รายงานการวิจัยฉบับสมบูรณ์

การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

Studying the effects of natural catastrophe such as flooding on the transmission of mosquito borne diseases such as dengue and malaria diseases in Thailand using mathematical modeling

นางสาว พันธนี พงศ์สัมพันธ์

(หัวหน้าโครงการ)

ได้รับทุนสนับสนุนงานวิจัยจากเงินงบประมาณแผ่นดิน

โครงการต่อเนื่อง 2 ปี ประจำปีงบประมาณ 2558

ตั้งแต่ เดือน ตุลาคม ปี 2557 ถึงเดือน กันยายน ปี 2559

คณะวิทยาศาสตร์

สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

รายงานการวิจัยฉบับสมบูรณ์

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สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

ชื่อโครงการ (ภาษาไทย) การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

ชื่อโครงการ(ภาษาอังกฤษ) Studying the effects of natural catastrophe such as flooding on the transmission of mosquito borne diseases such as dengue and malaria diseases in Thailand using mathematical modeling

แหล่งเงิน คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

โครงการต่อเนื่อง 2 ปี ประจำปีงบประมาณ 2558 จำนวนเงินที่ได้รับการสนับสนุน 500,000 บาท

ระยะเวลาทำการวิจัย 2 ปี ตั้งแต่ เดือน ตุลาคม ปี 2557 ถึงเดือน กันยายน ปี 2559

หัวหน้าโครงการ รองศาสตราจารย์ ดร.พันธนี พงศ์สัมพันธ์

ภาควิชาคณิตศาสตร์ คณะวิทยาศาสตร์

สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

e-mail: kppuntan@kmitl.ac.th

บทคัดย่อ

จากสถานการณ์อุทกภัยแต่ละครั้ง พื้นที่แต่ละแห่งจะเกิดสภาวะน้ำท่วมขัง ซึ่งเป็นแหล่งเพาะพันธุ์ของยุงชนิดต่างๆเป็นอย่างดี โดยเฉพาะยุงลายทำให้ประชาชนที่อยู่ในพื้นที่น้ำท่วมขังเสี่ยงเป็นโรคไข้เลือดออก ยุงลายมักจะชอบวางไข่ในน้ำที่นิ่งสะอาดและชอบกัดคนในเวลากลางวัน ทำให้หลังจากเกิดน้ำท่วมขังสักระยะหนึ่งเราจะพบผู้ป่วยโรคไข้เลือดออกเพิ่มขึ้นและอาจมีการแพร่ระบาดของโรคขยายเป็นวงกว้าง โดยเฉพาะในชุมชนที่แออัด โรคไข้เลือดออกเกิดจากเชื้อไวรัสเดงกี ซึ่งมี 4 ชนิด คือ DEN-1 DEN-2 DEN-3 และ DEN-4 โดยมียุงลายเป็นพาหะนำโรค อีกโรคหนึ่งที่พบว่าเป็นโรคที่เกิดขึ้นมาพร้อมกับน้ำท่วมคือโรคมาลาเรีย มาลาเรียเป็นโรคหรือสภาวะติดเชื้อในคนที่มีสาเหตุมาจากโปรโตซัว Genus *Plasmodium* เชื้อมาลาเรียที่จัดว่าเป็นปรสิตของคนมี 4 ชนิด ได้แก่ พลาสโมเดียมฟัลซิพารัม พลาสโมเดียมไวแวกซ์ พลาสโมเดียมมาลาริอี และพลาสโมเดียมโอวัลเล่ อาการของผู้ป่วยโรคมาลาเรียแต่ละคนจะขึ้นอยู่กับระยะฟักตัวของเชื้อ ชนิดของเชื้อ จำนวนของสปอโรซอยต์ที่ผู้ป่วยได้รับเข้าไป ภาวะภูมิต้านทานต่อเชื้อมาลาเรียของผู้ป่วย ภาวะที่ผู้ป่วยได้รับยาป้องกันมาลาเรียมาก่อน หรือได้รับยารักษามาลาเรียมาบ้างแล้ว ในงานวิจัยนี้ได้ทำการศึกษาแบบจำลองทางคณิตศาสตร์ที่สามารถนำมาอธิบายการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย นอกจากนั้นในงานวิจัยนี้ยังมีการศึกษาการกระจายของผู้ป่วยทั้งสองโรคนี้โดยใช้วิธีของการสร้างแบบจำลองการกระจายตามพื้นที่ (Spatial model) โดยพิจารณาถึงการเคลื่อนที่ของประชากร และหาค่าพารามิเตอร์เชิงตัวเลขในแบบจำลอง โดยการใช้ข้อมูลที่เก็บได้เพื่อเป็นประโยชน์ในการวิเคราะห์ลักษณะการระบาดของโรค

คำสำคัญ การระบาด ทฤษฎีการจำลองเชิงพลวัตมาตรฐาน น้ำท่วม แบบจำลองการกระจายตามพื้นที่ แบบจำลองทางคณิตศาสตร์ ภัยพิบัติ โรคไข้เลือดออก โรคมาลาเรีย

Research Title: Studying the effects of natural catastrophe such as flooding on the transmission of mosquito borne diseases such as dengue and malaria diseases in Thailand using mathematical modeling

Researcher: Assoc.Prof.Dr.Puntani Pongsumpun

Faculty: Faculty of Science **Department:** Department of Mathematics

King Mongkut's Institute of Technology Ladkrabang

ABSTRACT

After each flooding in Thailand, there are many areas appropriated for the growing of mosquitoes. *Aedes* Mosquitoes typically prefer to lay eggs in stagnant clean water and biting human for the daytime. After flooding, we found many dengue patients and may increase the spread of the disease. Dengue virus has four serotypes such as DEN-1 DEN-2 DEN-3 and DEN-4. Another disease that is a common disease that occurs with flooding is malaria. Malaria is an infectious disease that is caused by the protozoan Genus *Plasmodium* malaria parasite. Symptoms of malaria patients are depend on the type of infection, the incubation period, Immunity of each person, A condition of each patient receive anti-malaria drugs, etc. In this study, we formulate mathematical models that can be described the transmission of dengue disease and malaria with the flooding in Thailand. We also study the distribution of the disease by the spatial model with the movement of the population. Numerical simulations of our models are found to show the distribution of this disease. The set of parameters are found to reduce the outbreak of this disease. The collected data are used for analyzing the characteristics of this disease.

Keywords : Transmission, standard dynamical modeling theorem, flood, spatial model, mathematical model, catastrophe, dengue disease, malaria disease

กิตติกรรมประกาศ

ผู้วิจัยขอกราบขอบพระคุณ Professor Dr. I-Ming Tang และ Professor Dr.Marc A. Dubois เป็นอย่างสูง ที่กรุณาให้คำแนะนำต่างๆ ในการทำงานวิจัย พร้อมทั้งให้ความรู้และประสบการณ์ที่ดี

ขอขอบพระคุณคณาจารย์สาขาคณิตศาสตร์ รวมถึงเจ้าหน้าที่ประจำสาขาวิชาทุกท่านที่ช่วยเหลือในด้านการอำนวยความสะดวกเกี่ยวกับอุปกรณ์ที่จำเป็นต่างๆ

ขอกราบขอบพระคุณครอบครัว ที่ได้ให้การสนับสนุนทุกประการทางด้านการทำวิจัย และยังให้กำลังใจตลอดมาจนถึงปัจจุบัน และต้องขอขอบคุณเพื่อนๆ ทุกท่านที่ช่วยเหลือให้คำแนะนำต่างๆ จนงานวิจัยสำเร็จสมบูรณ์ยิ่งขึ้น

คุณค่าและประโยชน์อันพึงมีจากงานวิจัยฉบับนี้ ผู้จัดทำขออุทิศแด่ บิดา มารดา และผู้มีพระคุณทุกท่าน

สุดท้ายนี้ ผู้วิจัยขอกราบขอบพระคุณ คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง ที่ได้ให้ทุนสนับสนุนการทำงานวิจัยนี้

รองศาสตราจารย์ ดร. พันธนี พงศ์สัมพันธ์

สารบัญ

บทที่ 1
บทนำ

1.1 ความสำคัญและที่มาของปัญหาที่ทำการวิจัย

เนื่องจากประเทศไทยอยู่ในเขตร้อน หลายภาคจึงมักเกิดน้ำท่วมฉับพลันตามฤดูกาล อย่างในอุทกภัยครั้งล่าสุดที่เกิดขึ้นในปีพ.ศ.2554 ได้เริ่มขึ้นในระหว่างฤดูมรสุม ส่งผลให้เกิดฝนตกหนักทางภาคเหนือ และภาคตะวันออกเฉียงเหนือในประเทศไทย ภายในเวลาไม่นาน อุทกภัยได้ลุกลามไปยังแม่น้ำเจ้าพระยา ซึ่งส่งผลกระทบต่อหลายจังหวัดในภาคกลางรวมไปถึงจังหวัดกรุงเทพมหานครซึ่งเป็นเมืองหลวงของประเทศไทย [1] หลังจากน้ำซึ่งเข้าท่วมพื้นที่ต่างๆ เริ่มอยู่ในสภาพนิ่ง สิ่งที่ตามมาคือการเกิดเป็นแหล่งเพาะพันธุ์ของยุงหลายชนิดโดยเฉพาะยุงลาย [2] สภาพที่เกิดขึ้นนี้มีความคล้ายคลึงกับสภาพที่เกิดขึ้นหลังฝนตกและมีน้ำขังอยู่ในสถานที่ต่างๆ โดยยุงลายมักชอบวางไข่ในน้ำนิ่งที่สะอาดและชอบกัดคนในเวลากลางวัน หลังจากน้ำท่วมขังสักระยะหนึ่งจะพบผู้ป่วยโรคไข้เลือดออกเพิ่มขึ้น ซึ่งอาจเกิดการแพร่ระบาดของโรคในพื้นที่กว้างตามมาได้ นอกจากนั้นสภาพชุมชนที่แออัดอย่างค่ายผู้อพยพ การขาดสุขอนามัยที่ดี และการควบคุมประชากรยุงที่ไม่มีประสิทธิภาพ ล้วนส่งเสริมให้พบผู้ป่วยไข้เลือดออกเพิ่มขึ้นได้เสมอหลังเกิดน้ำท่วม โรคไข้เลือดออกเป็นโรคติดต่อที่มียุงลายเป็นพาหะนำโรค ปัจจุบันยังคงเป็นปัญหาสำคัญที่ทำให้ประชาชนป่วย และเสียชีวิตทุกปี มีแนวโน้มของการเกิดโรคสูงขึ้นเรื่อยๆอย่างน่าวิตก จากรายงานทางระบาดวิทยาของโรคไข้เลือดออก พบว่าวิวัฒนาการเกิดโรคเริ่มเปลี่ยนไป พบผู้ป่วยได้ตลอดปี จากเดิมพบเฉพาะฤดูฝน และพบผู้ป่วยทุกเพศ ทุกวัย ไม่เฉพาะแต่เด็กอายุต่ำกว่า 15 ปีเหมือนที่ผ่านมา โรคไข้เลือดออกเป็นโรคติดต่อที่เป็นปัญหาของประเทศไทยต่อเนื่องมานาน ที่ผ่านมาพบว่าการเกิดและระบาดของโรคมักเกิดปีเว้นปี ปีเว้นสองปี แต่ในช่วงระยะที่ผ่านมาการเกิดและระบาดของโรคมีแนวโน้มต่อเนื่อง จากรายงานการเกิดโรคในช่วง 2–3 ปีที่ผ่านมา การเกิดโรคพบผู้ป่วยทุกเดือนและความรุนแรงของโรคมีแนวโน้มรุนแรงขึ้น อัตราการป่วยและอัตราการเสียชีวิตสูงขึ้นด้วย อีกโรคหนึ่งที่พบว่าเป็นโรคที่เกิดขึ้นมาพร้อมกับน้ำท่วมคือโรคมาลาเรียซึ่งพบว่าเป็นโรคหนึ่งในจำนวนเก้าโรคที่มาพร้อมกับน้ำท่วมและคงอยู่หลังจากน้ำลดแล้ว [3] โรคมาลาเรียเป็นปัญหาสาธารณสุขที่สำคัญในประเทศไทย ยุงก้นปล่องเป็นพาหะนำโรคนี้ องค์การอนามัยโรคประมาณกันว่าในแต่ละปีจะมีผู้ป่วยเป็นโรคมาลาเรียถึงปีละ 300-400 ล้านคนทั่วโลก [4] และมีคนเสียชีวิตปีละประมาณ 1 ล้านคน ในแต่ละปีองค์การอนามัยโลกได้รายงานว่า ประชากรโลก 400 ล้านคนจะล้มป่วยเป็นไข้และมีอาการหนาวสั่นด้วยโรคมาลาเรีย และคน 2 ล้านคนจะเสียชีวิตด้วยโรคนี้ นั่นคือในทุก 30 วินาที จะมีคนเสียชีวิตด้วยโรคมาลาเรีย 1 คน องค์การสหประชาชาติยังได้รายงานอีกว่าผู้ป่วยของโรคนี้ส่วนใหญ่มักเป็นเด็กที่มีอายุน้อยกว่า 5 ปี โดยเฉพาะในกรณีครอบครัวที่ยากจนเหตุการณ์เสียชีวิตจะมีโอกาสเป็นไปได้สูง มาลาเรียเป็นโรคติดเชื้อในคนและสัตว์ที่เกิดจากยุง โรค

นี้เป็นผลจากการเพิ่มทวีสายพันธุ์ของเชื้อพลาสโมเดียม โรคมาลาเรียเป็นโรคที่เก่าแก่ขอุงคนอย่างน้อยมากกว่า 50,000 ปี โรคนี้แพร่กระจายในเขตร้อน ในทวีปแอฟริกา เอเชีย และอเมริกา'[5]

ในงานวิจัยนี้ ผู้วิจัย จะนำเสนอทางเลือกใหม่ในการลดการระบาดของโรคนี้ โดยการสร้างแบบจำลองทางคณิตศาสตร์สำหรับการแพร่ระบาดของทั้งสองโรคนี้กับการเกิดน้ำท่วมโดยพิจารณาถึงปัจจัยต่างๆที่เกี่ยวข้องกับการระบาดของทั้งสองโรคนี้ในประเทศไทย ศึกษาการกระจายของผู้ป่วยทั้งสองโรคนี้โดยวิธีของการสร้างแบบจำลองการกระจายตามพื้นที่ (Spatial model) หาค่าพารามิเตอร์เชิงตัวเลขในแบบจำลอง โดยการใช้ข้อมูลที่เก็บได้ เพื่อเป็นประโยชน์ในการวิเคราะห์ลักษณะการระบาดของโรคในครั้งต่อไปได้ ใช้วิธีการวิเคราะห์ทางคณิตศาสตร์มาใช้กับแบบจำลองที่ได้ พร้อมทั้งเสนอวิธีการลดการระบาดของทั้งสองโรคนี้ในประเทศไทย

1.2 วัตถุประสงค์ของโครงการวิจัย

1. เพื่อสร้างและพัฒนาแบบจำลองการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย
2. เพื่อวิเคราะห์และแสดงถึงปัจจัยที่มีผลทำให้เกิดการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วม เพื่อเป็นแนวทางในการลดและควบคุมการระบาดของโรคไข้เลือดออกและโรค
มาลาเรียในประเทศไทย
3. เพื่อแสดงให้เห็นว่าสามารถนำความรู้ ทฤษฎีทางคณิตศาสตร์ สถิติ ทฤษฎีการระบาดวิทยา และระบบสารสนเทศทางภูมิศาสตร์มาประยุกต์กับวิทยาศาสตร์ทางการแพทย์ได้
4. เพื่อถ่ายทอดเทคโนโลยี และความรู้ใหม่ๆ สู่ชุมชน
5. เพื่อผลิตผลงานวิจัยและนวัตกรรมใหม่ เพื่อความเป็นเลิศทางด้านวิชาการ และเป็นที่ยอมรับในระดับชาติและระดับนานาชาติ
6. เพื่อให้สอดคล้องกับโครงการวิจัยกับยุทธศาสตร์การพัฒนาประเทศตามแผน พัฒนาเศรษฐกิจ และสังคมแห่งชาติ ฉบับที่ 11 (พ.ศ. 2555-2559)

1.3 ขอบเขตของโครงการวิจัย

ศึกษาข้อมูล ลักษณะการแพร่ระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วม สร้างและพัฒนาแบบจำลองทางคณิตศาสตร์เพื่อนำมาอธิบายการแพร่ระบาดของทั้งสองโรคนี้กับการเกิดน้ำท่วมโดยพิจารณาถึงปัจจัยต่างๆที่เกี่ยวข้องกับการระบาดของทั้งสองโรคนี้ในประเทศไทย ตัวอย่างเช่น ระยะฟักตัวของเชื้อไวรัสแดงกีและเชื้อพลาสโมเดียม พฤติกรรมการวางไข่ของยุงลายและยุงก้นปล่องที่เกี่ยวข้องกับน้ำที่ท่วมขัง อายุของประชากร อัตราความเสี่ยงของประชากร

ที่มีต่อโรคไข้เลือดออกและโรคมาลาเรีย อัตราการถ่ายทอดเชื้อไวรัสแดงกีและเชื้อพลาสโมเดียม ระยะเวลาการมีภูมิคุ้มกันสำหรับเชื้อ แต่ละชนิดของไวรัสแดงกีและพลาสโมเดียม ปริมาณน้ำฝนที่ส่งผลให้เกิดน้ำท่วมและเป็นแหล่งเพาะพันธุ์ของยุง ฯลฯ ทำการวิเคราะห์ด้วยทฤษฎีทางคณิตศาสตร์ ใช้วิธีการหาคำตอบเชิงตัวเลขเป็นการทดสอบวิธีการที่นำมาวิเคราะห์ ต่อจากนั้นจะพัฒนาการสร้างแบบจำลองทางคณิตศาสตร์ของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมโดยศึกษาการกระจายของผู้ป่วยทั้งสองโรคนี้โดยใช้วิธีของการสร้างแบบจำลองการกระจายตามพื้นที่ (Spatial model) มาวิเคราะห์โดยพิจารณาถึงการระบาดของโรคกับการเดินทางของประชากร หลังจากนั้นหาค่าพารามิเตอร์เชิงตัวเลขในแบบจำลองโดยการใช้ข้อมูลที่เก็บได้ เพื่อเป็นประโยชน์ในการวิเคราะห์ลักษณะการระบาดของโรคในครั้งต่อไปได้ หลังจากนั้นจะนำมาทดสอบกับข้อมูลจริง สร้างทฤษฎีใหม่ที่เกี่ยวข้อง เมื่อได้ผลลัพธ์เป็นที่เรียบร้อยแล้ว สรุปผลที่ได้ และนำไปประยุกต์ใช้ในสถานการณ์จริงกับการเกิดน้ำท่วมว่าจะสามารถลดและควบคุมการระบาดของโรคนี้ให้น้อยลงได้อย่างไร

1.4 ประโยชน์ที่คาดว่าจะได้รับ

1. เพื่อเพิ่มความรู้ ความเข้าใจเกี่ยวกับโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วม
2. เพื่อสร้างแบบจำลองเชิงคณิตศาสตร์สำหรับศึกษาการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย
3. เพื่อนำคณิตศาสตร์มาประยุกต์ใช้ในการศึกษา การวิจัย ทางด้านแบบจำลองทางคณิตศาสตร์
4. เพื่อให้สอดคล้องกับแผนพัฒนาเศรษฐกิจและสังคมแห่งชาติ ฉบับที่ 11 ยุทธศาสตร์การพัฒนาคนสู่สังคมแห่งการเรียนรู้ตลอดชีวิตอย่างยั่งยืน ประเภทการวิจัยประยุกต์
5. เพื่อให้ผลที่ได้จากการวิเคราะห์แบบจำลองทางคณิตศาสตร์นำไปใช้ให้เป็นประโยชน์ทางการแพทย์ได้
6. เพื่อหาแนวทางใหม่ที่ช่วยในการลดการระบาดของโรค โดยใช้เทคนิคและทฤษฎีทางคณิตศาสตร์มาสร้างแบบจำลองเชิงคณิตศาสตร์สำหรับการระบาดของไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย ซึ่งอาจเป็นการช่วยลดงบประมาณในการควบคุมการระบาดของโรคนี้
7. ผลิตบทความตีพิมพ์เพื่อเผยแพร่ในระดับชาติ และนานาชาติ พร้อมทั้งผลิตบัณฑิต

1.5 ระเบียบวิธีการวิจัย

1. ศึกษาข้อมูลเบื้องต้นเกี่ยวกับโรคไข้เลือดออกและโรคมาลาเรีย
2. ค้นคว้าและรวบรวมข้อมูลของคนไข้โรคไข้เลือดออกและโรคมาลาเรียในประเทศไทย
3. ศึกษาปัจจัยต่างๆที่ทำให้เกิดการระบาดของโรคไข้เลือดออกและโรคมาลาเรียในประเทศไทย
4. ศึกษาหาความสัมพันธ์ระหว่างการเกิดน้ำท่วมในประเทศไทยกับการระบาดของโรคไข้เลือดออกและโรคมาลาเรีย
5. สร้างแบบจำลองทางคณิตศาสตร์สำหรับการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย
6. พัฒนาแบบจำลองทางคณิตศาสตร์สำหรับการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย
7. วิเคราะห์แบบจำลองทางคณิตศาสตร์สำหรับการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย พร้อมทั้งเขียนผลการวิจัยเพื่อการตีพิมพ์
8. สร้างทฤษฎีใหม่ๆ ที่เกี่ยวข้อง
9. หาคำตอบเชิงตัวเลข
10. ทดสอบทฤษฎีที่สร้างขึ้นมาใหม่
11. วิเคราะห์การกระจายของผู้ป่วยโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย
12. ใช้กระบวนการทางคณิตศาสตร์กับการระบาดของโรคเสนอหาค่าพารามิเตอร์เชิงตัวเลขในแบบจำลอง
13. ทดสอบผลที่ได้
14. สร้างทฤษฎีเกี่ยวกับการแพร่ระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย
15. เขียนผลการวิจัย

1.6 ทฤษฎีหรือกรอบแนวคิดของโครงการวิจัย (ภาคผนวก)

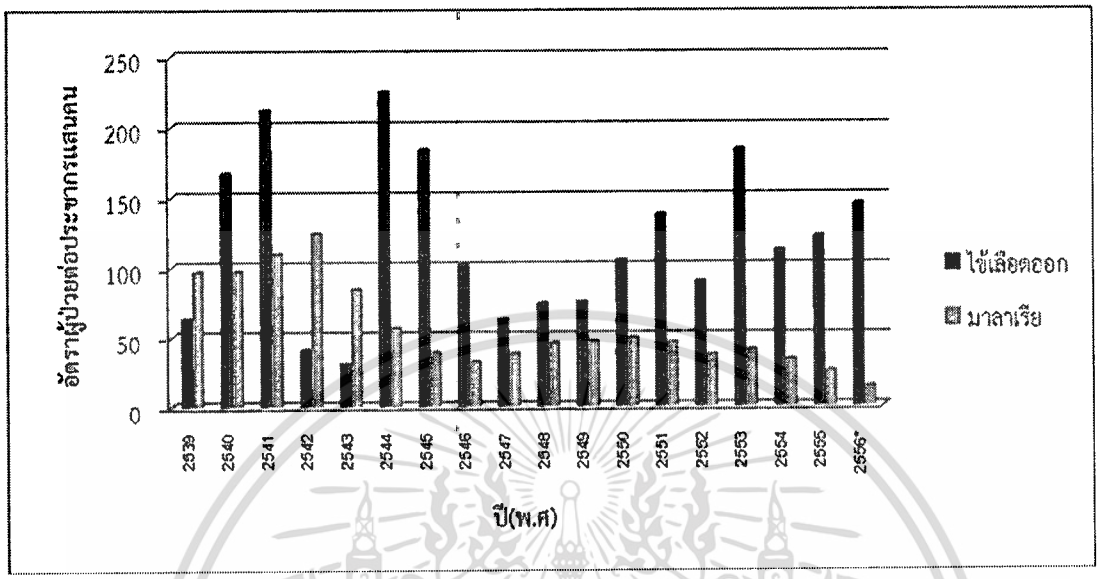
1. Standard Dynamical Analysis Method
2. The equilibrium state
3. The Routh-Hurwitz criteria
4. Local asymptotical stability
5. Global stability
6. Geographic Information System

บทที่ 2
โรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย

อุทกภัย คือ ภัยที่เกิดขึ้นเนื่องจากมีน้ำเป็นสาเหตุ อย่างเช่น น้ำท่วม น้ำป่า หรืออื่นๆ เป็นภัยธรรมชาติที่เกิดขึ้นมากที่สุดประมาณร้อยละ 40 ของภัยธรรมชาติทั้งหมดที่เกิดขึ้นทั่วโลก [21] ส่วนใหญ่เกิดในประเทศกำลังพัฒนาและเขตร้อน ร้อยละ 44 ของอุทกภัยธรรมชาติทั่วโลกล้วนมีผลกระทบต่อภูมิภาคเอเชีย ผลกระทบไม่เพียงแต่ทำให้เสียชีวิตและทำลายสิ่งก่อสร้าง แต่ยังรวมถึงผลกระทบต่อสังคม เศรษฐกิจ สุขภาพ การเปลี่ยนแปลงของโรคประจำถิ่น และการเปลี่ยนแปลงสภาพภูมิอากาศส่งผลให้อุทกภัยมีแนวโน้มที่จะเกิดถี่และรุนแรงขึ้นในหลายพื้นที่ทั่วโลก สาเหตุส่วนใหญ่เกิดจากฝนตกหนักต่อเนื่องเป็นเวลานาน แต่อาจมีสาเหตุจากพายุหมุนเขตร้อน ลมมรสุมมีกำลังแรง ร่องความกดอากาศต่ำมีกำลังแรง อากาศแปรปรวน หรือน้ำทะเลหนุน ทำให้อุทกภัยมีหลายรูปแบบและรุนแรงต่างกัน [22] ประเทศไทยอยู่ในเขตอิทธิพลของมรสุมตะวันตกเฉียงใต้และมรสุมตะวันออกเฉียงเหนือ ซึ่งพัดประมาณฤดูกาลละ 6 เดือน จากค่าเฉลี่ยย้อนหลังพบว่าเดือนพฤษภาคมเป็นเดือนที่เริ่มมีฝนตก และฝนตกหนักในช่วงเดือนพฤษภาคมถึงกรกฎาคม แต่ในช่วงเดือนกรกฎาคมถึงตุลาคมเกือบทุกภาคมีโอกาสเกิดอุทกภัยยกเว้นภาคใต้ ส่วนในช่วงปลายปีต่อเนื่องถึงต้นปีระหว่างเดือนพฤศจิกายนถึงมกราคมมีเฉพาะจังหวัดในภาคใต้ฝั่งตะวันออกที่มีโอกาสเกิดอุทกภัย จากการกำหนดขอบเขตพื้นที่จำแนกชั้นความรุนแรงของการเกิดน้ำท่วมซ้ำซากของประเทศไทยพบว่า ทั้งประเทศมีพื้นที่น้ำท่วมซ้ำซาก 52 จังหวัด 2,369 ตำบล(ร้อยละ 32.65) 9,210 หมู่บ้าน (ร้อยละ 12.29) ภาคเหนือ และภาคกลางมีสัดส่วนของตำบลและหมู่บ้านที่น้ำท่วมซ้ำซากมากที่สุด จากสถิติอุทกภัยที่ผ่านมาพบว่าทุกปีมีจังหวัดที่ประสบอุทกภัยมากกว่าครึ่งประเทศ สำหรับกรุงเทพมหานครซึ่งเป็นเมืองหลวงของประเทศไทยก็ประสบกับน้ำท่วมหลายครั้ง น้ำท่วมครั้งแรกเกิดขึ้นในปีพ.ศ.2485 เป็นเหตุการณ์น้ำท่วมที่รุนแรงที่สุดในประวัติศาสตร์ ก่อนที่จะมีการสร้างเขื่อนขนาดใหญ่เพื่อมากักเก็บน้ำ ต่อมาในปีพ.ศ.2518 เนื่องจากพายุดีเปรสชั่นได้พาดผ่านตอนบนลุ่มแม่น้ำเจ้าพระยาทำให้มีปริมาณน้ำสูงทางภาคกลางตอนบนจนเป็นเหตุให้น้ำไหลทะลักเข้าท่วมกรุงเทพมหานคร นอกจากนั้นกรุงเทพมหานครก็ได้ประสบกับปัญหาน้ำท่วมอีกหลายครั้ง ในปี พ.ศ.2521 พ.ศ.2523 พ.ศ.2526 พ.ศ.2529 พ.ศ.2533 พ.ศ.2537 พ.ศ.2538 พ.ศ.2539 พ.ศ.2541 และล่าสุดเมื่อปี พ.ศ.2554 [23] อุทกภัยในประเทศไทย พ.ศ.2554 หรือเรียกกันว่า มหาอุทกภัย เป็นอุทกภัยรุนแรงที่ส่งผลกระทบต่อบริเวณลุ่มแม่น้ำเจ้าพระยาและลุ่มน้ำโขง เริ่มตั้งแต่ปลายเดือนกรกฎาคมและสิ้นสุดเมื่อวันที่ 16 มกราคม พ.ศ. 2555 การเปลี่ยนแปลงของสิ่งแวดล้อมแต่ละครั้งมีผลกระทบต่อการเปลี่ยนแปลงของประชากร [24]

หลังจากสถานการณ์อุทกภัยแต่ละครั้ง พื้นที่แต่ละแห่งจะเกิดสภาวะน้ำท่วมขัง ซึ่งเป็นแหล่งเพาะพันธุ์ของยุงชนิดต่างๆเป็นอย่างดี โดยเฉพาะยุงลายทำให้ประชาชนที่อยู่ในพื้นที่น้ำท่วมขังเสี่ยงเป็นโรคไข้เลือดออก ยุงลายมักจะชอบวางไข่ในน้ำที่นิ่งสะอาดและชอบกัดคนในเวลากลางวัน ทำให้หลังจากเกิดน้ำท่วมขังสักระยะหนึ่งเราจะพบผู้ป่วยโรคไข้เลือดออกเพิ่มขึ้นและอาจมีการแพร่ระบาดของโรคขยายเป็นวงกว้าง โดยเฉพาะในชุมชนที่แออัด เช่น ศูนย์ผู้อพยพ ถ้ายิ่งขาดสุขอนามัยที่ดีและขาดการควบคุมประชากรยุงที่มีประสิทธิภาพจะยิ่งทำให้พบผู้ป่วยไข้เลือดออกเพิ่มขึ้นได้ หลังเกิดอุทกภัยน้ำท่วม โรคไข้เลือดออกมีสาเหตุมาจากเชื้อไวรัสเด่งกี ซึ่งมี 4 ชนิด คือ DEN-1 DEN-2 DEN-3 และ DEN-4 โดยมียุงลายเป็นพาหะนำโรค หลังจากยุงลายดูดเลือดของผู้ป่วยที่มีเชื้อไวรัสแดงกี และไปกัดคนอื่นต่อ อาการของผู้ป่วยไข้เลือดออกมี 3 ระยะ คือ ระยะไข้สูง ผู้ป่วยจะมีอาการไข้สูงนานประมาณ 3-7 วัน ระยะวิกฤต เป็นระยะที่ผู้ป่วยมีอาการไข้ลดลง ผู้ป่วยจำนวนหนึ่งจะมีการรั่วของน้ำเหลืองหรือพลาสมาออกจากเส้นเลือด ทำให้เกิดภาวะเลือดข้น และอาจมีความรุนแรงถึงขั้นทำให้ผู้ป่วยมีภาวะช็อกและเสียชีวิตได้และ ระยะพักฟื้น เป็นระยะที่ผู้ป่วยหายจากโรค อายุของผู้ป่วยไข้เลือดออกมีแนวโน้มสูงขึ้น ส่วนใหญ่จะเป็นในเด็กโตและผู้ใหญ่ที่อายุไม่มากนัก อีกโรคหนึ่งที่พบว่าเป็นโรคที่เกิดขึ้นมาพร้อมกับน้ำท่วมคือโรคมาลาเรีย มาลาเรียเป็นโรคหรือสภาวะติดเชื้อในคนที่มีสาเหตุมาจากโปรโตซัว Genus *Plasmodium* คำว่า malaria มาจากภาษาอิตาเลียน mal+aria แปลว่า bad air ถ้าเรียกตามหลักการเรียกชื่อโรคนี้ทางวิทยาศาสตร์ ควรเรียกว่า *Plasmodiosis* แต่คำนี้ไม่เป็นที่นิยมใช้กัน ส่วนในประเทศไทยก่อนที่จะรู้จักคำว่า มาลาเรีย มีชื่อที่ใช้เรียกโรคนี้ ได้แก่ ไข้ป่า ไข้จับสั่น ไข้ป้าง ไข้ร้อนเย็นและไข้ดอกสัก เชื้อมาลาเรียที่พบในปัจจุบันมีทั้งหมดกว่า 100 ชนิด ในจำนวนนี้มี 22 ชนิด ที่พบในสัตว์ชั้นสูง คือ ลิง และคน นอกนั้นเป็นเชื้อมาลาเรียของสัตว์จำพวกฟันแทะ ค้างคาว สัตว์ปีกและสัตว์เลื้อยคลาน เชื้อมาลาเรียที่จัดว่าเป็นปรสิตของคนมี 4 ชนิด ได้แก่ พลาสโมเดียมฟัลซิพารัม พลาสโมเดียมไวแวกซ์ พลาสโมเดียมมาลาริอี และพลาสโมเดียมโอวัลเล่ [4] ผู้ป่วยจะมีไข้สูงตลอดเวลา โดยเฉพาะในผู้ป่วยที่เป็นมาลาเรียครั้งแรก เนื่องจากในระยะแรกของการติดเชื้อมาลาเรีย เชื้ออาจเจริญไม่พร้อมกัน ซึ่งอาจเป็นผลมาจากการได้รับเชื้อในเวลาที่แตกต่างกัน เชื้อจึงเจริญในเม็ดโลหิตแดงไม่พร้อมกัน ทำให้เกิดมีเชื้อหลายระยะ การแตกของเม็ดโลหิตแดงจึงไม่พร้อมกัน ผู้ป่วยมาลาเรียในระยะแรกอาจมีไข้สูงตลอดวันแต่เมื่อผ่านไประยะหนึ่งแล้ว การแตกของเม็ดโลหิตแดงเกิดขึ้นพร้อมกัน ผู้ป่วยมีการจับไข้เป็นวาระสั่นเป็นเวลาแยกได้ชัดเจนตามชนิดของเชื้อมาลาเรีย อาการของผู้ป่วยโรคมาลาเรียแต่ละคนจะขึ้นอยู่กับระยะฟักตัวของเชื้อ ชนิดของเชื้อ จำนวนของสปอโรซอยต์ที่ผู้ป่วยได้รับเข้าไป ภาวะภูมิต้านทานต่อเชื้อมาลาเรียของผู้ป่วย ภาวะที่ผู้ป่วยได้รับยาป้องกันมาลาเรียมาก่อน หรือได้รับยารักษามาลาเรียมาบ้างแล้ว จากข้อมูลของผู้ป่วยโรคไข้เลือดออกและโรคมาลาเรียปี พ.ศ. 2539 ถึงเดือน

สิงหาคม ปี พ.ศ. 2556 จากสำนักระบาดวิทยา กรมควบคุมโรค กระทรวงสาธารณสุข พบการระบาดของทั้งสองโรคอย่างต่อเนื่องในประเทศไทย แสดงดังรูปที่ 1

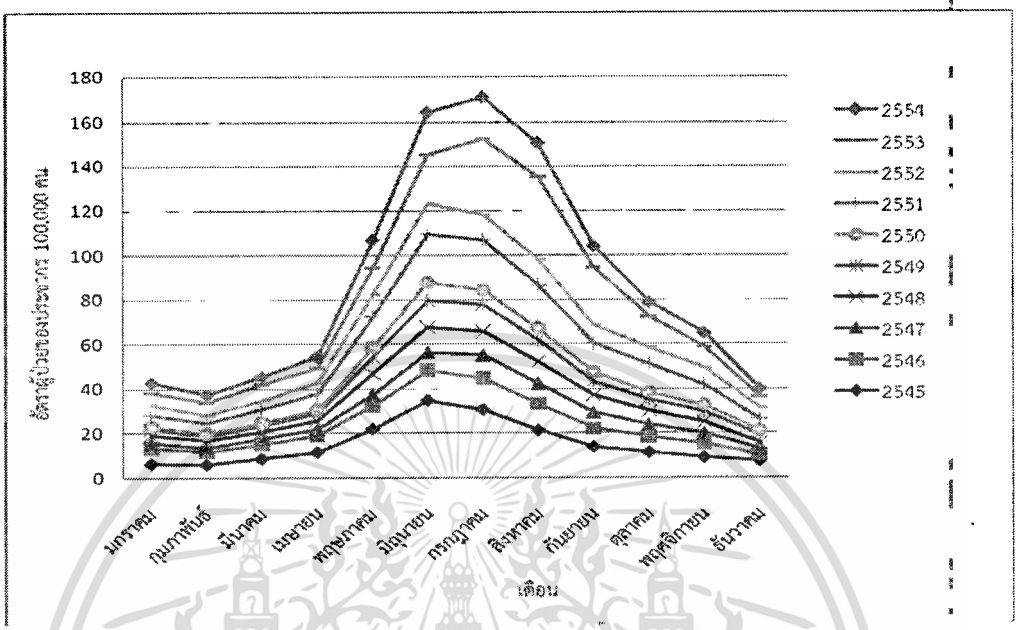


รูปที่ 1 สถานการณ์โรคไข้เลือดออกและโรคมาลาเรียในประเทศไทย ปีพ.ศ.2539 ถึงปี พ.ศ.2556 [25]

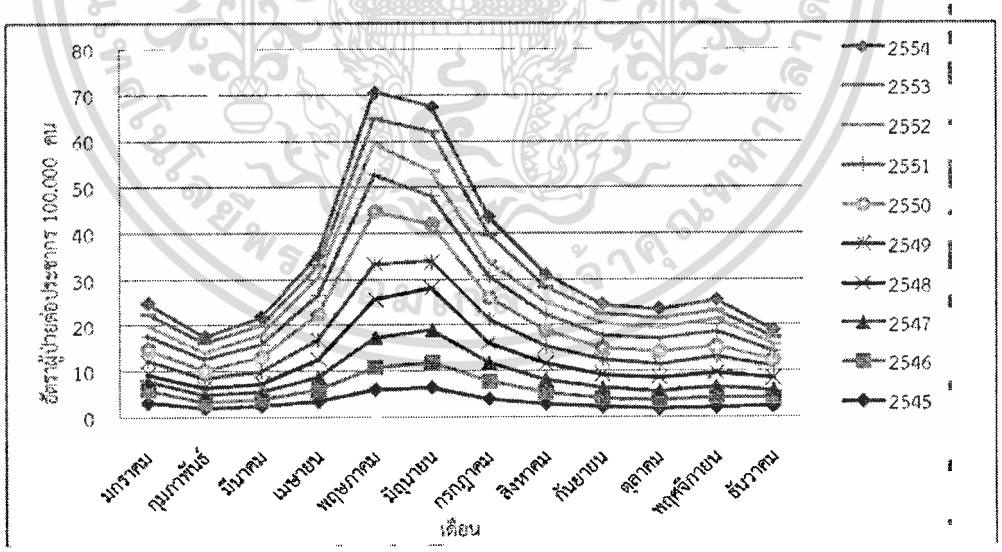
หมายเหตุ ปี 2556* หมายถึง 1 มกราคม - 6 สิงหาคม พ.ศ 2556

สำหรับสถานการณ์โรคไข้เลือดออกปี 2556 ข้อมูล ณ วันที่ 6 สิงหาคม พ.ศ.2556 มีผู้ป่วยโรคไข้เลือดออกสะสมรวม 93,034 ราย คิดเป็นอัตราป่วย 144.76 ต่อแสนประชากร จำนวนผู้ป่วยเพิ่มขึ้นจากปี พ.ศ.2555 ณ ช่วงเวลาเดียวกัน 3.2 เท่า

การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่น
โรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์



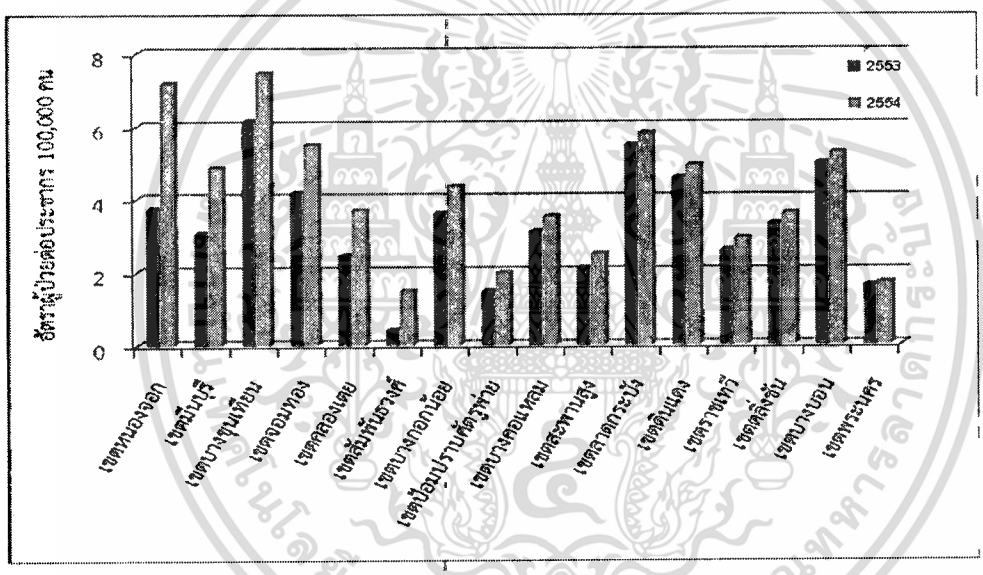
รูปที่ 2 สถานการณ์โรคไข้เลือดออกตามรายเดือนในประเทศไทยปีพ.ศ.2545 ถึงปีพ.ศ.2554 [25]



รูปที่ 3 สถานการณ์โรคมาลาเรียตามรายเดือนในประเทศไทยปีพ.ศ.2545 ถึงปีพ.ศ.2554 [25]

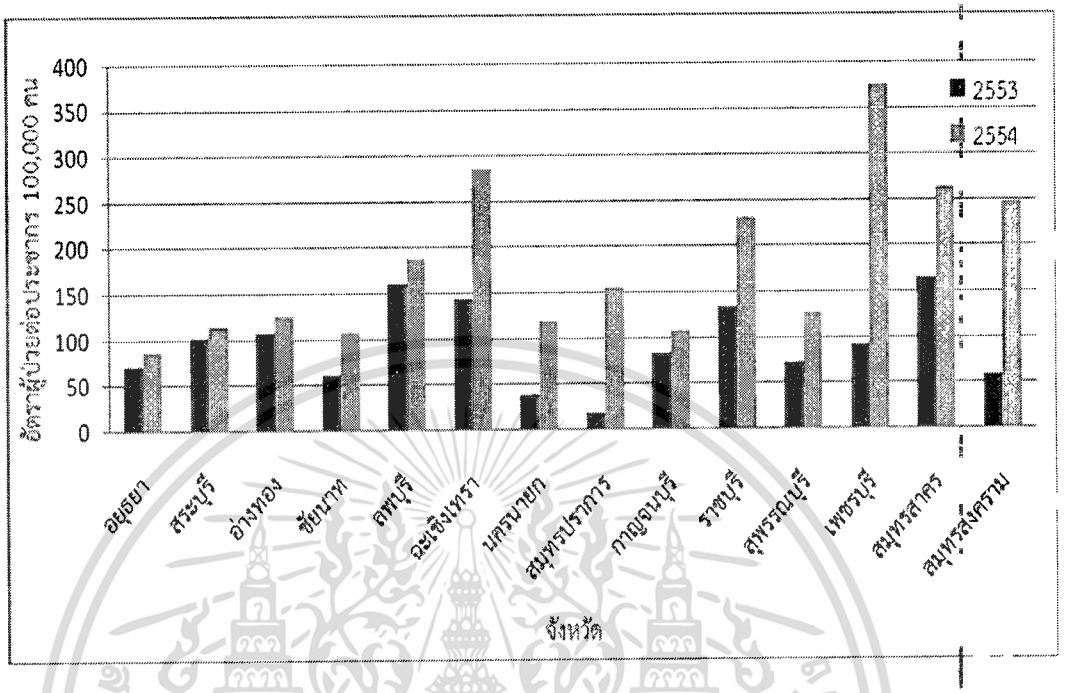
จากรูปที่ 2 และรูปที่ 3 จะเห็นได้ว่าการกระจายของผู้ป่วยเป็นไปตามฤดูกาล คือ พบผู้ป่วยจำนวนสูงสุดในช่วงฤดูฝน นั่นคือช่วงเดือนพฤษภาคมถึงเดือนกันยายน

ในประเทศไทยเกิดอุทกภัยหลายครั้ง สำหรับปี พ.ศ.2554 ถือว่าเป็นอุทกภัยครั้งรุนแรงที่สุดเป็นประวัติการณ์ ตั้งแต่ต้นปีจนถึงปลายปี และมีพื้นที่ประสบภัยกระจายตัวในทุกภาคของประเทศ โดยเฉพาะพื้นที่ภาคเหนือและภาคกลางที่เกิดน้ำท่วมหนักเป็นระยะเวลานาน ยิ่งไปกว่านั้นพื้นที่กรุงเทพมหานครและปริมณฑล เป็นพื้นที่หนึ่งซึ่งเกิดน้ำท่วมหนักในรอบ 70 ปี สำหรับการแพร่ระบาดของโรคที่มียุงเป็นพาหะซึ่งได้แก่โรคไข้เลือดออกและโรคมาลาเรียก็มีการเปลี่ยนแปลงเพิ่มขึ้นจากปีพ.ศ.2553 จากข้อมูลของผู้ป่วยโรคไข้เลือดออกและโรคมาลาเรียดังรูปที่ 4 ถึงรูปที่ 10 แสดงให้เห็นถึงจังหวัดที่มีอัตราของผู้ป่วยที่เพิ่มขึ้น

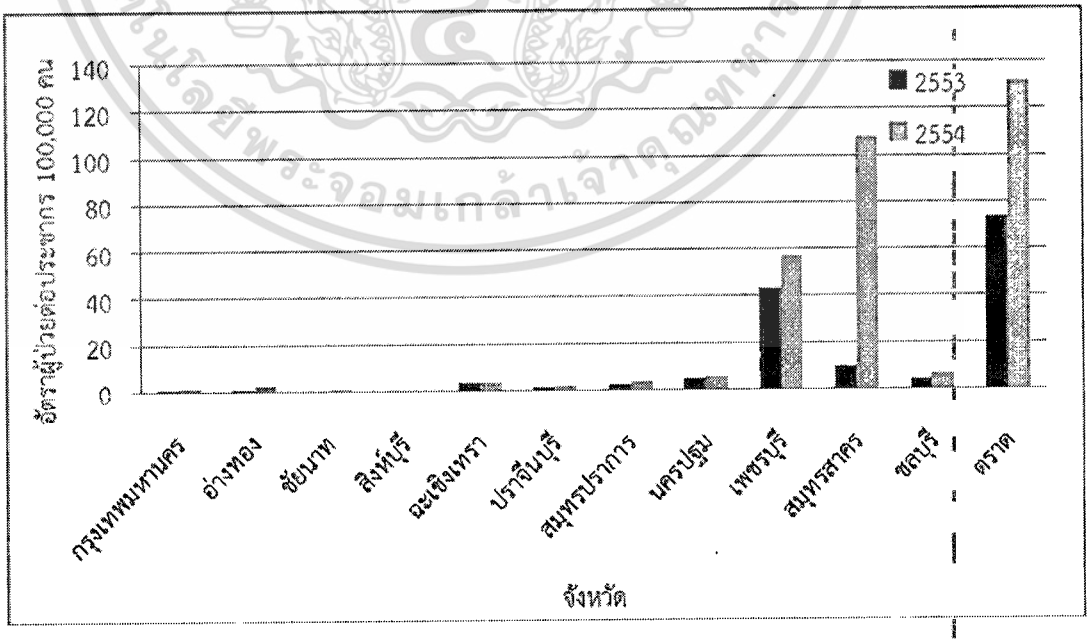


รูปที่ 4 แสดงผู้ป่วยโรคไข้เลือดออกในเขตของกรุงเทพมหานครที่มีอัตราผู้ป่วยในปีพ.ศ.2554 เพิ่มขึ้นจากปีพ.ศ.2553 [25]

การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่น โรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

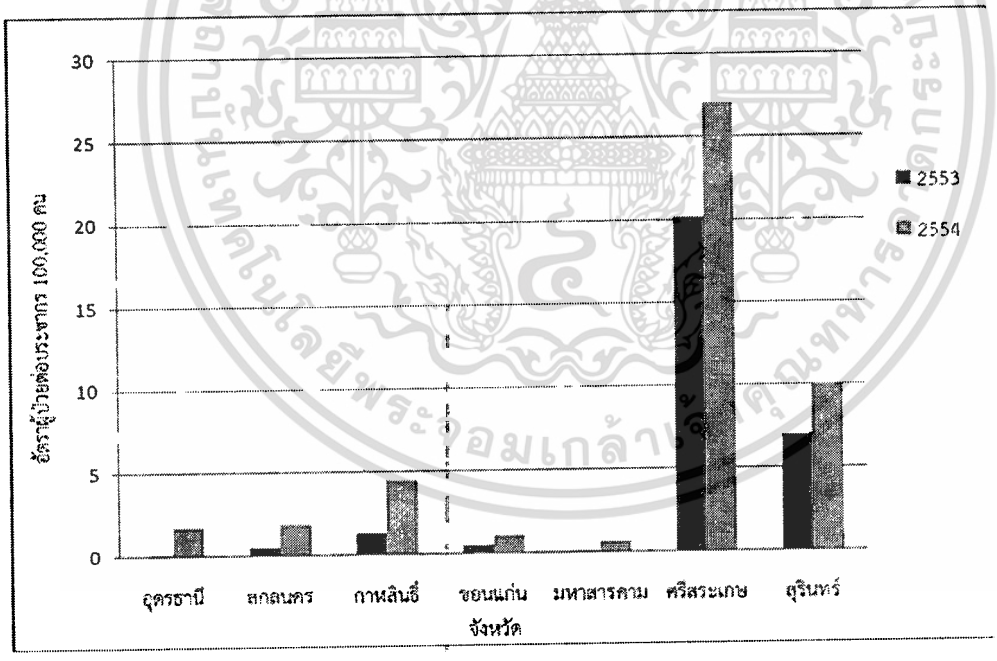


รูปที่ 5 แสดงผู้ป่วยโรคไข้เลือดออกในจังหวัดของภาคกลางที่มีอัตราผู้ป่วยในปีพ.ศ.2554 เพิ่มขึ้นจากปีพ.ศ.2553 [25]



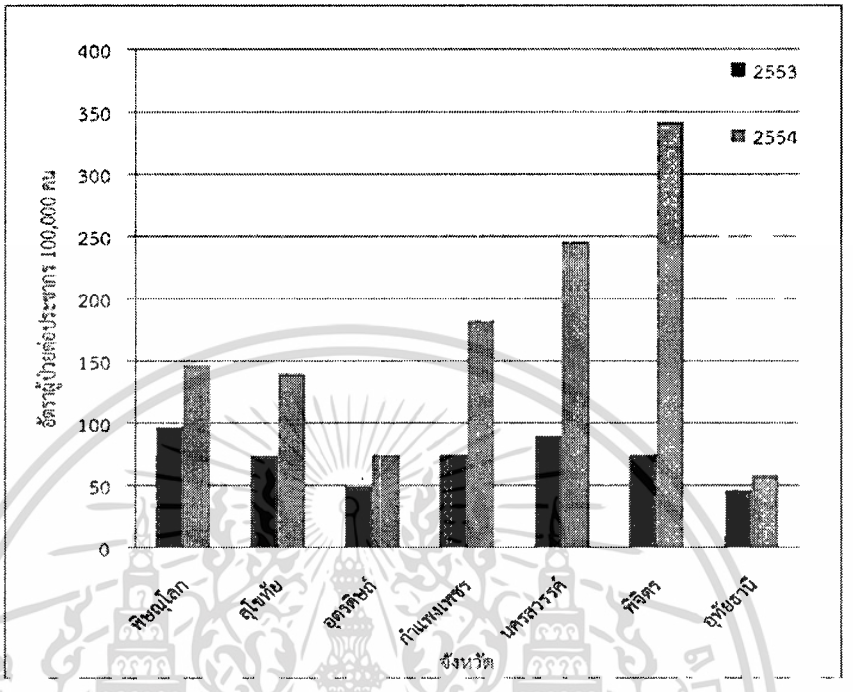
รูปที่ 6 แสดงผู้ป่วยโรคมาลาเรียในจังหวัดของภาคกลางที่มีอัตราผู้ป่วยในปีพ.ศ.2554 เพิ่มขึ้นจากปีพ.ศ.2553 [25]

รูปที่ 7 แสดงผู้ป่วยโรคไข้เลือดออกในจังหวัดของภาคตะวันออกเฉียงเหนือที่มีอัตราผู้ป่วยในปี พ.ศ.2554 เพิ่มขึ้นจากปีพ.ศ.2553 [25]

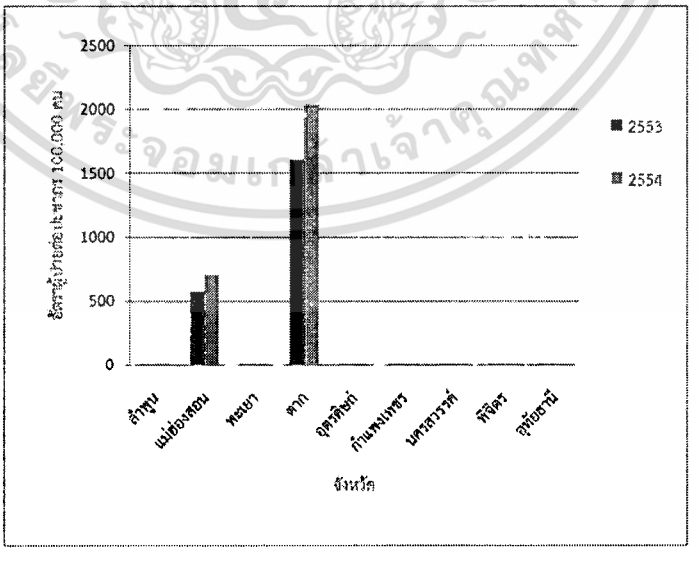


รูปที่ 8 แสดงผู้ป่วยโรคมาลาเรียในจังหวัดของภาคตะวันออกเฉียงเหนือที่มีอัตราผู้ป่วยในปี พ.ศ.2554 เพิ่มขึ้นจากปีพ.ศ.2553 [25]

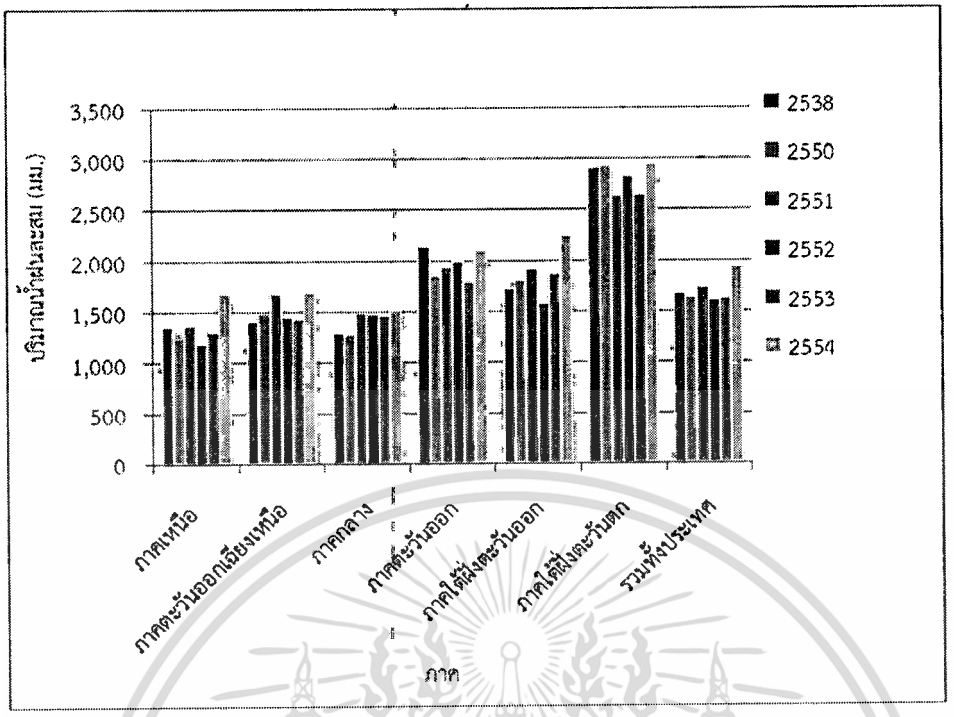
การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่น โรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์



รูปที่ 9 แสดงผู้ป่วยโรคไข้เลือดออกในจังหวัดของภาคเหนือที่มีอัตราผู้ป่วยในปีพ.ศ.2554 เพิ่มขึ้นจากปีพ.ศ.2553 [25]



รูปที่ 10 แสดงผู้ป่วยโรคมาลาเรียในจังหวัดของภาคเหนือที่มีอัตราผู้ป่วยในปีพ.ศ.2554 เพิ่มขึ้นจากปีพ.ศ.2553 [25]



รูปที่ 11 แสดงการเปรียบเทียบปริมาณน้ำฝนสะสมปีพ.ศ.2538 พ.ศ.2550 ถึงปีพ.ศ.2554 [26]

จากข้อมูลของสำนักระบาดวิทยา กระทรวงสาธารณสุขซึ่งแสดงดังรูปที่ 4 ถึงรูปที่ 10 จังหวัดที่มีการแพร่ระบาดของโรคที่เกิดจากยุงเป็นพาหะเพิ่มขึ้นส่วนใหญ่เป็นจังหวัดที่ประสบอุทกภัยในปี พ.ศ.2554 ปริมาณน้ำฝนสะสมในประเทศไทยแสดงดังรูปที่ 11 จะเห็นได้ว่าปีพ.ศ.2554 เป็นปีที่มีปริมาณน้ำฝนสะสมสูงเมื่อเปรียบเทียบกับปริมาณน้ำฝนสะสมของปีอื่นๆ จึงทำให้เกิดเป็นมหาอุทกภัยในปีพ.ศ.2554 ดังที่กล่าวมาข้างต้น จากสถานการณ์โรคที่เกิดจากการแพร่ระบาดของโรคที่มียุงเป็นพาหะ ซึ่งได้แก่โรคไข้เลือดออกและมาลาเรีย พบว่าผู้ป่วยทั้งสองโรคนี้มีการระบาดอย่างต่อเนื่องทุกๆ ปี โรคไข้เลือดออกและโรคมาลาเรียเป็น 2 ใน 9 โรคที่เกิดขึ้นภายหลังจากน้ำท่วม งบประมาณที่ใช้ในการรักษาผู้ป่วยสองโรคนี้มีเพิ่มขึ้นเรื่อยๆ นอกจากนั้นยังไม่มีวัคซีนที่สามารถป้องกันทั้งสองโรคนี้ได้อย่างมีประสิทธิภาพ ผู้วิจัยจึงเห็นว่าควรจะเสนอแนวทางใหม่ในการลดและควบคุมการระบาดของทั้งสองโรคนี้กับสถานการณ์การเกิดน้ำท่วมโดยใช้เทคนิคการสร้างแบบจำลองคณิตศาสตร์

แบบจำลอง (Model) หมายถึง ตัวแทนของลักษณะหรือพฤติกรรมของสิ่งที่สนใจ ใช้ในการนำเสนอเพื่อศึกษา หรือเลียนแบบเพื่อใช้ศึกษาปัญหานั้นๆ การจำลองแบบปัญหาเป็นวิธีการหนึ่งที่มีประสิทธิภาพอย่างมากที่นำมาช่วยสำหรับการศึกษา และวิเคราะห์หาผลลัพธ์ เพื่อนำไปใช้สำหรับการแก้ปัญหาในด้านต่างๆ ซึ่งมีระบบหรือขั้นตอนการทำงานที่มีความยุ่งยากซับซ้อน การจำลอง

แบบปัญหาเป็นเครื่องมือที่จะช่วยในการวิเคราะห์ และตัดสินใจเกี่ยวกับปัญหานั้นๆ แบบจำลองทางคณิตศาสตร์สำหรับการแพทย์ ได้มีบทบาทอย่างมากต่อการทำความเข้าใจ และแก้ปัญหาเกี่ยวกับโรค เพื่อศึกษา วิเคราะห์ และนำไปสู่การควบคุมการระบาดของโรค การสร้างแบบจำลองทางคณิตศาสตร์เริ่มมีบทบาทสำคัญต่อการแก้ปัญหาการระบาดของโรคต่างๆ [27-31] เช่น โรคไข้เลือดออก โรคมาลาเรีย โรคไข้หวัด ฯลฯ สำหรับงานวิจัยทางด้านแบบจำลองคณิตศาสตร์สำหรับการระบาดของโรคไข้เลือดออก และโรคมาลาเรียนั้นได้มีผู้พัฒนาแบบจำลองดังนี้คือ

ในปีพ.ศ.2541 Esteva และ Vargas ได้ศึกษาแบบจำลองโดยการกำหนดให้จำนวนประชากรคนและจำนวนยุงคงที่ [29] หลังจากนั้นได้ประยุกต์วิธีการของการจำลองเชิงพลวัตมาตรฐาน (standard dynamical modeling) มาวิเคราะห์ลักษณะของคำตอบในแบบจำลองทางคณิตศาสตร์พร้อมทั้งแสดงเงื่อนไขของตัวแปรที่ทำให้เกิดความเสถียรภายในของจุดสมดุลภายใต้สภาวะไร้โรค (disease free state) และสภาวะระบาดอย่างเรื้อรัง (disease endemic state) ผลลัพธ์เชิงตัวเลขของแบบจำลองได้ถูกนำมาแสดง เพื่อใช้ในการสนับสนุนสมมติฐานในการศึกษา และนำไปสู่วิธีการลดการระบาดของโรค

ปีพ.ศ.2542 Esteva และ Vargas ได้พัฒนาแบบจำลองทางคณิตศาสตร์ โดยแบ่งการพิจารณาคน และยุง โดยที่กำหนดให้จำนวนประชากรของคนไม่คงที่ [30] และกำหนดให้มีการติดเชื้อเพียงครั้งเดียว

ปีพ.ศ.2543 และพ.ศ.2546 Esteva และ Vargas ได้ศึกษาแบบจำลองทางคณิตศาสตร์โดยศึกษาความสัมพันธ์ของการติดเชื้อซ้ำและพิจารณาการถ่ายทอดเชื้อระหว่างยุง [32,33] และกำหนดให้จำนวนประชากรของคนและยุงคงที่

ปีพ.ศ.2550 ผู้วิจัยและคณะ [34] ได้ศึกษาและสร้างแบบจำลองทางคณิตศาสตร์ โดยพิจารณาการฟักตัวของเชื้อไวรัสเดงกี

ปีพ.ศ.2553 ผู้วิจัย และคณะ [35] ได้ศึกษาแบบจำลองทางคณิตศาสตร์ของการแพร่เชื้อโรคไข้เลือดออกโดยมียุงลายเป็นพาหะนำโรค และพิจารณาการระบาดของโรคนี้โดยให้การถ่ายทอดเชื้อของแต่ละฤดูกาลไม่เท่ากัน

การสร้างแบบจำลองทางคณิตศาสตร์สำหรับศึกษาโรคมาลาเรียเกิดขึ้นครั้งแรกในปี พ.ศ. 2454 โดย Ross [36] ต่อมาในปี พ.ศ. 2500 ได้มีการอธิบายเพิ่มเติมครั้งสำคัญในหนังสือของ Macdonald [37] โดยที่แบบจำลองแบบแรกนั้นเป็นการพิจารณาประชากรคนและประชากรยุง

ต่อมาในปี พ.ศ. 2517 แบบจำลองทางคณิตศาสตร์สำหรับโรคมาลาเรียนำมาศึกษาเพิ่มเติมโดยผู้ที่มีบทบาทสำคัญคือ Dietz, Molineaux และ Thomas [38] พวกเขาได้สร้างแบบจำลองทางคณิตศาสตร์เพื่อศึกษาแนวทางการควบคุมโรคมาลาเรียชนิดเชื้อพลาสโมเดียมฟัลซิพารัมและศึกษาถึงระดับภูมิคุ้มกันของประชากรโดยแสดงในรูปแบบของฟังก์ชัน และพวกเขาได้มีการนำข้อมูล

ของมาลาเรียในแอฟริกาที่ได้มาจากองค์การอนามัยโลก ตั้งแต่เดือนตุลาคม ปี พ.ศ.2513 มาทดสอบกับแบบจำลองของพวกเขา

หลังจากนั้น ในปี พ.ศ.2531 Aron [39] ได้ศึกษาเปรียบเทียบแบบจำลอง 2 แบบ โดยการศึกษาผลของการมีภูมิคุ้มกันต่อมาลาเรีย เขาได้แสดงให้เห็นถึงความแตกต่างในการหาแนวทางการควบคุมและลดการระบาดของโรค โดยแสดงให้เห็นว่าการระบาดของโรคจะลดลงถ้าเสริมสร้างภูมิคุ้มกันและเพิ่มอัตราการฟื้นไข้

ในปี พ.ศ.2534 Koella [40] ได้ใช้แบบจำลองทางคณิตศาสตร์ศึกษาการแพร่ระบาดของโรคมาลาเรีย จากสิ่งที่มีอิทธิพลต่อการแพร่ระบาดของโรคและในปีถัดมา Halloran และ Struchiner [41] ได้สร้างแบบจำลองเพื่อศึกษาคุณลักษณะเฉพาะเพื่อเป็นแนวทางการหาวัคซีนป้องกันโรคมาลาเรีย ต่อมาในปี พ.ศ.2539 Lindsay และ Birley [42] ได้ใช้แบบจำลองทางคณิตศาสตร์ศึกษาอิทธิพลผลกระทบของอุณหภูมิต่อการระบาดของโรคมาลาเรีย ชนิดเชื้อไวแวกซ์ ซึ่งผลที่ได้จากการศึกษาพบว่า การเพิ่มขึ้นของอุณหภูมิเพียงเล็กน้อยก็สามารถทำให้อัตราการแพร่ระบาดเพิ่มมากขึ้น

ในปี พ.ศ.2542 Ngwa และ Shu [43] ได้ศึกษาและวิเคราะห์ แบบจำลองของตัวแบบเชิงกำหนด (deterministic model) สำหรับการระบาดของโรคมาลาเรีย โดยการพิจารณากลุ่มประชากรคนและประชากรยุง พวกเขาได้ค้นพบเงื่อนไขของจุดสมดุล (equilibrium state) ที่นำไปสู่สภาวะการระบาดของโรคแบบไร้โรค (disease free state) และสภาวะการระบาดของโรคแบบเรื้อรัง (disease endemic state) จากค่าสืบพันธุ์พื้นฐาน ต่อมาในปี พ.ศ.2543 Yang [44] ได้อธิบายการแพร่ระบาดของโรคมาลาเรีย โดยการพิจารณากลุ่มประชากรคนและประชากรยุง ผลที่ได้จากการศึกษาคือ จุดสมดุลซึ่งได้จากการคำนวณจากค่าสืบพันธุ์พื้นฐานในเทอมของตัวแปรต่างๆ และในปีเดียวกันนั้นเอง Yang และ Ferreira [45] ได้ใช้แบบจำลองทางคณิตศาสตร์อธิบายและทำความเข้าใจเกี่ยวกับการแพร่ระบาดของโรค โดยการศึกษาอิทธิพลเพิ่มเติมจากการเปลี่ยนแปลงของอุณหภูมิ การรวมกลุ่มของประชากรคน และสภาวะเศรษฐกิจที่มีผลต่อการแพร่ระบาดของโรค

ในปี พ.ศ. 2544 Yang [46] ได้ศึกษาและวิเคราะห์แบบจำลองโดยการพิจารณากลุ่มประชากรที่ไวต่อการติดเชื้อโดยการพิจารณาช่วงอายุของการได้รับวัคซีน ซึ่งเป็นปัจจัยที่สำคัญยิ่งต่อการติดเชื้อ โดยการอธิบายการแพร่ระบาดด้วยสมการเชิงอนุพันธ์แบบไม่เชิงเส้น หลังจากนั้นในปี พ.ศ. 2546 Koella และ Boete [47] ได้อธิบายแบบจำลองโดยการพิจารณาประชากรยุงเป็นหลัก

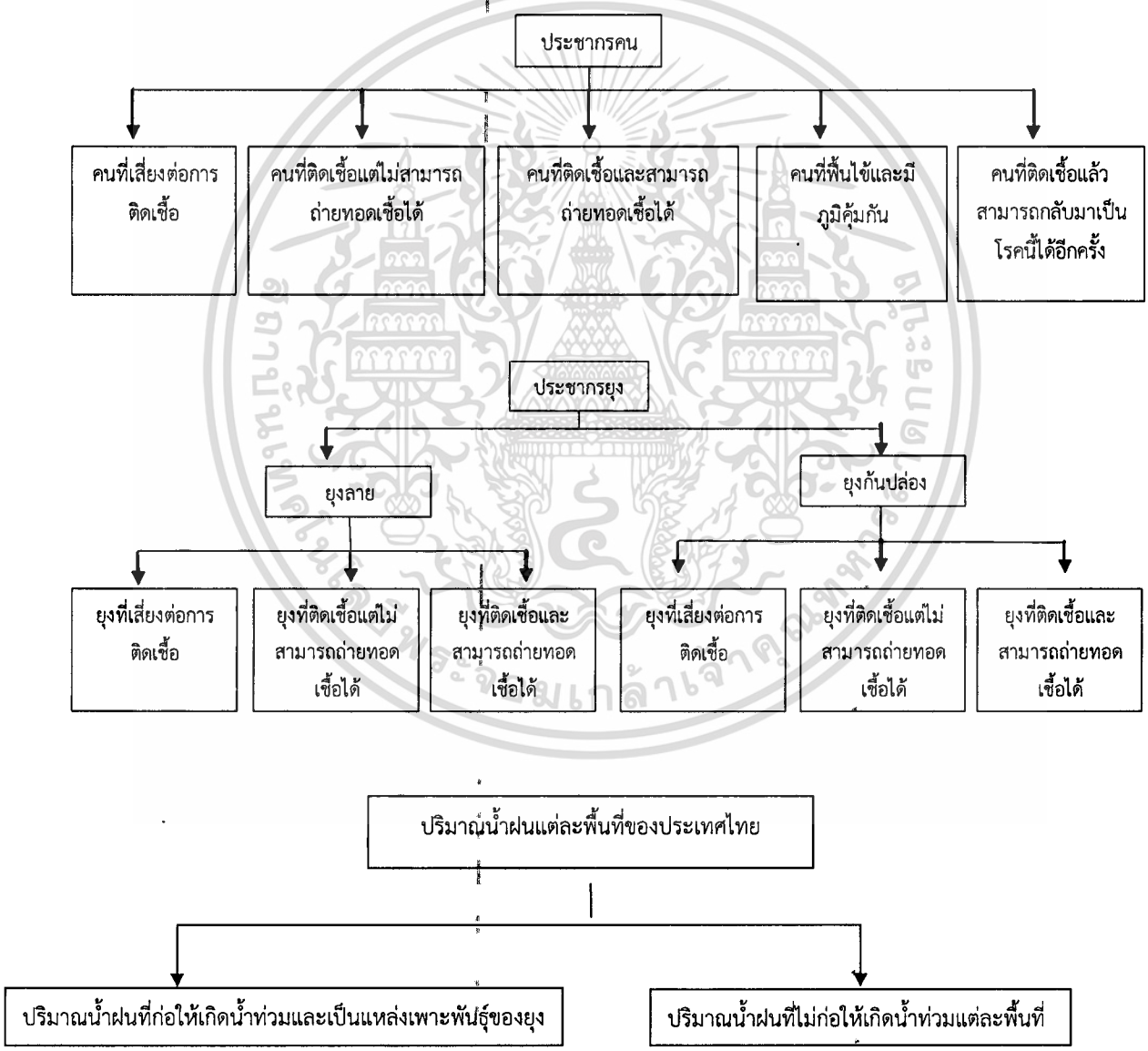
ในปี พ.ศ. 2547 Ngwa [48] ได้ศึกษาและวิเคราะห์แบบจำลองโดยการพิจารณาค่าสืบพันธุ์พื้นฐาน ผลที่ได้จากการศึกษาพบว่า ถ้าค่าสืบพันธุ์พื้นฐานน้อยกว่า 1 จะเกิดสภาวะไร้โรค ซึ่งเป็นการศึกษาโดยใช้แบบจำลองแบบกระบวนการสโทแคสติก (stochastic process) ในปี พ.ศ. 2550, ผู้วิจัยและคณะ [49] ได้ทำการศึกษาและพัฒนาแบบจำลองสำหรับการระบาดของโรคมาลาเรียชนิดไวแวกซ์ และได้แสดงเงื่อนไขของตัวพารามิเตอร์ที่ทำให้เกิดความเสถียรภายใน (local asymptotically stable) ของจุดสมดุลภายใต้สภาวะไร้โรค (disease free state) และสภาวะระบาดอย่างเรื้อรัง (disease endemic state) ผลลัพธ์เชิงตัวเลขของแบบจำลองได้ถูกนำมาแสดง เพื่อใช้ในการสนับสนุนสมมติฐานในการศึกษา ในปี พ.ศ.2551 ผู้วิจัยและคณะ [50] ได้ทำการวิเคราะห์เงื่อนไขที่ทำให้ เกิดพฤติกรรมการระบาดของโรคมาลาเรียชนิดไวแวกซ์แบ่งออกเป็นสองลักษณะ (Bifurcation) ในเวลาต่อมา ผู้วิจัยและคณะ [51] ได้ทำการศึกษาและพัฒนาแบบจำลองสำหรับการระบาดของโรคมาลาเรียชนิดไวแวกซ์ที่เกิดขึ้นในระดับชุมชน ต่อมาผู้วิจัยและคณะ [52] ได้ทำการศึกษาและพัฒนาแบบจำลองสำหรับการระบาดของโรคมาลาเรียชนิดฟัลซิพารัม และชนิดไวแวกซ์ ที่เกิดขึ้นในประเทศไทย ในเวลาต่อมาผู้วิจัยและคณะ [53] ได้ทำการศึกษาและพัฒนาแบบจำลองสำหรับการระบาดของโรคมาลาเรียโดยพิจารณาการระบาดเมื่อมีการเดินทางของชาวพม่าเพื่อมาเป็นแรงงานในประเทศไทย และได้แสดงสภาวะการระบาดของโรคที่แตกต่างกันเมื่อมีอัตราการเดินทางของแรงงานชาวพม่าที่แตกต่างกัน

สำหรับงานวิจัยที่เกี่ยวกับการสร้างแบบจำลองทางคณิตศาสตร์ที่เกี่ยวข้องกับการเกิดน้ำท่วมในประเทศไทยก็เป็นการสร้างแบบจำลองทางคณิตศาสตร์เพื่อศึกษาและทำนายการเกิดน้ำท่วมเท่านั้น [54,55]

จากงานวิจัยที่เกี่ยวกับการสร้างแบบจำลองทางคณิตศาสตร์ของโรคที่มียุงเป็นพาหะซึ่งได้แก่โรคไข้เลือดออกและโรคมาลาเรียที่ผ่านมานั้นยังไม่มีงานวิจัยที่ได้ดำเนินการสร้างแบบจำลองทางคณิตศาสตร์ที่สามารถนำมาอธิบายการระบาดของโรคไข้เลือดออกและโรคมาลาเรียกับการเกิดน้ำท่วมในประเทศไทย นอกจากนั้นในงานวิจัยนี้ยังมีการศึกษาการกระจายของผู้ป่วยทั้งสองโรคนี้โดยใช้วิธีของการสร้างแบบจำลองการกระจายตามพื้นที่ (Spatial model) โดยพิจารณาถึงการเคลื่อนที่ของประชากร และยังได้มีการนำเสนอการหาค่าพารามิเตอร์เชิงตัวเลขในแบบจำลอง เพื่อเป็นประโยชน์ในการวิเคราะห์ลักษณะการระบาดของทั้งสองโรคนี้

บทที่ 3
แบบจำลองทางคณิตศาสตร์

ผู้วิจัยพิจารณาการสร้างแบบจำลองทางคณิตศาสตร์ โดยพิจารณาในประชากรคน และประชากรยุง โดยแบบจำลองนี้ ผู้วิจัยสร้างและพัฒนาขึ้นมาใหม่ โดยพิจารณากระบวนการ และเหตุผลทางชีวภาพของการระบาดสำหรับโรคไข้เลือดออกและโรคมาลาเรีย รวมทั้งผลกระทบจากน้ำท่วมที่มีผลต่อการระบาดของโรคก็นำมาพิจารณาด้วย แผนภาพแสดงแนวคิดของตัวแปรที่จะนำมาศึกษารวมทั้งวิเคราะห์ในงานวิจัยนี้คือ



รูปที่ 12 แผนภาพแสดงตัวแปรที่ใช้ในงานวิจัยนี้

ในงานวิจัยฉบับนี้จะดำเนินการสร้างแบบจำลองคณิตศาสตร์แบบต่างๆ ซึ่งจะแสดงในบทที่ 4 โดยการใช้ระบบสมการเชิงอนุพันธ์มาอธิบายการระบาดของโรคนี้ ตัวแปรที่สร้างขึ้นในงานวิจัยฉบับนี้สอดคล้องกับรูปที่ 12 พร้อมทั้งเพิ่มปัจจัยต่างๆ ที่มีผลต่อการระบาดของโรคนี้ ซึ่งคือ ระยะฟักตัวของเชื้อไวรัส อัตราความเสี่ยงที่ทำให้คนสามารถติดเชื้อนี้ได้ อัตราการมีภูมิคุ้มกันของคน อัตราการเกิด อัตราการถ่ายทอดเชื้อจากผู้ที่เป็นพาหะของโรคนี้ทั้งบุคคลที่แสดงอาการของโรคและไม่แสดงอาการ อัตราที่คนไข้ที่เป็นโรคนี้แล้วสามารถกลับมาเป็นโรคนี้ได้อีกครั้งหนึ่ง อัตราการเสียชีวิตของบุคคลที่เคยและไม่เคยเป็นโรคนี้มาก่อน และพารามิเตอร์อื่นๆที่มีผลต่อการเกิดน้ำท่วม นำผลที่ได้ศึกษาดูว่ามีความเหมาะสมกับการระบาดของทั้งสองโรคนี้ในประเทศไทยหรือยัง ถ้ายังไม่เหมาะสม ทำการพัฒนาใหม่ให้เหมาะสม ต่อจากนั้นจะทำการศึกษาการกระจายของผู้ป่วยทั้งสองโรคนี้โดยใช้วิธีของการสร้างแบบจำลองการกระจายตามพื้นที่ (Spatial model) มาวิเคราะห์โดยพิจารณาถึงการระบาดของโรคกับการเดินทางของประชากร ใช้ข้อมูลของผู้ป่วยโรคไข้เลือดออกและโรคมาลาเรียที่ได้รับความร่วมมือจากสำนักระบาดวิทยา กระทรวงสาธารณสุข และข้อมูลที่เกี่ยวข้องกับปริมาณน้ำฝนซึ่งส่งผลกระทบต่ออุทกภัยในประเทศไทยได้รับความร่วมมือจากสำนักพัฒนาอุตุนิยมวิทยา กรมอุตุนิยมวิทยา เพื่อเป็นประโยชน์ในการวิเคราะห์ลักษณะการระบาดของโรคในครั้งต่อไปได้ นำผลที่ได้ มาทดสอบกับข้อมูลจริง สร้างทฤษฎีใหม่ที่เกี่ยวข้อง เมื่อได้ผลลัพธ์เป็นที่เรียบร้อยแล้ว สรุปผลที่ได้ วิเคราะห์และสรุปผลที่ได้จากการวิเคราะห์แบบจำลองทางคณิตศาสตร์ของการระบาดของโรค พร้อมทั้งเสนอแนวทางในการลดการระบาดของโรคนี้โดยอ้างอิงความรู้ ทฤษฎีทางคณิตศาสตร์และวิทยาศาสตร์การแพทย์

บทที่ 4

การวิเคราะห์แบบจำลองทางคณิตศาสตร์ของโรคไข้เลือดออกและโรคมาลาเรีย กับการเกิดน้ำท่วมในประเทศไทย

ในงานวิจัยฉบับนี้ได้ทำการสร้างและวิเคราะห์แบบจำลองทางคณิตศาสตร์แบบต่างๆ ดังนี้

4.1. แบบจำลองที่ 1 แบบจำลองของโรคไข้เลือดออกโดยที่ไม่ได้คำนึงถึงสภาพแวดล้อมแต่พิจารณาถึงยุงที่ติดเชื้อมาตั้งแต่เกิด [56]

We formulate the mathematical model by considering infected vector by both biting of infected human and vector-born infection. The human and vector population are related in this study, which human populations are separated into three classes, susceptible, infected and recovered human while the vector populations are separated into two classes, susceptible and infected vector populations. The transmission of dengue fever is shown in Figure1.1.

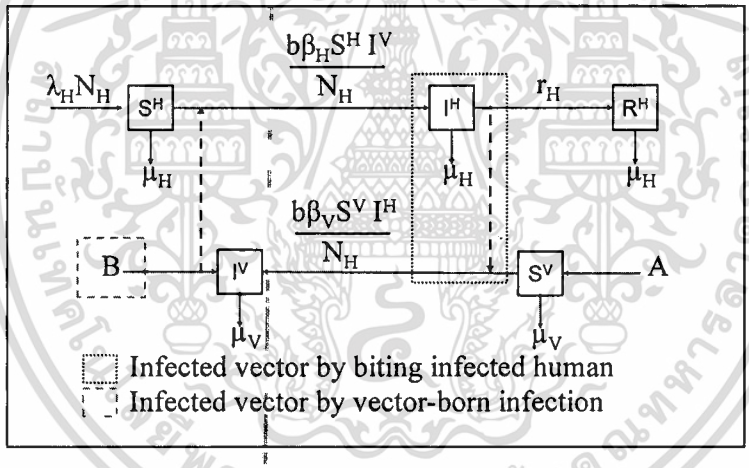


Figure 1.1: Diagram of model (1)

Let:

$S^H(t)$ = Number of susceptible humans at time t,
$I^H(t)$ = Number of infected humans at time t,
$R^H(t)$ = Number of recovered humans at time t,
$S^V(t)$ = Number of susceptible vector population at time t,
$I^V(t)$ = Number of infected vector population at time t,
A = Recruitment rate of vector population,
B = Vector-born rate of vector population.

The dengue fever transmission model with vector-born infection can be explained by the following equation:

$$\frac{dS^H}{dt} = \lambda_H N_H - \frac{b\beta_H}{N_H} S^H I^V - \mu_H S^H \quad (1)$$

$$\frac{dI^H}{dt} = \frac{b\beta_H}{N_H} S^H I^V - (\mu_H + r_H) I^H \quad (2)$$

$$\frac{dR^H}{dt} = \mu_H I^H - \mu_H R^H \quad (3)$$

$$\frac{dS^V}{dt} = A - \frac{b\beta_V}{N_H} S^V I^H - \mu_V S^V \quad (4)$$

$$\frac{dI^V}{dt} = B + \frac{b\beta_V}{N_H} S^V I^H - \mu_V I^V \quad (5)$$

และมีเงื่อนไข

$$N_H = S^H + I^H + R^H \quad (6)$$

$$N_V = S^V + I^V \quad (7)$$

where:

N_H = Total number the human population,

λ_H = Birth rate of the human population,

b = Biting rate of the vector population,

β_H = Transmission probability of dengue virus from vector population to human population,

β_V = Transmission probability of dengue virus from human population to vector population,

μ_H = Death rate of the human population,

μ_V = Death rate of the vector population,

r_H = Recovery rate of the human population.

The total number of human and vector are assumed to be constant. It means that the rate of change of vector and human population are zero. It can be expressed as following:

$$\frac{dS^H}{dt} + \frac{dI^H}{dt} + \frac{dR^H}{dt} = 0 \quad (8)$$

$$\frac{dS^V}{dt} + \frac{dI^V}{dt} = 0 \quad (9)$$

So

$$N_V = (A + B)/\mu_V \quad (10)$$

$$\lambda_H = \mu_H \quad (11)$$

We define new variables:

$$S_H = \frac{S^H}{N_H}, I_V = \frac{S^H}{N_H}, R_V = \frac{R^H}{N_H}, S_V = \frac{S^V}{N_V}, I_V = \frac{S^V}{N_V} \quad (12)$$

Therefore, we have

$$\frac{dS_H}{dt} = \mu_H(1 - S_H) - \frac{b\beta_H S_H I_V N_V}{N_H} \quad (13)$$

$$\frac{dI_H}{dt} = \frac{b\beta_H S_H I_V N_V}{N_H} - (\mu_H + r_H) I_H \quad (14)$$

$$\frac{dI_V}{dt} = \frac{B}{N_V} + b\beta_V S_V I_H - \mu_V I_V \quad (15)$$

The equilibrium points can be found by setting the right hand side of our equations to zero. Then we have following solutions.

$$E_1 = (S_H^{1*}, I_H^{1*}, I_V^{1*}) \quad (16)$$

$$E_2 = (S_H^{2*}, I_H^{2*}, I_V^{2*}) \quad (17)$$

$$S_H^{1*} = \frac{N_H \mu_H}{bd_1 N_V \mu_H + N_H \mu_{H_1}} \quad (18)$$

?? $$S_H^{2*} = \frac{N_H \mu_H}{bd_2 N_V \mu_H + N_H \mu_H} \quad (19)$$

$$I_H^{1*} = \frac{bd_1 \beta_H N_V \mu_H}{(\mu_H + r_H)(bd_1 N_V \beta_H + N_H \mu_H)} \quad (20)$$

$$I_H^{2*} = \frac{bd_2 \beta_H N_V \mu_H}{(\mu_H + r_H)(bd_2 N_V \beta_H + N_H \mu_H)} \quad (21)$$

$$I_V^{1*} = d_1 \quad (22)$$

$$I_V^{2*} = d_2 \quad (23)$$

and

$$d_1 = \frac{M + R_0 M}{N}$$

$$d_2 = \frac{M - R_0 M}{N}$$

$$M = b^2 N_V^2 \beta_H \beta_V \mu_H + N_V(\mu_H + r_H)(b\beta_H \beta_V - N_H \mu_H \mu_V)$$

$$N = 2bN_V^2 \beta_H (b\beta_V \mu_H + (\mu_H + r_H)\mu_V)$$

$$R_0 = \frac{\sqrt{N_V^2(4bN_H \beta_H \beta_V \mu_H(\mu_H + r_H)(b\beta_V \mu_H) + (\mu_H + r_H)\mu_V) + (b\beta_H \beta_V (r_H + \mu_H + bN_V \mu_H) - N_N \mu_H (\mu_H + r_H)\mu_V)^2}}{b^2 N_V^2 \beta_H \beta_V \mu_H + N_V(\mu_H + r_H)(b\beta_H \beta_V - N_H \mu_H \mu_V)}$$

The local stability of the equilibrium point is calculated by Jacobian matrix of equations (13) – (15). The eigenvalues will indicate the local stability. The equilibrium solution is local

stability when all eigenvalues are negative real parts. The eigenvalues of Jacobian matrix are determined by solving:

$$\det(J - \lambda I) = 0$$

where

J = The Jacobian matrix of the equilibrium point,
λ = The eigenvalue,
I = The identity matrix.

All eigenvalues are determined by following:

$$(\lambda^3 + e_0\lambda^2 + e_1\lambda + e_2) = 0 \quad (25)$$

Routh-Hurwitz criteria is used to analyze the local stability of equilibrium point. The solution is local stability when the conditions are satisfied by following:

$$(e_0 > 0), (e_1 > 0) \text{ และ } (e_0 e_1 > e_2) \quad (26)$$

By solving equation (13) – (15) and (24) – (25), it can be found that all conditions are complied with equation (26). Thus, we can conclude that equilibrium point E_1 is local stable.

The basic reproductive number of the dengue fever in this study is $\sqrt{R_0}$. It is the average number of secondary case that one case can produce into a susceptible human. In case of R_0 value more than one, the endemic equilibrium is stable. Numerical solutions of equations (13) – (15) are presented the dengue fever situation. The computer software package is used to analyze in this investigated. The values of parameters are as following $A = 400$,

$B = 200$,
$N_H = 10{,}000$,
$b = 1/3$ day^{-1},
$\beta_H = 0.75$,
$\beta_V = 1.00$,
$\mu_H = 0.0000391$ day^{-1},
$\mu_V = 0.075$ day^{-1},
$r_H = 0.1428$ day^{-1}.

All eigenvalues of Jacobian matrix from equations (13) – (15) are determined by equation (24) and we obtained the characteristic equation as below:

$$(-\lambda^3 - 0.21457\lambda^2 - 0.0603873\lambda - 6.3884 * 1 \quad (27)$$

The results of calculated values are: $\lambda_1 = -0.181491, \lambda_2 = -0.0319781, \lambda_3 = -0.00110074$ and $R_0 = 1.07768$. All eigenvalues are negative that leads to the equilibrium state. R_0 is more than 1 that leads to be the endemic state. The solutions oscillate to the endemic equilibrium points $S_H^{1*} = 0.060569$, $I_H^{1*} = 0.000257$, $I_V^{1*} = 0.002870$.

The time series solutions of susceptible human, infected human and infected vector populations are shown in Figure 2.

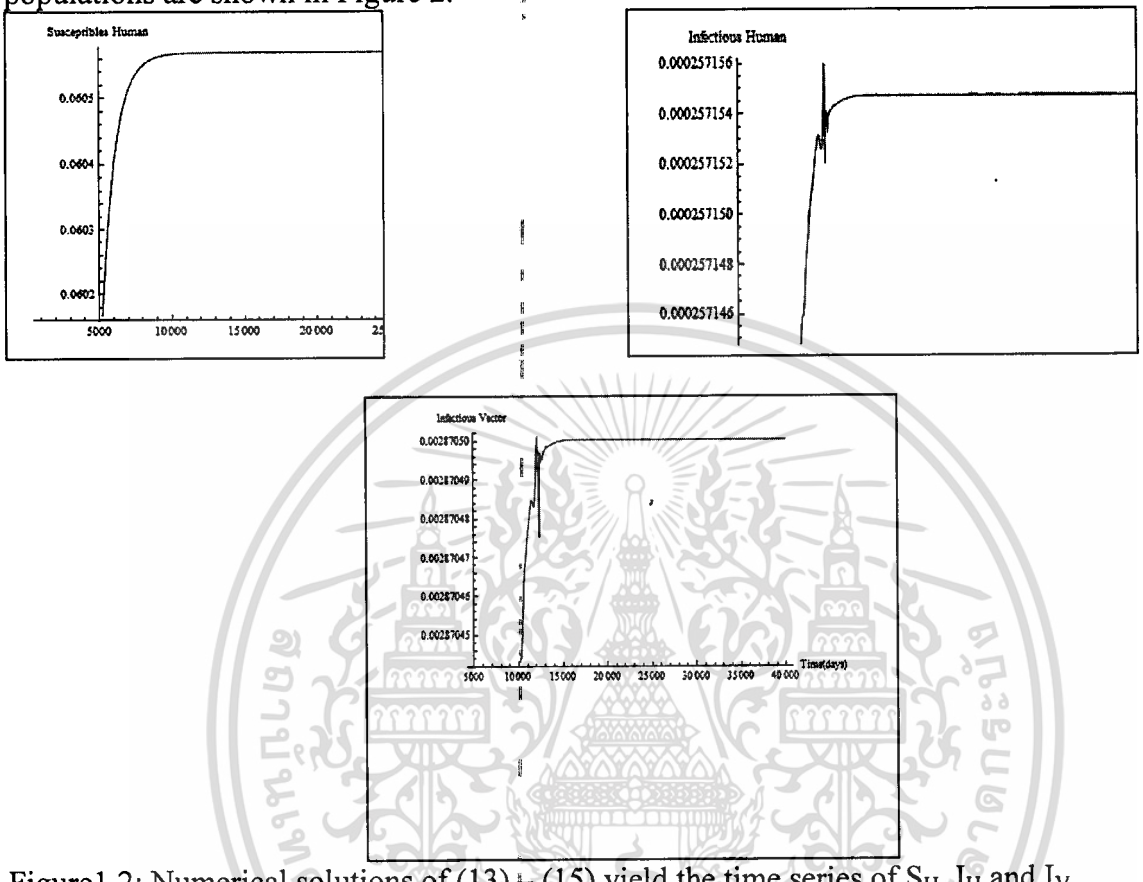
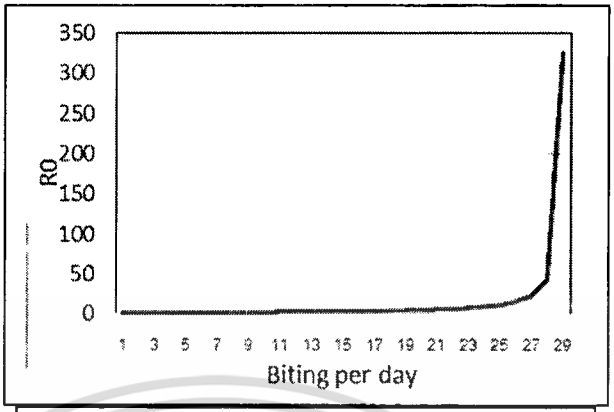
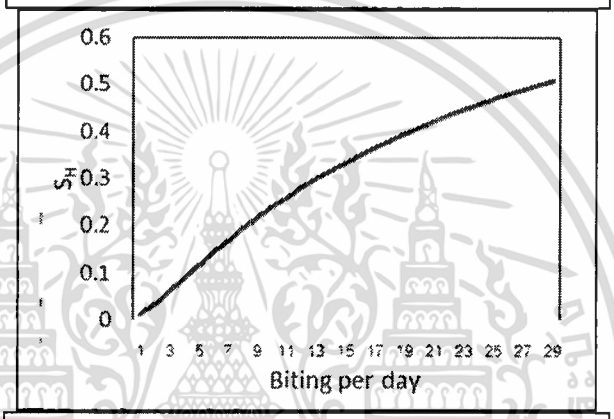
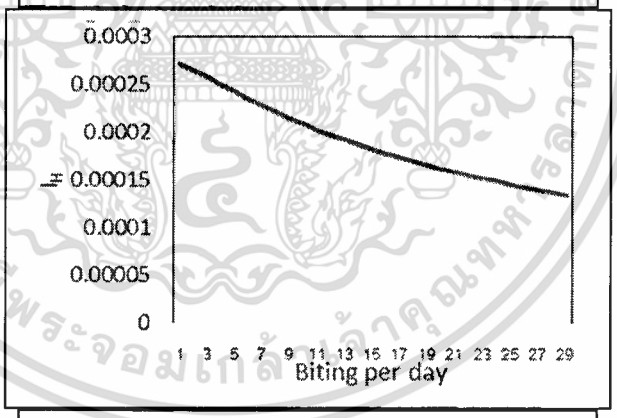


Figure1.2: Numerical solutions of (13) – (15) yield the time series of S_H, I_H and I_V

The relationship between mosquito biting and R_0, susceptible human, infected human and infected vector populations are shown in Fig1.3. If the mosquito biting is increased, the values of R_0 and S_H will increase while I_H and I_V will increase as below.







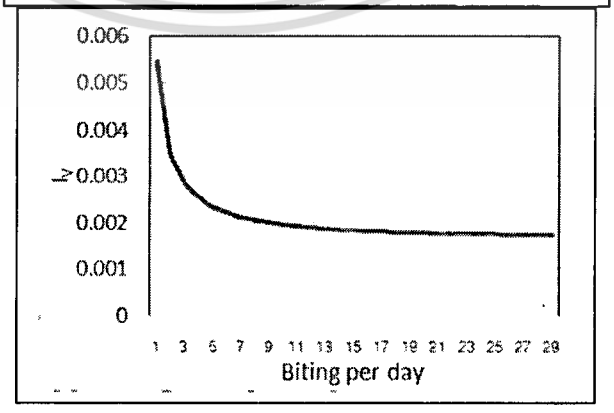


Figure 1.3: Relationship of mosquito biting and R_0, S_H, I_H and I_V

For first model, we can conclude that the values of parameters are satisfied with Routh – Hurwitz criteria and the numerical solutions converge to the endemic equilibrium point E_1 (0.060569, 0.000257, 0.002870). Figure3 shows time series solution of S_H, I_H and I_V. The simulations of the biting rate of mosquitoes are investigated and the results show in Figure 1.4. The value of R_0 can control by decreasing the mosquitoes biting. The basic reproductive numbers are used to control the transmission of dengue fever. The effective way to control the dengue fever is decreased the carry capacity of the environment of mosquitoes such as mosquitoes breeding sites and decreased the mosquitoes biting.

In this model, we propose and analyze the transmission dynamics of SIR modeling for dengue with vector – born infection. We consider vector population both the recruitment rate of mosquitoes and mosquitoes-born infection. We found the endemic equilibrium state and we can reduce the human susceptibility to the dengue fever that can reduce the outbreak of dengue fever.

4.2. แบบจำลองที่ 2 แบบจำลองของโรคไข้เลือดออกโดยที่ไม่ได้คำนึงถึงสภาพแวดล้อมแต่พิจารณาถึงยุงที่ติดเชื้อมาตั้งแต่เกิด และพิจารณาถึงการฟักตัวของเชื้อ [57]

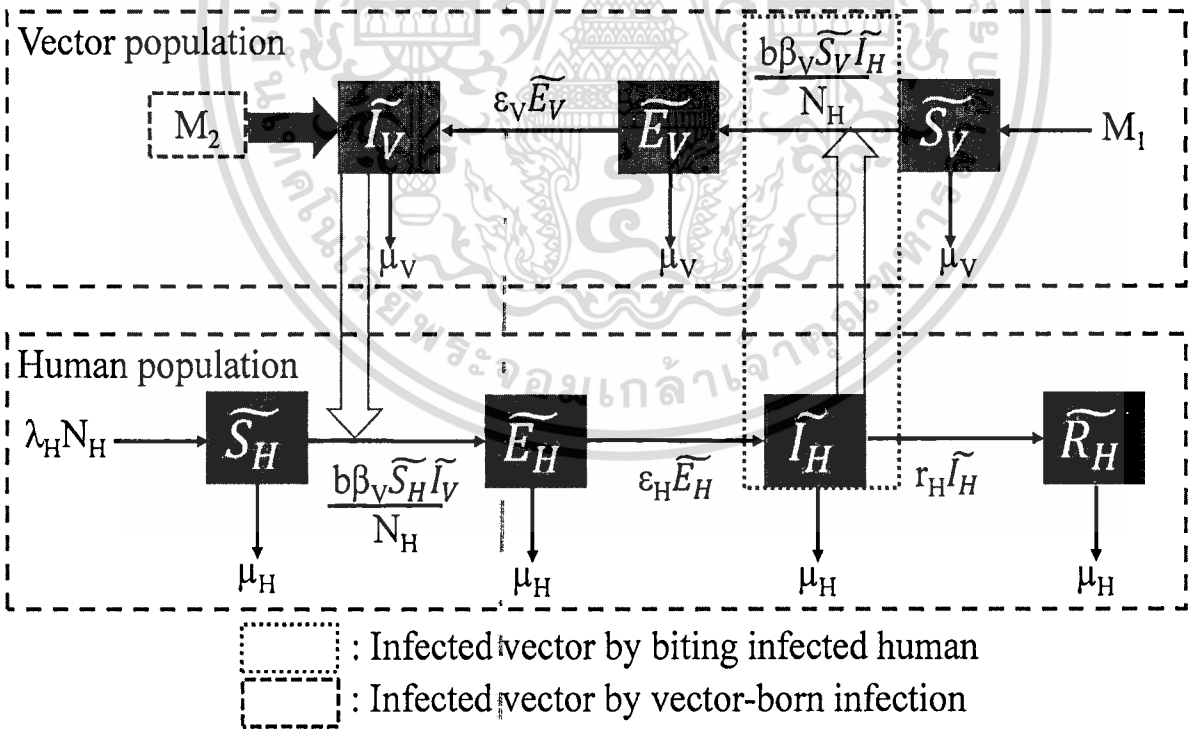


Figure 4.4: Diagram of our model.

Let:

$\tilde{S}_H(t)$ = Number of susceptible human population at time t,

$\tilde{E}_H(t)$ = Number of exposed human population at time t,

$\tilde{I}_H(t)$ = Number of infected human population at time t,

$\tilde{R}_H(t)$ = Number of recovered human population at time t,

$\tilde{S}_V(t)$ = Number of susceptible vector population at time t,

$\tilde{E}_V(t)$ = Number of exposed vector population at time t,

$\tilde{I}_V(t)$ = Number of infected vector population at time t,

M_1 = Constant recruitment rate,

M_2 = Number of new infected vector.

The dengue disease transmission model of both population groups can be explained by following equations:

$$d\tilde{S}_H / dt = \lambda_H N_H - (b\beta_H / N_H)\tilde{S}_H \tilde{I}_V - \mu_H \tilde{S}_H \quad (2.1)$$

$$d\tilde{E}_H / dt = (b\beta_H / N_H)\tilde{S}_H \tilde{I}_V - (\varepsilon_H + \mu_H)\tilde{E}_H \quad (2.2)$$

$$d\tilde{I}_H / dt = \varepsilon_H \tilde{E}_H - (\mu_H + \gamma_H)\tilde{I}_H \quad (2.3)$$

$$d\tilde{R}_H / dt = \gamma_H \tilde{I}_H - \mu_H \tilde{R}_H \quad (2.4)$$

$$d\tilde{S}_V / dt = M_1 - (b\beta_V / N_H)\tilde{S}_V \tilde{I}_H - \mu_V \tilde{S}_V \quad (2.5)$$

$$d\tilde{E}_V / dt = (b\beta_V / N_H)\tilde{S}_V \tilde{I}_H - (\varepsilon_V + \mu_V)\tilde{E}_V \quad (2.6)$$

$$d\tilde{I}_V / dt = M_2 + \varepsilon_V \tilde{E}_V - \mu_V \tilde{I}_V \quad (2.7)$$

with the conditions:

$$N_H = \tilde{S}_H + \tilde{E}_H + \tilde{I}_H + \tilde{R}_H \quad (2.8)$$

$$N_V = \tilde{S}_V + \tilde{E}_V + \tilde{I}_V \tag{2.9}$$

where:

N_H = Total number of human population,

N_V = Total number of vector population,

λ_H = Birth rate of human population,

b = Biting rate of vector population,

β_H = Transmission probability of dengue virus from vector population to human population,

β_V = Transmission probability of dengue virus from human population to vector population,

ε_H = Intrinsic incubation rate,

ε_V = Extrinsic incubation rate,

μ_H = Death rate of human population,

μ_V = Death rate of vector population,

γ_H = Recovery rate of the human population.

The assumption of our model is the total human and vector population are constant. This indicates that the rate of change for human and vector population are zero. The results are:

$$d\tilde{S}_H / dt + d\tilde{E}_H / dt + \tilde{I}_H / dt + d\tilde{R}_H / dt = 0 \tag{2.10}$$

$$d\tilde{S}_V / dt + d\tilde{E}_V / dt + d\tilde{I}_V / dt = 0. \tag{2.11}$$

From the preceeding equations, we can obtain the following equations:

$$N_V = (M_1 + M_2) / \mu_V \tag{2.12}$$

$$\lambda_H = \mu_H. \tag{2.13}$$

We normalized equations (2.1) – (2.9) in order to analyze the model by using the conditions as following:

$$S_H = \tilde{S}_H / N_H, E_H = \tilde{E}_H / N_H, I_H = \tilde{I}_H / N_H, R_H = \tilde{R}_H / N_H \tag{2.14}$$

$$S_V = \tilde{S}_V / N_V, E_V = \tilde{E}_V / N_V, I_V = \tilde{I}_V / N_V. \tag{2.15}$$

Therefore, the necessary conditions of the system are follows:

$$1 = S_H + E_H + I_H + R_H \tag{2.16}$$

$$1 = S_V + E_V + I_V. \tag{2.17}$$

The mathematical model of equation (2.1) – (2.7) can be reduced to the following equations:

$$dS_H / dt = \mu_H (1 - S_H) - (b\beta_H / N_H) S_H I_V N_V \tag{2.18}$$

$$dE_H / dt = (b\beta_H / N_H) S_H I_V N_V - (\varepsilon_H + \mu_H) E_H \tag{2.19}$$

$$dI_H / dt = \varepsilon_H E_H - (\mu_H + \gamma_H) I_H \tag{2.20}$$

$$dE_V / dt = b\beta_V S_V I_H - (\varepsilon_V + \mu_V) E_V \tag{2.21}$$

$$dI_V / dt = M_2 / N_V + \varepsilon_V E_V - \mu_V I_V \tag{2.22}$$

The mathematical model is analyzed and investigated to find the equilibrium points and system stability. The equilibrium points are calculated by setting the right hand side of equation (2.18) – (2.22) equal to zero. The system stability is determined by eigenvalues and basic reproductive number. After we solved equation (2.18) – (2.22), we can obtain equilibrium points E_1 and E_2 as follows:

$$E_1 = (S_H^{1*}, E_H^{1*}, I_H^{1*}, E_V^{1*}, I_V^{1*}) \tag{2.23}$$

$$E_2 = (S_H^{2*}, E_H^{2*}, I_H^{2*}, E_V^{2*}, I_V^{2*}) \tag{2.24}$$

$$S_H^{1*} = A / [B((R_0 D_1^2 / D_2) - D_2) + A] \tag{2.25}$$

$$S_H^{2*} = A / [B((R_0 D_1^2 / D_2) + D_2) + A] \tag{2.26}$$

$$E_H^{1*} = B((R_0 D_1^2 / D_2) - D_2)\mu_H / [K_2(B((R_0 D_1^2 / D_2) - D_2) + A)] \quad (2.27)$$

$$E_H^{2*} = B((R_0 D_1^2 / D_2) + D_2)\mu_H / [K_2(B((R_0 D_1^2 / D_2) + D_2) + A)] \quad (2.28)$$

$$I_H^{1*} = B((R_0 D_1^2 / D_2) - D_2)(\varepsilon_H - \mu_H)\mu_H / [F_2(B((R_0 D_1^2 / D_2) - D_2) + A)] \quad (2.29)$$

$$I_H^{2*} = B((R_0 D_1^2 / D_2) + D_2)(\varepsilon_H - \mu_H)\mu_H / [F_2(B((R_0 D_1^2 / D_2) - D_2) + A)] \quad (2.30)$$

$$E_V^{1*} = N_1 / N_2 \quad (2.31)$$

$$E_V^{2*} = P_1 / (P_2 P_3) \quad (2.32)$$

$$I_V^{1*} = (R_0 D_1^2 / D_2) - D_2 \quad (2.33)$$

$$I_V^{2*} = (R_0 D_1^2 / D_2) + D_2 \quad (2.34)$$

$$J(S_H, E_H, I_H, E_V, I_V) = \begin{bmatrix} -\mu_H - \frac{b\beta_H}{N_H} I_V N_V & 0 & 0 & 0 & -\frac{b\beta_H}{N_H} S_H N_V \\ \frac{b\beta_H}{N_H} I_V N_V & -(\varepsilon_H + \mu_H) & 0 & 0 & \frac{b\beta_H}{N_H} S_H N_V \\ 0 & \varepsilon_H & -(\mu_H + r_H) & 0 & 0 \\ 0 & 0 & b\beta_V S_V & -(\varepsilon_V + \mu_V) & 0 \\ 0 & 0 & 0 & \varepsilon_V & -\mu_V \end{bmatrix} \quad (2.35)$$

where:

$R_0 = D_1 / D_2$

$D_1 = M(M_1 b\beta_H \varepsilon_V C + K_1(L + J)$

$D_2 = \sqrt{M^2(C^2G^2 + 2CGK_1(L-J) + K_1^2(L-J)^2)}$

$A = N_H \mu_H \mu_V$

$$B = b(M_1 + M_2)\beta_H$$

$$C = b\beta_V(\varepsilon_H - \mu_H)\mu_H$$

$$F = \gamma_H(\varepsilon_H - \mu_H)$$

$$G = M_1 b\beta_H \varepsilon_V$$

$$H = M_2 b\beta_H$$

$$J = N_H \gamma_H \mu_H (\varepsilon_H + \mu_H)\mu_V^2$$

$$L = M_2 b^2 \beta_H \beta_V (\varepsilon_H - \mu_H)\mu_H + M_2 b\gamma_H \beta_H (\varepsilon_H + \mu_H)\mu_V$$

$$K_1 = (\varepsilon_V + \mu_V)$$

$$K_2 = (\varepsilon_H + \mu_H)$$

$$M = M_1 + M_2$$

$$N_1 = BC((R_0 D_1^2 / D_2) - D_2)(1 + (R_0 D_1^2 / D_2) - D_2)$$

$$N_2 = [-B((R_0 D_1^2 / D_2) - D_2)(C + F\varepsilon_V) + F(-B((R_0 D_1^2 / D_2) - D_2)\mu_V + A\varepsilon_V) + AF\mu_V$$

$$P_1 = BC((R_0 D_1^2 / D_2) + D_2)(-1 + (R_0 D_1^2 / D_2) + D_2)$$

$$P_2 = F(B((R_0 D_1^2 / D_2) + D_2) + A)$$

$$P_3 = K_1 + [(BC((R_0 D_1^2 / D_2) + D_2) / F(B((R_0 D_1^2 / D_2) + D_2) + A)]$$

In order to determine the local stability of the steady states, we evaluate the Jacobian matrix of equations (2.18) – (2.22). The results are shown as follows:

The characteristic equation is determined in order to evaluate the eigenvalues, which the solution can be obtained by solving *det* $(J_{Ei}-\lambda I) = 0$ where
J_{Ei} = The Jacobian matrix at equilibrium point *Ei (i =1, 2),*
λ = The eigenvalue,
I = The identity matrix.

The solution of equation (2.35) will be set in the form of characteristic equation as below:

$$(\lambda^5 + e_1\lambda^4 + e_2\lambda^3 + e_3\lambda^2 + e_4\lambda^1 + e_5) = 0 \qquad (2.36)$$

when:

$e_1 = Y + Z + \mu_H$

$e_2 = Z(Y + \mu_H) + X$

$e_3 = (Y + Q + X(1 + \mu_H)$

$e_4 = (Y\varepsilon_V(r_H\varepsilon_H + T + S) + Q_1) + (R_1 + Q_1\mu_H)$

$e_5 = YR + \mu_H(YT\varepsilon_V + R)$

where:

$X = 2\varepsilon_V\mu_H + \mu_H^2 + \varepsilon_V\mu_V + 4\mu_H\mu_V + \mu_V^2 + \varepsilon_H(\varepsilon_V + \mu_H + 2\mu_V) + r_H(\varepsilon_H + \varepsilon_V + \mu_H + 2\mu_V)$

$Y = [b(-1 + M_2)I_V\beta_H]/(N_H\mu_V)$

$Z = r_H + \varepsilon_H + \varepsilon_V + 2(\mu_H + \mu_V)$

$Q = \varepsilon_V(r_H + \mu_H)(\varepsilon_H + \mu_H) + (2r_H\varepsilon_H + r_H\varepsilon_V + \varepsilon_H\varepsilon_V + 2(r_H + \varepsilon_H + \varepsilon_V)\mu_H + 2\mu_H^2)\mu_V + (r_H + \varepsilon_H + 2\mu_H)\mu_H^2$

$Q_1 = (2r_H\varepsilon_H + r_H\varepsilon_V + \varepsilon_H\varepsilon_V + 2(r_H + \varepsilon_H + \varepsilon_V)\mu_H + 2\mu_H^2)\mu_V + (r_H + \varepsilon_H + 2\mu_H)\mu$

$R = (r_H + \mu_H)(\varepsilon_H + \mu_H)\mu_V(\varepsilon_V + \mu_V) + \varepsilon_V(r_H + \mu_H)(\varepsilon_H + \mu_H)$

$R_1 = (r_H + \mu_H)(\varepsilon_H + \mu_H)\mu_V(\varepsilon_V + \mu_V)$

$S = (r_H + \varepsilon_H)\mu_H + \mu_H^2$

$T = ((b / I_V)(-1 + E_V + I_V)S_S\beta_H)\varepsilon_H$

The solutions of equation (36) will be solved by using the Routh-Hurwitz criteria in order to analyze the local stability of equilibrium point. The equilibrium points are local stability when all eigenvalues have negative real parts and the following conditions are satisfied:

$$e_1 > 0, e_2 > 0, e_3 > 0, e_4 > 0, e_5 > 0 \tag{2.37}$$

$$e_1 e_2 e_3 > e_3^2 + e_1^2 e_4 \tag{2.38}$$

$$(e_1 e_4 - e_5)(e_1 e_2 e_3 - e_3^2 - e_1^2 e_4) > e_5 (e_1 e_2 - e_3)^2 + e_1 e_5^2 \tag{2.39}$$

After we check the above three conditions by Mathematica, we found that the endemic equilibrium state is locally stable. It can be seen that the coefficients e_0, e_1, e_2, e_3, e_4 and e_5 satisfy the Routh-Hurwitz criteria for local stability of equations (37) – (39) and $R_0>1$. As the results, the endemic equilibrium states are local stability for $R_0>1$ where $R_0 = M(M_1 b\beta_H \varepsilon_V C + K_1(L-J))/[\sqrt{M^2(C^2G^2 + 2CGK_1(L-J) + K_1^2(L+J)^2)}]$. The basic reproductive number of dengue disease is $\sqrt{R_0}$ which is the average number of secondary patients that one patient can produce in a susceptible human.

We consider the dynamic transmission of dengue disease using SEIR model which focus on infectious vectors caused both by biting of infected humans and vectors born infection. A computer software package was used for analysis in this investigation and the numerical solutions of equations (2.18) – (2.22) are presented.

The parameter values to simulate the behavior of our model are follows: the life expectancy is 70 years for human, the mean life of mosquito is 13.5 days, the mosquito can bite the susceptible human three times per one day, and the recovery of infected human is 7 days. We assumed that the human intrinsic incubation rate of human is greater than the death rate of human population; $\varepsilon_H > \mu_H$. The other parameters are arbitrary chosen.

As the results, the values of parameters are as follows: $M_1 = 400$, $M_2 = 200$, $N_H = 10{,}000$, $b = 1/3$ day-1, $\beta_H = 0.75$, $\beta_V = 1.00$, $\mu_H = 0.0000391$ day-1, $\mu_V = 0.075$ day-1, $r_H = 0.1428$ day-1, $\varepsilon_V = 0.0607$, $\varepsilon_H = 0.1$. Therefore, the characteristic equation are follows:

$$(\lambda^5 + 0.516102\lambda^4 + 0.104296\lambda^3 + 0.0103068\lambda^2 + 0.000497936\lambda^1 + 9.4232 * 10^{-6}) = 0$$

The solutions of the equilibrium above equation are: $\lambda 1$ = -0.147004, $\lambda 2$ = -0.116491, $\lambda 3$ = -0.11498, $\lambda 4$ = -0.0688138 - 0.00710395i, $\lambda 5$ = -0.0688138 + 0.00710395i, and $R0$ = 1.00111. All eigenvalues has negative and $R0$ is greater than one that leads to the endemic equilibrium state. Thus, the solutions oscillate to the endemic equilibrium points; $S_H^* = 0.000554$, $E_H^* = 0.000391$, $I_H^* = 0.000273$, $E_V^* = 0.000346$, $I_V^* = 0.333629$.

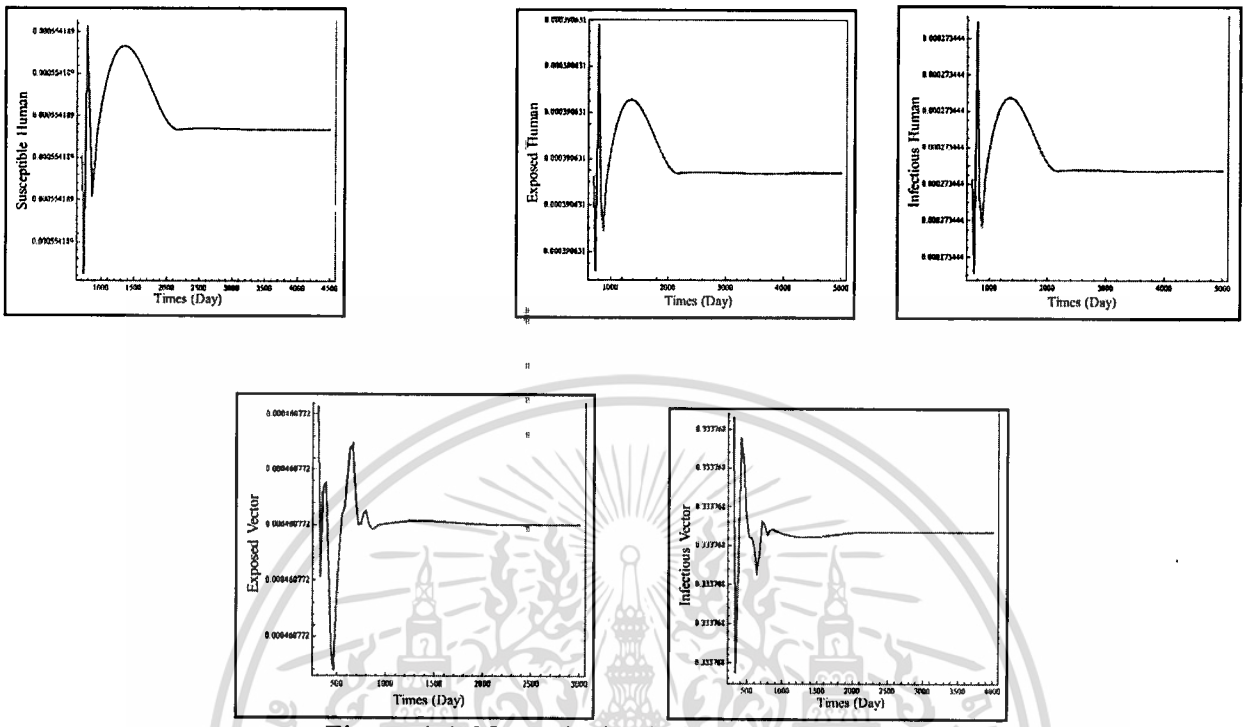


Figure 4.4: Numerical solutions of our model.

We propose model and analyze the transmission dynamics of SEIR model for dengue disease. We consider the transmission of dengue virus caused by both biting infected human and vector born infection. The vector population consider both recruitment rate of mosquitoes and mosquitoes born infection. Mathematical model of the system is formulated in order to investigate the stability of the model.

As the results, we found the endemic equilibrium state and we found the parameters which can reduce the outbreak of dengue disease. The R0 value can be controlled by decreasing the mosquitoes biting and the basic reproductive numbers are used to reduce the transmission of dengue disease. The effective way to control dengue disease is to decrease the carry capacity of the environment to support mosquitoes, especially mosquito breeding sites, and to decrease the mosquitoes' biting.

4.3. แบบจำลองที่ 3แบบจำลองของโรคไข้เลือดออกโดยคำนึงถึงปริมาณน้ำฝนที่มีผลต่อยุงที่เกิดใหม่ [58]

In this model, we use the knowledge of mathematical model to formulate our model. The variables and parameters in our model are defined in the following table:

Table 3.1: Definitions of variables and parameters in our model.

Variable/Parameter	Definition
S_h	The number of susceptible human population
I_h	The number of infectious human population
R_h	The number of recovered human population

O_v	The number of mosquitoes' eggs
S_v	The number of susceptible mosquitoes
I_v	The number of infectious mosquitoes
B	The biting rate of mosquitoes
β_h	The transmission probability of dengue virus from mosquitoes to human population
β_v	The transmission probability of dengue virus from human to mosquitoes
N_h	The size of human population
N_v	The size of mosquitoes
a_h	The birth rate of human population
μ_h	The death rate of human population
μ_v	The death rate of vector population
e_h	The recovery rate of human population
α	The percentage of mosquitoes' eggs which can be susceptible mosquitoes
b_{ov}	The rate of new mosquitoes' eggs per 1 volume of raining
n_r	The volume of raining

The diagram of our dynamical equations can be described by following figure:

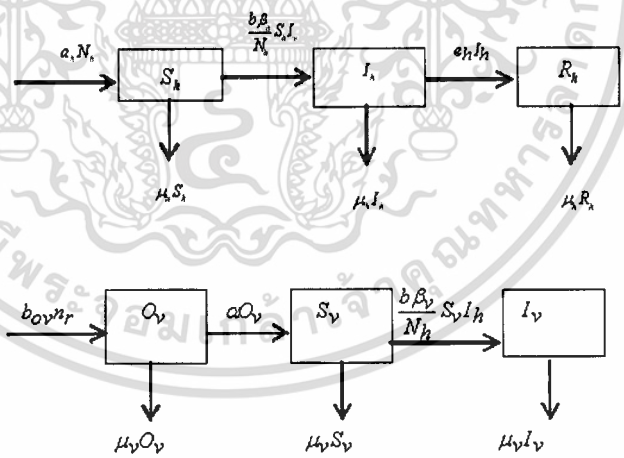


Figure 3.2 Diagram of our equations.

The system of differential equations for describing dengue disease is given by following equations.

For human population:

$$\frac{dS_h}{dt} = a_h N_h - \frac{b\beta_h}{N_h} S_h I_v - \mu_h S_h \tag{3.1}$$

$$\frac{dI_h}{dt} = \frac{b\beta_h}{N_h} S_h I_v - (e_h + \mu_h) I_h \tag{3.2}$$

$$\frac{dR_h}{dt} = e_h I_h - \mu_h R_h \tag{3.3}$$

with a condition $S_h + I_h + R_h = N_h$.

For vector population:

$$\frac{dO_v}{dt} = b_{ov} n_r - (\alpha + \mu_v) O_v, \tag{3.4}$$

$$\frac{dS_v}{dt} = \alpha O_v - \frac{b\beta_v}{N_h} S_v I_h - \mu_v S_v, \tag{3.5}$$

$$\frac{dI_v}{dt} = \frac{b\beta_v}{N_h} S_v I_h - \mu_v I_v, \tag{3.6}$$

with a condition $O_v + S_v + I_v = N_v$.

We reduced our equations by letting

$$s_h = \frac{S_h}{N_h}, i_h = \frac{I_h}{N_h}, r_h = \frac{R_h}{N_h}, \tag{3.7}$$

$$o_v = \frac{O_v}{N_v}, s_v = \frac{S_v}{N_v}, i_v = \frac{I_v}{N_v}. \tag{3.8}$$

The normalized equations become

$$\frac{ds_h}{dt} = \mu_h (1 - s_h) - \frac{b\beta_h}{N_h}\left(\frac{b_{ov} n_r}{\mu_v}\right) i_v s_h, \tag{3.9}$$

$$\frac{di_h}{dt} = \frac{b\beta_h}{N_h}\left(\frac{b_{ov} n_r}{\mu_v}\right) i_v s_h - i_h (e_h + \mu_h), \tag{3.10}$$

$$\frac{ds_v}{dt} = -(b\beta_v i_h + \mu_v) s_v + \alpha(1 - s_v - i_v), \tag{3.11}$$

$$\frac{di_v}{dt} = b\beta_v i_h s_v - \mu_v i_v \tag{3.12}$$

where $s_h + i_h + r_h = 1, o_v + s_v + i_v = 1$.

Our assumption is the total human and total vector populations have constant sizes. This means that rates of change for human and vector populations equal to zero. Thus, we have the following equations:

$$\frac{dN_h}{dt} = 0 \text{ and } \frac{dN_v}{dt} = 0. \tag{3.13}$$

Then we obtain the relations:

$$a_h = \mu_h \text{ and } N_v = \frac{b_{ov} n_r}{\mu_v}. \tag{3.14}$$

To analyze our model, we use standard dynamical modeling method to find steady states and their local stabilities.

The steady states are obtained by setting (9)-(12) equal to zero. We obtain two steady states:

i) Disease free steady state: $(1, 0, \frac{\alpha}{\alpha + \mu_v}, 0)$

ii) Endemic disease state: $(s_h^*, i_h^*, s_v^*, i_v^*)$

where

$$s_h^* = \frac{\mu_v(\alpha+\mu_v)(b\beta_v\mu_h + (e_h+\mu_h)\mu_v)N_h}{b\beta_v(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\beta_h b_{ov} n_r)}, \quad (3.15)$$

$$i_h^* = \frac{-\mu_h(e_h+\mu_h)\mu_v^2(\alpha+\mu_v)N_h + \alpha b^2\beta_h b_{ov}\beta_v\mu_h n_r}{b\beta_v(e_h+\mu_h)(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\beta_h b_{ov} n_r)}, \quad (3.16)$$

$$s_v^* = \frac{(e_h+\mu_h)\mu_v(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\ b\beta_h b_{ov}\beta_v n_r)}{b\beta_h(e_h+\mu_h)(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\beta_h b_{ov} n_r)}, \quad (3.17)$$

$$i_v^* = \frac{-\mu_h(e_h+\mu_h)\mu_v^2(\alpha+\mu_v)N_h + \alpha b^2\beta_h b_{ov}\beta_v\mu_h n_r}{b\beta_h b_{ov}(\alpha+\mu_v)(b\beta_v\mu_h + (e_h+\mu_h)\mu_v)n_r}. \quad (3.18)$$

We let

$$G_1(s_h, i_h, s_v, i_v) = \mu_h(1-s_h) - \frac{b\beta_h}{N_h}\left(\frac{b_{ov}n_r}{\mu_v}\right)i_v s_h, \quad (3.19)$$

$$G_2(s_h, i_h, s_v, i_v) = \frac{b\beta_h}{N_h}\left(\frac{b_{ov}n_r}{\mu_v}\right)i_v s_h - i_h(e_h+\mu_h), \quad (3.20)$$

$$G_3(s_h, i_h, s_v, i_v) = -(b\beta_v i_h + \mu_v)s_v + \alpha(1-s_v-i_v), \quad (3.21)$$

$$G_4(s_h, i_h, s_v, i_v) = b\beta_v i_h s_v - \mu_v i_v \quad (3.22)$$

The local stability of each steady state is determined by the sign of all real parts of eigenvalues for each steady state. If the sign of real parts give the negative, then that steady state is local stability. The eigenvalues (θ) are produced from the solutions of the following characteristic equation:

$$\det(J - \theta I) = 0$$

where $J = \begin{pmatrix} \frac{\partial G_1}{\partial s_h} & \frac{\partial G_1}{\partial i_h} & \frac{\partial G_1}{\partial s_v} & \frac{\partial G_1}{\partial i_v} \\ \frac{\partial G_2}{\partial s_h} & \frac{\partial G_2}{\partial i_h} & \frac{\partial G_2}{\partial s_v} & \frac{\partial G_2}{\partial s_v} \\ \frac{\partial G_3}{\partial s_h} & \frac{\partial G_3}{\partial i_h} & \frac{\partial G_3}{\partial s_v} & \frac{\partial G_3}{\partial i_v} \\ \frac{\partial G_4}{\partial s_h} & \frac{\partial G_4}{\partial i_h} & \frac{\partial G_4}{\partial s_v} & \frac{\partial G_4}{\partial i_v} \end{pmatrix}$ and I is the identity matrix. (3.23)

After calculating our equations(3.19)-(3.22), the Jacobian matrix(J) is defined by

We consider two cases:

Case I: Disease free steady state: the characteristic equation is

$$(\theta+\mu_h)(\theta+\alpha+\mu_v)(\theta^2 + B_1\theta + B_0) = 0 \quad (3.24)$$

where

$B_1 = e_h + \mu_h + \mu_v,$

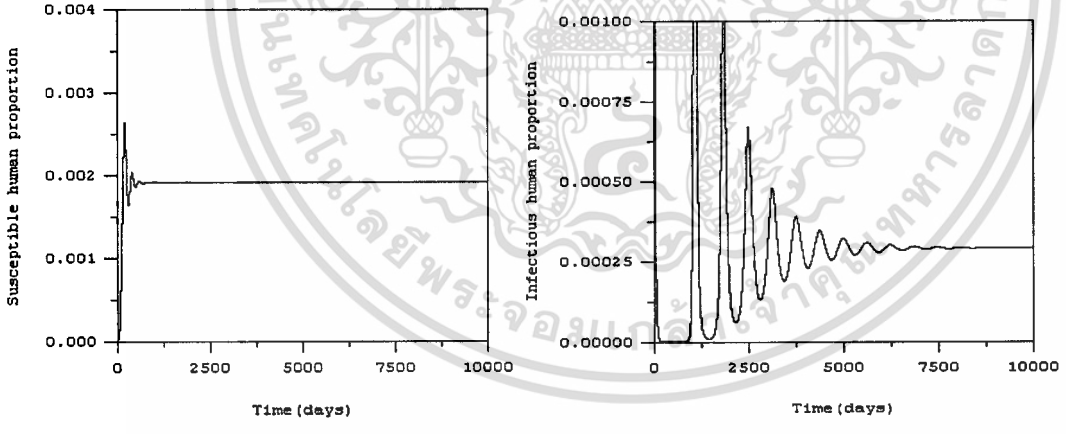
$$B_0 = (e_h + \mu_h)\mu_v - \frac{\alpha b^2 \beta_h \beta_v b_{ov} n_r}{\alpha \mu_v N_h + \mu_v^2 N_h}.$$

From evaluating all eigenvalues, the real parts of all eigenvalues have negative signs when $R_0 < 1$

where $$R_0 = \frac{\alpha b^2 \beta_h \beta_v b_{ov} n_r}{(e_h + \mu_h)\mu_v^2(\alpha + \mu_v)N_h}. \quad (3.25)$$

Case II: Endemic disease state: the characteristic equation is calculated in the same method as the disease free state. The real parts of all eigenvalues have negative signs when $R_0 > 1$, where R_0 is defined in (25). To explain the local stability of the steady states clearly, we use the numerical simulations on the next section.

In this section, we use numerical solution to confirm our analytical results. We simulate our equations(9)-(12) by using the conditions of endemic disease steady state. The parameters are follows: $\mu_h = 1/(365 \times 65)$ corresponds to the life cycle 65 years of human. $b = 1/3$ corresponds to the 3 times per day of biting for the vector. $\mu_v = 1/14$ satisfy to the life cycle 14 days of vectors. $e_h = 1/7$ corresponds to the 7 days of recovering for human. The other parameters are arbitrary chosen: $\beta_h = 0.75$, $\beta_v = 1.0$, $b_{ov} = 500$, $n_r = 100$, $\alpha = 0.8$, $N_h = 100{,}000$ and $R_0 = 52.47$.



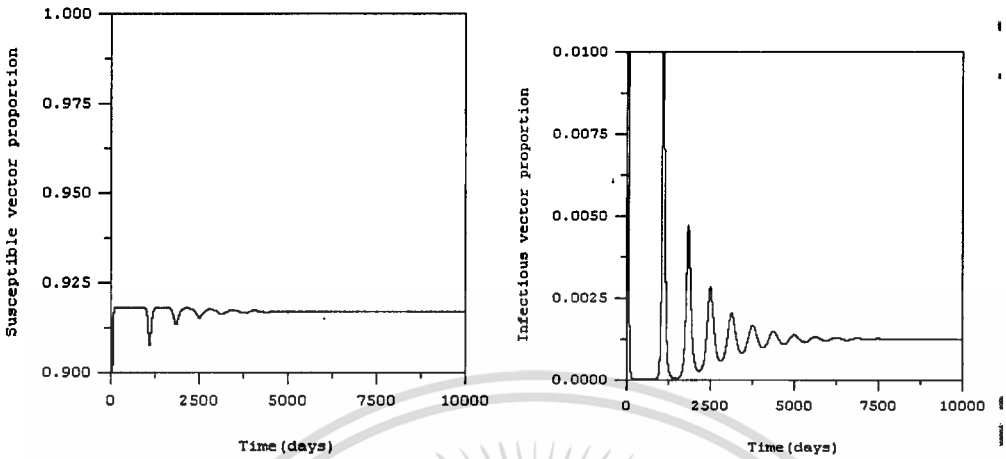
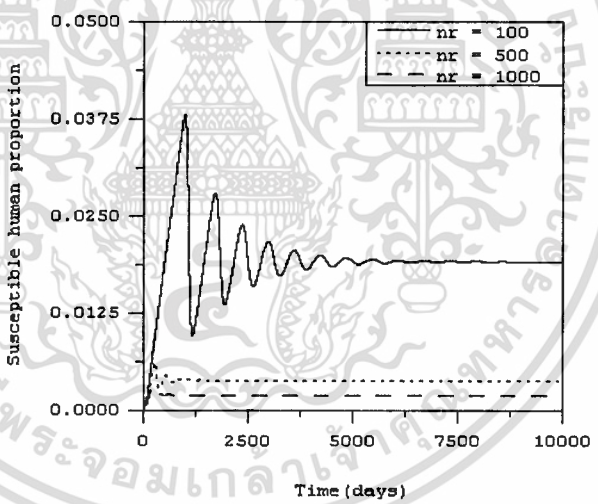


Figure 3.3 Numerical solutions of our equations(3.9)-(3.12). The conditions of parameters are satisfied to the endemic disease state. The solution converges to the endemic steady state(0.0019, 0.00029, 0.91677, 0.00126).

We can see that the solutions converge to the endemic steady state when $R_0 > 1$.

Furthermore, we analyze the parameter n_r (the volume of raining) as shown in Figure4.



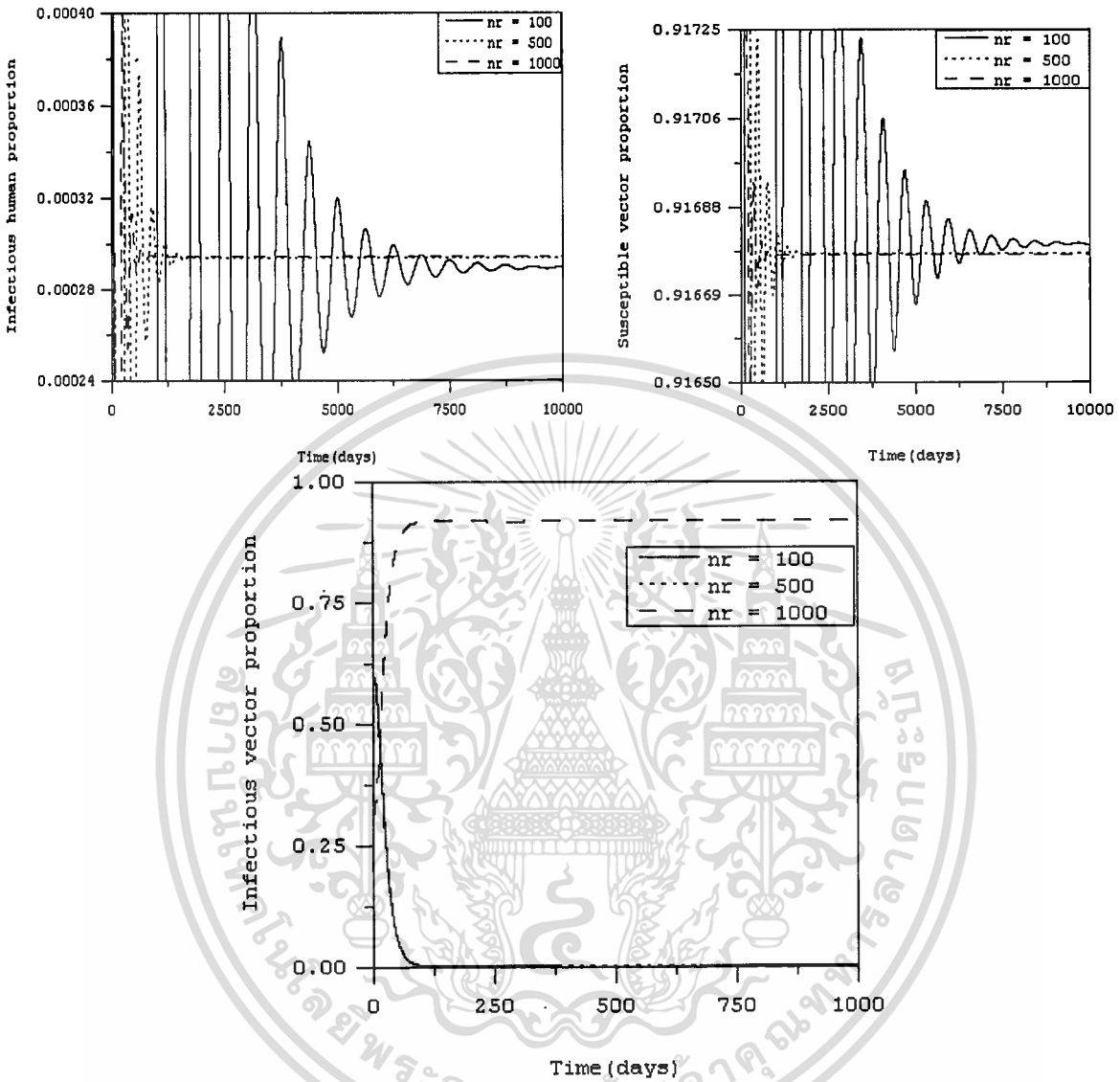


Figure 3.4 Numerical solutions of susceptible human, infectious human, susceptible vector and infectious vector populations when there are the different volumes of raining.

We analyze the model of dengue disease with the volume of raining in this study. The basic reproductive number is defined in the form of R_0 is given by

$$R_0 = \frac{\alpha b^2 \beta_h \beta_v b_{ov} n_r}{(e_h + \mu_h)\mu_v^2(\alpha + \mu_v)N_h}. \qquad (3.26)$$

From (26), we can see that the three effects α (percentage of mosquitoes' eggs which can be susceptible mosquitoes), b_{ov} (The rate of new mosquitoes' eggs per 1 volume of raining) and n_r (volume of raining) are proportional to the basic reproductive number as shown in Figure5 to Figure7.

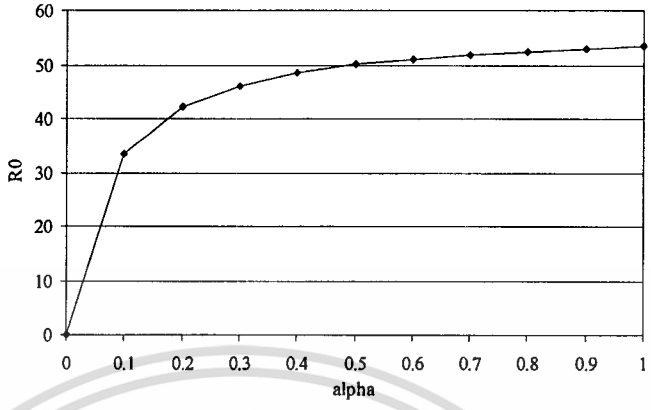


Figure 3.5 Numerical solutions of R_0 versus α. The other parameters are same as Figure 3.3.

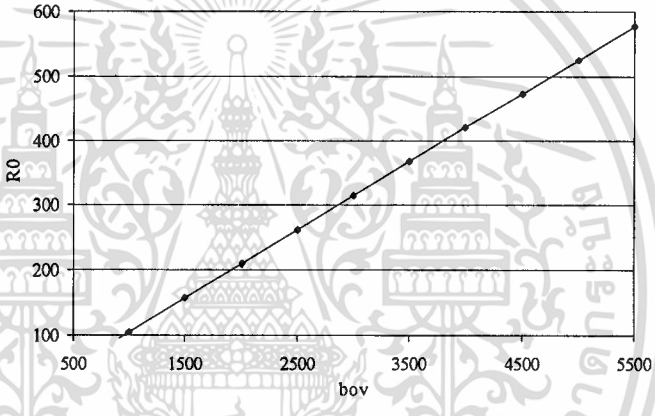


Figure 3.6 Numerical solutions of R_0 versus b_{ov}. The other parameters are same as Figure 3.3.

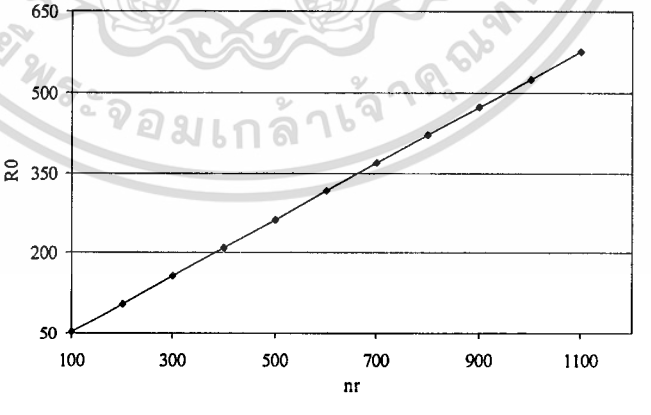


Figure 3.7 Numerical solutions of R_0 versus n_r. The other parameters are same as Figure 3.3.

We can see that the infectious human and vector proportions are higher and the smaller proportions of susceptible human and susceptible vector proportions when there is the higher

volume of raining as shown in Figure 3.4. This is fact because when there is the higher volume of raining, the temperature and humidity are appropriated for growth of dengue virus.

4.4. แบบจำลองที่ 4 แบบจำลองของโรคไข้เลือดออกที่พิจารณาความแตกต่างระหว่างพื้นที่ที่มีน้ำท่วมกับพื้นที่ที่ไม่มีน้ำท่วม [59]

In this study, we formulate the mathematical model for describing the transmission of this disease by using SIR(Susceptible-Infectious-Recovered) model for human and SI(Susceptible-Infectious) model for vector population. We assume SIR model for human and SI for vector population because vector can not recover from infection. We suppose that there are the different transmission rates for the different areas. The transmission diagram of dengue disease is given as follows:

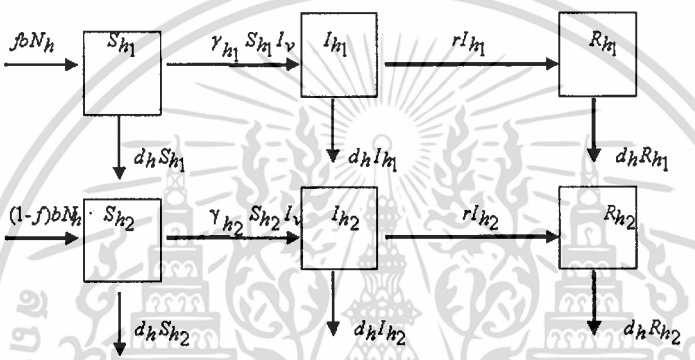


Figure 4.1. Transmission diagram for human population.

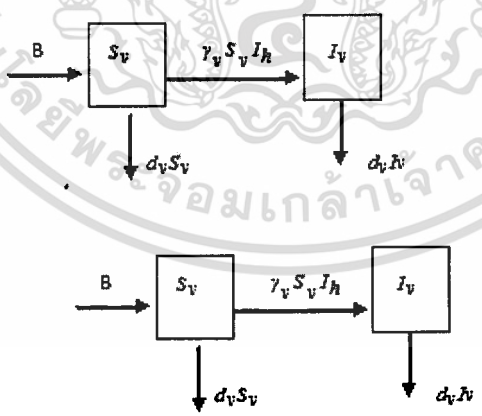


Figure 4.2. Transmission diagram for vector population.

From the above figures, the dynamical transmission model can be written as

$$
\begin{aligned}
\frac{d}{dt}S_{h_1} &= fbN_h - \gamma_{h_1} S_{h_1} I_v - d_h S_{h_1} \\
\frac{d}{dt}I_{h_1} &= \gamma_{h_1} S_{h_1} I_v - (r+d_h) I_{h_1} \\
\frac{d}{dt}R_{h_1} &= rI_{h_1} - d_h R_{h_1} \\
\frac{d}{dt}S_{h_2} &= (1-f)bN_h - \gamma_{h_2} S_{h_2} I_v - d_h S_{h_2} \\
\frac{d}{dt}I_{h_2} &= \gamma_{h_2} S_{h_2} I_v - (r+d_h) I_{h_2} \\
\frac{d}{dt}R_{h_2} &= rI_{h_2} - d_h R_{h_2} \\
\frac{d}{dt}S_v &= B - \gamma_v S_v I_h - d_v S_v \\
\frac{d}{dt}I_v &= \gamma_v S_v I_h - d_v I_v
\end{aligned}
\qquad (4.1)
$$

where $I_h = I_{h_1} + I_{h_2}$,

$N_h = S_{h_1} + I_{h_1} + R_{h_1} + S_{h_2} + I_{h_2} + R_{h_2}$,

$N_v = S_v + I_v$. (4.2)

The variables and parameters are described in the following table.

The variables and parameters in our model are defined in the following table:

Table1: Definitions of variables and parameters for our model.

variable/parameter	definition
S_{h_1}	Number of susceptible human in the flooding area
I_{h_1}	Number of infectious human in the flooding area
R_{h_1}	Number of recovered human in the flooding area
S_{h_2}	Number of susceptible human in the non flooding area
I_{h_2}	Number of infectious human in the non flooding area
R_{h_2}	Number of recovered human in the non flooding area
I_h	Total infectious human
S_v	Number of susceptible vector
I_v	Number of infectious vector
f	Probability of human who stay in flooding area
b	Birth rate of human population
d_h	Death rate of human population
N_h	Total number of human population

N_v	Total vector population
γ_{h_1}	Transmission rate of dengue virus from vector to human population in flooding area
γ_{h_2}	Transmission rate of dengue virus from vector to human population in non flooding area
r	Recovery rate
B	Constant recruitment rate of vector population
γ_v	Transmission rate of dengue virus from human to vector population
d_v	Death rate of vector population

We suppose that the total human and vector population have constant sizes. Then rates of change for human and vector population are zero. Thus $\frac{d}{dt}N_h = 0$ and, then we have $b = d_h$ and $N_v = \frac{B}{d_v}$. This means that birth and death rate is equivalent for human population. The number of vector population is ratio between constant recruitment rate of vector and death rate of vector population.

To simplify our model, we introduce new variables by letting

$$s_{h1} = \frac{S_{h1}}{N_T},\ i_{h1} = \frac{I_{h1}}{N_T},\ r_{h1} = \frac{R_{h1}}{N_T}\ s_{h2} = \frac{S_{h2}}{N_T},\ i_{h2} = \frac{I_{h2}}{N_T},\ r_{h2} = \frac{R_{h2}}{N_T}$$

and $s_v = \frac{S_v}{Nv},\ i_v = \frac{I_v}{Nv}$, then we obtain the following equations:

$$\begin{aligned}
\frac{d}{dt}s_{h1} &= bf - (b + \gamma_{h1} i_v (B/d_v))s_{h1} \\
\frac{d}{dt}i_{h1} &= -i_{h1}(b+r) + \gamma_{h1} i_v (B/d_v)s_{h1} \\
\frac{d}{dt}r_{h1} &= ri_{h1} - brh_1 \\
\frac{d}{dt}s_{h2} &= -\gamma_{h2} i_v (B/d_v)s_{h2} + b(1 - f - s_{h2}) \\
\frac{d}{dt}i_{h2} &= -i_{h2}(b+r) + \gamma_{h2} i_v (B/d_v)s_{h2} \\
\frac{d}{dt}i_v &= \gamma_v (i_{h1} + i_{h2})N_h (1 - i_v) - d_v i_v
\end{aligned} \tag{4.3}$$

After setting (3) to zero, we obtain steady states. The steady states of our equations are follows:

i) Disease free state: $e_1 = (f,0,0,1-f,0,0)$ (4.4)

ii) Endemic disease state: $e_2 = (s\tilde{h}_1, i\tilde{h}_1, r\tilde{h}_1, s\tilde{h}_2, i\tilde{h}_2, i\tilde{v})$

(4.5)

where

$$\tilde{i_v} = \frac{b(BM - bd_v^2(B(\gamma_{h_1}+\gamma_{h_2})+d_v(b+r)R_0)) + \sqrt{\begin{matrix} b^2B^2(4d_v^3\gamma_{h_1}\gamma_{h_2}(b+r)(b(d_v+\gamma_v N_h)+d_v r)(R_0-1) \\ +(-M+bd_v^2(\gamma_{h_1}+\gamma_{h_2}+\frac{d_v(b+r)R_0}{B}))^2) \end{matrix}}}{2B^2\gamma_{h_1}\gamma_{h_2}(b(d_v+\gamma_v N_h)+d_v r)},$$

$$\tilde{s_{h_1}} = \frac{bd_v f}{bd_v + B\gamma_{h_1}\tilde{i_v}}, \tilde{i_{h_1}} = \frac{B\gamma_{h_1}\tilde{i_v}\tilde{s_{h_1}}}{d_v(b+r)}, \tilde{r_{h_1}} = \frac{r}{b}\tilde{i_{h_1}}, \tilde{s_{h_2}} = \frac{d_v b(1-f)}{bd_v + B\gamma_{h_2}\tilde{i_v}}, \tilde{i_{h_2}} = \frac{B\gamma_{h_2}\tilde{i_v}\tilde{s_{h_2}}}{d_v(b+r)}.$$

To determine the local stability of our equations, we check the sign of eigenvalues. The eigenvalues are the solutions of characteristic equations: $\det(J-\lambda I)=0$; where J is the jacobian matrix of (4.3) , I is the identity matrix. If all eigenvalues have negative real parts, then that steady state will be local stability.

For disease free steady state: Jacobian matrix is defined by

$$J_0 = \begin{pmatrix} -b & 0 & 0 & 0 & -\frac{Bf\gamma_{h_1}}{d_v} \\ 0 & -b-r & 0 & 0 & \frac{Bf\gamma_{h_1}}{d_v} \\ 0 & 0 & -b & 0 & -\frac{B(1-f)\gamma_{h_2}}{d_v} \\ 0 & 0 & 0 & -b-r & \frac{B(1-f)\gamma_{h_2}}{d_v} \\ 0 & \gamma_v N_h & 0 & \gamma_v N_h & -d_v \end{pmatrix}. \quad (4.6)$$

Jacobian matrix for endemic steady state is given by

$$J = \begin{pmatrix} -b-\frac{B\gamma_{h_1}}{d_v}\tilde{i_v} & 0 & 0 & 0 & -\frac{B\gamma_{h_1}}{d_v}\tilde{s_{h_1}} \\ \frac{B\gamma_{h_1}}{d_v}\tilde{i_v} & -b-r & 0 & 0 & \frac{B\gamma_{h_1}}{d_v}\tilde{s_{h_1}} \\ 0 & 0 & -b-\frac{B\gamma_{h_2}}{d_v}\tilde{i_v} & 0 & -\frac{B\gamma_{h_2}}{d_v}\tilde{s_{h_2}} \\ 0 & 0 & \frac{B\gamma_{h_2}}{d_v}\tilde{i_v} & -b-r & \frac{B\gamma_{h_2}}{d_v}\tilde{s_{h_2}} \\ 0 & \gamma_v(1-\tilde{i_v})N_h & 0 & \gamma_v(1-\tilde{i_v})N_h & -d_v-\gamma_v(\tilde{i_{h_1}}+\tilde{i_{h_2}})N_h \end{pmatrix} \quad (4.7)$$

We check the sign of all eigenvalues for disease free steady state and endemic steady state, then we conclude that the disease free steady state is local stability for $R_0<1$ and endemic steady state is local stability for $R_0>1$; where $R_0 = \frac{B(f(\gamma_{h_1}-\gamma_{h_2})+\gamma_{h_2})\gamma_v N_h}{d_v^2(b+r)}$.

We show our analytical results by numerical solutions for endemic disease state. We simulate our equations by using parameters as shown in Figure4.3.

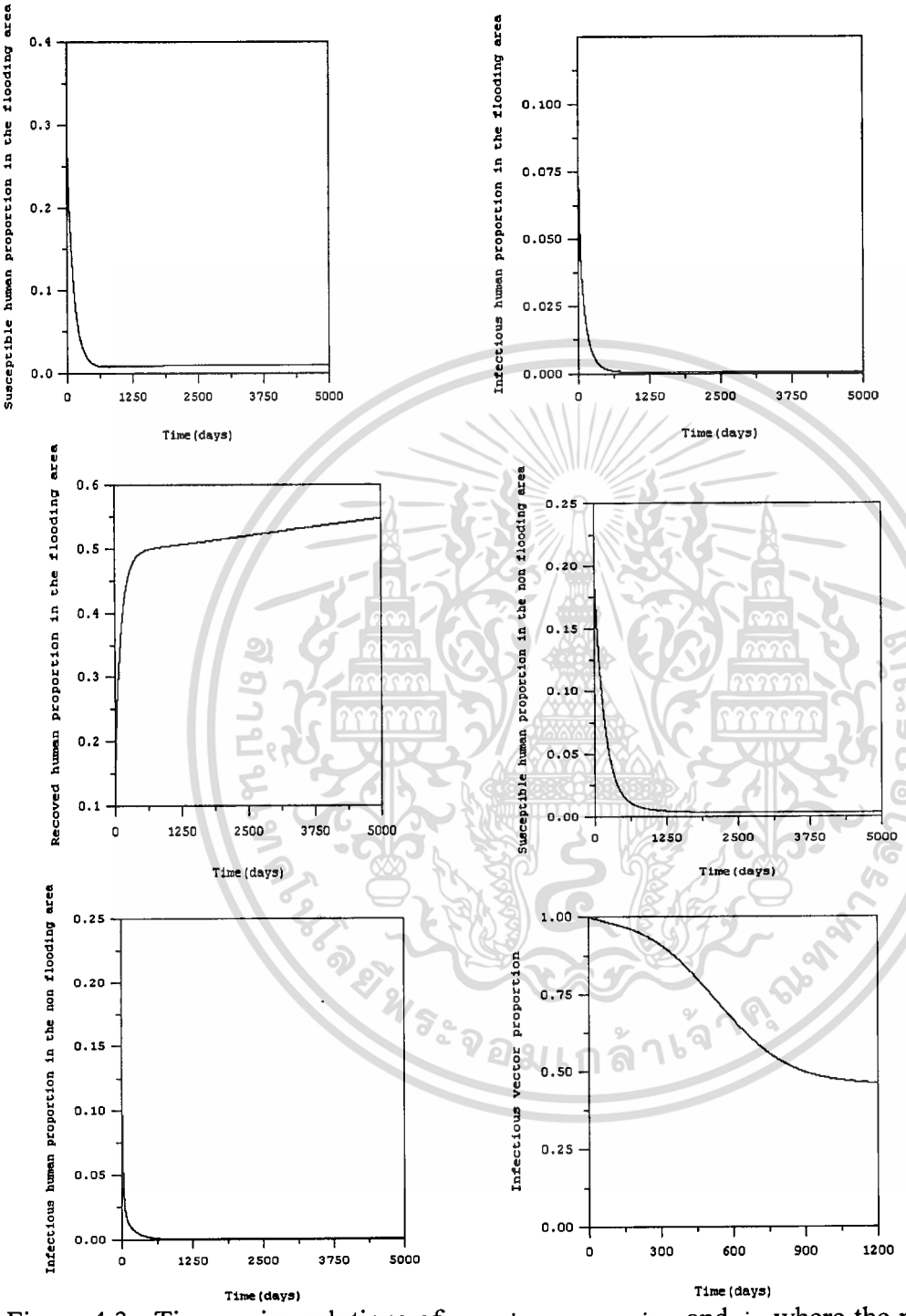


Figure 4.3 . Time series solutions of $s_{h_1}, i_{h_1}, r_{h_1}, s_{h_2}, i_{h_2}$ and i_v where the parameters are given by f = 0.8,b=1/(365*65), N_h=100, $\gamma_{h_1} = 0.0000006$, $\gamma_{h_2} = 0.0000004$, r = 1/20, B = 1,000, γ_v=0.7, d_v=1/14 and $R_0 = 137$. The solutions converge to the endemic disease state(0.009, 0.0007, 0.55, 0.003, 0.00016, 0.45). We can see that the solutions converge to the endemic disease state.

In this study, we consider the transmission of dengue disease in flooding and non flooding areas. Standard dynamical modeling method is used in this paper. We found equilibrium states and determine the conditions for local stability. The basic reproductive number is used for reduce the transmission of many diseases .

The basic reproductive number of this disease is defined by

$$R_0 = \frac{B(f(\gamma_{h_1} - \gamma_{h_2}) + \gamma_{h_2})\gamma_v N_h}{d_v^2(b+r)}.$$

We can see that the transmission rate of dengue disease in flooding area, probability of people who stay in flooding area, the constant recruitment rate of vector and the transmission rate of dengue disease from human to vector effect to the basic reproductive number. If the transmission rate of dengue disease is high, the basic reproductive number is high too. Moreover, we simulate our model by input the different values of probabilities of people who stay in flooding area. The results are shown in Figure4.4.

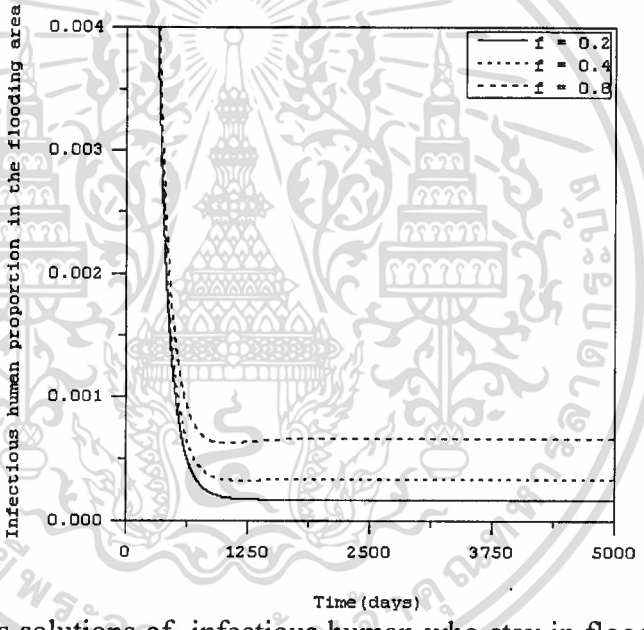


Figure 4.4 . Time series solutions of infectious human who stay in flooding area when there is the different probabilities of people who stay in flooding areas.

From Figure4.4, we can see that the infectious human proportion who stay in the area where there is the more probability of flooding will be greater than the infectious human proportion who stay in the area where there is the less probability of flooding. The results correspond to the real life situation. The results of this study suggest the way for controlling this disease.

4.5. แบบจำลองที่ 5 แบบจำลองของโรคมาลาเรียเมื่อพิจารณาการเกิดน้ำท่วมในประเทศไทย [60]

We study the transmission of Malaria with flooding in Thailand by formulating the differential equations. We use the knowledge of mathematical model to describe the transmission of this disease. We consider the dynamical equations of human and mosquitoes. The differential equations for describing the transmission of this disease is

$$S_n'(t) = hN_n - \gamma_n S_n I_v - dS_n \tag{5.1}$$

$$E_n'(t) = \gamma_n S_n I_v - \frac{1}{II_n} E_n - dE_n \tag{5.2}$$

$$I_n'(t) = \frac{1}{II_n} E_n - (\gamma + d) I_n \tag{5.3}$$

$$R_n'(t) = \gamma I_n - dR_n \tag{5.4}$$

$$S_{v_f}'(t) = A_f - \gamma_{v_f} S_{v_f} I_n - d_v S_{v_f} \tag{5.5}$$

$$I_{v_f}'(t) = \gamma_{v_f} S_{v_f} I_n - d_v I_{v_f} \tag{5.6}$$

$$S_{v_{nf}}'(t) = A_{nf} - \gamma_{v_{nf}} S_{v_{nf}} I_n - d_v S_{v_{nf}} \tag{5.7}$$

$$I_{v_{nf}}'(t) = \gamma_{v_{nf}} S_{v_{nf}} I_n - d_v I_{v_{nf}} \tag{5.8}$$

where $N_n = S_n + E_n + I_n + R_n$, $N_{v_f} = S_{v_f} + I_{v_f}$ and $N_{v_{nf}} = S_{v_{nf}} + I_{v_{nf}}$.

The variables and parameters in our equations are described as follows:

$S_n(t)$ is the size of susceptible human population at time t,

$E_n(t)$ is the size of exposed human population at time t,

$I_n(t)$ is the size of infectious human population at time t,

$R_n(t)$ is the size of recovered human population at time t,

$S_{v_f}(t)$ is the size of susceptible mosquito during the flood at time t,

$I_{v_f}(t)$ is the size of infectious mosquito during the flood at time t,

$S_{v_{nf}}(t)$ is the size of susceptible mosquito during the non-flood at time t,

$I_{v_f}(t)$ is the size of infectious mosquito during the non-flood at time t,

h is the birth rate of human population,

d is the death rate of human population,

γ_n is the transmission rate of *Plasmodium malaria* from mosquito to human,

II_n is the incubation period of *Plasmodium malaria* in human,

N_n is the size of human population,

N_{v_f} is the size of mosquitoes during flooding time,

$N_{v_{nf}}$ is the size of mosquitoes during non-flooding time,

γ is the recovery rate of human population,

A_f is the constant recruitment rate of mosquitoes during flooding time,

A_{nf} is the constant recruitment rate of mosquitoes during non-flooding time,

γ_{v_f} is the transmission rate of *Plasmodium malaria* from human to mosquitoes during flooding time,

$\gamma_{v_{nf}}$ is the transmission rate of *Plasmodium malaria* from human to mosquitoes during non-flooding time,

d_v is the death rate of mosquitoes,

Suppose that the size of human and mosquitoes are constant, then

$N'_n = S'_n + E'_n + I'_n + R'_n = 0$, $N'_{v_f} = S'_{v_f} + I'_{v_f} = 0$ and $N'_{v_{nf}} = S'_{v_{nf}} + I'_{v_{nf}} = 0$.

From the above equations,
we get h = d, $N_{v_f} = A_f / d_v$ and $N_{v_{nf}} = A_{nf} / d_v$.

Normalizing the above equations by letting $s_n = S_n / N_n$, $e_n = E_n / N_n$, $i_n = I_n / N_n$, $r_n = R_n / N_n$,
$s_{v_f} = S_{v_f} / N_v$, $i_{v_f} = I_{v_f} / N_v$, $s_{v_f} = S_{v_f} / N_{v_f}$, $i_{v_f} = I_{v_f} / N_{v_f}$,
$s_{v_{nf}} = S_{v_{nf}} / N_{v_{nf}}$, $i_{v_{nf}} = I_{v_{nf}} / N_{v_{nf}}$.

Thus, the reduced equations become:

$$s'_n(t) = h - (d + \gamma_n i_v) s_h \tag{5.9}$$

$$e'_n(t) = \gamma_n s_n i_v - \frac{1}{II_n} e_n - d e_n \tag{5.10}$$

$$i'_n(t) = \frac{1}{II_n} e_n - (\gamma + d) i_n \tag{5.11}$$

$$i'_{v_f}(t) = \gamma_{v_f} s_{v_f} i_n N_n - d_v i_{v_f} \tag{5.12}$$

$$i'_{v_{nf}}(t) = \gamma_{v_{nf}} s_{v_{nf}} i_n N_n - d_v i_{v_{nf}} \tag{5.13}$$

The standard dynamical method is used for analysis our model. Steady states of our equations are found by setting (9)-(13) to zero, then we obtain the steady states:

i) Disease free steady state: (1,0,0,0,0) and

ii) Endemic steady state: $(s_n, e_n, i_n, i_{v_f}, i_{v_{nf}})$ where

$$s^*_n = \frac{h}{h + \gamma_n (i^*_{v_f} + i^*_{v_{nf}})}, \quad e^*_n = \frac{\gamma_n II_n i^*_v s^*_h}{1 + d II_n},$$

$$i^*_{v_f} = \frac{\gamma_{v_f} \mathrm{N_h}}{(h+\gamma) II_n (d_v + \gamma_{v_f} i^*_n \mathrm{N_h})} e^*_n \text{ and } i^*_{v_{nf}} = \frac{\gamma_{v_f} \mathrm{N_h}}{(h+\gamma) II_n d_v + e^*_n \gamma_{v_{nf}} \mathrm{N_h}} e^*_n$$

where

$$i^*_n = \frac{1}{2(d+\gamma)(d+2\gamma_n)\gamma_{v_f}\gamma_{v_{nf}}(1+d\mathrm{II_n})\mathrm{N_h^2}} \Big(-d_v(d+\gamma)(d+\gamma_n)(\gamma_{v_f}+\gamma_{v_{nf}})(1+d\mathrm{II_n})\mathrm{N_h}$$

$$+ 2\gamma_n\gamma_{v_f}\gamma_{v_{nf}}\mathrm{N_h^2} + \sqrt{\begin{array}{l}(\mathrm{N_h^2}((d_v(d+\gamma)(d+\gamma_n)(\gamma_{v_f}+\gamma_{v_{nf}})(1+d\mathrm{II_n}) - 2\gamma_n\gamma_{v_f}\gamma_{v_{nf}}\mathrm{N_h})^2 \\ - 4d_v(d+\gamma)(d+2\gamma_n)\gamma_{v_f}\gamma_{v_{nf}}(1+d\mathrm{II_n})(dd_v(d+\gamma)(1+d\mathrm{II_n}) \\ - \gamma_n(\gamma_{v_f}+\gamma_{v_{nf}})\mathrm{hN_h}))))\end{array}} \tag{5.14}$$

By using Standard dynamical modeling method, the local stability of each steady state is determined by considering the signs of eigenvalues. If the signs of all eigenvalues give negative, then we can conclude that that steady state is local stability [8-10]. The characteristic equation is defined by following equation:

$$|\mathrm{J} - \kappa \mathrm{I}| = 0$$

where $|\mathrm{A}|$ means determinant of A, J is the Jacobian matrix, κ is the eigenvalues and I is the identity matrix .

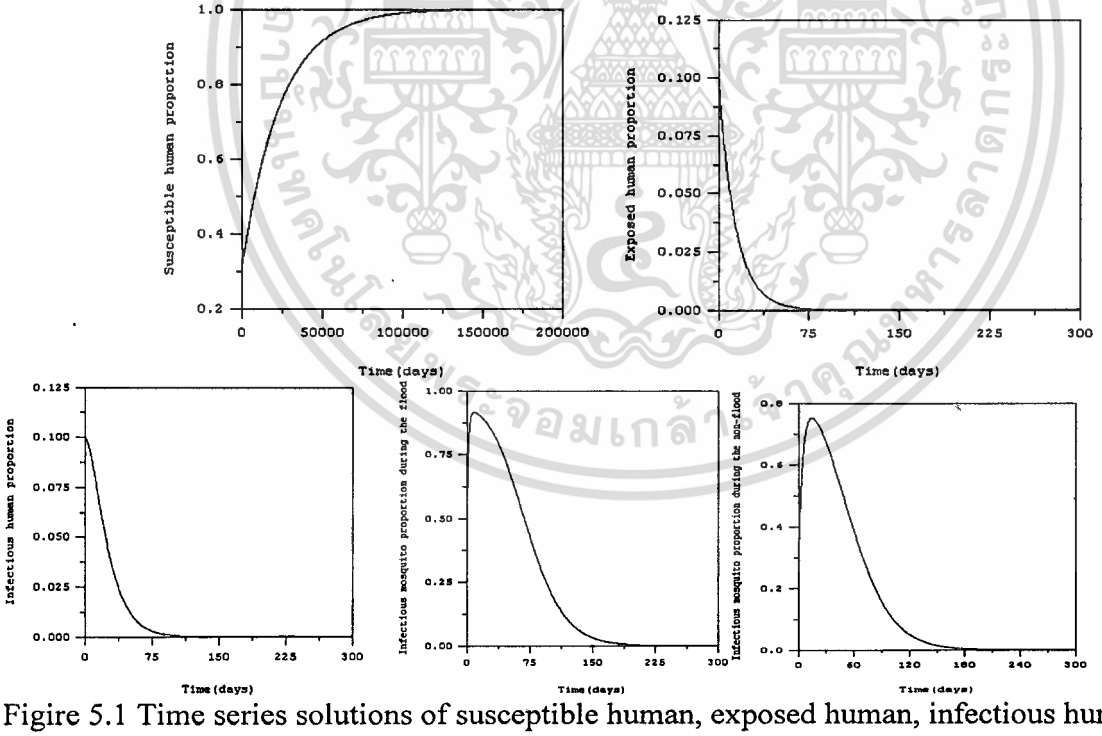
After evaluating our model, the condition for negative real parts of eigenvalues is $R_0 > 1$, where

$$R_0 = \frac{\gamma_n N_n(\gamma_{v_f} + \gamma_{v_{nf}})}{d_v(d+\gamma)(1+d\mathrm{II}_\mathrm{n})}.$$

Therefore, we can conclude that the disease free steady state is local stability for $R_0 < 1$ and the endemic steady state is local stability for $R_0 > 1$.

Numerical method is used for solving numerical solutions of (9)-(13). We simulate our equations for disease free and endemic regions.

For disease free region:



Figire 5.1 Time series solutions of susceptible human, exposed human, infectious human, infectious mosquito during flooding time and infectious mosquito during non-flooding time on disease free region. The solutions converge to (1,0,0,0,0)

For endemic region:

The parameters are follows:

$h = 1/(365\times 65)$ corresponds to the life cycle 65 years of human. $\gamma_n = 0.006$, $\gamma_{v_f} = 0.008$, $\gamma_{v_{n_f}} = 0.002$ and $N_h = 10{,}000$ are arbitrary chosen parameters. $d_v = 1/45$ corresponds to 45 days life time of *Anopheles* mosquitoes. $II_n = 14$ corresponds to 14 days of incubation period of *Plasmodium malaria* in human. $\gamma = 1/14$ corresponds to the 14 days of recovering of human and $R_0 = 493$.

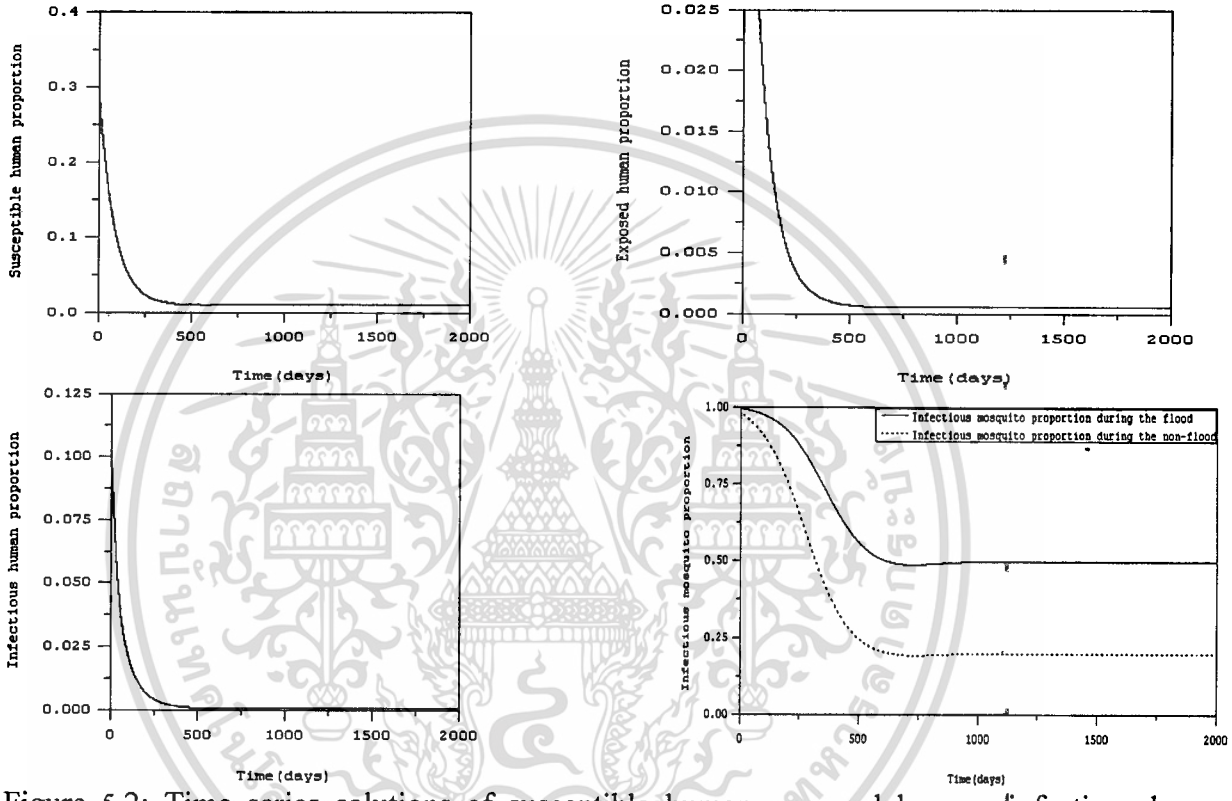
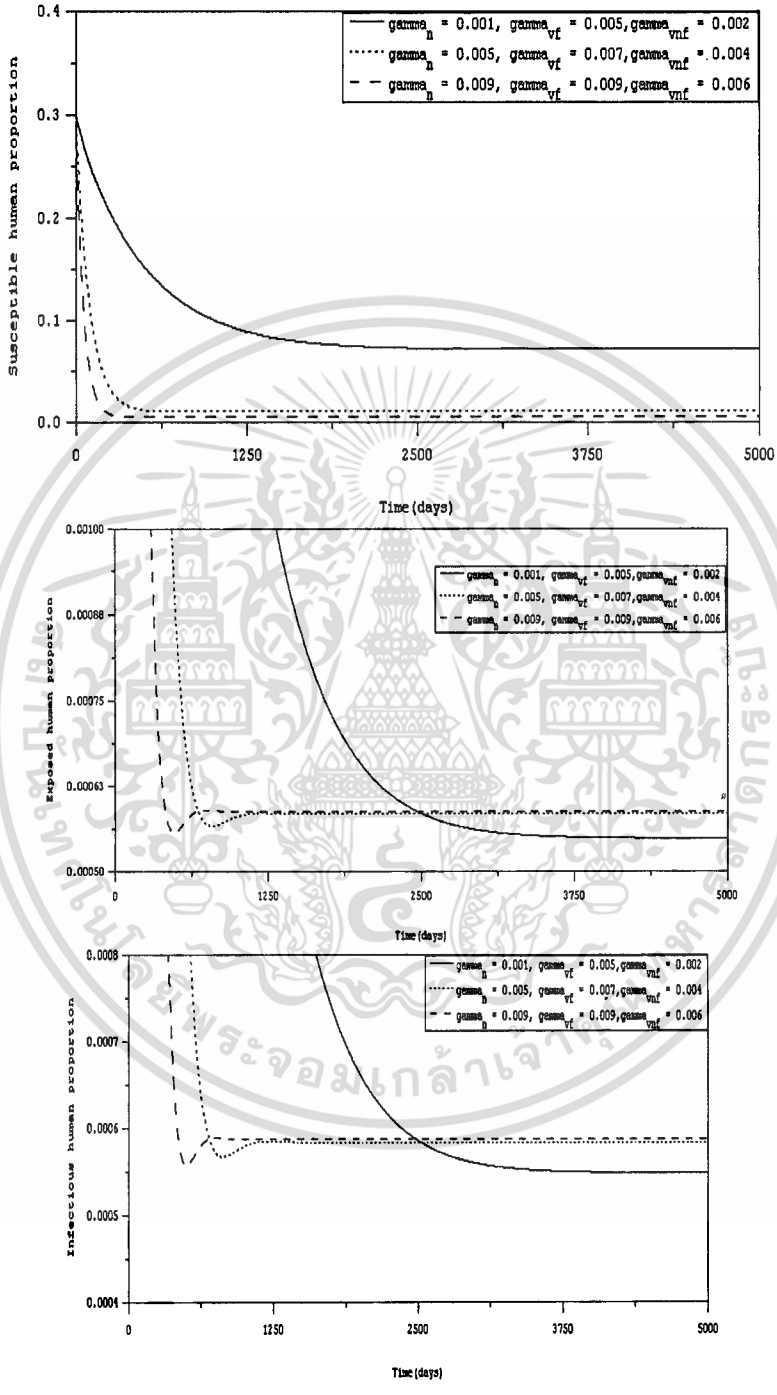


Figure 5.2: Time series solutions of susceptible human, exposed human, infectious human, infectious mosquito during flooding time and infectious mosquito during non-flooding time on endemic region. The solutions converge to (0.01,0.0006,0.0006,0.5,0.2)

From the above figures, we can see that the solutions converge to the disease free steady state for $R_0 < 1$. For $R_0 > 1$, the solutions converge to the endemic steady state.

In this study, we formulate the model of Malaria transmission with the influence of flooding in Thailand. Condition for local stabilities of disease free steady state and endemic steady state is defined by R_0, where $R_0 = \dfrac{\gamma_n N_n(\gamma_{v_f} + \gamma_{v_{n_f}})}{d_v(d+\gamma)(1+d\mathrm{II}_n)}$. (5.15)

The basic reproductive number is given as $R_0' = \sqrt{R_0}$, defined as the average number of secondary casesproduced from primary cases .From (5.15), we can see that the transmission rates of *Plasmodium* Malaria (γ_n, γ_{v_f} and $\gamma_{v_{n_f}}$) effect to the basic reproductive number. If we can reduce the transmission rate of this disease, then we can reduce the outbreak of the disease. Next, we simulate our solutions for different values of transmission rates.



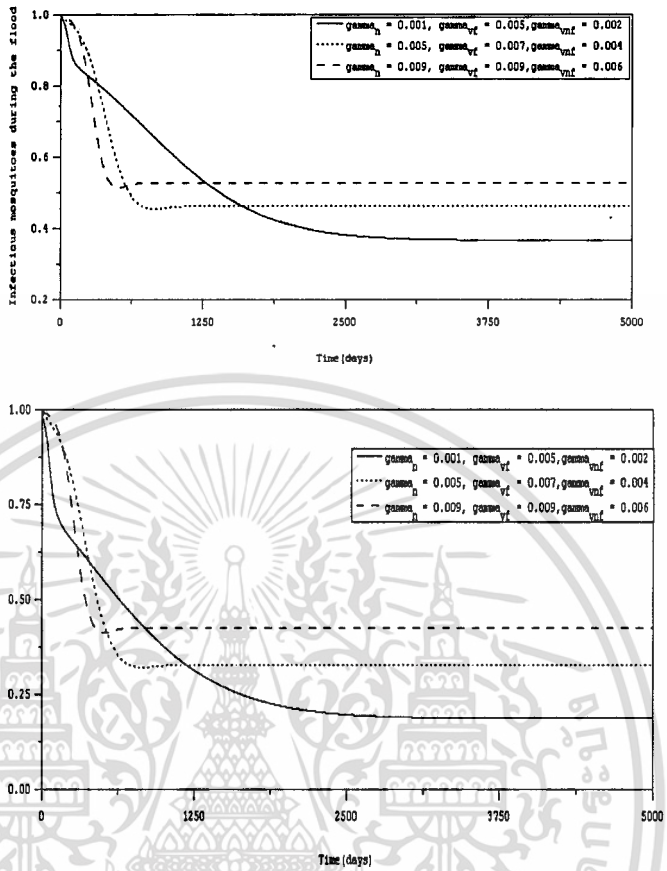


Figure 5.3: Time series solutions of susceptible human, exposed human, infectious human, infectious mosquito during flooding time and infectious mosquito during non-flooding time for the different sets of transmission rates.

We can see that when the transmission rates are higher, the steady state solutions of exposed and infectious groups are increasing but the steady state solutions of susceptible group is decreasing. From our simulations, we can see that the infectious proportion during flooding time is higher than the infectious proportion during non-flooding time. This is true because mosquitoes in the flooding time can grow faster than mosquitoes in the non-flooding time.

4.6. แบบจำลองที่ 6 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงชนิดของยุงลาย [61]

The SIR and SI mathematical model simulates the spread of dengue virus between host and vector. The age structure into a disease model is to human population into two classes , child (c) and adults (a), then we modify it by incorporating the different behaviors of *Aedes aegypti* and *Aedes albopictus*. In Figure 1 , we show the age distribution of the incidence rates in one province in Thailand during 2002 – 2012 epidemic. As we see , most cases occur in children under the age of 15. However , a small number of cases do occur in older people. Similar distributions are seen in the other provinces in the country.

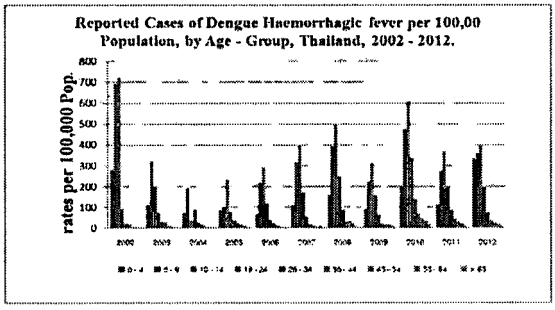


Figure6.1. Age distribution of the 2002 – 2012 Dengue fever incidence rates in Thailand.

This model with age structure , the dynamics of each component of the human is given by

$$\frac{dS_c}{dt} = P_c N_{tc} - \beta_{ac}(1+\alpha_a \sin\varepsilon t) I_{va1} S_c - \beta_{bc}(1+\alpha_b \sin\varepsilon t) I_{vb1} S_c - \mu_d S_c \quad (6.1a)$$

$$\frac{dI_{c1}}{dt} = \beta_{ac}(1+\alpha_a \sin\varepsilon t)\, I_{va1} S_c - \kappa_{c1} I_{c1} - \mu_d I_{c1} \quad (6.1b)$$

$$\frac{dI_{c2}}{dt} = \beta_{bc}(1+\alpha_b \sin\varepsilon t) I_{vb1} S_c - \kappa_{c2} I_{c2} - \mu_d I_{c2} \quad (6.1c)$$

$$\frac{dR_c}{dt} = \kappa_{c1} I_{c1} + \kappa_{c2} I_{c2} - \mu_d R_c \quad (6.1d)$$

$$\frac{dS_a}{dt} = P_a N_{ta} - \beta_{aa}(1+\alpha_a \sin\varepsilon t) I_{va2} S_a - \beta_{ba}(1+\alpha_b \sin\varepsilon t) I_{vb2} S_a - \mu_d S_a \quad (6.1e)$$

$$\frac{dI_{a1}}{dt} = \beta_{aa}(1+\alpha_a \sin\varepsilon t)\, I_{va2} S_a - \kappa_{a1} I_{a1} - \mu_d I_{a1} \quad (6.1f)$$

$$\frac{dI_{a2}}{dt} = \beta_{ba}(1+\alpha_b \sin\varepsilon t) I_{vb2} S_a - \kappa_{a2} I_{a2} - \mu_d I_{a2} \quad (6.1g)$$

$$\frac{dR_a}{dt} = \kappa_{a1} I_{a1} + \kappa_{a2} I_{a2} - \mu_d R_a \quad (6.1h)$$

where S_c , I_{c1} , I_{c2} , R_c are the numbers of susceptible child , infected from *Aedes aegypti* and *Aedes albopictus* in child , and recovered child. S_a , I_{a1} , I_{a2} , R_a are the numbers of susceptible adult , infected from *Aedes aegypti* and *Aedes albopictus* in adult, and recovered adult , respectively ; N_t, the total population (N_{tc}, the total population in child and N_{ta}, the total population in adult , two this to be constant) ; P_c and P_a , the birth rate , in child and in adult ; β_{ac} ,the transmission probability of dengue virus from *Aedes aegypti* to child, β_{bc} , the transmission probability of dengue virus from *Aedes albopictus* to child and β_{aa} , the transmission probability of dengue virus from *Aedes aegypti* to adult , β_{ba} , the transmission probability of dengue virus from *Aedes albopictus* to adult ; κ_{c1} , is the rate at which the infected child of *Aedes aegypti* recover , κ_{c2} , is the rate at which the infected child of *Aedes albopictus* recover and κ_{a1} , is the rate at which the infected adult of *Aedes aegypti* recover , κ_{a2} , is the rate at which the infected adult of *Aedes albopictus* recover ,and μ_d is the natural death rate of human population. α_a, the measure of influence on the transmission process from human population to *Aedes aegypti* and α_b,the measure of influence on the

transmission process from human population to *Aedes albopictus*; ρ_{va} , the measure of influence on the transmission process from *Aedes aegypti* to human population and ρ_{vb} , the measure of influence on the transmission process from *Aedes albopictus* to human population .

It we add equations (6.1a) –(6.1h) together , we get

$$\frac{dN_t}{dt} = \frac{dN_{tc}}{dt} + \frac{dN_{ta}}{dt}$$
$$= (S_c + I_{c1} + I_{c2} + R_c) + (S_a + I_{a1} + I_{a2} + R_a)$$

For the total human populations in child and adult to be constant sizes, i.e., $\frac{dN_{tc}}{dt} = 0$ and $\frac{dN_{ta}}{dt} = 0$, the birth rate would have to be equal to the death rate, $P_c = P_a = \mu_d$ in child and adult ,respectively .

where N_{tc} is the total number of child and is equal to $S_c + I_{c1} + I_{c2} + R_c$

N_{ta}, the total population in adult and is equal to $S_a + I_{a1} + I_{a2} + R_a$

The Dynamics of the mosquitoes is described by

$$\frac{dS_{va1}}{dt} = A_{va1} - \lambda_{va1}(1 + \rho_{va}\sin\varepsilon t) I_{c1} S_{va1} - \mu_{va1} S_{va1} \quad (6.2a)$$

$$\frac{dI_{va1}}{dt} = \lambda_{va1}(1 + \rho_{va}\sin\varepsilon t) I_{c1} S_{va1} - \mu_{va1} I_{va1} \quad (6.2b)$$

$$\frac{dS_{va2}}{dt} = A_{va2} - \lambda_{va2}(1 + \rho_{va}\sin\varepsilon t) I_{a1} S_{va2} - \mu_{va2} S_{va2} \quad (6.2c)$$

$$\frac{dI_{va2}}{dt} = \lambda_{va2}(1 + \rho_{va}\sin\varepsilon t) I_{a1} S_{va2} - \mu_{va2} I_{va2} \quad (6.2d)$$

$$\frac{dS_{vb1}}{dt} = A_{vb1} - \lambda_{vb1}(1 + \rho_{vb}\sin\varepsilon t) I_{c2} S_{vb1} - \mu_{vb1} S_{vb1} \quad (6.2e)$$

$$\frac{dI_{vb1}}{dt} = \lambda_{vb1}(1 + \rho_{vb}\sin\varepsilon t) I_{c2} S_{vb1} - \mu_{vb1} I_{vb1} \quad (6.2f)$$

$$\frac{dS_{vb2}}{dt} = A_{vb2} - \lambda_{vb2}(1 + \rho_{vb}\sin\varepsilon t) I_{a2} S_{vb2} - \mu_{vb2} S_{vb2} \quad (6.2g)$$

$$\frac{dI_{vb2}}{dt} = \lambda_{vb2}(1 + \rho_{vb}\sin\varepsilon t) I_{a2} S_{vb2} - \mu_{vb2} I_{vb2} \quad (6.2h)$$

where S_{va1} ,and I_{va1} are the number of susceptible and infected in *Aedes aegypti* of child, respectively; μ_{va1}, the death rate of the mosquitoes; A_{va1}, the carrying capacity of the environment (for mosquitoes) and λ_{va1} is the probability that a dengue virus transmitted to the *Aedes aegypti* from an infected human. S_{va2} ,and I_{va2} are the number of susceptible and infected in *Aedes aegypti* of adult, respectively; μ_{va2} , the death rate of the mosquitoes; A_{va2} , the carrying capacity of the environment (for mosquitoes) and λ_{va2} is the probability that a dengue virus transmitted to the *Aedes aegypti* from an infected human. S_{vb1} ,and I_{vb1} are the number of susceptible and infected in *Aedes albopictus* of child, respectively; μ_{vb1}, the death rate of the mosquitoes; A_{vb1}, the carrying capacity of the environment (for mosquitoes) and λ_{vb1} is the probability that a dengue virus transmitted to the *Aedes albopictus* from an infected human. S_{vb2} ,and I_{vb2} are the number of susceptible and infected in *Aedes albopictus* of adult,

respectively; μ_{vb2}, the death rate of the mosquitoes; A_{vb2}, the carrying capacity of the environment (for mosquitoes) and λ_{vb2} is the probability that a dengue virus transmitted to the *Aedes albopictus* from an infected human. If we add equations (6.2a) – (6.2h) together, we get

$$\frac{d(S_{va1}+I_{va1})}{dt} = A_{va1}-\mu_{va1}N_{va1} \tag{6.3a}$$

$$\frac{d(S_{va2}+I_{va2})}{dt} = A_{va2}-\mu_{va2}N_{va2} \tag{6.3b}$$

$$\frac{d(S_{vb1}+I_{vb1})}{dt} = A_{vb1}-\mu_{vb1}N_{vb1} \tag{6.3c}$$

$$\frac{d(S_{vb2}+I_{vb2})}{dt} = A_{vb2}-\mu_{vb2}N_{vb2} \tag{6.3d}$$

where N_{va1} and N_{va2} are the numbers of *Aedes aegypti* in child and adult respectively , which is equal to $S_{va1}+I_{va1}$ and $S_{va2}+I_{va2}$. N_{vb1} and N_{vb2} are the numbers of *Aedes albopictus* in child and adult respectively, which is equal to $S_{vb1}+I_{vb1}$ and $S_{vb2}+I_{vb2}$. If the numbers of mosquitoes are also constant each other (6.3a) – (6.3d) gives $N_{va1}=A_{va1}/\mu_{va1}$, $N_{va2}=A_{va2}/\mu_{va2}$, $N_{vb1}=A_{vb1}/\mu_{vb1}$ and $N_{vb2}=A_{vb2}/\mu_{vb2}$.

We normalize parameter (6.1a) – (6.1h) and (6.2a) – (6.2h) by writing $S'_c=\frac{S_c}{N_{tc}}$, $I'_{c1}=\frac{I_{c1}}{N_{tc}}$, $I'_{c2}=\frac{I_{c2}}{N_{tc}}$, $R'_c=\frac{R_c}{N_{tc}}$ in child and $S'_a=\frac{S_a}{N_{ta}}$, $I'_{a1}=\frac{I_{a1}}{N_{ta}}$, $I'_{a2}=\frac{I_{a2}}{N_{ta}}$, $R'_a=\frac{R_a}{N_{ta}}$ in adult. $S'_{va1}=\frac{S_{va1}}{N_{va1}}$, $I'_{va1}=\frac{I_{va1}}{N_{va1}}$, $S'_{va2}=\frac{S_{va2}}{N_{va2}}$, $I'_{va2}=\frac{I_{va2}}{N_{va2}}$, $S'_{vb1}=\frac{S_{vb1}}{N_{vb1}}$, $I'_{vb1}=\frac{I_{vb1}}{N_{vb1}}$, $S'_{vb2}=\frac{S_{vb2}}{N_{vb2}}$ and $I'_{vb2}=\frac{I_{vb2}}{N_{vb2}}$, then the reduced equations become

$$\frac{d}{dt}S'_c=\mu_d-\beta_{ac}(1+\alpha_a\sin\varepsilon t)I'_{va1}N_{va1}S'_c-\beta_{bc}(1+\alpha_b\sin\varepsilon t)I'_{vb1}N_{vb1}S'_c-\mu_dS'_c \tag{6.4a}$$

$$\frac{d}{dt}I'_{c1}=\beta_{ac}(1+\alpha_a\sin\varepsilon t)\,I'_{va1}N_{va1}\,S'_c-\kappa_{c1}I'_{c1}-\mu_dI'_{c1} \tag{6.4b}$$

$$\frac{d}{dt}I'_{c2}=\beta_{bc}(1+\alpha_b\sin\varepsilon t)I'_{vb1}N_{vb1}\,S'_c-\kappa_{c2}I'_{c2}-\mu_dI'_{c2} \tag{6.4c}$$

$$\frac{d}{dt}S'_a=\mu_d-\beta_{aa}(1+\alpha_a\sin\varepsilon t)I'_{va2}N_{va2}S'_a-\beta_{ba}(1+\alpha_b\sin\varepsilon t)I'_{vb2}N_{vb2}S'_a-\mu_dS'_a \tag{6.4d}$$

$$\frac{d}{dt}I'_{a1}=\beta_{aa}(1+\alpha_a\sin\varepsilon t)\,I'_{va2}\,N_{va2}S'_a-\kappa_{a1}I'_{a1}-\mu_dI'_{a1} \tag{6.4e}$$

$$\frac{d}{dt}I'_{a2}=\beta_{ba}(1+\alpha_b\sin\varepsilon t)I'_{vb2}N_{vb2}\,S'_a-\kappa_{a2}I'_{a2}-\mu_dI'_{a2} \tag{6.4f}$$

$$\frac{d}{dt}I'_{va1}=\lambda_{va1}(1+\rho_{va}\sin\varepsilon t)\,I'_{c1}\,N_{tc}S'_{va1}-\mu_{va1}I'_{va1} \tag{6.4g}$$

$$\frac{d}{dt}I'_{va2}=\lambda_{va2}(1+\rho_{va}\sin\varepsilon t)\,I'_{a1}\,N_{ta}S'_{va2}-\mu_{va2}I'_{va2} \tag{6.4h}$$

$$\frac{d}{dt}I'_{vb1}=\lambda_{vb1}(1+\rho_{vb}\sin\varepsilon t)\,I'_{c2}\,N_{tc}S'_{vb1}-\mu_{vb1}I'_{vb1} \tag{6.4i}$$

$$\frac{d}{dt}I'_{vb2}=\lambda_{vb2}(1+\rho_{vb}\sin\varepsilon t)\,I'_{a2}\,N_{ta}S'_{vb2}-\mu_{vb2}I'_{vb2} \tag{6.4j}$$

The dynamical equations with conditions for $S'_c + I'_{c1} + I'_{c2} + R'_c = 1$, $S'_a + I'_{a1} + I'_{a2} + R'_a = 1$, $S_{va1} + I_{va1} = 1$, $S'_{va2} + I'_{va2} = 1$, $S'_{vb1} + I'_{vb1} = 1$ and $S'_{vb2} + I'_{vb2} = 1$.

The equilibrium states $(S'_c, I'_{c1}, I'_{c2}, S'_a, I'_{a1}, I'_{a2}, I'_{va1}, I'_{vb1}, I'_{va2}, I'_{vb2})$ are obtained by setting the right hand side of (6.4a) – (6.4j) to zero. They are two group independent ,therefore divide into groups equilibrium states to be child and adult, follows $(S'_c, I'_{c1}, I'_{c2}, I'_{va1}, I'_{vb1})$ and $(S'_a, I'_{a1}, I'_{a2}, I'_{va2}, I'_{vb2})$. Doing this, we get Four equilibrium states,

A. The two group disease free equilibrium state

$S_0 = (1, 0, 0, 0, 0, 1, 0, 0, 0, 0)$

A1. the disease free equilibrium state $S_{c0} = (1, 0, 0, 0, 0)$ in child.

A2. the disease free equilibrium state $S_{a0} = (1, 0, 0, 0, 0)$ in adult.

B. The two group endemic equilibrium state

$\hat{S} = (S^*_c, I^*_{c1}, I^*_{c2}, I^*_{va1}, I^*_{vb1}, S^*_a, I^*_{a1}, I^*_{a2}, I^*_{va2}, I^*_{vb2})$

B1. the endemic state

$S_{c1} = (S^*_c, I^*_{c1}, I^*_{c2}, I^*_{va1}, I^*_{vb1})$ in child , where

$$S^*_c = \frac{(N_{tc}\mu_d\lambda_{vb1} + (\kappa_{c2}+\mu_d)\mu_{vb1} + N_{tc}\mu_d\lambda_{vb1}\rho_{vb}\sin\varepsilon t)}{(N_{tc}\lambda_{vb1}(I^*_{vd}N_{vd}\beta_{ac} + N_{vb1}\beta_{bc} + \mu_d + (I^*_{vd}N_{vd}\alpha_a\beta_{ac} + N_{vb1}\alpha_b\beta_{bc})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t)))} \quad (6.5a)$$

$$I^*_{c1} = \frac{I^*_{vd}N_{vd}\beta_{ac}(1+\alpha_a\sin\varepsilon t)(N_{tc}\mu_d\lambda_{vb1} + (\kappa_{c2}+\mu_d)\mu_{vb1} + N_{tc}\mu_d\lambda_{vb1}\rho_{vb}\sin\varepsilon t))}{(N_{tc}\lambda_{vb1}(\kappa_{c1}+\mu_d)(I^*_{vd}N_{vd}\beta_{ac} + N_{vb1}\beta_{bc} + \mu_d + (I^*_{vd}N_{vd}\alpha_a\beta_{ac} + N_{vb1}\alpha_b\beta_{bc})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))} \quad (6.5b)$$

$$I^*_{c2} = \frac{(I^*_{vb1}N_{vb1}\beta_{bc}(1+\alpha_b\sin\varepsilon t)(N_{tc}\lambda_{vb1}\mu_d + (\kappa_{c2}+\mu_d)\mu_{vb1} + N_{tc}\lambda_{vb1}\mu_d\rho_{vb}\sin\varepsilon t))}{(N_{tc}\lambda_{vb1}(\kappa_{c2}+\mu_d)(I^*_{vd}N_{vd}\beta_{ac} + I^*_{vb1}N_{vb1}\beta_{bc} + \mu_d + (I^*_{vd}N_{vd}\alpha_a\beta_{ac} + N_{vb1}\alpha_b\beta_{bc})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))} \quad (6.5c)$$

$$\begin{aligned} I^*_{va1} = {} & [(2(-2\lambda_{vb1}\mu_d(\kappa_{c1}+\mu_d)\mu_{va1} + 2N_{va1}\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{vb1} + N_{va1}\alpha_a\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{vb1}\rho_{va} \\ & - N_{vb1}\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{va1}(2+\alpha_b\rho_{vb}) + N_{tc}N_{va1}\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d(2+\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb}))) - \\ & - 2(N_{va1}\alpha_a\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{vb1}\rho_{va} - N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{va1}\rho_{vb} + N_{tc}N_{va1}\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d \\ & (\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb})))\cos 2\varepsilon t + (4(N_{va1}\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{vb1}(\alpha_a+\rho_{va}) - \lambda_{vb1}\mu_d(\kappa_{c1}+\mu_d)\mu_{va1} \\ & - N_{vb1}\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{va1}(\alpha_b+\rho_{vb})) + N_{tc}N_{va1}\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d(4(\rho_{va}+\rho_{vb}) + \alpha_a(4+3\rho_{va}\rho_{vb})))\sin\varepsilon t \\ & - N_{tc}N_{va1}\alpha_a\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d\rho_{va}\rho_{vb}\sin\varepsilon t)] / [(2N_{va1}\beta_{ac}(1+\alpha_a\sin\varepsilon t)(2\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{va1} \\ & + 2\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{vb1}(\kappa_{c2}+\mu_d)\mu_{vb1} + N_{tc}\mu_d\lambda_{va1}\lambda_{vb1}(2+\rho_{va}\rho_{vb}) - N_{tc}\mu_d\lambda_{va1}\lambda_{vb1}\rho_{va}\rho_{vb}\cos 2\varepsilon t \\ & + 2(\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{vb1}\rho_{va} + \lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{va1}\rho_{vb} + N_{tc}\mu_d\lambda_{va1}\lambda_{vb1}(\rho_{va}+\rho_{vb}))\sin\varepsilon t))] \end{aligned} \quad (6.5d)$$

$$\begin{aligned} I^*_{vb1} = {} & [(N_{tc}N_{vb1}\beta_{ac}\lambda_{vb1}\mu_d - (I^*_{va1}N_{va1}\beta_{ac} + \mu_d)(\kappa_{c2}+\mu_d)\mu_{vb1} + \sin\varepsilon t(-I^*_{va1}N_{va1}\alpha_a\beta_{ac}(\kappa_{c2}+\mu_d)\mu_{vb1} + \\ & N_{tc}N_{vb1}\beta_{bc}\lambda_{vb1}\mu_d(\alpha_b+\rho_{vb}) + N_{tc}N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}\mu_d\rho_{vb}\sin\varepsilon t)))] / [N_{vb1}\beta_{bc}(1+\alpha_b\sin\varepsilon t) \\ & (N_{tc}\lambda_{vb1}\mu_d + (\kappa_{c2}+\mu_d)\mu_{vb1} + N_{tc}\lambda_{vb1}\mu_d\rho_{vb}\sin\varepsilon t))] \end{aligned} \quad (6.5e)$$

B2. the endemic state

$S_{a1} = (S^*_a, I^*_{a1}, I^*_{a2}, I^*_{va2}, I^*_{vb2})$ in adult, where

$$S^*_a = \frac{(N_{ta}\mu_d\lambda_{vb2} + (\kappa_{a2}+\mu_d)\mu_{vb2} + N_{ta}\mu_d\lambda_{vb2}\rho_{vb}\sin\varepsilon t)}{(N_{ta}\lambda_{vb2}(I^*_{va2}N_{va2}\beta_{aa} + N_{vb2}\beta_{ba} + \mu_d + (I^*_{va2}N_{va2}\alpha_a\beta_{aa} + N_{vb2}\alpha_b\beta_{ba})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t)))} \quad (6.6a)$$

$$I^*_{a1} = \frac{I^*_{va2}N_{va2}\beta_{aa}(1+\alpha_a\sin\varepsilon t)(N_{ta}\mu_d\lambda_{vb2} + (\kappa_{a2}+\mu_d)\mu_{vb2} + N_{ta}\mu_d\lambda_{vb2}\rho_{vb}\sin\varepsilon t))}{(N_{ta}\lambda_{vb2}(\kappa_{a1}+\mu_d)(I^*_{va2}N_{va2}\beta_{aa} + N_{vb2}\beta_{ba} + \mu_d + (I^*_{va2}N_{va2}\alpha_a\beta_{aa} + N_{vb2}\alpha_b\beta_{ba})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))} \quad (6.6b)$$

$$I^*_{a2} = \frac{(I^*_{vb2}N_{vb2}\beta_{ba}(1+\alpha_b\sin\varepsilon t)(N_{ta}\lambda_{vb2}\mu_d + (\kappa_{a2}+\mu_d)\mu_{vb2} + N_{ta}\lambda_{vb2}\mu_d\rho_{vb}\sin\varepsilon t))}{(N_{ta}\lambda_{vb2}(\kappa_{a2}+\mu_d)(I^*_{va2}N_{va2}\beta_{aa} + I^*_{vb2}N_{vb2}\beta_{ba} + \mu_d + (I^*_{va2}N_{va2}\alpha_a\beta_{aa} + N_{vb2}\alpha_b\beta_{ba})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))} \quad (6.6c)$$

$$I^*_{va2} = [(2(-2\lambda_{vb2}\mu_d(\kappa_{a1}+\mu_d)\mu_{va2}+2N_{va2}\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{vb2}+N_{va2}\alpha_a\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{vb2}\rho_{va}$$
$$-N_{vb2}\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{va2}(2+\alpha_b\rho_{vb})+N_{ta}N_{va2}\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d(2+\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb})))-$$
$$-2(N_{va2}\alpha_a\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{vb2}\rho_{va}-N_{vb2}\alpha_b\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{va2}\rho_{vb}+N_{ta}N_{va2}\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d$$
$$(\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb})))\cos 2\varepsilon t+(4(N_{va2}\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{vb2}(\alpha_a+\rho_{va})-\lambda_{vb2}\mu_d(\kappa_{a1}+\mu_d)\mu_{va2}$$
$$-N_{vb2}\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{va2}(\alpha_b+\rho_{vb}))+N_{ta}N_{va2}\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d(4(\rho_{va}+\rho_{vb})+\alpha_a(4+3\rho_{va}\rho_{vb})))\sin\varepsilon t$$
$$-N_{ta}N_{va2}\alpha_a\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d\rho_{va}\rho_{vb}\sin\varepsilon t)]/[(2N_{va2}\beta_{aa}(1+\alpha_a\sin\varepsilon t)(2\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{va2}$$
$$+2\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{vb2}(\kappa_{a2}+\mu_d)\mu_{vb2}+N_{ta}\mu_d\lambda_{va2}\lambda_{vb2}(2+\rho_{va}\rho_{vb})-N_{ta}\mu_d\lambda_{va2}\lambda_{vb2}\rho_{va}\rho_{vb}\cos 2\varepsilon t$$
$$+2(\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{vb2}\rho_{va}+\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{va2}\rho_{vb}+N_{ta}\mu_d\lambda_{va2}\lambda_{vb2}(\rho_{va}+\rho_{vb}))\sin\varepsilon t))] \quad (6.6d)$$

$$I^*_{vb2} = [(N_{ta}N_{vb2}\beta_{ad}\lambda_{vb2}\mu_d-(I^*_{va2}N_{va2}\beta_{aa}+\mu_d)(\kappa_{a2}+\mu_d)\mu_{vb2}+\sin\varepsilon t(-I^*_{va2}N_{va2}\alpha_a\beta_{aa}(\kappa_{a2}+\mu_d)\mu_{vb2}+$$
$$N_{ta}N_{vb2}\beta_{ad}\lambda_{vb2}\mu_d(\alpha_b+\rho_{vb})+N_{ta}N_{vb2}\alpha_b\beta_{bd}\lambda_{vb2}\mu_d\rho_{vb}\sin\varepsilon t))]/[N_{vb2}\beta_{bd}(1+\alpha_b\sin\varepsilon t)$$
$$(N_{ta}\lambda_{vb2}\mu_d+(\kappa_{a2}+\mu_d)\mu_{vb2}+N_{ta}\lambda_{vb2}\mu_d\rho_{vb}\sin\varepsilon t))] \quad (6.6e)$$

The local stability of each equilibrium state is determined from Jacobian matrix of right hand side of the above set of differential equations evaluated at the equilibrium state.

Proposition A. If $E_0^*<1$ and $E_0''>1$ when $\varepsilon=0$, then the equilibrium S_{c0} in child and S_{a0} in adult are locally asymptotically stable.

Proof.

For the disease free equilibrium state in child S_{c0} = (1 , 0 , 0 , 0 ,0) and in adult S_{a0} = (1, 0 , 0 , 0 ,0).

The system defined by equations (4a) – (4j), the Jacobian matrix evaluated at S_{c0} and S_{a0} are 5 x 5 matrix respectively, given by

$$J_c=\begin{bmatrix} -(\mu_d) & 0 & 0 & -\beta_{ac}(1+\alpha_c\sin(\varepsilon t))N_{va} & -\beta_{bc}(1+\alpha_c\sin(\varepsilon t))N_{va} \\ 0 & -(\kappa_{c1}+\mu_d) & 0 & \beta_{ac}(1+\alpha_c\sin(\varepsilon t))N_{va} & 0 \\ 0 & 0 & -(\kappa_{c2}+\mu_d) & 0 & \beta_{bc}(1+\alpha_c\sin(\varepsilon t))N_{va} \\ 0 & \lambda_{va}(1+\rho_a\sin(\varepsilon t)) & 0 & -\mu_{va} & 0 \\ 0 & 0 & \lambda_{vb}(1+\rho_a\sin(\varepsilon t)) & 0 & -\mu_{vb} \end{bmatrix} \quad (6.7a)$$

$$J_a=\begin{bmatrix} -(\mu_d) & 0 & 0 & -\beta_{aa}(1+\alpha_a\sin(\varepsilon t))N_{va} & -\beta_{ba}(1+\alpha_a\sin(\varepsilon t))N_{va} \\ 0 & -(\kappa_{a1}+\mu_d) & 0 & \beta_{aa}(1+\alpha_a\sin(\varepsilon t))N_{va} & 0 \\ 0 & 0 & -(\kappa_{a2}+\mu_d) & 0 & \beta_{ba}(1+\alpha_a\sin(\varepsilon t))N_{va} \\ 0 & \lambda_{va}(1+\rho_a\sin(\varepsilon t)) & 0 & -\mu_{va} & 0 \\ 0 & 0 & \lambda_{vb}(1+\rho_a\sin(\varepsilon t)) & 0 & -\mu_{vb} \end{bmatrix} \quad (6.7b)$$

The eigenvalues are obtained by solving the matrix equations, $\det|\eta I-J|=0$ to evaluate the determinant, we get the following characteristic equations:

$$(\eta+\mu_d)(\eta^4+W_1\eta^3+W_2\eta^2+W_3\eta+W_4)=0 \quad (6.8a)$$

$$(\eta+\mu_d)(\eta^4+F_1\eta^3+F_2\eta^2+F_3\eta+F_4)=0 \quad (6.8b)$$

where

$$W_1=\kappa_{c1}+\kappa_{c2}+2\mu_d+\mu_{va1}+\mu_{vb1}\ , \quad (6.9a)$$

$$W_2=-N_{va1}\beta_{ac}\lambda_{va1}-N_{vb1}\beta_{bc}\lambda_{vb1})+\mu_d^2+2\mu_d\mu_{va1}+2\mu_d\mu_{vb1}+\mu_{va1}\mu_{vb1}+\kappa_{c2}(\mu_d+\mu_{va1}+\mu_{vb1})+\kappa_{c1}(\kappa_{c2}+\mu_d+\mu_{va1}+\mu_{vb1}), \quad (6.9b)$$

$$W_3=(\kappa_{c1}+\mu_d)(\kappa_{c2}+\mu_d)\mu_{va1}-N_{vb1}\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d+\mu_{va1})+((\kappa_{c1}+\mu_d)(\kappa_{c2}+\mu_d)+(\kappa_{c1}+\kappa_{c2}+2\mu_d)\mu_{va1})\mu_{vb1}-N_{va1}\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d+\mu_{vb1})+(\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d+\mu_{vb1})), \quad (6.9c)$$

$$W_4=(N_{va1}\beta_{ac}\lambda_{va1}-(\kappa_{c1}+\mu_d)\mu_{va1})(N_{vb1}\beta_{bc}\lambda_{vb1}+(\kappa_{c2}+\mu_d)\mu_{vb1})\ , \quad (6.9d)$$

$$F_1=\kappa_{a1}+\kappa_{a2}+2\mu_d+\mu_{va2}+\mu_{vb2}\ , \quad (6.9e)$$

$$F_2=-N_{va2}\beta_{ad}\lambda_{va2}-N_{vb2}\beta_{bd}\lambda_{vb2})+\mu_d^2+2\mu_d\mu_{va2}+2\mu_d\mu_{vb2}+\mu_{va2}\mu_{vb2}+\kappa_{a2}(\mu_d+\mu_{va2}+\mu_{vb2})+\kappa_{a1}(\kappa_{a2}+\mu_d+\mu_{va2}+\mu_{vb2})\ , \quad (6.9f)$$

$$F_3=(\kappa_{a1}+\mu_d)(\kappa_{a2}+\mu_d)\mu_{va2}-N_{vb2}\beta_{bd}\lambda_{vb2}(\kappa_{a1}+\mu_d+\mu_{va2})+((\kappa_{a1}+\mu_d)(\kappa_{a2}+\mu_d)+(\kappa_{a1}+\kappa_{a2}+2\mu_d)\mu_{va2})\mu_{vb2}-N_{va2}\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d+\mu_{vb2})+(\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d+\mu_{vb2}))\ , \quad (6.9g)$$

$$F_4 = (N_{va2}\beta_{ad}\lambda_{va2} - (\kappa_{a1}+\mu_d)\mu_{va2})(N_{vt2}\beta_{td}\lambda_{vt2} + (\kappa_{a2}+\mu_d)\mu_{vt2}) \quad (6.9h)$$

From the characteristic equation , equation (6.8a) –(6.8b) , we see that one eigenvalue are $\eta_c = -\mu_d$ and $\eta_a = -\mu_d$, all of these eigenvalues are negative, if $E_0^* < 1$. Next, we check of these are negative. The sign of other four eigenvalues can be ascertained by the use of solving the equation $(\eta^4 + W_1\eta^3 + W_2\eta^2 + W_3\eta + W_4) = 0$ and $(\eta^4 + F_1\eta^3 + F_2\eta^2 + F_3\eta + F_4) = 0$. The remaining four eigenvalues have negative real parts if they satisfy Routh-Hurwitz criteria (6.9a) - (6.9h), each equilibrium state is locally asymptotically stable if the following conditions are satisfied,

$$W_1 \text{ and } F_1 > 0 \quad (6.10a)$$

$$W_3 \text{ and } F_3 > 0 \quad (6.10b)$$

$$W_4 \text{ and } F_4 > 0 \quad (6.10c)$$

$$W_1W_2W_3 > W_3^2 + W_1^2W_4 \text{ and } F_1F_2F_3 > F_3^2 + F_1^2F_4 \quad (6.10d)$$

After we use Mathematica to show the conditions in the locally asymptotically stable , we can see that W_1 and F_1 are always positive . For the equations given by (6.9a) – (6.9h), we show these conditions by using the following figure :

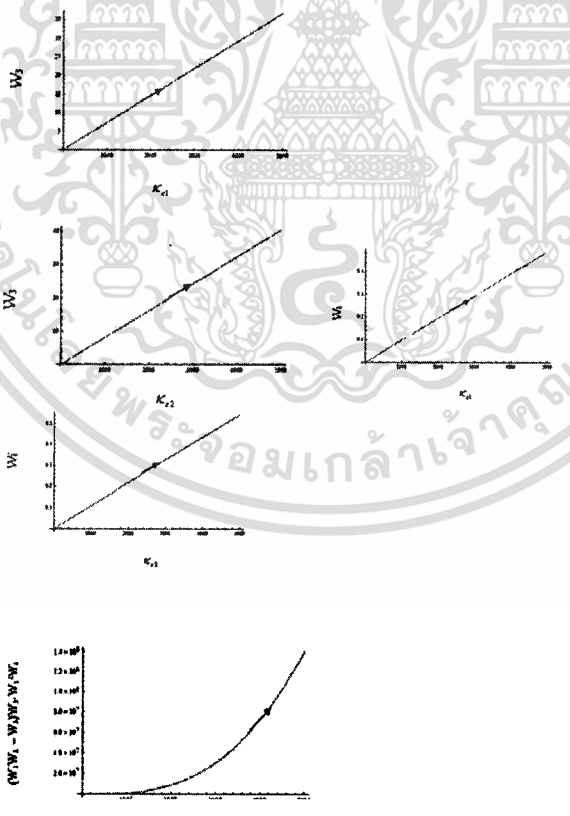


Figure6.2. The parameter spaces for the disease free equilibrium state for equation $(\eta^4+W_1\eta^3+W_2\eta^2+W_3\eta+W_4)=0$ and $(\eta^4+F_1\eta^3+F_2\eta^2+F_3\eta+F_4)=0$,which satisfies the Routh-Hurwitz conditions , show onto (W_3, κ_{c1}), (W_3, κ_{c2}), (W_4, κ_{c1}), (W_4, κ_{c2}),$((W_1W_2-W_3)W_3-W_1^2W_4, \kappa_{c1})$, $((W_1W_2-W_3)W_3-W_1^2W_4, \kappa_{c2})$, (F_3, κ_{a1}), (F_3, κ_{a2}), (F_4, κ_{a1}), (F_4, κ_{a2}),$((F_1F_2-F_3)F_3-F_1^2F_4, \kappa_{a1})$, $((F_1F_2-F_3)F_3-F_1^2F_4, \kappa_{a2})$, , respectively. The values of parameter are follows: From the above figure, the Routh-Hurwitz conditions are satisfies for $E_0''>1$

a) $\kappa_{c1}=1/(17/2), \kappa_{c2}=1/(19/2), \mu_d=1/(365*74.6)$ day^1, $\mu_{va1}=1/45$, $\mu_{vb1}=1/37$, $N_{tc}=9000$, $N_{va1}=4000$, $N_{vb1}=5500$, $\beta_{ac}=0.00769$, $\beta_{bc}=0.000246$, $\lambda_{va1}=0.00000576$, $\lambda_{vb1}=0.00000335$, $\alpha_a=0.07$, $\alpha_b=0.067$,and $N_t=100000$.

b) $\kappa_{a1}=1/(19/2), \kappa_{a2}=1/(21/2), \mu_d=1/(365*74.6)$ day^1, $\mu_{va2}=1/40$, $\mu_{vb2}=1/34$, $N_{ta}=6000$, $N_{va2}=3000$, $N_{vb2}=4100$, $\beta_{aa}=0.000045$, $\beta_{ba}=0.000067$, $\lambda_{va2}=0.0066$, $\lambda_{vb2}=0.00235$, $\alpha_a=0.07$, $\alpha_b=0.067$,and $N_t=100000$. From the above figures , the Routh-Hurwitz conditions are satisfies for $E_0''>1$.

C. Endemic disease state

Proposition B. If $E_0^*>1$,when $\varepsilon=0$,then the equilibrium state $\hat{S}=(S_c^*, I_{c1}^*, I_{c2}^*, I_{va1}^*, I_{vb1}^*, S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*)$ is locally asymptotically stable.

Proof. For the endemic disease equilibrium state $S_{c1} = (S_c^*, I_{c1}^*, I_{c2}^*, I_{va1}^*, I_{vb1}^*)$ in child and $S_{a1} = (S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*)$, we obtain the characteristic equation:

$$(\eta^5+D_1\eta^4+D_2\eta^3+D_3\eta^2+D_4\eta+D_5)=0 \quad \text{in child} \tag{6.11a}$$

$$(\eta^5+G_1\eta^4+G_2\eta^3+G_3\eta^2+G_4\eta+G_5)=0 \quad \text{in adult} \tag{6.11b}$$

where

$$D_1 = N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \kappa_{c1}+\kappa_{c2}+3\mu_d+\mu_{va1}+\mu_{vb1} \tag{6.12a}$$

$$\begin{aligned} D_2 = {} & \kappa_{c1}\kappa_{c2}+2\kappa_{c1}\mu_d+2\kappa_{c2}\mu_d+3\mu_d^2+\kappa_{c1}\mu_{va1}+\kappa_{c2}\mu_{va1}+3\mu_d\mu_{va1}+ \\ & (\kappa_{c1}+\kappa_{c2}+3\mu_d+\mu_{va1})\mu_{vb1}+N_{va1}\beta_{ac}(-(\lambda_{va1}\mu_d/N_{va1}\beta_{ac}\theta_1+N_{vb1}\beta_{bc}\theta_2\mu_d)+\theta_1(\kappa_{c1}+\kappa_{c2}+2\mu_d \\ & +(\lambda_{va1}\mu_d/N_{va1}\beta_{ac}\theta_1+N_{vb1}\beta_{bc}\theta_2\mu_d)+\mu_{va1}+\mu_{vb1}))+N_{vb1}\beta_{bc}(-(\lambda_{vb1}\mu_d/N_{va1}\beta_{ac}\theta_1+N_{vb1}\beta_{bc}\theta_2\mu_d)+ \\ & \theta_2(\kappa_{c1}+\kappa_{c2}+2\mu_d+(\lambda_{vb1}\mu_d/N_{va1}\beta_{ac}\theta_1+N_{vb1}\beta_{bc}\theta_2\mu_d)\mu_{va1}+\mu_{vb1})) \end{aligned} \tag{6.12b}$$

$$\begin{aligned} D_3 = {} & \frac{1}{N_{va1}\beta_{ac}\theta_1+N_{vb1}\beta_{bc}\theta_2+\mu_d}(N_{va1}^2\beta_{ac}^2\theta_1^2(\mu_d^2+2\mu_d\mu_{va1}+2\mu_d\mu_{vb1}+\mu_{va1}\mu_{vb1}+\kappa_{c2}(\mu_d+\mu_{va1}+\mu_{vb1}) \\ & +\kappa_{c1}(\kappa_{c2}+\mu_d+\mu_{va1}+\mu_{vb1}))+N_{vb1}^2\beta_{bc}^2\theta_2^2(\mu_d^2+2\mu_d\mu_{va1}+2\mu_d\mu_{vb1}+\mu_{va1}\mu_{vb1}+\kappa_{c2}(\mu_d+\mu_{va1}+\mu_{vb1}) \\ & +\kappa_{c1}(\kappa_{c2}+\mu_d+\mu_{va1}+\mu_{vb1}))+\mu_d(\kappa_{c2}(\mu_d^2+\mu_{va1}\mu_{vb1}+2\mu_d(\mu_{va1}+\mu_{vb1}))+\mu_d(\mu_d^2+3\mu_{va1}\mu_{vb1}+3\mu_d(\mu_{va1}+\mu_{vb1}))+ \\ & \kappa_{c1}(\mu_d^2+\mu_{va1}\mu_{vb1}+2\mu_d(\mu_{va1}+\mu_{vb1})+\kappa_{c2}(\mu_d+\mu_{va1}+\mu_{vb1})))+N_{vb1}\beta_{bc}(-\lambda_{vb1}\mu_d(\kappa_{c1}+2\mu_d+\mu_{va1})+\theta_2(\mu_d(2\mu_d \\ & (\kappa_{c2}+\lambda_{vb1}+\mu_d)+(3\kappa_{c2}+\lambda_{vb1}+5\mu_d)\mu_{va1})+(\kappa_{c2}(3\mu_d+\mu_{va1})+\mu_d(5\mu_d+4\mu_{va1}))\mu_{vb1}+\kappa_{c2}(2\mu_d+\mu_{va1}+\mu_{vb1}))))+ \\ & N_{va1}\beta_{ac}(-\lambda_{va1}\mu_d(\kappa_{c2}+2\mu_d+\mu_{vb1})+\theta_1(\kappa_{c2}\mu_d(\lambda_{va1}+2\mu_d+3\mu_{va1})+\kappa_{c2}(3\mu_d+\mu_{va1})\mu_{vb1}+ \\ & \mu_d(2\mu_d(\lambda_{va1}+\mu_d)+5\mu_d\mu_{va1}+(\lambda_{va1}+5\mu_d+4\mu_{va1})\mu_{vb1})+\kappa_{c1}(2\mu_d^2+\mu_{va1}\mu_{vb1}+3\mu_d(\mu_{va1}+\mu_{vb1})+\kappa_{c2}(2\mu_d+\mu_{va1}+\mu_{vb1})))+ \\ & N_{vb1}\beta_{bc}(-\theta_2\lambda_{va1}\mu_d+\theta_1(-\lambda_{vb1}\mu_d+\theta_2(\mu_d(\lambda_{va1}+\lambda_{vb1}+2\mu_d+4\mu_{va1})+2(2\mu_d+\mu_{vb1})\mu_{vb1}+2\kappa_{c2} \\ & (\mu_d+\mu_{va1}+\mu_{vb1})+2\kappa_{c1}(\kappa_{c2}+\mu_d+\mu_{va1}+\mu_{vb1})))))) \end{aligned} \tag{6.12c}$$

$$D_4 = \kappa_{c1}\kappa_{c2}\mu_d\mu_{va1} + \kappa_{c1}\mu_d^2\mu_{va1} + \kappa_{c2}\mu_d^2\mu_{va1} + \mu_d^3\mu_{va1} + \kappa_{c1}\kappa_{c2}\mu_d\mu_{vb1} + \kappa_{c1}\mu_d^2\mu_{vb1} + \kappa_{c2}\mu_d^2\mu_{vb1} + \mu_d^3\mu_{vb1}$$
$$+ \kappa_{c1}\kappa_{c2}\mu_{va1}\mu_{vb1} + 2\kappa_{c1}\mu_d\mu_{va1}\mu_{vb1} + 2\kappa_{c2}\mu_d\mu_{va1}\mu_{vb1} + 3\mu_d^2\mu_{va1}\mu_{vb1} + \frac{1}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d}$$
$$N_{vb1}\beta_{bc}((-1+\theta_2)\lambda_{vb1}\mu_d^2(\mu_d + 2\mu_{va1}) + \theta_2(N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d)(\mu_d(\kappa_{c2} + \mu_d)\mu_{va1} + (\mu_d(\kappa_{c2} + \mu_d) +$$
$$+(\kappa_{c2} + 2\mu_d)\mu_{va1})\mu_{vb1}) + \kappa_{c1}((-1+\theta_2)\lambda_{vb1}\mu_d(\mu_d + 2\mu_{va1}) + \theta_2(N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d)((\kappa_{c2} + \mu_d)\mu_{va1} +$$
$$(\kappa_{c2} + \mu_d + \mu_{va1})\mu_{vb1}))) + N_{va1}\beta_{ac}(-\frac{\kappa_{c2}\lambda_{va1}\mu_d^2}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \frac{\theta_1\kappa_{c2}\lambda_{va1}\mu_d^2}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} -$$
$$\frac{\lambda_{va1}\mu_d^3}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \frac{\theta_1\lambda_{va1}\mu_d^3}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \theta_1\kappa_{c1}\kappa_{c2}\mu_{va1} + \theta_1\kappa_{c1}\mu_d\mu_{va1} + \theta_1\kappa_{c2}\mu_d\mu_{va1}$$
$$+\theta_1\mu_d^2\mu_{va1} + \theta_1\kappa_{c1}\kappa_{c2}\mu_{vb1} + \theta_1\kappa_{c1}\mu_d\mu_{vb1} + \theta_1\kappa_{c2}\mu_d\mu_{vb1} + \theta_1\mu_d^2\mu_{vb1} - \frac{\kappa_{c2}\lambda_{va1}\mu_d\mu_{vb1}}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} +$$
$$\frac{\theta_1\kappa_{c2}\lambda_{va1}\mu_d\mu_{vb1}}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} - \frac{2\lambda_{va1}\mu_d^2\mu_{vb1}}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \frac{2\theta_1\lambda_{va1}\mu_d^2\mu_{vb1}}{N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \theta_1\kappa_{c1}\mu_{va1}\mu_{vb1} +$$
$$\theta_1\kappa_{c2}\mu_{va1}\mu_{vb1} + 2\theta_1\mu_d\mu_{va1}\mu_{vb1} + \frac{1}{(N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d)^2}N_{vb1}\beta_{bc}\mu_d(N_{va1}\beta_{ac}\theta_1(-\theta_1\lambda_{vb1}(\kappa_{c1} + \mu_d + \mu_{va1})$$
$$+\theta_2((-1+\theta_1)\kappa_{c2}\lambda_{va1} - \lambda_{va1}(\mu_d + \mu_{vb1}) + \theta_1(\lambda_{vb1}(\kappa_{c1} + \mu_d + \mu_{va1}) + \lambda_{va1}(\mu_d + \mu_{vb1})))) + N_{vb1}\beta_{bc}\theta_2(-\theta_1\lambda_{vb1} \quad (6.12d)$$
$$(\kappa_{c1} + \mu_d + \mu_{va1}) + \theta_2((-1+\theta_1)\kappa_{c2}\lambda_{va1} - \lambda_{va1}(\mu_d + \mu_{vb1}) + \theta_1(\lambda_{vb1}(\kappa_{c1} + \mu_d + \mu_{va1}) + \lambda_{va1}(\mu_d + \mu_{vb1}))))$$
$$+\mu_d(-\lambda_{vb1}(-\lambda_{va1} + \theta_1(\kappa_{c1} + \lambda_{va1} + \mu_d + \mu_{va1})) + \theta_2((-1+\theta_1)\kappa_{c2}\lambda_{va1} - \lambda_{va1}(\lambda_{vb1} + \mu_d + \mu_{vb1}) +$$
$$\theta_1(\kappa_{c1}\lambda_{vb1} + \lambda_{vb1}(\mu_d + \mu_{va1}) + \lambda_{va1}(\lambda_{vb1} + \mu_d + \mu_{vb1}))))))$$

$$D_5 = \frac{1}{(N_{va1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d)^2}(N_{va1}^3\beta_{ac}^3\theta_1^3(\kappa_{c1} + \mu_d)(\kappa_{c2} + \mu_d)\mu_{va1}\mu_{vb1} + (N_{vb1}\beta_{bc}\theta_2 + \mu_d)(\kappa_{c1} \quad (6.12e)$$
$$\mu_{va1}(N_{vb1}\beta_{bc}(-1+\theta_2)\lambda_{vb1}\mu_d^2 + (N_{vb1}\beta_{bc}\theta_2 + \mu_d)^2(\kappa_{c2} + \mu_d)\mu_{vb1}) + N_{va1}^2\beta_{ac}^2\theta_1(N_{vb1}\beta_{bc}\theta_1(-1+\theta_2)\lambda_{vb1}\mu_d$$
$$(\kappa_{c1} + \mu_d)\mu_{va1} + (N_{vb1}\beta_{bc}\theta_2 + \mu_d)(\kappa_{c2} + \mu_d)((-1+\theta_1)\lambda_{va1}\mu_d + 3\theta_1(\kappa_{c1} + \mu_d)\mu_{va1})\mu_{vb1}) + N_{va1}\beta_{ac}(\mu_d^2(\kappa_{c2} + \mu_d)$$
$$((-1+\theta_1)\lambda_{va1}\mu_d + 3\theta_1(\kappa_{c1} + \mu_d)\mu_{va1})\mu_{vb1}) + N_{vb1}^2\beta_{bc}^2\theta_2(\theta_1(-1+\theta_2)\lambda_{vb1}\mu_d(\kappa_{c1} + \mu_d)\mu_{va1} + \theta_2(\kappa_{c2} + \mu_d)$$
$$((-1+\theta_1)\lambda_{va1}\mu_d + 3\theta_1(\kappa_{c1} + \mu_d)\mu_{va1})\mu_{vb1}) + N_{vb1}\beta_{bc}\mu_d((-1+\theta_2)\lambda_{vb1}\mu_d + 2\theta_1(\kappa_{c1} + \mu_d)\mu_{va1}) + 2\theta_2(\kappa_{c2} + \mu_d)$$
$$((-1+\theta_1)\lambda_{va1}\mu_d + 3\theta_1(\kappa_{c1} + \mu_d)\mu_{va1})\mu_{vb1})))$$

$$G_1 = N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \kappa_{a1} + \kappa_{a2} + 3\mu_d + \mu_{va2} + \mu_{vb2} \quad (6.12f)$$

$$G_2 = \kappa_{a1}\kappa_{a2} + 2\kappa_{a1}\mu_d + 2\kappa_{a2}\mu_d + 3\mu_d^2 + \kappa_{a1}\mu_{va2} + \kappa_{a2}\mu_{va2} + 3\mu_d\mu_{va2} +$$
$$(\kappa_{a1} + \kappa_{a2} + 3\mu_d + \mu_{va2})\mu_{vb2} + N_{va2}\beta_{aa}(-(\lambda_{va2}\mu_d / N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4\mu_d) + \theta_3(\kappa_{a1} + \kappa_{a2} + 2\mu_d \quad (6.12g)$$
$$+(\lambda_{va2}\mu_d / N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4\mu_d) + \mu_{va2} + \mu_{vb2})) + N_{vb2}\beta_{ba}(-(\lambda_{vb2}\mu_d / N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4\mu_d) +$$
$$\theta_4(\kappa_{a1} + \kappa_{a2} + 2\mu_d + (\lambda_{vb2}\mu_d / N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4\mu_d)\mu_{va2} + \mu_{vb2}))$$

$$G_3 = \frac{1}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d}(N_{va2}^2\beta_{aa}^2\theta_3^2(\mu_d^2 + 2\mu_d\mu_{va2} + 2\mu_d\mu_{vb2} + \mu_{va2}\mu_{vb2} + \kappa_{a2}(\mu_d + \mu_{va2} + \mu_{vb2}) \quad (6.12h)$$
$$+\kappa_{a1}(\kappa_{a2} + \mu_d + \mu_{va2} + \mu_{vb2})) + N_{vb2}^2\beta_{ba}^2\theta_4^2(\mu_d^2 + 2\mu_d\mu_{va2} + 2\mu_d\mu_{vb2} + \mu_{va2}\mu_{vb2} + \kappa_{a2}(\mu_d + \mu_{va2} + \mu_{vb2})$$
$$+\kappa_{a1}(\kappa_{a2} + \mu_d + \mu_{va2} + \mu_{vb2})) + \mu_d(\kappa_{a2}(\mu_d^2 + \mu_{va2}\mu_{vb2} + 2\mu_d(\mu_{va2} + \mu_{vb2})) + \mu_d(\mu_d^2 + 3\mu_{va2}\mu_{vb2} + 3\mu_d(\mu_{va2} + \mu_{vb2})) +$$
$$\kappa_{a1}(\mu_d^2 + \mu_{va2}\mu_{vb2} + 2\mu_d(\mu_{va2} + \mu_{vb2}) + \kappa_{a2}(\mu_d + \mu_{va2} + \mu_{vb2}))) + N_{vb2}\beta_{ba}(-\lambda_{vb2}\mu_d(\kappa_{a1} + 2\mu_d + \mu_{va2}) + \theta_4(\mu_d(2\mu_d$$
$$(\kappa_{a2} + \lambda_{vb2} + \mu_d) + (3\kappa_{a2} + \lambda_{vb2} + 5\mu_d)\mu_{va2}) + (\kappa_{a2}(3\mu_d + \mu_{va2}) + \mu_d(5\mu_d + 4\mu_{va2}))\mu_{vb2} + \kappa_{a2}(2\mu_d + \mu_{va2} + \mu_{vb2}))) +$$
$$N_{va2}\beta_{aa}(-\lambda_{va2}\mu_d(\kappa_{a2} + 2\mu_d + \mu_{vb2}) + \theta_3(\kappa_{a2}\mu_d(\lambda_{va2} + 2\mu_d + 3\mu_{va2}) + \kappa_{a2}(3\mu_d + \mu_{va2})\mu_{vb2} +$$
$$\mu_d(2\mu_d(\lambda_{va2} + \mu_d) + 5\mu_d\mu_{va2} + (\lambda_{va2} + 5\mu_d + 4\mu_{va2})\mu_{vb2}) + \kappa_{a1}(2\mu_d^2 + \mu_{va2}\mu_{vb2} + 3\mu_d(\mu_{va2} + \mu_{vb2}) + \kappa_{a2}(2\mu_d + \mu_{va2} + \mu_{vb2}))) +$$
$$N_{vb2}\beta_{ba}(-\theta_4\lambda_{va2}\mu_d + \theta_3(-\lambda_{vb2}\mu_d + \theta_4(\mu_d(\lambda_{va2} + \lambda_{vb2} + 2\mu_d + 4\mu_{va2}) + 2(2\mu_d + \mu_{vb2})\mu_{vb2} + 2\kappa_{a2}$$
$$(\mu_d + \mu_{va2} + \mu_{vb2}) + 2\kappa_{a1}(\kappa_{a2} + \mu_d + \mu_{va2} + \mu_{vb2}))))))$$

$$G_4 = \kappa_{a1}\kappa_{a2}\mu_d\mu_{va2} + \kappa_{a1}\mu_d^2\mu_{va2} + \kappa_{a2}\mu_d^2\mu_{va2} + \mu_d^3\mu_{va2} + \kappa_{a1}\kappa_{a2}\mu_d\mu_{vb2} + \kappa_{a1}\mu_d^2\mu_{vb2} + \kappa_{a2}\mu_d^2\mu_{vb2} + \mu_d^3\mu_{vb2}$$
$$+ \kappa_{a1}\kappa_{a2}\mu_{va2}\mu_{vb2} + 2\kappa_{a1}\mu_d\mu_{va2}\mu_{vb2} + 2\kappa_{a2}\mu_d\mu_{va2}\mu_{vb2} + 3\mu_d^2\mu_{va2}\mu_{vb2} + \frac{1}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d}$$
$$N_{vb2}\beta_{ba}((-1+\theta_4)\lambda_{vb2}\mu_d^2(\mu_d + 2\mu_{va2}) + \theta_4(N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d)(\mu_d(\kappa_{a2} + \mu_d)\mu_{va2} + (\mu_d(\kappa_{a2} + \mu_d) +$$
$$+(\kappa_{a2} + 2\mu_d)\mu_{va2})\mu_{vb2}) + \kappa_{a1}((-1+\theta_4)\lambda_{vb2}\mu_d(\mu_d + 2\mu_{va2}) + \theta_4(N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d)((\kappa_{a2} + \mu_d)\mu_{va2} +$$
$$(\kappa_{a2} + \mu_d + \mu_{va2})\mu_{vb2}))) + N_{va2}\beta_{aa}(-\frac{\kappa_{a2}\lambda_{va2}\mu_d^2}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} + \frac{\theta_3\kappa_{a2}\lambda_{va2}\mu_d^2}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} -$$
$$\frac{\lambda_{va2}\mu_d^3}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} + \frac{\theta_3\lambda_{va2}\mu_d^3}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} + \theta_3\kappa_{a1}\kappa_{a2}\mu_{va2} + \theta_3\kappa_{a1}\mu_d\mu_{va2} + \theta_3\kappa_{a2}\mu_d\mu_{va2}$$
$$+\theta_3\mu_d^2\mu_{va2} + \theta_3\kappa_{a1}\kappa_{a2}\mu_{vb2} + \theta_2\kappa_{a1}\mu_d\mu_{vb2} + \theta_3\kappa_{a2}\mu_d\mu_{vb2} + \theta_3\mu_d^2\mu_{vb2} - \frac{\kappa_{a2}\lambda_{va2}\mu_d\mu_{vb2}}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} +$$
$$\frac{\theta_3\kappa_{a2}\lambda_{va2}\mu_d\mu_{vb2}}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} - \frac{2\lambda_{va2}\mu_d^2\mu_{vb2}}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} + \frac{2\theta_3\lambda_{va2}\mu_d^2\mu_{vb2}}{N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d} + \theta_3\kappa_{a1}\mu_{va2}\mu_{vb2} +$$
$$\theta_3\kappa_{a2}\mu_{va2}\mu_{vb2} + 2\theta_3\mu_d\mu_{va2}\mu_{vb2} + \frac{1}{(N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d)^2}N_{vb2}\beta_{ba}\mu_d(N_{va2}\beta_{aa}\theta_3(-\theta_3\lambda_{vb2}(\kappa_{a1} + \mu_d + \mu_{va2})$$
$$+\theta_4((-1+\theta_3)\kappa_{a2}\lambda_{va2} - \lambda_{va2}(\mu_d + \mu_{vb2}) + \theta_3(\lambda_{vb2}(\kappa_{a1} + \mu_d + \mu_{va2}) + \lambda_{va2}(\mu_d + \mu_{vb2})))) + N_{vb2}\beta_{ba}\theta_4(-\theta_3\lambda_{vb2}$$
$$(\kappa_{a1} + \mu_d + \mu_{va2}) + \theta_4((-1+\theta_3)\kappa_{a2}\lambda_{va2} - \lambda_{va2}(\mu_d + \mu_{vb2}) + \theta_3(\lambda_{vb2}(\kappa_{a1} + \mu_d + \mu_{va2}) + \lambda_{va2}(\mu_d + \mu_{vb2}))))$$
$$+\mu_d(-\lambda_{vb2}(-\lambda_{va2} + \theta_3(\kappa_{a1} + \lambda_{va2} + \mu_d + \mu_{va2})) + \theta_4((-1+\theta_3)\kappa_{a2}\lambda_{va2} - \lambda_{va2}(\lambda_{vb2} + \mu_d + \mu_{vb2}) +$$
$$\theta_3(\kappa_{a1}\lambda_{vb2} + \lambda_{vb2}(\mu_d + \mu_{va2}) + \lambda_{va2}(\lambda_{vb2} + \mu_d + \mu_{vb2}))))))) \quad (6.12i)$$

$$G_5 = \frac{1}{(N_{va2}\beta_{aa}\theta_3 + N_{vb2}\beta_{ba}\theta_4 + \mu_d)^2}(N_{va2}^3\beta_{aa}^3\theta_3^3(\kappa_{a1} + \mu_d)(\kappa_{a2} + \mu_d)\mu_{va2}\mu_{vb2} + (N_{vb2}\beta_{ba}\theta_4 + \mu_d)(\kappa_{a1} + \mu_d)$$
$$\mu_{va2}(N_{vb2}\beta_{ba}\beta_{aa}(-1+\theta_4)\lambda_{vb2}\mu_d^2 + (N_{vb2}\beta_{ba}\theta_4 + \mu_d)^2(\kappa_{a2} + \mu_d)\mu_{vb2}) + N_{va2}^2\beta_{aa}^2\theta_3(N_{vb2}\beta_{ba}\theta_3(-1+\theta_4)\lambda_{vb2}\mu_d \quad (6.12\,j)$$
$$(\kappa_{a1} + \mu_d)\mu_{va2} + (N_{vb2}\beta_{ba}\theta_4 + \mu_d)(\kappa_{a2} + \mu_d)((-1+\theta_3)\lambda_{va2}\mu_d + 3\theta_3(\kappa_{a1} + \mu_d)\mu_{va2})\mu_{vb2}) + N_{va2}\beta_{aa}(\mu_d^2(\kappa_{a2} + \mu_d)$$
$$((-1+\theta_3)\lambda_{va2}\mu_d + 3\theta_3(\kappa_{a1} + \mu_d)\mu_{va2})\mu_{vb2}) + N_{vb2}^2\beta_{ba}^2\theta_4(\theta_3(-1+\theta_4)\lambda_{vb2}\mu_d(\kappa_{a1} + \mu_d)\mu_{va2} + \theta_4(\kappa_{a2} + \mu_d)$$
$$((-1+\theta_3)\lambda_{va2}\mu_d + 3\theta_3(\kappa_{a1} + \mu_d)\mu_{va2})\mu_{vb2}) + N_{vb2}\beta_{ba}\mu_d((-1+\theta_4)\lambda_{vb2}\mu_d + 2\theta_3(\kappa_{a1} + \mu_d)\mu_{va2}) + 2\theta_4(\kappa_{a2} + \mu_d)$$
$$((-1+\theta_3)\lambda_{va2}\mu_d + 3\theta_3(\kappa_{a1} + \mu_d)\mu_{va2})\mu_{vb2})))$$

with

$$\theta_1 = \frac{(N_{tc}N_{va}\beta_{ac}\lambda_{va}\lambda_{vb}\mu_d - \lambda_{vb}(N_{vb}\beta_{bc} + \mu_d)(\kappa_{c1} + \mu_d)\mu_{va} + N_{va}\beta_{ac}\lambda_{va}(\kappa_{c2} + \mu_d)\mu_{vb})}{(N_{va}\beta_{ac}(N_{tc}\lambda_{va}\lambda_{vb}\mu_d + \lambda_{vb}(\kappa_{c1} + \mu_d)\mu_{va} + \lambda_{va}(\kappa_{c2} + \mu_d)\mu_{vb}))} \quad (6.13a)$$

$$\theta_2 = \frac{N_{tc}N_{vb1}\beta_{bc}\lambda_{vb1}\mu_d - (N_{va1}\beta_{ac}\theta_1 + \mu_d)(\kappa_{c2} + \mu_d)\mu_{vb1}}{N_{vb1}\beta_{bc}(N_{tc}\lambda_{vb1}\mu_d + (\kappa_{c2} + \mu_d)\mu_{vb1})} \quad (6.13b)$$

$$\theta_3 = \frac{(N_{tc}N_{va}\beta_{ac}\lambda_{va}\mu_d - \lambda_{va}(N_{vb}\beta_{bc} + \mu_d)(\kappa_{c1} + \mu_d)\mu_{vb} + N_{va}\beta_{ac}\lambda_{va}(\kappa_{c2} + \mu_d)\mu_{vb})}{(N_{va}\beta_{ac}(N_{tc}\lambda_{va}\lambda_{vb}\mu_d + \lambda_{va}(\kappa_{c1} + \mu_d)\mu_{vb} + \lambda_{va}(\kappa_{c2} + \mu_d)\mu_{vb}))} \quad (6.13c)$$

$$\theta_4 = \frac{N_{tc}N_{vb2}\beta_{bc}\lambda_{vb2}\mu_d - (N_{va2}\beta_{ac}\theta_3 + \mu_d)(\kappa_{c2} + \mu_d)\mu_{vb2}}{N_{vb2}\beta_{ba}(N_{tc}\lambda_{vb2}\mu_d + (\kappa_{a2} + \mu_d)\mu_{vb2})} \quad (6.13d)$$

From the characteristic equation (6.11a) –(6.11b) , The remaining eigenvalues are found by solving $(\eta^5 + D_1\eta^4 + D_2\eta^3 + D_3\eta^2 + D_4\eta + D_5) = 0$ in child and in adult $(\eta^5 + G_1\eta^4 + G_2\eta^3 + G_3\eta^2 + G_4\eta + G_5) = 0$. The remaining five eigenvalues have negative real parts if they satisfy Routh-Hurwitz criteria (6.12a) - (6.12j)[17], each equilibrium state is locally asymptotically stable if the following conditions are satisfied,

$$\det H_1 = T_1 > 0 \quad (6.14a)$$
$$\det H_2 = T_1T_2 - T_3 > 0 \quad (6.14b)$$
$$\det H_3 = T_1T_2T_3 - T_3^2 - T_1^2T_4 > 0 \quad (6.14c)$$
$$\det H_4 = T_1T_2T_3T_4 - T_3^2T_4 - T_1^2T_4^2 > 0 \quad (6.14d)$$
$$\det H_5 = T_1T_2T_3T_4T_5 - T_3^2T_4T_5 - T_1^2T_4^2T_5 - T_1T_2^2T_5^2 + T_2T_3T_5^2 + 2T_1T_4T_5^2 - T_5^3 > 0 \quad (6.14e)$$

We check the stability of endemic equilibrium state by using the Routh-Hurwitz conditions (6.14a) – (6.14e), we can present the above conditions by following graphs.

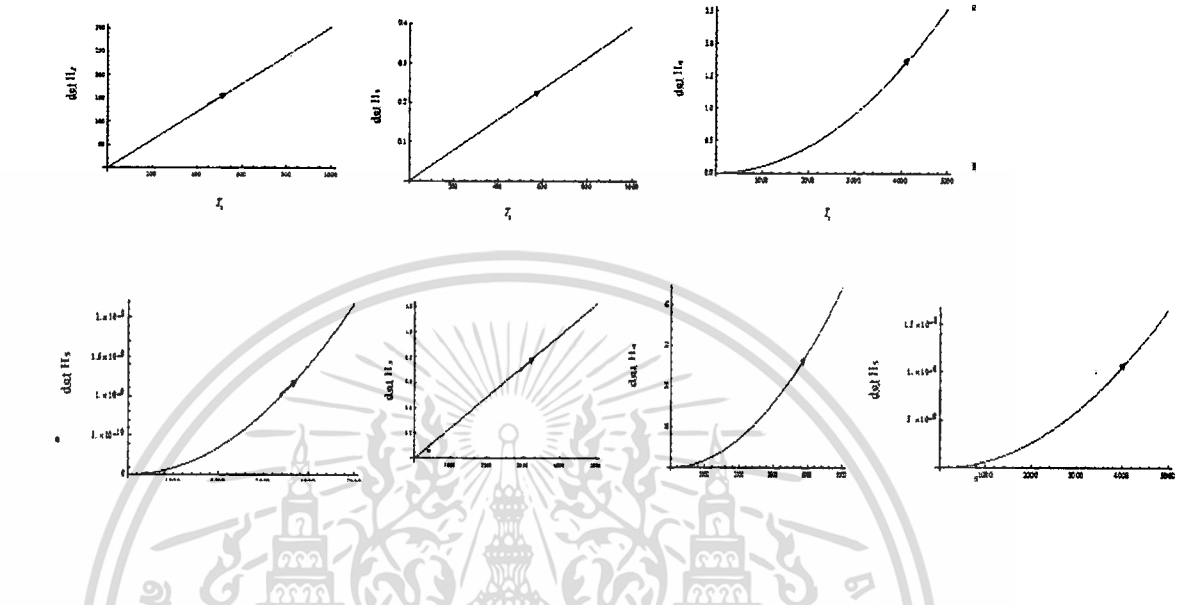


Figure6.3. The parameter spaces for endemic disease equilibrium state which satisfies the Routh-Hurwitz conditions with the value of parameters: respectively , for with $(\eta^5 + D_1\eta^4 + D_2\eta^3 + D_3\eta^2 + D_4\eta + D_5) = 0$ and $(\eta^5 + G_1\eta^4 + G_2\eta^3 + G_3\eta^2 + G_4\eta + G_5) = 0$, which satisfies the Routh-Hurwitz conditions , plotted onto ($detH_2$, κ_{c1}), (det H_3 , κ_{c1}), (det H_4 , κ_{c1}), (det H_5 , κ_{c1}), ($detH_2$, κ_{a1}), (det H_3 , κ_{a1}),(det H_4 , κ_{a1}) and (det H_5 , κ_{a1}) , respectively. The values of parameter are follows: From the above figure, the Routh-Hurwitz conditions :

a) $\kappa_{c1} = 1/(17/2), \kappa_{c2} = 1/(19/2), \mu_d = 1/(365*74.6)$ day^{-1}, $\mu_{va1} = 1/45$, $\mu_{vb1} = 1/30$, $N_{tc} = 6000$, $N_{va1} = 5000$, $N_{vb1} = 2500$, $\beta_{ac} = 0.2$, $\beta_{bc} = 0.0714$, $\lambda_{va1} = 0.00000000576$, $\lambda_{vb1} = 0.00000435$, $\alpha_a = 0.08$, $\alpha_b = 0.047$, and $N_t = 100000$.

b) $\kappa_{a1} = 1/(19/2), \kappa_{a2} = 1/(21/2), \mu_d = 1/(365*746)$ day^{-1}, $\mu_{va2} = 1/36$, $\mu_{vb2} = 1/30$, $N_{ta} = 4000$, $N_{va2} = 7000$, $N_{vb2} = 4300$, $\beta_{aa} = 0.1667$, $\beta_{ba} = 0.125$, $\lambda_{va2} = 0.00000000176$, $\lambda_{vb2} = 0.000000835$, $\alpha_a = 0.07$, $\alpha_b = 0.027$, and $N_t = 100000$. From the above figures , the Routh-Hurwitz conditions are satisfies for $E_0^* > 1$.

We consider the numerical solutions for transmission dengue virus , the main effect of introducing an age structure onto the model is to change the definition of the basic reproduction rate. Using the values of the parameters in this study are detetmined by the real life observations. The values of the parameters are as follows: $\mu_d = 1/(365*74.6)$ day^{-1}, corresponding to life expectancy of 74.6 years for human; $\kappa_{c1} = 1/(17/2)$ and $\kappa_{c2} = 1/(19/2)$ corresponding to the recovery rate of child human population due to biting of *Aedes aegypti* and *Aedes albopictus*, respectively. $\kappa_{a1} = 1/(19/2)$ and $\kappa_{a2} = 1/(21/2)$ corresponding to

the recovery rate of adult human population due to biting of *Aedes aegypti* and *Aedes albopictus*, respectively. The other parameters are arbitrary chosen. Numerical solutions of

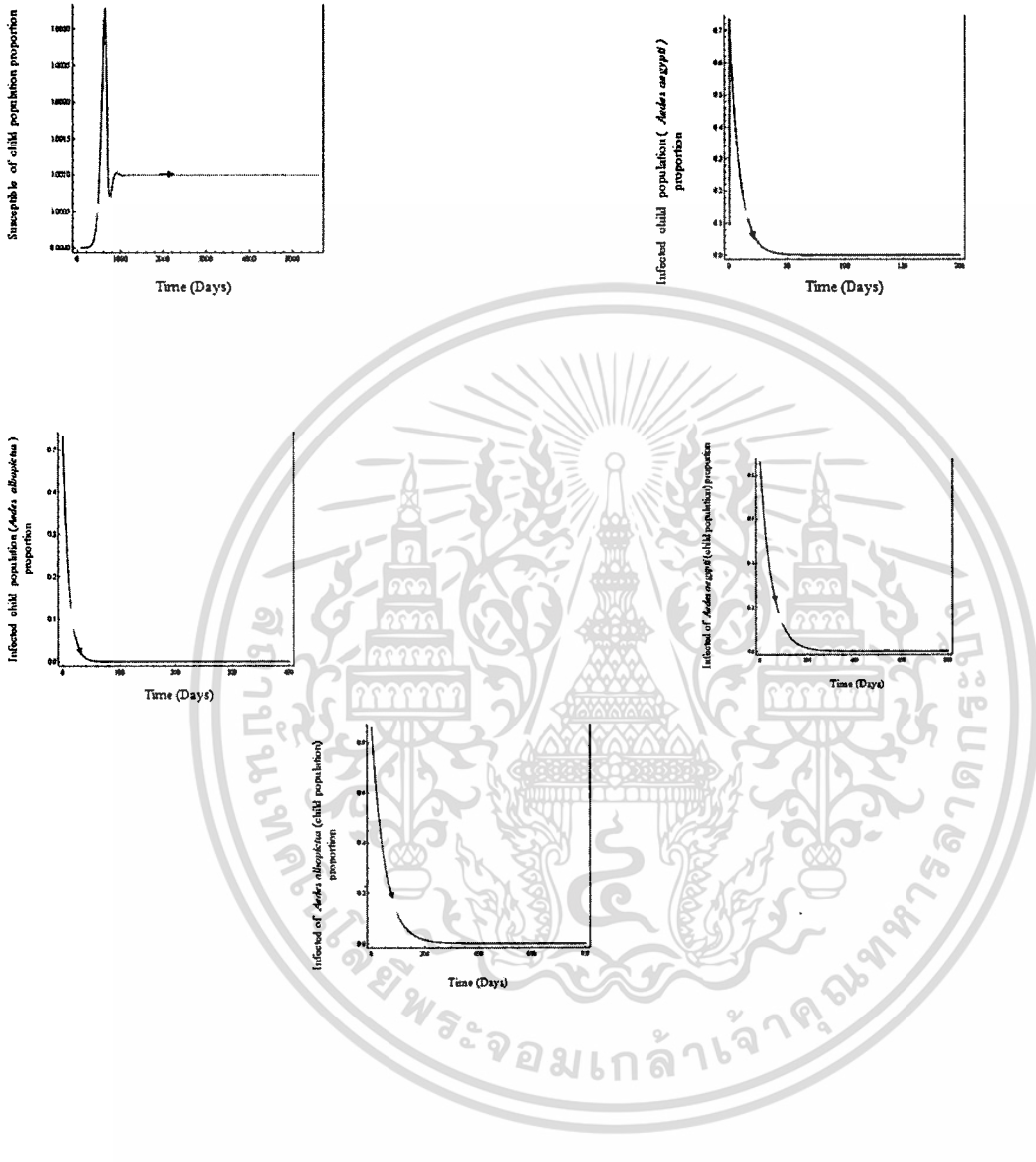


Figure6.4 . Numerical solution demonstrates the solution trajectories, projected of S_c, I_{c1} , I_{c2} , I_{va1} and I_{vb1} respectively . For $E_0^* < 1$, when S_{0c} = 0.000023944 with of parameters are: $\mu_{va1} = 1/49$, $\mu_{vb1} = 1/39$, $N_{tc} = 71000$, N_{va1} = 5800, $N_{vb1} = 10000$, $\beta_{ac} = 0.0239$, β_{bc} = 0.0333, $\lambda_{va1} = 0.00000000000347$, $\lambda_{vb1} = 0.0000\,000675$, $\alpha_a = 0.07$, $\alpha_b = 0.027$,and $N_t = 100000$ .The proportions of populations $(S_c'$, I_{c1}' , I_{c2}' , I_{va1}' , $I_{vb1}')$ approach to the disease free equilibrium state (1,0,0,0,0).

Case A.2, in child , when $\varepsilon = 0$:

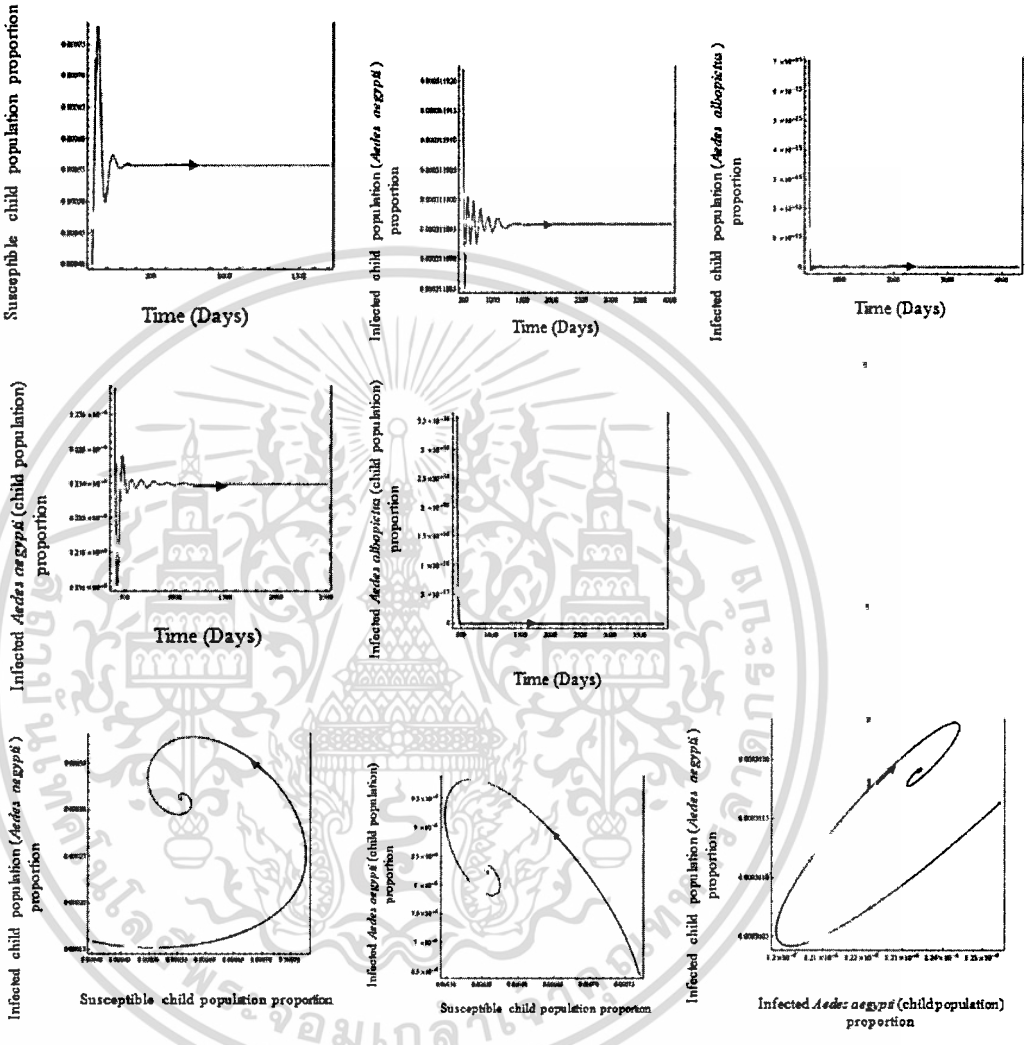


Figure6.5 . Numerical solution of yield the time series solutions of the susceptible , infected and infected vector populations. Values of parameters in the model are: $\mu_{va1} = 1/7$, $\mu_{vb1} = 1/14$, $N_{tc} = 50000$, $N_{va1} = 32000$, $N_{vb1} = 17000$, $\beta_{ac} = 0.2$, $\beta_{bc} = 0.125$, $\lambda_{va1} = 0.0000000058$, $\lambda_{vb1} = 0.00000000465$, $\alpha_a = 0.026$, $\alpha_b = 0.009$,and $N_t = 100000$, when $S_{0c} = 174.473$.

a) There are $S_c^*, I_{c1}^*, I_{c2}^*, I_{va1}^*, I_{vb1}^*$.

b) There are projected onto $(S_c^*, I_{c1}^*), (S_c^*, I_{va1}^*), (I_{va1}^*, I_{c1}^*)$.

The solutions oscillate to the endemic equilibrium state $S_c^* = 0.000556913$, $I_{c1}^* = 0.000311896$, $I_{c2}^* = 1.6622 \times 10^{-14}$, $I_{va1}^* = 8.23484 \times 10^{-6}$ and $I_{vb1}^* = 7.38289 \times 10^{-17}$,respectively.

Case B.1, in adult , when $\varepsilon = 0$:

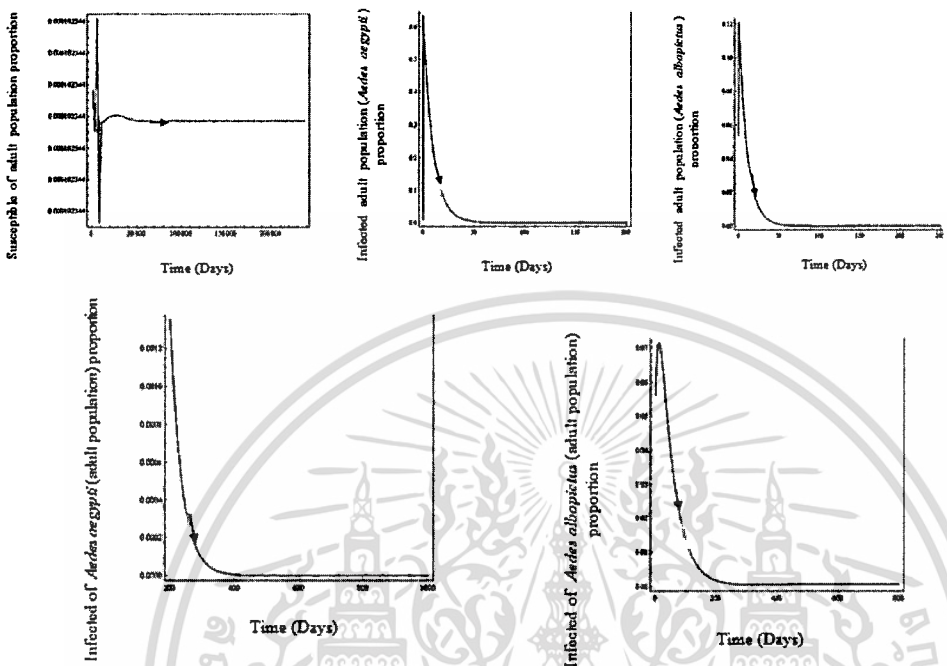


Figure6.6. Numerical solution demonstrates the solution trajectories, projected of S_a, I_{a1} , I_{a2} , I_{va2} and I_{vb2} respectively . For $E_0^* < 1$, when $S_{0a} = 0.0307919$ with of parameters are: $\mu_{va2} = 1/36$, $\mu_{vb2} = 1/46$, $N_{ta} = 61000$, $N_{va2} = 4800$, $N_{vb2} = 10000$, $\beta_{aa} = 0.03225$, $\beta_{ba} = 0.02941$, $\lambda_{va2} = 0.000000000076$, $\lambda_{vb2} = 0.000000000664$, $\alpha_a = 0.04$, $\alpha_b = 0.06$,and $N_t = 100{,}000$ .The proportions of populations $(S'_a$, I'_{a1} , I'_{a2} , I'_{va2} , $I'_{vb2})$ approach to the disease free equilibrium state (1,0,0,0,0).

Case B.2, in adult , when $\varepsilon = 0$:

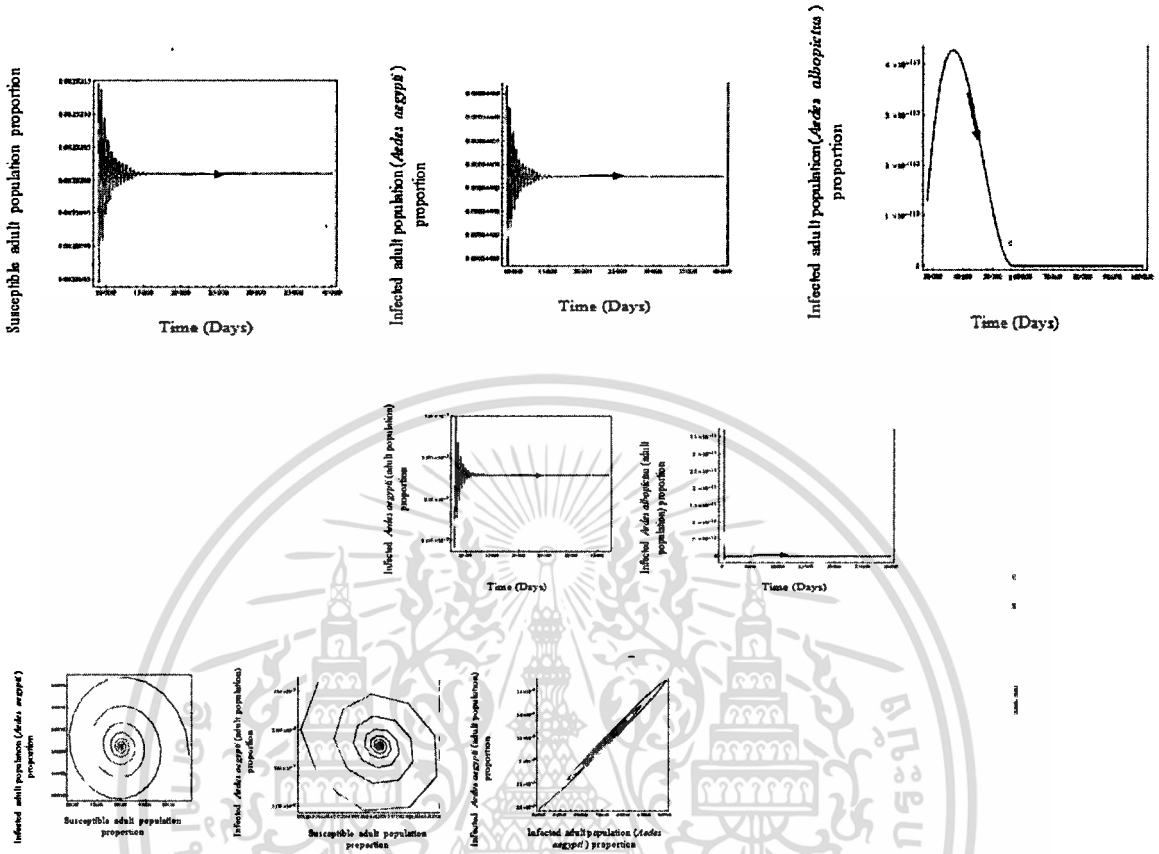


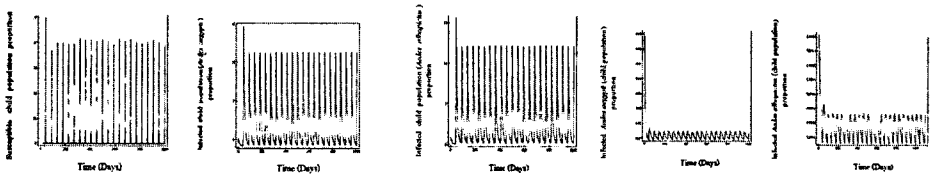
Figure6.7 . Numerical solution of yield the time series solutions of the susceptible , infected and infected vector populations. Values of parameters in the model are:
$\mu_{va2} = 1/7$, $\mu_{vb2} = 1/13$, $N_{ta} = 30000$, $N_{va2} = 37000$, $N_{vb2} = 19000$, $\beta_{aa} = 0.25$, $\beta_{ba} = 0.1428$,
$\lambda_{va2} = 0.0000000044$, $\lambda_{vb2} = 0.000000000335$, $\alpha_a = 0.02$, $\alpha_b = 0.07$, and $N_t = 100000$, when
$S_{0a} = 21.7785$.

a) There are $S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*$.

b)There are projected onto $(S_a^*, I_{a1}^*), (S_a^*, I_{va2}^*), (I_{va2}^*, I_{a1}^*)$.

The solutions oscillate to the endemic equilibrium state
$S_c^* = 0.0123201$, $I_{c1}^* = 0.0003444$, $I_{c2}^* = 6.9961 \times 10^{-14}$, $I_{val}^* = 3.18294 \times 10^{-7}$ and $I_{vb1}^* = 1.40069 \times 10^{-16}$,respectively.

Case C , in child , when $\varepsilon \neq 0$:



a)

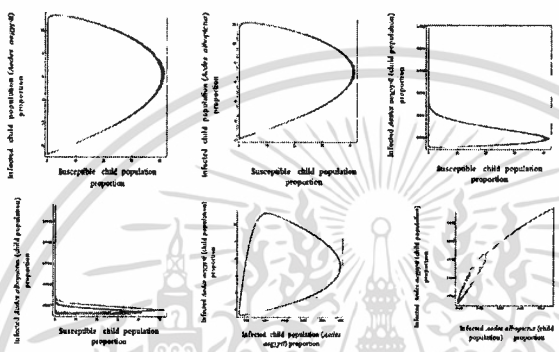


Figure6.8. Numerical solution of yield the time series solutions of the susceptible , infected and infected vector populations. Values of parameters in the model are: $\mu_{va1}=1/7$, $\mu_{vb1}=1/14$, $N_{tc}=50000$, $N_{va1}=32000$, $N_{vb1}=17000$, $\beta_{ac}=0.2$, $\beta_{bc}=0.125$, $\lambda_{va1}=0.0000000028$, $\lambda_{vb1}=0.000000000165$, $\alpha_a=0.005$, $\alpha_b=0.004$, and $N_t=100000$, when $S_{0c}=22.8627$.

a) There are $S_c^*, I_{c1}^*, I_{c2}^*, I_{va1}^*, I_{vb1}^*$.

b)There are projected onto $(S_c^*, I_{c1}^*), (S_c^*, I_{c2}^*), (S_c^*, I_{va1}^*), (S_c^*, I_{vb1}^*), (I_{va1}^*, I_{c1}^*), (I_{va1}^*, I_{vb1}^*)$.

The solutions oscillate to the endemic equilibrium state . The behaviors of $(S_c^*, I_{c1}^*, I_{c2}^*, I_{va1}^*, I_{vb1}^*)$ are limit cycles.

Case D , in adult , when $\varepsilon \neq 0$

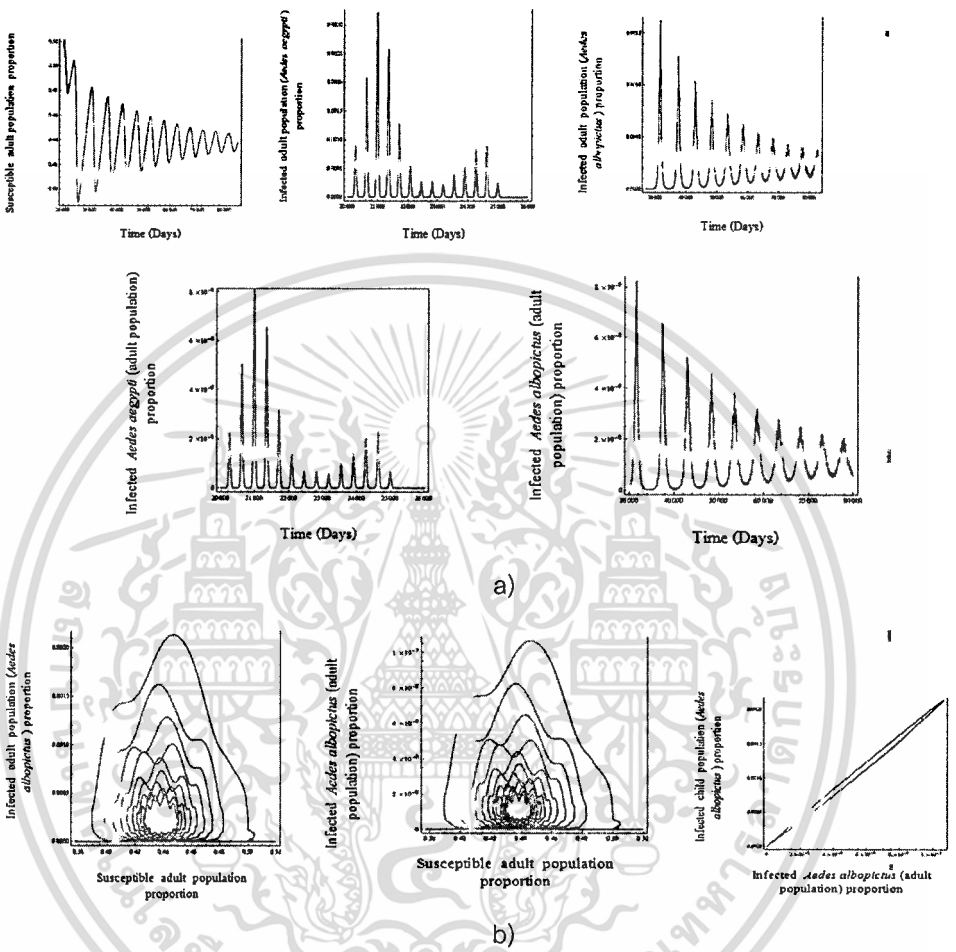


Figure6.9 . Numerical solution of yield the time series solutions of the susceptible , infected and infected vector populations. Values of parameters in the model are: $\mu_{va2}=1/7$, $\mu_{vb2}=1/16$, $N_{ta}=50000$, $N_{va2}=34000$, $N_{vb2}=30000$, $\beta_{aa}=0.25$, $\beta_{ba}=0.1428$, $\lambda_{va2}=0.0000000075$, $\lambda_{vb2}=0.000000000625$, $\alpha_a=0.02$, $\alpha_b=0.07$,and $N_t=100000$; when $S_{0a}=9.26764$.

a) There are $S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*$.

b) There are projected onto $(S_a^*, I_{a2}^*), (S_a^*, I_{vb2}^*), (I_{vb2}^*, I_{a2}^*)$.

The solutions oscillate to the endemic equilibrium state . The behaviors of $(S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*)$ are limit cycles.

Several investigations have been conducted using the SIR and SI model. The Particular SIR and SI model which proves most suitable for the states of child and adult in

two mosquitoes (*Aedes aegypti* and *Aedes albopictus*) are the model in obtained appropriate for the data reported in Thailand. We describe the result :

A1. S_0

In addition , the basic reproduction number of model (6.4a) – (6.4j) is defined as follows :

$$S_0 = \max \left\{ \frac{2N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{va1}\rho_{vb} + N_{va1}\beta_{ac}\lambda_{va1}(2(N_{tc}\lambda_{vb1}\mu_d + (\kappa_{c2}+\mu_d)\mu_{vb1})(2+\alpha_a\rho_{va}) + 2N_{tc}\lambda_{vb1}\mu_d(\alpha_a+\rho_{va}))}{(2\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{va1}(2\mu_d + N_{vb1}\beta_{bc}(2+\alpha_b\rho_{vb})) + 2N_{va1}\beta_{ac}\lambda_{va1}(\alpha_a(\kappa_{c2}+\mu_d)\mu_{vb1}\rho_{va} + N_{tc}\lambda_{vb1}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb})))}, \right.$$

$$\left. \frac{2N_{vb2}\alpha_b\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{va2}\rho_{vb} + N_{va2}\beta_{aa}\lambda_{va2}(2(N_{ta}\lambda_{vb2}\mu_d + (\kappa_{a2}+\mu_d)\mu_{vb2})(2+\alpha_a\rho_{va}) + 2N_{ta}\lambda_{vb2}\mu_d(\alpha_a+\rho_{va}))}{(2\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{va2}(2\mu_d + N_{vb2}\beta_{ba}(2+\alpha_b\rho_{vb})) + 2N_{va2}\beta_{aa}\lambda_{va2}(\alpha_a(\kappa_{a2}+\mu_d)\mu_{vb2}\rho_{va} + N_{ta}\lambda_{vb2}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb})))} \right\}$$

Searching for S_0 this rate shows how many infections will occur among child and adult as a result of an infection by a mosquitoes. Using the initial values and parameter values from data , the obtained result of threshold parameter value S_0 for S_{0c} and S_{0a} can be rewritten in mathematical form as follows:

$$S_{0c} = \frac{2N_{vb}\alpha_b\beta_{bc}\lambda_{vb}(\kappa_{c1}+\mu_d)\mu_{va}\rho_{vb} + N_{va}\beta_{ac}\lambda_{va}(2(N_{tc}\lambda_{vb}\mu_d + (\kappa_{c2}+\mu_d)\mu_{vb})(2+\alpha_a\rho_{va}) + 2N_{tc}\lambda_{vb}\mu_d(\alpha_a+\rho_{va}))}{(2\lambda_{vb}(\kappa_{c1}+\mu_d)\mu_{va}(2\mu_d + N_{vb}\beta_{bc}(2+\alpha_b\rho_{vb})) + 2N_{va}\beta_{ac}\lambda_{va}(\alpha_a(\kappa_{c2}+\mu_d)\mu_{vb}\rho_{va} + N_{tc}\lambda_{vb}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb})))}$$ in child

$$S_{0a} = \frac{2N_{va}\alpha_b\beta_{ba}\lambda_{vb}(\kappa_{a1}+\mu_d)\mu_{va}\rho_{vb} + N_{va}\beta_{aa}\lambda_{va}(2(N_{ta}\lambda_{vb}\mu_d + (\kappa_{a2}+\mu_d)\mu_{vb})(2+\alpha_a\rho_{va}) + 2N_{ta}\lambda_{vb}\mu_d(\alpha_a+\rho_{va}))}{(2\lambda_{va}(\kappa_{a1}+\mu_d)\mu_{va}(2\mu_d + N_{vb}\beta_{ba}(2+\alpha_b\rho_{vb})) + 2N_{va}\beta_{aa}\lambda_{va}(\alpha_a(\kappa_{a2}+\mu_d)\mu_{vb}\rho_{va} + N_{ta}\lambda_{vb}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb})))}$$ in adult

The reproductive rate depends on the number of infected mosquitoes I_{va1}, I_{vb1} in child and I_{va2}, I_{vb2} in adult . Determination of value S_0 depends on the value of I_{va1}, I_{vb1} in child and I_{va2}, I_{vb2} in adult by replacing some of the different values show in Table 1, the difference between these values .

I_{va1} value	I_{vb1} value	I_{va2} value	I_{vb2} value	S_0 value
0.00	0.00036	-	-	0.06795
-	-	2.3860x1	$6.44744\text{x}10^{-7}$	0.00310
2.5065	1.4099	0^{-18}	-	187.646
-	-	8.96405	6.10816	416.752

Table 6.1. Determination of the values S_0 of infected mosquitoes

Above , if the number of infected of mosquitoes is less than one $I_{va1} < 1$, $I_{vb1} < 1$ and $I_{va2} < 1, I_{vb2} < 1$, then the values $S_0 < 1$. If the number of infected of mosquitoes is more than one $I_{va1} > 1$, $I_{vb1} > 1$ and $I_{va2} > 1, I_{vb2} > 1$, then the values $S_0 > 1$, so that the transmission of dengue virus cased more than one person to be infected with dengue virus.

A2. We consider value are α_a , α_b , ρ_{va} *and* ρ_{vb} in (6.4a) – (6.4j) . The value of them , Be the change of transmitting disease dengue. Which we use numbers instead of parameters in the model such values as follows : $\alpha_a = 0.2$, $\alpha_b = 0.4$, $\rho_{va} = 0.02$, $\rho_{vb} = 0.1$ in child and

$\alpha_a = 0.4$, $\alpha_b = 0.07$, $\rho_{va} = 0.7$, $\rho_{vb} = 0.01$ in adult. The solution of the system model (6.4a) – (6.4j) oscillate to the limit cycle occurs for α_a, α_b, ρ_{va} *and* ρ_{vb}. Thus the dynamic behaviors of age structured populations occur while the seasonal variation of the mosquitoes (*Aedes aegypti* and *Aedes albopictus*) ,So that, It can be seen that the dynamic behavior of the endemic state change while the influence of the model.

4.7. แบบจำลองที่ 7 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงชนิดของยุงลายและฤดูกาล [62]

In recent decades, mathematical models were developed to investigate the infectious epidemiology. Most of the models incorporate several factors of the disease to predict the possible magnitude of the outbreaks. The moisture content, temperature, season and rainfall are influence to the mosquito development. Dengue infection is endemic in Thailand. From the data of Dengue cases rate and deaths rate in 2001 – 2013, we can see that most dengue patients are occurred in rainy season. We can see as shown in figure 7.1.

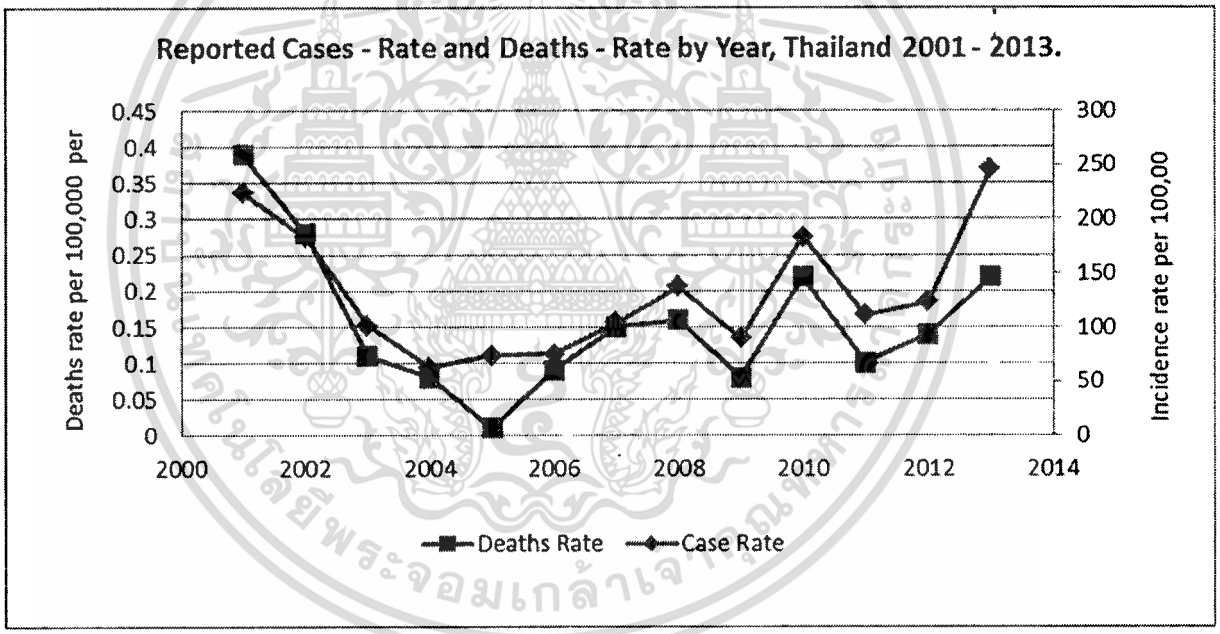


Figure7.1. The reports cases rate and deaths rate of dengue disease in Thailand by year during 2001 – 2013.[Ministry of public health, 2001-2013]

In this paper, we develop the transmission of dengue disease by formulating the mathematical models. We used SIRS model for analyzing and finding the method to decrease the outbreak of this disease. We analyze dengue model of seasonality compartment (rainy season, winter season and summer season).

The model consists of the standard SIRS model, where S, I ,R denote the number of susceptible, infectious, and recovered hosts, respectively. The mathematical modeling for dengue disease describes the relevance of human and mosquito population. In this study, we assume that the total human and mosquito population have constant sizes. Hence, the set of ordinary differential equations (ODEs) representing the *SIRS* model is given by:

The dynamics of human population are given by

$$\frac{d\bar{S}_r}{dt} = RN_T - \tau \frac{b_{v\to hr}}{N_{Tr}+g}\bar{I}_v\bar{S}_r - \eta_d\bar{S}_r + \theta\bar{R}_r \quad (7.1a)$$

$$\frac{d\bar{I}_r}{dt} = \tau \frac{b_{v\to hr}}{N_{Tr}+g}\bar{I}_v\bar{S}_r - \eta_d\bar{I}_r - \gamma\bar{I}_r \quad (7.1b)$$

$$\frac{d\bar{R}_r}{dt} = \gamma\bar{I}_r - \eta_d\bar{R}_r - \theta\bar{R}_r \quad (7.1c)$$

$$\frac{d\bar{S}_w}{dt} = WN_T - \tau \frac{b_{v\to hw}}{N_{Tw}+g}\bar{I}_v\bar{S}_w - \eta_d\bar{S}_w + \theta\bar{R}_w \quad (7.1d)$$

$$\frac{d\bar{I}_w}{dt} = \tau \frac{b_{v\to hw}}{N_{Tw}+g}\bar{I}_v\bar{S}_w - \eta_d\bar{I}_w - \gamma\bar{I}_w \quad (7.1e)$$

$$\frac{d\bar{R}_w}{dt} = \gamma\bar{I}_w - \eta_d\bar{R}_w - \theta\bar{R}_w \quad (7.1f)$$

$$\frac{d\bar{S}_s}{dt} = SN_T - \tau \frac{b_{v\to hs}}{N_{Ts}+g}\bar{I}_v\bar{S}_s - \eta_d\bar{S}_s + \theta\bar{R}_s \quad (7.1g)$$

$$\frac{d\bar{I}_s}{dt} = \tau \frac{b_{v\to hs}}{N_{Ts}+g}\bar{I}_v\bar{S}_s - \eta_d\bar{I}_s - \gamma\bar{I}_s \quad (7.1h)$$

$$\frac{d\bar{R}_s}{dt} = \gamma\bar{I}_s - \eta_d\bar{R}_s - \theta\bar{R}_s \quad (7.1i)$$

The variables are defined as follows: $\bar{S}_r$ is the number of susceptible human population in rainy season, $\bar{I}_r$ is the number of infectious human population in rainy season, $\bar{R}_r$ is the number of recovered human population in rainy season, $\bar{S}_w$ is the number of susceptible human population in winter season, $\bar{I}_w$ is the number of infectious human population in winter season, $\bar{R}_w$ is the number of recovered human population in winter season, $\bar{S}_s$ is the number of susceptible human population in summer season, $\bar{I}_s$ is the number of infectious human population in summer season, $\bar{R}_s$ is the number of recovered human population in summer season.

The dynamics of the mosquito population are given by :

$$\frac{d\bar{S}_v}{dt} = V - (\tau(\frac{b_{hr\to v}}{N_{Tr}+g}\bar{I}_r) + \tau(\frac{b_{hw\to v}}{N_{Tw}+g}\bar{I}_w) + \tau(\frac{b_{hs\to v}}{N_{Ts}+g}\bar{I}_s))\bar{S}_v - \eta_d\bar{S}_v \quad (7.2a)$$

$$\frac{d\bar{I}_v}{dt} = (\tau(\frac{b_{hr\to v}}{N_{Tr}+g}\bar{I}_r) + \tau(\frac{b_{hw\to v}}{N_{Tw}+g}\bar{I}_w) + \tau(\frac{b_{hs\to v}}{N_{Ts}+g}\bar{I}_s))\bar{S}_v - \eta_d\bar{I}_v \quad (7.2b)$$

we define

Table1: Definitions of variables and parameters for our model.

variable/parameter	definition
$\bar{S}_v$	the number of susceptible mosquito population
$\bar{I}_v$	the number of infectious mosquito population
N_T	the total human population
N_{Tr}	the total human population in rainy season

N_{Tw}	the total human population in winter season
N_{Ts}	the total human population in summer season
N_v	the total mosquito population
η_d	the natural death rate of human population
R	the birth rate of human population in rainy season
W	the birth rate of human population in winter season
S	the birth rate of human population in summer season
$b_{v\to hr}$	the transmission probability of dengue disease from mosquito to human in rainy season
$b_{v\to hw}$	the transmission probability of dengue disease from mosquito to human in winter season
$b_{v\to hs}$	the transmission probability of dengue disease from mosquito to human in summer season
$b_{v\to hs}$	the transmission probability of dengue disease from mosquito to human in summer season
$b_{hr\to v}$	the transmission probability of dengue disease from human to mosquito in rainy season
$b_{hw\to v}$	the transmission probability of dengue disease from human to mosquito in winter season
$b_{hs\to v}$	the transmission probability of dengue disease from human to mosquito in summer season
γ	the recovery rate of human population
τ	the biting rate of mosquito population
θ	the infection rate of human population
g	the number of other animals available as blood sources

We suppose that $N_r=\bar{S}_r+\bar{I}_r+\bar{R}_r$, $N_w=\bar{S}_w+\bar{I}_w+\bar{R}_w$, $N_s=\bar{S}_s+\bar{I}_s+\bar{R}_s$ and $N_v=\bar{S}_v+\bar{I}_v$.

We assume the total human and mosquito populations have constant sizes $\frac{dN_{Tr}}{dt}=0$ in rainy season, $\frac{dN_{Tw}}{dt}=0$ in winter season, $\frac{dN_{Ts}}{dt}=0$ in summer season and $\frac{dN_v}{dt}=0$.

$S_r=\frac{\bar{S}_r}{N_{Tr}}$, $I_r=\frac{\bar{I}_r}{N_{Tr}}$, $R_r=\frac{\bar{R}_r}{N_{Tr}}$, $S_w=\frac{\bar{S}_w}{N_{Tw}}$, $I_w=\frac{\bar{I}_w}{N_{Tw}}$, $R_w=\frac{\bar{R}_w}{N_{Tw}}$, $S_s=\frac{\bar{S}_s}{N_{Ts}}$, $I_s=\frac{\bar{I}_s}{N_{Ts}}$, $R_s=\frac{\bar{R}_s}{N_{Ts}}$,

$S_v=\frac{\bar{S}_v}{N_v}$, $I_v=\frac{\bar{I}_v}{N_{vr}}$

The total human and mosquito populations have constant sizes. Thus rates of change for human and mosquito populations equal to zero. Thus, the birth and death rates are equivalent for human populations , the total mosquito equal to $\frac{V}{\eta_v}$.

The reduced equations become :

$$\frac{dS_r}{dt}=R-\tau\frac{b_{v\to hr}}{N_{Tr}+g}I_v\left(\frac{V}{\eta_v}\right)S_r-\eta_d S_r+\theta(1-S_r-I_r) \qquad (7.3a)$$

$$\frac{dI_r}{dt} = \tau \frac{b_{v\to hr}}{N_{Tr}+g} I_v \left(\frac{V}{\eta_v}\right) S_r - \eta_d I_r - \gamma I_r \qquad (7.3b)$$

$$\frac{dS_w}{dt} = W - \tau \frac{b_{v\to hw}}{N_{Tw}+g} I_v \left(\frac{V}{\eta_v}\right) S_w - \eta_d S_w + \theta(1 - S_w - I_w) \qquad (7.3c)$$

$$\frac{dI_w}{dt} = \tau \frac{b_{v\to hw}}{N_{Tw}+g} I_v \left(\frac{V}{\eta_v}\right) S_w - \eta_d I_w - \gamma I_w \qquad (7.3d)$$

$$\frac{dS_s}{dt} = S - \tau \frac{b_{v\to hs}}{N_{Ts}+g} I_v \left(\frac{V}{\eta_v}\right) S_s - \eta_d S_s + \theta(1 - S_s - I_s) \qquad (7.3e)$$

$$\frac{dI_s}{dt} = \tau \frac{b_{v\to hs}}{N_{Ts}+g} I_v \left(\frac{V}{\eta_v}\right) S_s - \eta_d I_s - \gamma I_s \qquad (7.3f)$$

$$\frac{dI_v}{dt} = \left(\tau\left(\frac{b_{hr\to v}}{N_{Tr}+g} I_r N_{Tr}\right) + \tau\left(\frac{b_{hw\to v}}{N_{Tw}+g} I_w N_{Tw}\right) + \tau\left(\frac{b_{hs\to v}}{N_{Ts}+g} I_s N_{Ts}\right)\right) S_v - \eta_d I_v \qquad (7.3g)$$

from conditions $S_r + I_r + R_r = 1$, $S_w + I_w + R_w = 1$, $S_s + I_s + R_s = 1$ and $S_v + I_v = 1$.

Analysis of the Mathematical Model

From the above equations, we find two equilibrium states; the disease free equilibrium state $A_0 = (1,0,1,0,1,0,0)$ and the endemic disease equilibrium state $A_1 = (S_r', I_r', S_w', I_w', S_s', I_s', I_v')$ where

$$S_r' = \frac{(\gamma+\eta_d)\eta_v(R+\theta)}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_1}$$

$$I_r' = \frac{I_v' V(R+\theta)\tau\varpi_1}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_1}$$

$$S_w' = \frac{(\gamma+\eta_d)\eta_v(W+\theta)}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_2}$$

$$I_w' = \frac{I_v' V(W+\theta)\tau\varpi_2}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_2}$$

$$S_s' = \frac{(\gamma+\eta_d)\eta_v(S+\theta)}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_3}$$

$$I_s' = \frac{I_v' V(R+\theta)\tau\varpi_3}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_3}$$

and

$$I_v' = 1 - \frac{\eta_v}{\eta_v I_r' N_{Tr}\eta_1\tau + \eta_v I_w' N_{Tw}\eta_2\tau + \eta_v I_s' N_{Ts}\eta_3\tau}$$

with

$$\varpi_1 = \frac{b_{v\to hr}}{N_{Tr}+g}, \quad \varpi_2 = \frac{b_{v\to hw}}{N_{Tw}+g}, \quad \varpi_3 = \frac{b_{v\to hs}}{N_{Ts}+g},$$

$$\eta_1 = \frac{b_{hr\to v}}{N_{Tr}+g}, \quad \eta_2 = \frac{b_{hw\to v}}{N_{Tw}+g}, \quad \eta_3 = \frac{b_{hs\to v}}{N_{Ts}+g},$$

The reproductive number, E_0 is defined by $E_0 = \frac{\sum_{i=1}^{\alpha} \eta_i \varpi_i N_{T_i}}{N_T}$. The parameters are defined as follows: $\eta_d = 1/(365*74.61), \gamma = 1/4.5, \theta = 1/((180+365)/2)$. We suppose that $\gamma_1 = <N_T><\eta_i><\varpi_i>\tau^2$. Thus, we obtain $E_0 = \frac{3.961x10^{25}\gamma_1}{8.8083x10^{22}}$. $<N_T>$ the weighted average defined as $<N_T> = N_{Tr} + N_{Tw} + N_{Ts}$, $<\eta_i>$ when $i = 1,2,3$ and $<\varpi_i>$ when $i = 1,2,3$. Which is η_i the efficiency of the transmission of the dengue virus to the mosquito from human in each season (rainy, winter, summer).

We are interested in transmission of dengue disease with the season. The values of the parameter used in this study are as follows: $\eta_d = 1/(365*74.61)$ per day corresponds to a life expectancy of 74.61 years in human. The other parameters are arbitrarily chosen. We presented the numerical solutions of (7.3a) – (7.3g) for endemic equilibrium state on the follows figures.

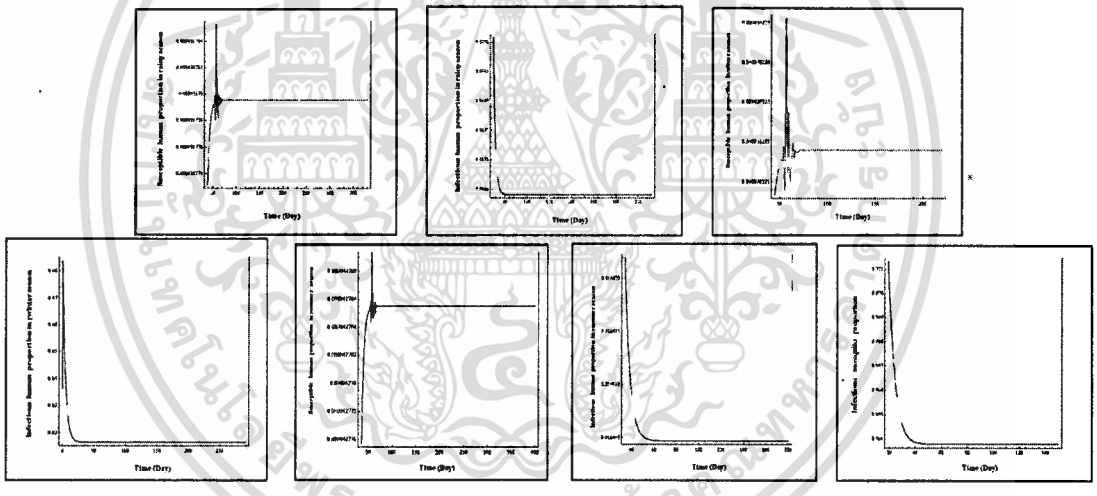


Figure 7.2. Numerical solutions of (7.3a)-(7.3g), demonstrate the times series of each human population, for $E_0 > 1$ in rainy season, in winter and in summer. $N_{tr} = 190{,}000$, $N_{tw} = 95{,}000$, $N_{ts} = 30{,}000$, $N_v = 20{,}000$, $\eta_d = 1/(365*74.61)$, $\gamma = 1/4.5$, $\tau = 35$, $\eta_v = 1/4$, $\theta = 1/((180+365)/2)$, $g = 3{,}800$ and $R_0 = 2.13674$.

From the above figures we can see that the solutions converge to the disease free state for $E_0 < 1$. If $E_0 > 1$ the solutions oscillate to the disease endemic state.

When the value of E_0 is lowered such as lowering the weighted average efficacy $<\varpi_i>$ or changing the transmission probability of dengue disease from mosquito to human $<\eta_i>$ or changing the transmission probability of dengue disease from human to mosquito in the

difference season. The incidence rate at the equilibrium state A_0 , can be determined by setting the time rate of change of the different season (by using equations 7.3a – 7.3g) and the equivalent equations for the infected and recovered to zero.

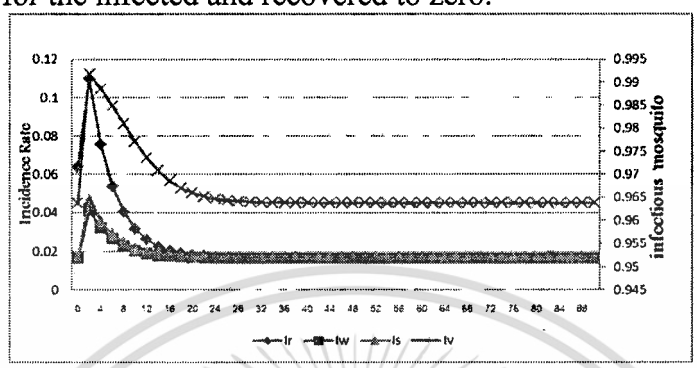


Figure 3. The value of solutions of each human population, for in infective rainy season, winter season and summer season. $\eta_d = 1/(365*74.61), \gamma = 1/4.5, \eta_v = 1/4, \theta = 1/((180+365)/2)$.

From Figure 7.3, the variables are $\bar{I}_r, \bar{I}_w, \bar{I}_s$ and $\bar{I}_v$. The number of infectious mosquito population affect the value of $\bar{I}_r, \bar{I}_w$ and $\bar{I}_s$. When are the number of infectious mosquito population increase will do the number of infectious population of different season.

4.8. แบบจำลองที่ 8 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงประเภทของการเกิดโรคไข้เลือดออก [63]

We analyze the data of dengue cases in Thailand between 1992 and 2012 by fitting curves. We denote x_i as the i^{th} year and $f(x_i)$ as the number of dengue cases (DF, DHF,DSS) of i^{th} year .Here, we use the polynomial curve fitting to find the best analytical approximated equations.

Consider the general form of Polynomial order j

$$f(x_i) = a + b_1 x_i + b_2 x_i^2 + b_3 x_i^3 + \ldots + b_j x_i^j = a + \sum_{k=1}^{j} b_k x_i^k \qquad (8.1)$$

where a, $b_1, b_2, \ldots, bj$ are some coefficients; i = 1,2,3,…,n and n is the total data sets. Error-Least squares approach is the method to find the general form of the Error -Least squares approach. We define

$$err = \sum_{i=1}^{n} (d_i)^2 \qquad (8.2)$$

where $d_i = y_i - f(x_i)$; i = 1,2,3,…,n; y_i is the real data of dengue cases in each year and $f(x_i)$ is the approximated number of dengue cases from fitting curves.

Thus,

$$err = \sum_{i=1}^{n} (y_i - f(x_i))^2 \qquad (8.3)$$

then we obtain;

$$err = \sum_{i=1}^{n} (y_i - (a + \sum_{k=1}^{j} b_k x_i^k))^2 \qquad (8.4)$$

Coefficient of determination is the proportion of variability in a data set. The value of R^2 is always positive and it is between 0 and 1. If this value is closed to 1, then the model is appropriated. We define

$$R^2 = \frac{\sum_{i=1}^{n}(f(x_i)-\bar{y})^2}{\sum_{i=1}^{n}(y_i-\bar{y})^2} \qquad (8.5)$$

where $\bar{y}$ is the average of real data. From the data of dengue cases (DF, DHF,DSS), we found the polynomial equations and coefficient of determination (R^2) as follows:

Polynomial equations	R^2
$0.2497x^2 - 0.2908x + 27.197$	0.3871
$0.0033x^3 + 0.1797x^2 + 0.1159x + 26.637$	0.3872
$-0.0776x^4 + 2.1759x^3 - 19.895x^2 + 68.243x - 36.679$	0.6209
$0.0208x^5 - 0..8073x^4 + 11.453x^3 - 71.702x^2 + 188.68x + 121.74$	0.7743
$-0.0011.x^6 + 0.068x^5 - 1.15714x^4 + 17.452x^3 - 95.067x^2 + 229.68x - 145.46$	0.778

Table 1. Polynomial equations and R^2 of DF cases by year (2000 – 2012)

Polynomial equations	R^2
$0.468x^2 - 9.0354x + 105.69$	0.0834
$0.1337x^3 - 2.3393x^2 + 7.2739x + 83.235$	0.1031
$-0.1925x^4 + 5.5232x^3 - 52.138x^2 + 176.27x - 73.831$	0.4993
$0.056x^5 - 2.1508x^4 + 30.422x^3 - 191.18x^2 + 499.5x + 302.12$	0.8036
$-0.0115x^6 + 0.5402x^5 - 10.001x^4 + 92.048x^3 - 431.21x^2 + 920.72x + 545.86$	0.9117

Table 2. Polynomial equations and R^2 of DHF cases by year (2000 – 2012)

Polynomial equations	R^2
$0.0213x^2 - 0.3056x + 3.1742$	0.0402
$0.0032x^3 - 0.046x^2 + 0.0851x + 2.6362$	0.0495
$-0.0077x^4 + 0.22x^3 - 2.0495x^2 + 6.8846x - 3.6831$	0.5755
$0.0013x^5 - 0.053x^4 + 0.7956x^3 - 5.2638x^2 + 14.357x - 8.9605$	0.7089
$-0.0002x^6 + 0.0106x^5 - 0.2032x^4 + 1.9749x^3 - 9.8569x^2 + 22.417x - 13.625$	0.7414

Table 3. Polynomial equations and R^2 of DSS cases by year (2000 – 2012)

Polynomial equations	R^2
$-0.000004x^2 + 0.0006x - 0.0013$	0.0013
$-0.0000008x^3 + 0.0002x^2 - 0.0006x\,0.0004$	0.4
$-0.0000002x^4 - 0.000006x^3 + 0.0007x^2 - 0.0025x + 0.0023$	0.4712

$0.00000009x^5 - 0.000003x^4 + 0.0004x^3 - 0.002x^2 + 0.0041x - 0.0026$	0.6631
$-0.000000002x^6 + 0.0000002x^5 - 0.000005x^4 + 0.0005x^3 - 0.0026x^2 + 0.0052x - 0.0032$	0.6642

Table 4. Polynomial equations and R^2 of DF deaths by year (2000 – 2012)

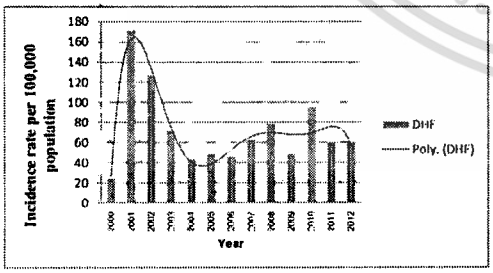
Polynomial equations	R^2
$0.0006x^2 - 0.0106x + 0.0788$	0.1412
$0.0001x^3 - 0.0017x^2 + 0.0029x + 0.0602$	0.1649
$-0.000009x^4 + 0.0025x^3 - 0.024x^2 + 0.0784x - 0.01$	0.3036
$0.000005x^5 - 0.0018x^4 + 0.024x^3 - 0.1441x^2 + 0.3578x - 0.2073$	0.7019
$-0.000001x^6 + 0.0005x^5 - 0.0088x^4 + 0.0798x^3 - 0.3595x^2 + 0.7356x - 0.4259$	0.8544

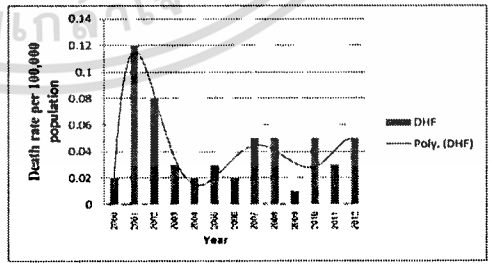
Table 5. Polynomial equations and R^2 of DHF deaths by year (2000 – 2012)

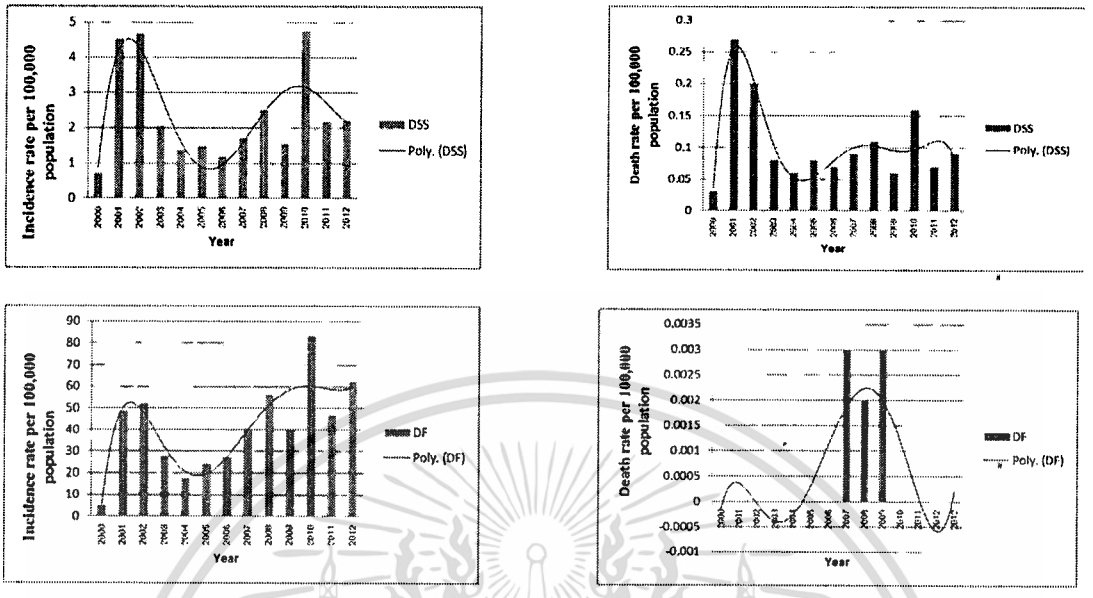
Polynomial equations	R^2
$0.0008x^2 - 0.0147x + 0.1606$	0.0796
$0.0002x^3 - 0.0033x^2 + 0.0091x + 0.1278$	0.0944
$-0.0003x^4 + 0.0084x^3 - 0.0788x^2 + 0.2653x - 0.1103$	0.415
$0.000009x^5 - 0.0036x^4 + 0.05x^3 - 0.3112x^2 + 0.8056x - 0.4918$	0.7144
$-0.000002x^6 + 0.001x^5 - 0.0176x^4 + 0.1605x^3 - 0..7418x^2 + 1.5612x - 0.9291$	0.837

Table 6. Polynomial equations and R^2 of DSS deaths by year (2000 – 2012)

From the above tables, the appropriated equations are 6 th order polynomial equations because R^2 converges to 1.







a) b)

Figure8.1 The real data and the corresponding fitted curves of dengue disease (DHF,DSS ,DF) in Thailand (a)Cases and (b) Deaths by Year).

Mathematical Model

In this study, we assume that the total human and mosquito populations have constant sizes. The human population is divided into susceptible, infected and recovered classes. The model considers transmission of dengue virus in human and mosquito population:

The dynamics of human population are given by

$$\frac{d}{dx}Ds(t) = \gamma P_h - \tau_h Ds(t) - \alpha_1 \frac{\theta \varpi_{FH}}{P_h + c} Ds(t) Ai(t) - (1-\alpha_1)\frac{\theta \varpi_{HH}}{P_h + c} Ds(t) Ai(t) \quad (8.6.1)$$

$$\frac{d}{dx}Fi(t) = \alpha_1 \frac{\theta \varpi_{FH}}{P_h + c} Ds(t) Ai(t) - \tau_h Fi(t) - \delta_1 Fi(t) \quad (8.6.2)$$

$$\frac{d}{dx}Hi(t) = (1-\alpha_1)\frac{\theta \varpi_{HH}}{P_h + c} Ds(t) Ai(t) - \tau_h Hi(t) - \beta Hi(t) - (1-\beta) Hi(t) \quad (8.6.3)$$

$$\frac{d}{dx}HFi(t) = \beta Hi(t) - \tau_h HFi(t) - \delta_2 HFi(t) \quad (8.6.4)$$

$$\frac{d}{dx}Si(t) = (1-\beta) Hi(t) - \tau_d Si(t) - \tau_h Si(t) - \delta_3 Si(t) \quad (8.6.5)$$

$$\frac{d}{dx}Dr(t) = \delta_1 Fi(t) + \delta_2 Hi(t) + \delta_3 Si(t) - \tau_h Dr(t) \quad (8.6.6)$$

We define

$Ds(t)$ is the number of susceptible human population at time t,

$Fi(t)$ is the number of DF infectious human at time t,

$Hi(t)$ is the number of infectious human who be suspected with DHF infection,

$HFi(t)$ is the number of DHF infectious human at time t,
$Si(t)$ is the number of DSS infectious human at time t,
$Dr(t)$ is the number of recovered human population at time t.

The dynamics of the mosquito population are given by :

$$\frac{d}{dx}As(t) = P_v - \frac{\theta \varpi_{FV}}{P_h + c} Fi(t)\,As(t) + \frac{\theta \varpi_{HV}}{P_h + c} Hi(t)\,As(t) - \tau_v As(t) \qquad (8.7.1)$$

$$\frac{d}{dx}Ai(t) = \frac{\theta \varpi_{FV}}{P_h + c} Fi(t)\,As(t) + \frac{\theta \varpi_{HV}}{P_h + c} Hi(t)\,As(t) - \tau_v Ai(t) \quad . \qquad (8.7.2)$$

We define

$As(t)$ is the number of susceptible mosquito population at time t,
$Ai(t)$ is the number of infectious mosquito population at time t.

The parameters of our equations are defined as follows:

P_h is the total human population,
P_v is the constant recruitment rate of mosquito population,
γ is the birth rate of human population,
θ is the biting rate of mosquito population,
α_1 is the probability of infection with DF,
$1-\alpha_1$ is the probability of infection with DHF,
β is the probability of patient with type DHF plasma leakage is not in shock,
$1-\beta$ is the probability of patient with type DHF plasma leakage in shock,
c is the number of other animals available as blood sources,
τ_h is the natural death rate of human population,
τ_d is the death rate of human population due to the disease,
τ_v is the death rate of mosquito population,
ϖ_{FH} is the transmission probability of DF from mosquito to human ,
ϖ_{HH} is the transmission probability of DHF from mosquito to human,
ϖ_{FV} is the transmission probability of DF from human to mosquito,
ϖ_{HV} is the transmission probability of DHF from human to mosquito,
δ_1 is the recovery rate of human population from DF infection,
δ_2 is the recovery rate of human population from DHF infection,
δ_1 is the recovery rate of human population from DSS infection.

We suppose that $P_h = Ds + Fi + Hi + HFi + Si + Dr$ and $N_v = As + Ai$, we assume the total human and mosquito populations have constant sizes $\frac{d}{dt}P_h = 0$ and $\frac{d}{dt}P_v = 0$

Equilibrium Points:

The equilibrium points $(Ds^*, Fi^*, Hi^*, HFi^*, Si^*, Dr^*, As^*, Ai^*)$ are found by setting the right hand side of (8.1.1) – (8.1.6) and (8.7.1) – (8.7.2) equal to zero. The system has two possible

equilibrium points: disease free equilibrium point and endemic disease equilibrium point. This gives

1) Disease free equilibrium point: $S_0 = (\frac{P_h\gamma}{\tau_h},0,0,0,0,0,\frac{P_v}{\tau_v},0)$

2) Endemic disease equilibrium point: $S_1 = (Ds^*, Fi^*, Hi^*, HFi^*, Si^*, Dr^*, As^*, Ai^*)$ where

$$Ds^* = \frac{P_h\gamma}{Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h} \tag{8.8.1}$$

$$Fi^* = \frac{Ai P_h\alpha_1\gamma\varepsilon_1}{(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_1+\tau_h)} \tag{8.8.2}$$

$$Hi^* = \frac{Ai P_h(-1+\alpha_1)\gamma\varepsilon_2}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)} \tag{8.8.3}$$

$$HFi^* = \frac{Ai P_h(-1+\alpha_1)\beta\gamma\varepsilon_2}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_2+\tau_h)} \tag{8.8.4}$$

$$Si^* = \frac{Ai P_h(-1+\alpha_1)(-1+\beta)\gamma\varepsilon_2}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_2+\tau_h+\tau_d)} \tag{8.8.5}$$

$$Dr^* = \frac{Ai P_h\gamma\left(-\frac{\alpha_1\varepsilon_1\delta_1}{\delta_1+\tau_h}-\frac{(-1+\alpha_1)\beta\varepsilon_2\delta_2}{(1+\tau_h)(\delta_2+\tau_h)}-\frac{(-1+\alpha_1)\beta\varepsilon_2\delta_3}{(1+\tau_h)(\delta_3+\tau_h+\tau_d)}\right)}{\tau_h(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)} \tag{8.8.6}$$

$$As^* = \frac{P_v}{\frac{Ai P_h\gamma(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1+(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4)\tau_h)}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_1+\tau_h)}+\tau_v} \tag{8.8.7}$$

$$Ai^* = \frac{P_vP_h\gamma(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1+(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4)\tau_h)-\tau_h(1+\tau_h)(\delta_1+\tau_h)\tau_v^2)}{(\tau_v(P_h\gamma(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1+(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4)\tau_h)+(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)(1+\tau_h)(\delta_1+\tau_h)\tau_v))} \tag{8.8.8}$$

with $\varepsilon_1 = \frac{(\theta\varpi_{FH})}{(P_h+c)}, \varepsilon_2 = \frac{(\theta\varpi_{HH})}{(P_h+c)}, \varepsilon_3 = \frac{(\theta\varpi_{FV})}{(P_h+c)}, \varepsilon_4 = \frac{(\theta\varpi_{HV})}{(P_h+c)}$

and

$$D_0 = \frac{P_vP_h\gamma\alpha_1(\varepsilon_1\varepsilon_3(1+\tau_h)+\varepsilon_2\varepsilon_4(\delta_1+\tau_h))}{(\delta_1+\tau_h)(P_vP_h\gamma\varepsilon_2\varepsilon_4+\tau_h(1+\tau_h)\tau_v^2)}$$

It can be seen from the above equations that the steady state solution is positive for $D_0 > 1$.

The local stability of each equilibrium point is determined by the sign of eigenvalues for each steady state. If all eigenvalues have negative real parts, then that steady state is local stability. The eigenvalues are obtained by solving the following characteristic equation

$$\det(J-\psi I_8)=0$$

where I_8 the identity matrix dimension 8x8 .

For the disease free steady state $S_0 = (\frac{P_h\gamma}{\tau_h},0,0,0,0,0,\frac{P_v}{\tau_v},0)$, the *Jacobian* matrix is given by

$$\begin{bmatrix}
(-(\tau_h)-(\alpha_1\varepsilon_1 Ai)-((1-\alpha_1)(\varepsilon_2)Ai))-\psi & 0 & 0 & 0 & 0 & 0 & 0 & -(\alpha_1\varepsilon_1 Ds)-((1-\alpha_1)(\varepsilon_2)Ds) \\
(\alpha_1\varepsilon_1 Ai) & (-(\tau_h)-(\delta_1))-\psi & 0 & 0 & 0 & 0 & 0 & (\alpha_1\varepsilon_1 Ds) \\
((1-\alpha_1)(\varepsilon_2)Ai)) & 0 & (-(\tau_h)-(\beta)-(1-\beta))-\psi & 0 & 0 & 0 & 0 & ((1-\alpha_1)(\varepsilon_2)Ds) \\
0 & 0 & \beta & (-(\tau_h)-(\delta_2))-\psi & 0 & 0 & 0 & 0 \\
0 & 0 & (1-\beta) & 0 & (-(\tau_h)-(\tau_d)-(\delta_3))-\psi & 0 & 0 & 0 \\
0 & \delta_1 & 0 & \delta_2 & \delta_3 & -(\tau_h)-\psi & 0 & 0 \\
0 & -(\varepsilon_3 As) & -(\varepsilon_4 As) & 0 & 0 & 0 & (-(\varepsilon_3 Fi)-(\varepsilon_4 Hi)-(\tau_v))-\psi & 0 \\
0 & (\varepsilon_3 As) & (\varepsilon_4 As) & 0 & 0 & 0 & (\varepsilon_3 Fi)+(\varepsilon_4 Hi) & (-\tau_v)-\psi
\end{bmatrix}$$

where

$\psi = -\tau_h$, $\psi = -\tau_h, \psi = -\tau_h - \delta_2, \psi = -\tau_h - \delta_3 - \tau_d, \psi = -\tau_v$,

The characteristic equation is defined by $\psi^3 + A_1\psi^2 + A_2\psi + A_3$.

where

$A_1 = 1 + \delta_1 + 2\tau_h + \tau_v$,

$$A_2 = (1+\tau_h) + (\delta_1 + \tau_h) - \frac{P_h P_v \gamma (\alpha_1\varepsilon_1\varepsilon_3 + \varepsilon_2\varepsilon_4 - \alpha_1\varepsilon_2\varepsilon_4)}{\tau_h\tau_v} + (1 + \delta_1 + 2\tau_h)\tau_v,$$

$$A_3 = \frac{1}{\tau_h\tau_v}(-P_h P_v \gamma(\alpha_1\varepsilon_1\varepsilon_3 - (-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1 + (\alpha_1\varepsilon_1\varepsilon_3 + \varepsilon_2\varepsilon_4 - \alpha_1\varepsilon_2\varepsilon_4)\tau_h) + \tau_h(1+\tau_h)(\delta_1+\tau_h)\tau_v^2$$

We check the sign of eigenvalues by using Routh Hurwitz criteria can impact eigenvalues with negative real parts. If the characteristic equation satisfy Routh Hurwitz criteria, we can say that the steady state is local stability. Thus, this disease free state will be local stability when $D_0 < 1$.On similarly method, we found that the disease endemic state will be local stability when $D_0 > 1$.

The parameters are given as follows: $\tau_h = 1/(365*74.6)$ corresponds to the life expectancy of 74.6 years for human, $\delta_1 = 1/5$ corresponds to the 5 days at which quarantine human change to be recovered human for DF, $\delta_2 = 1/6$ corresponds to the 6 days at which quarantine human change to be recovered human for DHF, $\delta_3 = 1/3$ corresponds to the 3 days at which quarantine human change to be recovered human for DSS. The other parameters are arbitrary chosen.

Cases1. $D_0 < 1$;

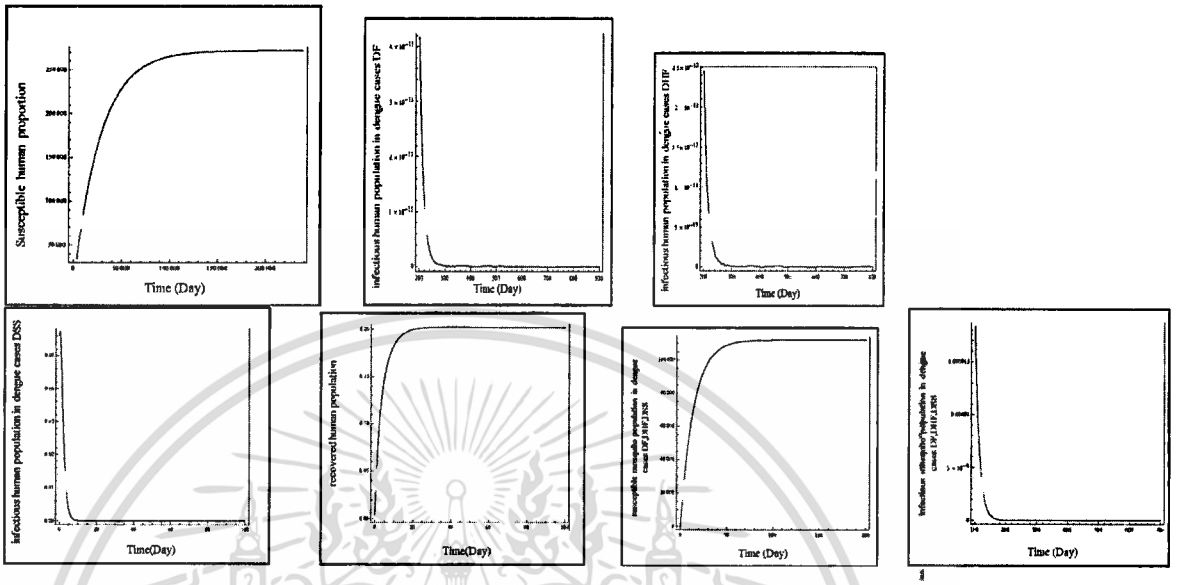


Figure 8.2. Times series solutions of susceptible, DF infectious human, DHF infectious human, DSS infectious human, susceptible mosquito population, infectious mosquito population, respectively. The parameters are
$\tau_h = 1/(365*74.6)$, $\delta_1 = 1/5$, $\delta_2 = 1/6$, $\delta_3 = 1/3$, $P_h = 100{,}000$, $P_v = 8000$, $\omega_{FH} = 1/8$, $\omega_{HH} = 1/10$, $\omega_{FV} = 1/3$, $\omega_{HV} = 1/7$, $\tau_d = 1/2$, $\alpha_1 = 0.7$, $\beta = 0.007$, $D_0 = 0.319108$. The solutions converge to the disease free states (272290, 0, 0, 0, 0, 0, 98000, 0)

Cases2. $D_0 > 1$;

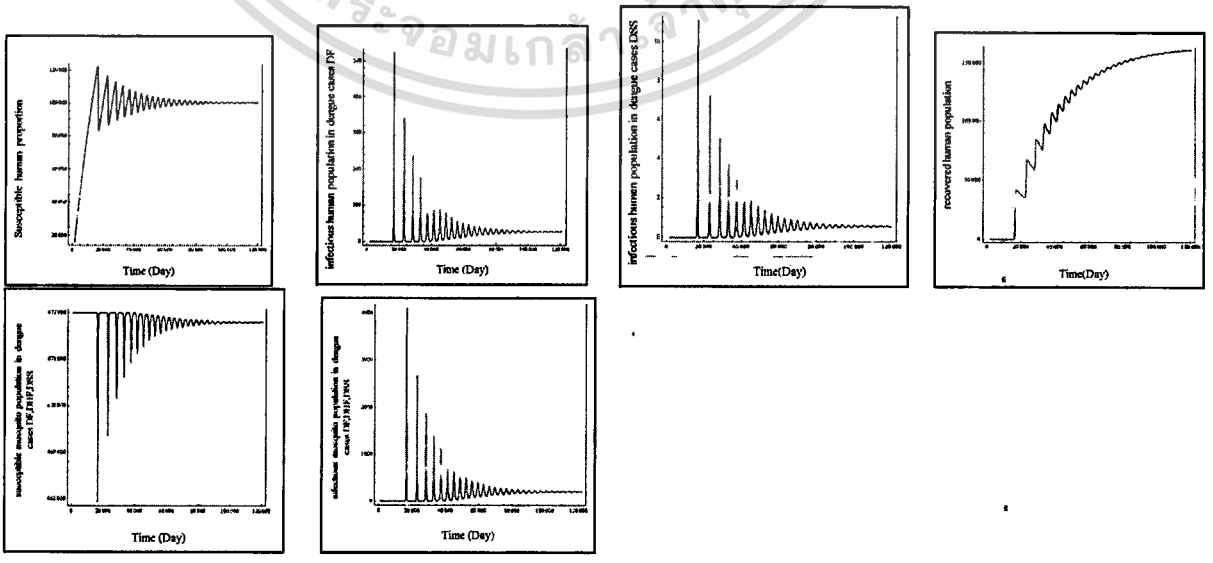


Figure8.3.Times series solutions of susceptible, DF infectious human, DHF infectious human, DSS infectious human, susceptible mosquito population, infectious mosquito population, respectively. The parameters are $\tau_h = 1/(365*74.6)$, $\delta_1 = 1/5$, $\delta_2 = 1/6$, $\delta_3 = 1/3$, $P_h = 100{,}000$, $P_v = 48000$, $\omega_{FH} = 1/8$, $\omega_{HH} = 1/10$, $\omega_{FV} = 1/3$, $\omega_{HV} = 1/7$, $\tau_d = 1/2$, $\alpha_1 = 0.9$, $\beta = 0.04$, $D_0 = 2.3622$. The solutions oscillate to the endemic disease states (100182, 26.1172, 0.515961, 0.113488, 0.550336, 164588, 671749, 206.223).

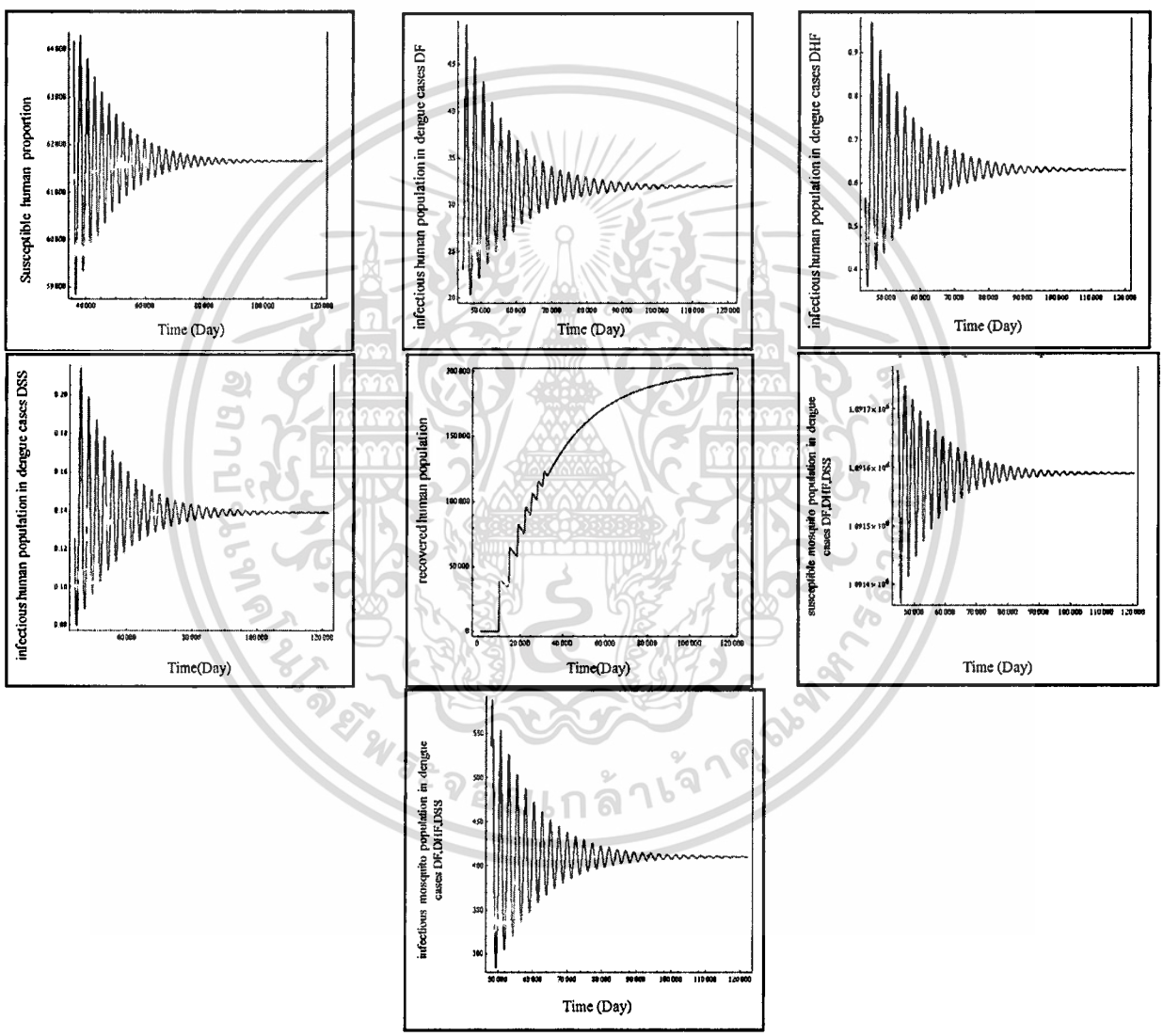


Figure8.4. Times series solutions of susceptible , DF infectious human, DHF infectious human, DSS infectious human, susceptible mosquito population, infectious mosquito population, respectively. The parameters are $\tau_h = 1/(365*74.6)$, $\delta_1 = 1/5$, $\delta_2 = 1/6$, $\delta_3 = 1/3$, $P_h = 100{,}000$, $P_v = 78000$, $\omega_{FH} = 1/8$, $\omega_{HH} = 1/10$, $\omega_{FV} = 1/3$, $\omega_{HV} = 1/7$, $\tau_d = 1/2$, $\alpha_1 = 0.7$,

$\beta=0.007$, $D_0=3.43912$. The solutions oscillate to the endemic disease states (61654.8, 31.9637, 0.631462, 0.138894, 0.673532, 201432, 0.000001091, 410.1).

When value of probability of infection with DF (α_1) and probability of patient with type DHF plasma leakage is not in shock (β),as a results Figure3 converge to endemic faster than Figure8.4.

In this study, we constructed the mathematical model of dengue cases (DF,DHF,DSS) and analyzed the results by using standard dynamical modeling method. The basic reproductive number is defined by D_0.From Figure3 ,parameter values are $\alpha_1=0.9$, $\beta=0.04$ and Figure4, parameter values are $\alpha_1=0.7$, $\beta=0.007$,so that the convergence of the graph are different. The others parameter were ,too. Therefore, we know that , when values α_1 (the probability of infection with DF) and β (the probability of patient with type DHF plasma leakage is not in shock), the convergence to endemic state are different. The time series parameter inference shows different dynamic behaviours, depending on the data collection to be described via the modeling approaches. The output of this model should introduce the way for reducing the transmission of this disease.

4.9. แบบจำลองที่ 9 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงอุณหภูมิของสิ่งแวดล้อม [64]

We formulate our model by separating the population into 2 groups such as human and vector populations. Human is separated into 3 groups such as susceptible, infected and recovered groups. Vector is separated into 2 groups such as susceptible and infected groups. We separate the infected human into 2 classes. Class of infected human population when the temperature is 28-35 ^{0}C and class of infected vector population when the temperature is not 28-35 ^{0}C. The variables and parameters of our model is described as follows:

variable/parameter	definition
S	Number of susceptible human
I_{t_a}	Number of infected humanwhen the temperature is 28-35 ^{0}C
I_{t_b}	Number of infected humanwhen the temperature is not 28-35 ^{0}C
R	Number of recovered human
S_v	Number of susceptible vector
I_v	Number of infectious vector
b	Birth rate of human
N_T	Total human
μ_h	Death rate of human population
β_{t_a}	Transmission rate of dengue virus from vector to human population when the temperature is 28-35 ^{0}C
β_{t_b}	Transmission rate of dengue virus from vector to human

	population when the temperature is not 28-35 ^{0}C
r	Recovery rate of human population
C_v	Constant recruitment rate of vector population
β_v	Transmission rate of dengue virus from human to vector population
μ_v	Death rate of vector population

Using the knowledge of mathematical model and the transmission behavior of this disease, we can obtain the differential equations as follows:
For human population:

$$\begin{aligned}
\frac{d}{dt}S &= bN_T - (\beta_{t_a} + \beta_{t_b})SI_v - \mu_h S \\
\frac{d}{dt}I_{t_a} &= \beta_{t_a} SI_v - (r+\mu_h)I_{t_a} \\
\frac{d}{dt}I_{t_b} &= \beta_{t_b} SI_v - (r+\mu_h)I_{t_b} \\
\frac{d}{dt}R &= r(I_{t_a} + I_{t_b}) - \mu_h R
\end{aligned} \tag{9.1}$$

For vector population:

$$\begin{aligned}
\frac{d}{dt}S_v &= C_v - \beta_v S_v(I_{t_a} + I_{t_b}) - \mu_v S_v \\
\frac{d}{dt}I_v &= \beta_v S_v(I_{t_a} + I_{t_b}) - \mu_v I_v
\end{aligned} \tag{9.2}$$

with the conditions: $N_T = S + I_{t_a} + I_{t_b} + R$ and $N_v = S_v + I_v$.
We normalize our equations (1)-(2) by introducing the new variables:

$$s = \frac{S}{N_T}, i_{t_a} = \frac{I_{t_a}}{N_T}, i_{t_b} = \frac{I_{t_b}}{N_T}, r_h = \frac{R}{N_T}, s_v = \frac{S_v}{N_v} \text{ and } i_v = \frac{I_v}{N_v}. \tag{9.3}$$

Note that $s, i_{t_a}, i_{t_b}, r_h, s_v$ and i_v are the fractions of susceptible human, infected human when the temperature is 28-35 ^{0}C, infected human when the temperature is not 28-35 ^{0}C, recovered human, susceptible vector and infectious vector, respectively.

S	Number of susceptible human
I_{t_a}	Number of infected humanwhen the temperature is 28-35 ^{0}C
I_{t_b}	Number of infected humanwhen the temperature is not 28-35 ^{0}C
R	Number of recovered human

The reduced equations become

$$\begin{aligned}
\frac{d}{dt}s &= \mu_h(1-s)-(\beta_{t_a}+\beta_{t_b})(C_v/\mu_v)s i_v \\
\frac{d}{dt}i_{t_a} &= \beta_{t_a}(C_v/\mu_v)s i_v-(r+\mu_h)i_{t_a} \\
\frac{d}{dt}I_{t_b} &= \beta_{t_b}(C_v/\mu_v)s i_v-(r+\mu_h)i_{t_b} \\
\frac{d}{dt}i_v &= \beta_v(1-i_{t_a}-i_{t_b})(i_{t_a}+i_{t_b})N_T-\mu_v i_v
\end{aligned} \qquad (9.4)$$

with the conditions: $1=s+i_{t_a}+i_{t_b}+r_h$ and $1=s_v+i_v$.

To follow the method of dynamical modeling method, the steady states of our equations are found. They are from setting (9.4) to zero, thus the steady states are (1,0,0,0) and the positive steady state $(s^*,i^*_{t_a},i^*_{t_b},i^*_v)$ is defined by

$$s^*=\frac{\mu_h\mu_v}{(\beta_{t_a}+\beta_{t_b})C_v i^*_v+\mu_h\mu_v}, i^*_{t_a}=\frac{\beta_{t_a}C_v i^*_v s^*}{\mu_v(\mu_h+r)}, i^*_{t_b}=\frac{\beta_{t_b}C_v i^*_v s^*}{\mu_v(\mu_h+r)} \text{ where}$$

i^*_v is found from solving (9.5).

$$\begin{aligned}
&\mu_h^2\mu_v(((\beta_{t_a}+\beta_{t_b})C_v i^*_v+\mu_h\mu_v)^2-(\beta_{t_a}+\beta_{t_b})\beta_v C_v\mu_h N_T)+\mu_h((\beta_{t_a}+\beta_{t_b})C_v i^*_v+\mu_h\mu_v) \\
&-(\beta_{t_a}+\beta_{t_b})\beta_v C_v N_T)r+\mu_v((\beta_{t_a}+\beta_{t_b})C_v i^*_v+\mu_h\mu_v)^2 r^2=0
\end{aligned} \qquad (9.5)$$

Next, we check the local stability of each steady state by looking the sign of eigenvalues, where the eigenvalues are evaluated by $\det(J-\lambda I)=0$; $\det(J-\lambda I)=0$; I is the identity matrix. If all eigenvalues have negative real parts, then that steady state will be local stability.
For the first steady state(disease free state) : (1,0,0,0), jacobian matrix is given by

$$J_1=\begin{pmatrix}
-\mu_h & 0 & 0 & -\dfrac{(\beta_{t_a}+\beta_{t_b})C_v}{\mu_v} \\
0 & -\mu_h-r & 0 & \dfrac{\beta_{t_a}C_v}{\mu_v} \\
0 & 0 & -\mu_h-r & \dfrac{\beta_{t_b}C_v}{\mu_v} \\
0 & \beta_v N_T & \beta_v N_T & -\mu_v
\end{pmatrix}.$$

The eigenvalues are

$$-\mu_h,-\mu_h-r,\frac{1}{2\mu_v}(-\mu_h\mu_v-\mu_v^2-\mu_v r\pm\sqrt{\mu_v(4(\beta_{t_a}+\beta_{t_b})\beta_v C_v N_T+\mu_v(\mu_h+\mu_v+r)^2)}).$$

We can see that all eigenvalues have negative real parts when $A_0<1$;

where $A_0 = \dfrac{(\beta_{t_a} + \beta_{t_b})\beta_v C_v N_T}{\mu_v^2(\mu_h + r)}$.

The positive steady state(endemic state): $(s^*, i^*_{t_a}, i^*_{t_b}, i^*_v)$;

Jacobian matrix is defined by

$$J_2 = \begin{pmatrix} -\mu_h - \dfrac{(\beta_{t_a}+\beta_{t_b})C_v}{\mu_v} i_v^* & 0 & 0 & \dfrac{(\beta_{t_a}+\beta_{t_b})C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)} \\ \dfrac{\beta_{t_a}C_v}{\mu_v} i_v^* & -\mu_h - r & 0 & \dfrac{\beta_{t_a}C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)} \\ \dfrac{\beta_{t_b}C_v}{\mu_v} i_v^* & 0 & -\mu_h - r & \dfrac{\beta_{t_b}C_v}{\mu_v} \\ 0 & \dfrac{(\beta_{t_a}+\beta_{t_b})\beta_v C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)(r+\mu_h)} N_T i_v^* & \beta_v N_T\left(1 - \dfrac{2(\beta_{t_a}+\beta_{t_b})C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)(r+\mu_h)}\right) & -\mu_v \\ & + \beta_v N_T\left(1 - \dfrac{(\beta_{t_a}-\beta_{t_b})C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)(r+\mu_h)}\right) i_v^* & & \end{pmatrix}.$$

Using the same method as before, eigenvalues are obtained by solving $\lambda^3 + A\lambda^2 + B\lambda + C = 0$;

where $A = \dfrac{(\beta_{t_a} + \beta_{t_b})C_v i_v^* + \mu_v(2\mu_h + \mu_v + r)}{\mu_v}$,

$$B = -\frac{1}{L_4\mu_v((\beta_{t_a} + \beta_{t_b})C_v i_v^* + \mu_h\mu_v)^2}((-\beta_{t_a}^3 - \beta_{t_b}^3)C_v^3 i_v^{*3} L_3 L_4$$
$$- \beta_{t_b} C_v\mu_v(L_4\mu_h\mu_v(-i_v^* L_1 + \beta_v\mu_h N_T(\mu_h - r))) - L_4\mu_h^2\mu_v^3(\mu_h(\mu_h + 2\mu_v) + (\mu_h + \mu_v)r)$$
$$- \beta_{t_a} C_v(-3\beta_{t_b}^2 C_v^2 i_v^{*3} L_3 L_4 + L_4\mu_h\mu_v^2(-i_v^* L_1 + \beta_v\mu_h N_T) + \beta_{t_a} C_v i_v^*(3\beta_{t_a} C_v i_v^* L_3 L_4$$
$$+ \mu_v(i_v^* L_2 L_4 + \beta_v\mu_h N_T(\mu_h - r))) - 2\beta_{t_b} C_v i_v^*\mu_v(i_v^* L_2 L_4 - \beta_v\mu_h N_T r))),$$

$$C = \frac{\mu_h(((\beta_{t_a} + \beta_{t_b})C_v i_v^* + \mu_h\mu_v)^2 - (\beta_{t_a} + \beta_{t_b})\beta_v C_v\mu_h N_T}{(\beta_{t_a} + \beta_{t_b})C_v i_v^* + \mu_h\mu_v} + ((\beta_{t_a} + \beta_{t_b})C_v i_v^* + \mu_h\mu_v)r$$
$$+ \frac{2(\beta_{t_a}^2 + \beta_{t_a}\beta_{t_b} + \beta_{t_b}^2)\beta_v C_v^2 i_v^*\mu_h^3 N_T}{((\beta_{t_a} + \beta_{t_b})C_v i_v^* + \mu_h\mu_v)^2(\mu_h + r)},$$

where

$$L_1 = 3\mu_h^2 + 5\mu_h\mu_v + 3\mu_h r + 2\mu_v r,$$
$$L_2 = 3\mu_h^2 + 4\mu_h\mu_v + 3\mu_h r + \mu_v r,$$
$$L_3 = \mu_h + \mu_v + r,$$
$$L_4 = \mu_h + r$$

From Routh Hurwitz criteria, the eigenvalues have negative real parts when the following conditions are satisfied:

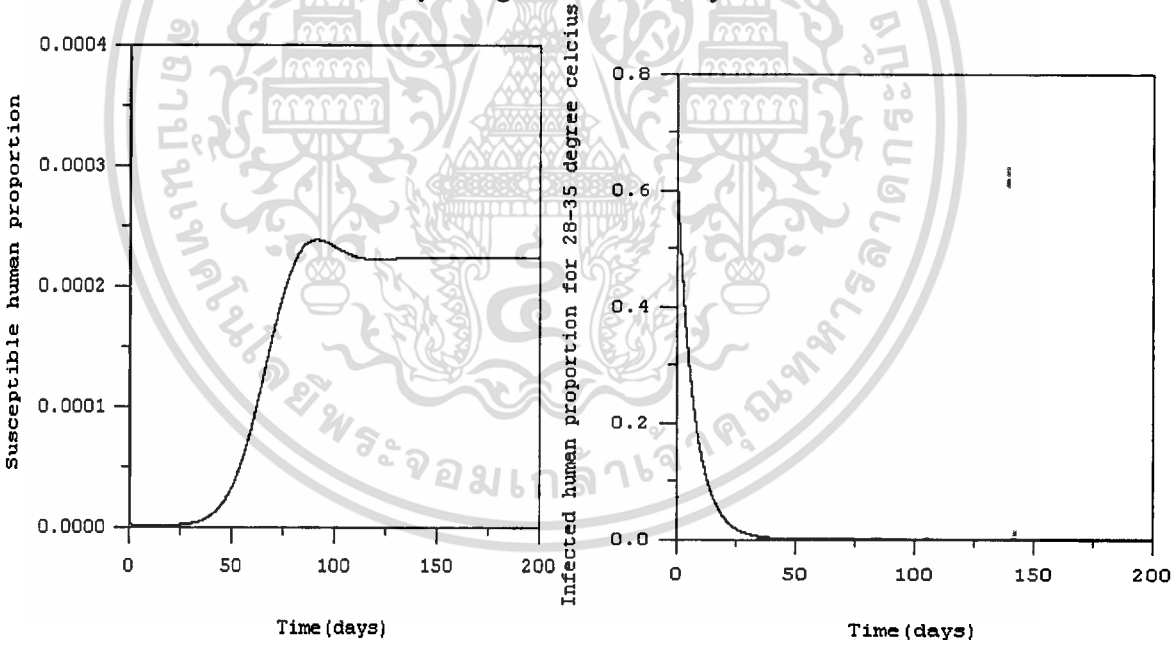
i) $A > 0$
ii) $C > 0$
iii) $AB > C$.

From our evaluations, we can say that the above conditions are satisfied when $A_0 > 1$;

where $A_0 = \dfrac{(\beta_{t_a} + \beta_{t_b})\beta_v C_v N_T}{\mu_v^2(\mu_h + r)}$.

We can conclude that the first steady state is local stability when $A_0 < 1$ and the second steady state is local stability when $A_0 > 1$.

Next, we show our results by using numerical analysis.



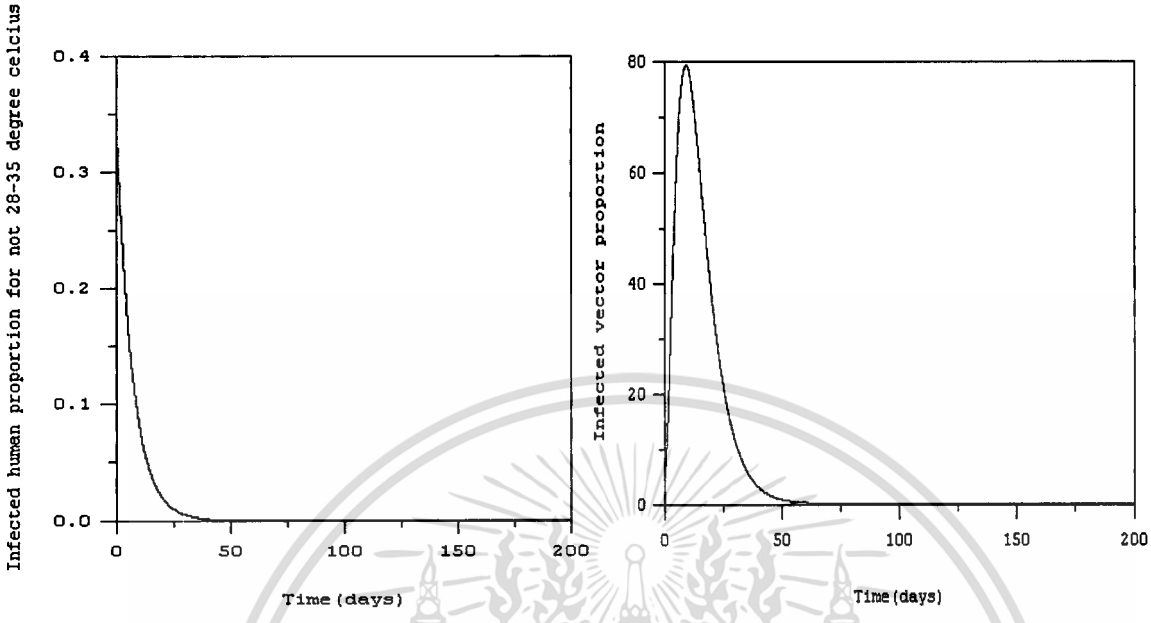


Figure 9.1. Time series of each population group for $A_0 = 4{,}480$ The parameters used in this study are μ_h = 0.0000457, μ_v = 0.25, β_{t_a} = 0.0007, β_{t_b} = 0.0003, β_v = 1, r = 0.1428, N_T = 100, C_v = 400. The solutions converge to the steady state (0.000223266,0.000223893,0.000095,0.127899).

From figure 9.1, it can be seen that the solutions converge to the endemic steady state for $A_0 > 1$.

The threshold number is defined by $A_0 = \dfrac{(\beta_{t_a} + \beta_{t_b})\beta_v C_v N_T}{\mu_v^2(\mu_h + r)}$. For $A_0 < 1$, the disease free state is local stability and the endemic state is local stability for $A_0 > 1$.The basic reproductive number is defined by $\hat{A}_0 = \sqrt{A_0}$, it represents the average number of secondary cases produced from primary cases. This values are used for reduced the outbreak of this disease. Next, we compare the behavior of solutions for the different total human population.

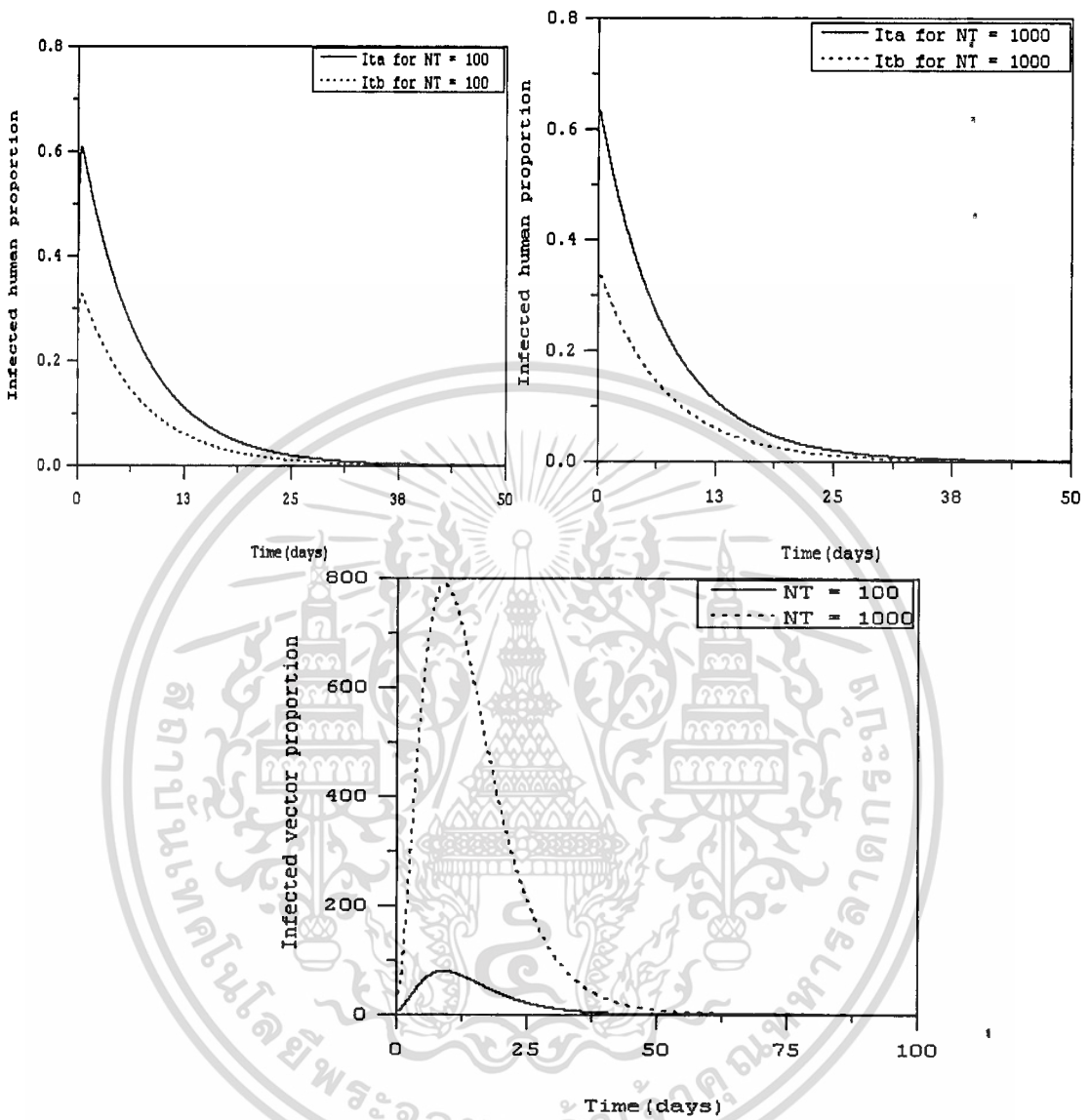


Figure 9.2.Comparison of numerical results for the different total human population: $N_T = 100$ and $N_T = 1000$.

We can see that the fraction of vector population and the outburst time are depending on the total human population. The fraction of dengue cases are depending on the temperature, as we can see from figure 9.2. The fraction of dengue cases for 28-35 ^{0}C are greater than the other temperatures because the appropriated temperature for the growth of mosquito population.

4.10. แบบจำลองที่ 10 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงชนิดของยุงลายและปริมาณน้ำฝน [65]

Our model is formulated by considering the two species of vectors, *Aedes albopictus* and *Aedes aegypti*. Each species is separated in to 3 classes, Eggs(O), Exposed(E) and Infectious(I) classes. The volume of raining effects to the number of eggs' mosquitoes. The dynamical equations are explained as follows:

For *Aedes albopictus* vector,

$$O'_A(t) = va_1A - a_2O_A(t) - \mu_A O_A(t), \tag{10.1}$$

$$E'_A(t) = a_2O_A(t) - \frac{1}{EP_A}E_A(t) - \mu_A E_A(t), \tag{10.2}$$

$$I'_A(t) = \frac{1}{EP_A}E_A(t) - \mu_A I_A(t). \tag{10.3}$$

with $N_A(t) = O_A(t) + E_A(t) + I_A(t)$.

For *Aedes aegypti* vector,

$$O'_B(t) = vb_1B - b_2O_B(t) - \mu_B O_B(t), \tag{10.4}$$

$$E'_B(t) = b_2O_B(t) - \frac{1}{EP_B}E_B(t) - \mu_B E_B(t), \tag{10.5}$$

$$I'_A(t) = \frac{1}{EP_B}E_B(t) - \mu_B I_B(t). \tag{10.6}$$

with $N_B(t) = O_B(t) + E_B(t) + I_B(t)$.

We define varaiables and parameters as follows:

$O_A(t)$ is the number of eggs' *Aedes albopictus* vector.

$O_B(t)$ is the number of eggs' *Aedes aegypti* vector.

$E_A(t)$ is the number of exposed *Aedes albopictus* vector.

$E_B(t)$ is the number of exposed *Aedes aegypti* vector.

$I_A(t)$ is the number of infectious *Aedes albopictus* vector.

$I_B(t)$ is the number of infectious *Aedes aegypti* vector.

v is the probability of producing eggs' mosquitoes at the time of raining.

a_1 is the rate of producing eggs per 1 *Aedes albopictus* vector.

b_1 is the rate of producing eggs per 1 *Aedes aegypti* vector.

a_2 is the survival rate of eggs of *Aedes albopictus* vector.

b_2 is the survival rate of eggs of *Aedes aegypti* vector

A is the constant recruitment rate of *Aedes albopictus* vector.

B is the constant recruitment rate of *Aedes aegypti* vector.

EP_A is the incubation period of *Aedes albopictus* vector.

EP_B is the incubation period of *Aedes aegypti* vector.

μ_A is the death rate of *Aedes albopictus* vector.

μ_B is the death rate of *Aedes aegypti* vector.

N_A is the total number of *Aedes albopictus* vector.

N_B is the total number of *Aedes aegypti* vector.

To reduce our equations, we introduce the new variables: $\tilde{O}_A(t), \tilde{O}_B(t), \tilde{E}_A(t), \tilde{E}_B(t), \tilde{I}_A(t)$ and

$\tilde{I}_B(t)$ as the proportion of each population group that is

$\tilde{O}_A(t) = O_A(t)/N_A, \tilde{O}_B(t) = O_B(t)/N_B, \tilde{E}_A(t) = E_A(t)/N_A, \tilde{E}_B(t) = E_B(t)/N_B, \tilde{I}_A(t) = I_A(t)/N_A$ and $\tilde{I}_B(t) = I_B(t)/N_A$. Then we obtain 4 reduced equations:

where $\tilde{O}_A(t) + \tilde{E}_A(t) + \tilde{I}_A(t) = 1$ and $\tilde{O}_B(t) + \tilde{E}_B(t) + \tilde{I}_B(t) = 1$.

The standard dynamical modeling method is used in this study. First, we find equilibrium states by setting eqs.(10.7) – (10.10) to zero, then we get an equilibrium state $(\tilde{O}_A', \tilde{E}_A', \tilde{O}_B', \tilde{E}_B')$ where

$$\tilde{O}_A' = \frac{Aa_1 v}{(a_2 + \mu_A)N_A},$$

$$\tilde{I}_A' = \frac{Aa_1 a_2 v}{(a_2 + \mu_A)(\mu_A + EP_A \mu_A^2)N_A},$$

$$\tilde{O}_B' = \frac{Bb_1 v}{(b_2 + \mu_B)N_B},$$

$$\tilde{I}_B' = \frac{Bb_1 b_2 v}{(b_2 + \mu_B)(\mu_B + EP_B \mu_b^2)N_B}.$$

To determine the local stability of this equilibrium state, we evaluate the eigenvalues (λ) from

$\det(J - \lambda I) = 0$; where J is the Jacobian matrix and I is the identity matrix.

J is defined by

$$J=\begin{pmatrix} \frac{\partial F_1}{\partial \tilde{O}_A} & \frac{\partial F_1}{\partial \tilde{I}_A} & \frac{\partial F_1}{\partial \tilde{O}_B} & \frac{\partial F_1}{\partial \tilde{I}_B} \\ \frac{\partial F_2}{\partial \tilde{O}_A} & \frac{\partial F_2}{\partial \tilde{I}_A} & \frac{\partial F_2}{\partial \tilde{O}_B} & \frac{\partial F_2}{\partial \tilde{I}_B} \\ \frac{\partial F_3}{\partial \tilde{O}_A} & \frac{\partial F_3}{\partial \tilde{I}_A} & \frac{\partial F_3}{\partial \tilde{O}_B} & \frac{\partial F_3}{\partial \tilde{I}_B} \\ \frac{\partial F_4}{\partial \tilde{O}_A} & \frac{\partial F_4}{\partial \tilde{I}_A} & \frac{\partial F_4}{\partial \tilde{O}_B} & \frac{\partial F_4}{\partial \tilde{I}_B} \end{pmatrix}$$

$$F_1(t)=-(a_2+\mu_A)O_A(t)+\frac{Aqv}{N_A}, \tag{10.7}$$

$$F_2(t)=(1/EP_A)(1-O_A(t)-I_A(t))-I_A(t)\mu_A, \tag{10.8}$$

$$F_3(t)=-(b_2+\mu_b)O_B(t)+\frac{Bhv}{N_B}, \tag{10.9}$$

$$F_4(t)=(1/EP_B)(1-O_B(t)-I_B(t))-I_B(t)\mu_B, \tag{10.10}$$

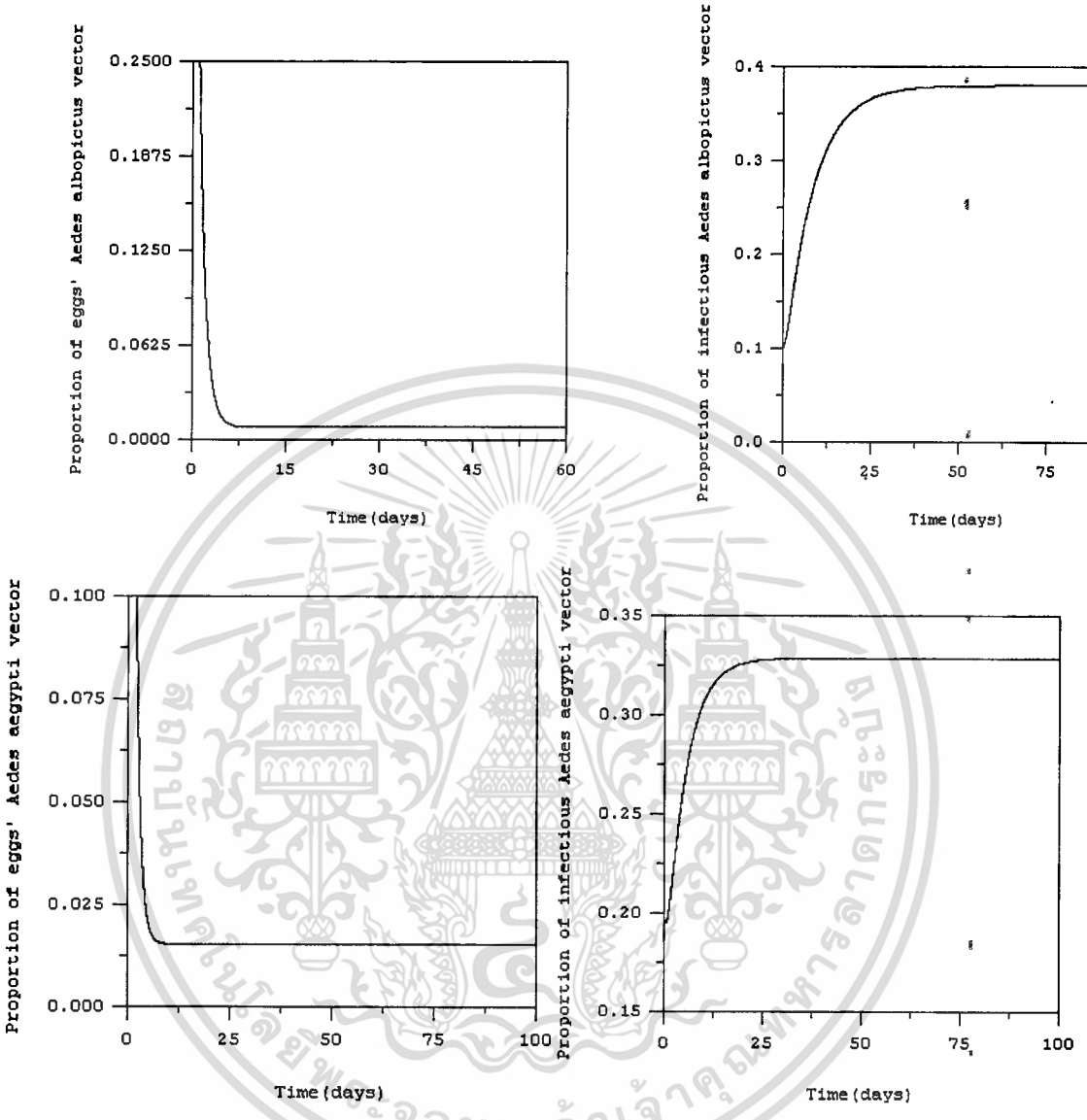
After calculation, the characteristic equation of our equilibrium state is

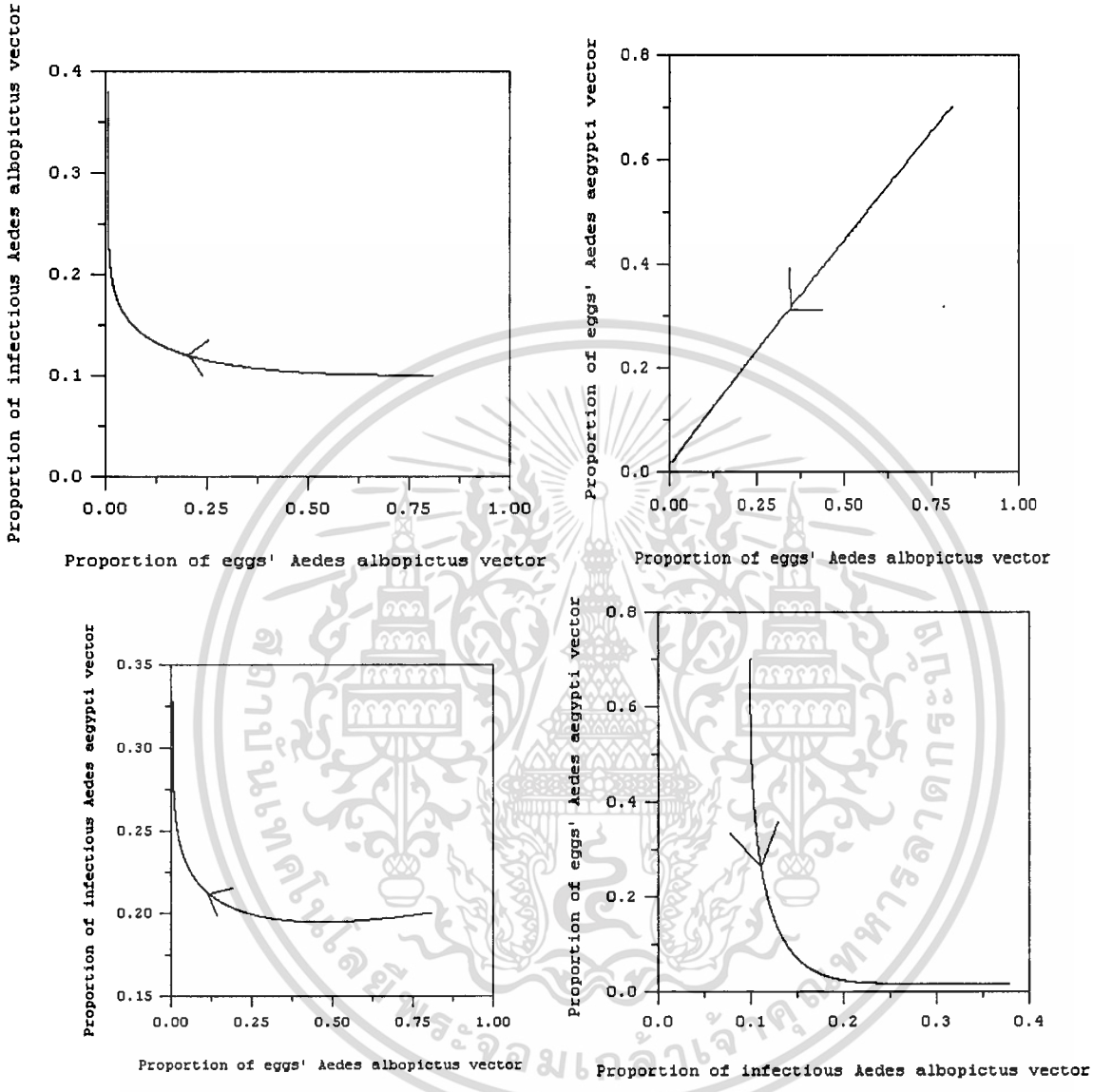
$$(\lambda^2+(a_2+1/EP_A+2\mu_A)\lambda+a_2/EP_A+a_2\mu_A+\mu_A/EP_A+\mu_A^2)$$
$$(\lambda^2+(b_2+1/EP_B+2\mu_B)\lambda+a_2/EP_B+a_2\mu_B+\mu_B/EP_B+\mu_B^2) = 0. \tag{10.11}$$

The eigenvalues are $\lambda_1=-a_2-\mu_A$, $\lambda_2=-(1/EP_A)(1+EP_A\mu_A)$, $\lambda_3=-b_2-\mu_b$ and $\lambda_2=-(1/EP_B)(1+EP_B\mu_B)$.

From local stability theorem, the equilibrium state is local stability when the eigenvalues give the negative signs, It can be seen that all eigenvaluaes are negative. Therefore, we can conclude that the equilibrium state is local stability.

Next, we show the results by using numerical results. The parameters used in this study follow the real situations.





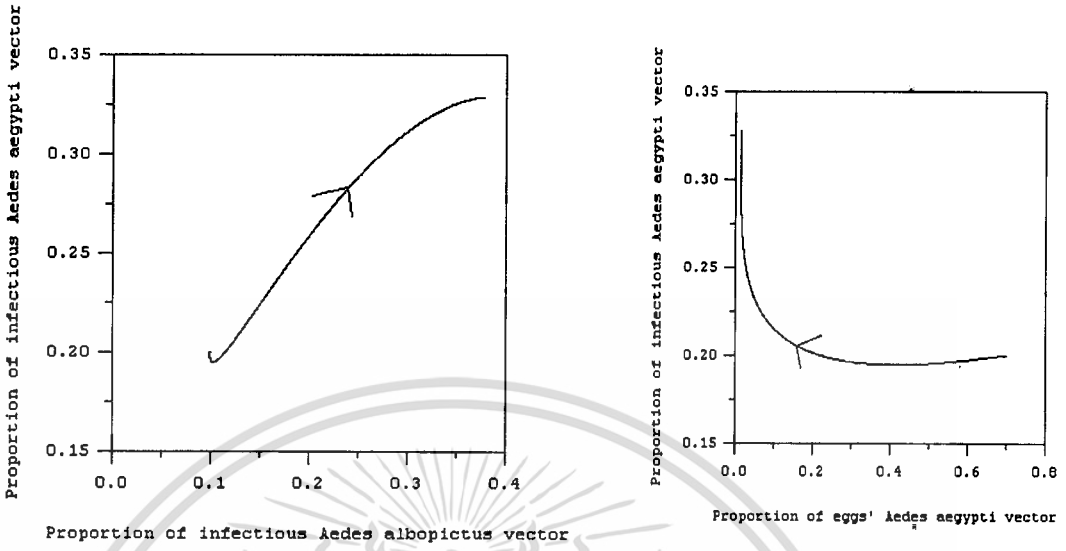


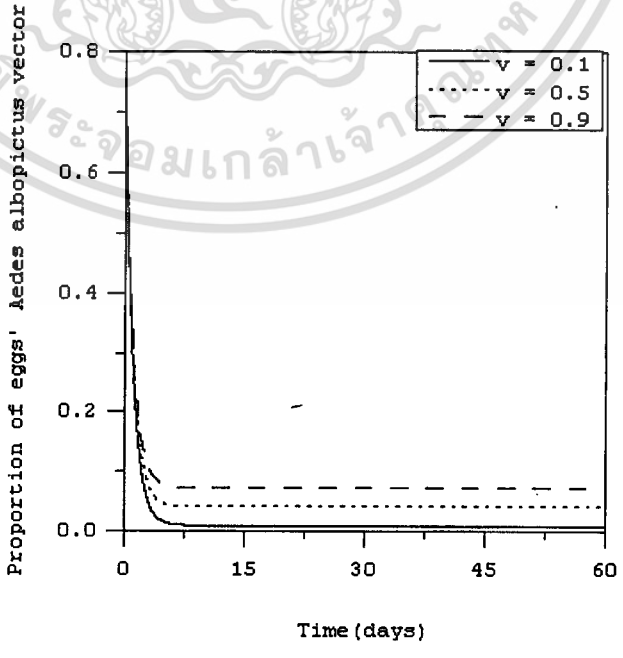
Figure10.1. Numerical solutions of our equations(10.7)-(10.10). The parameters used in this study are

v =0.1, $a_1 = 0.8$, A=7,000, $a_2 = 0.9$, $\mu_A = 1/13$, $EP_A = 21$, $b_1 = 0.6$, B = 10,000, $b_2 = 0.8$, $\mu_B = 1/7$,

$EP_B = 14$.

We will see that the solutions converge to the equilibrium state (0.00787402,0.379342,0.0151515,0.328283) corresponding to the analytical results.

Mathematical model is formulated corresponding to the characteristics of dengue disease.The effect of raining is considered in this study. Mathematics is applied to many diseases. We simulate our solutions when there are the different probabilities of producing eggs' mosquitoes at the time of raining.



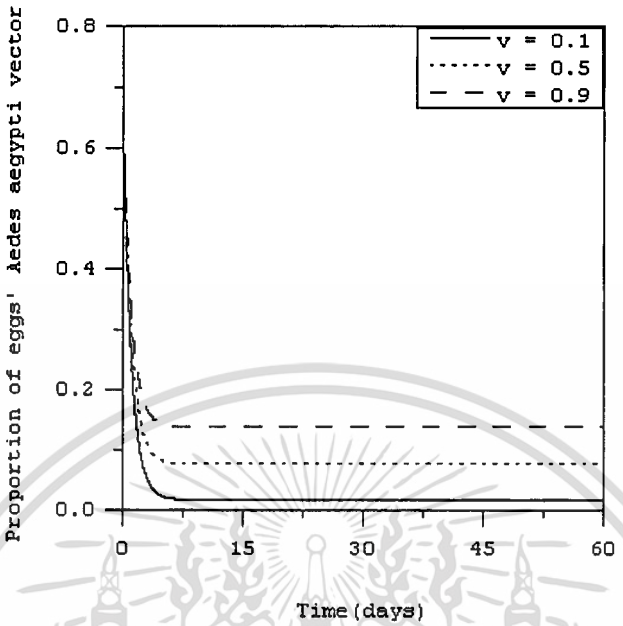


Figure10.2. Time series solutions of proportion of eggs' *Aedes albopictus* and *Aedes aegypti* vectors for the different probability of producing eggs' mosquitoes at the time of raining.

From Figure10.2, we can see that the volume of raining effects to the eggs of two species of vectors(*Aedes albopictus* and *Aedes aegypti*). When there is the higher volume of raining, the higher proportion of vectors. This corresponding to the real situation in Thailand.

4.11 แบบจำลองที่ 11 แบบจำลองของโรคไข้เลือดออกเมื่อประชากรมีการเดินทางโดยพิจารณาพื้นที่ที่มีน้ำท่วมในประเทศไทย [66]

Dengue virus is transmitted between human and mosquitoes. We assume that people can move between houses. The mosquitoes can fly to any houses. In the beginning, there is only one dengue case and he/she can stay in any house. The people can travel to any house but at the ending day, he/she will come back to the house same as the beginning day. The flood effects to the transmission of dengue virus, thus the rate of flooding is considered in our model. The discrete dynamical equations can be described as the following equations:

$$S'(t) = \mu_h N(t) - (\beta_h S(t) I(t) + \beta_o S(t)) - dS(t)$$

$$I'(t) = (\beta_h S(t) I(t) + \beta_o S(t)) + \alpha R(t) + A_I - (r+d) I(t)$$

$$R'(t) = rI(t) - (\alpha + d) R(t)$$

The parameters are defined as in the following table:
Table 11.1: The definitions of variables/parameters in our dynamical equations.

Variable/Parameter	Definition
$Sh_{t,k}$	Number of susceptible persons of k^{th}house at time t.
$Ih_{t,k}$	Number of infectious persons of k^{th} house at time t.
$Rh_{t,k}$	Number of recovered persons of k^{th} house at time t.
φ	Percentage of flooding.
$Sv_{t,k}$	Number of susceptible vector of k^{th} house at time t.
$Iv_{t,k}$	Number of infectious vector of k^{th} house at time t.
$Rv_{t,k}$	Number of recovered vector of k^{th} house at time t.
f_h	Infectious rate of dengue virus from vector to human.
r	The distant of flying 's mosquito.
r_{max}	The maximum distant of flying 's mosquito
w	The rate at which the recovered persons can become to be susceptible persons.
a	The recovery rate of human.
f_v	Infectious rate of dengue virus from human to vector.
μ_v	The death rate of vector.

Our dynamical equations are calculated by simulating the different set of parameters. The solutions are shown in the next section.

We simulate the different sets of parameters. The considered parameters are Percentage of flooding(φ),Infectious rate of dengue virus from vector to human(f_h),The distant of flying 's mosquito(r) and Infectious rate of dengue virus from human to vector(f_v). The different sets of parameters are shown in the following table. The results are the total number of dengue cases from all houses.

Table 11.2: The different set of parameters are used in this simulation.

Parameter	Values			
φ	80%	60%	40%	20%
f_h	0.9	0.6	0.3	0.1
r	400	300	200	100
f_v	1.0	0.75	0.5	0.25

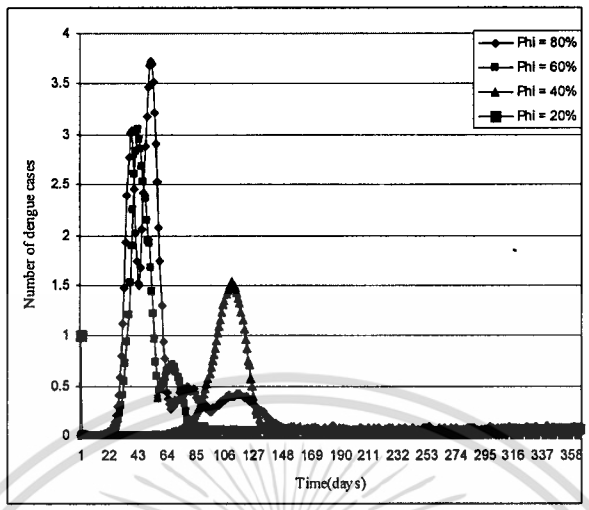


Figure 11.2. The number of dengue case when there is the different Percentage of flooding.

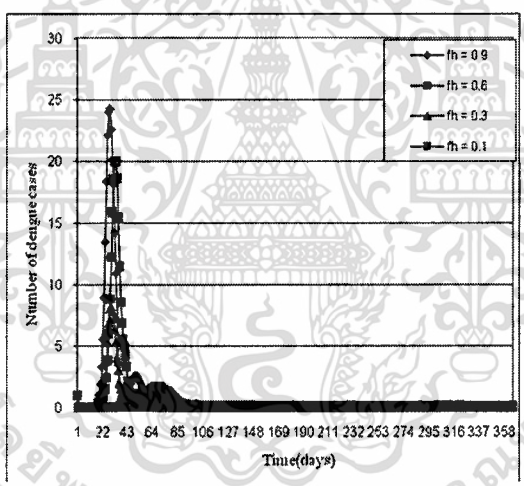


Figure 11.3. The number of dengue case when there is the different Infectious rate of dengue virus from vector to human.

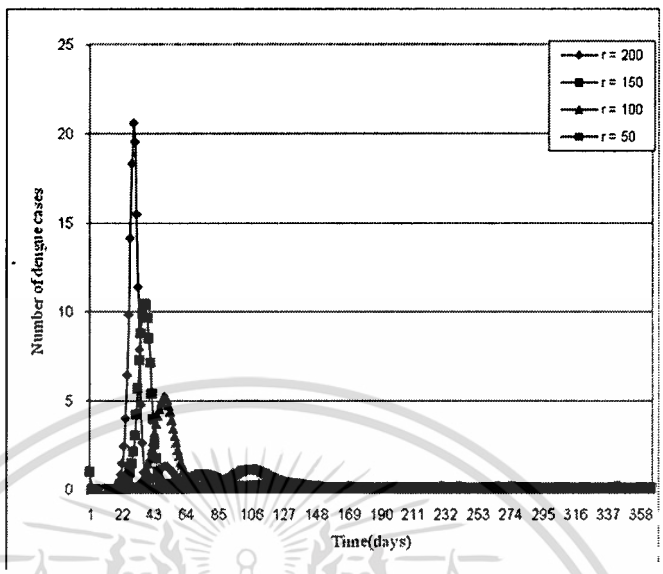


Figure 11.4. The number of dengue case when there is the different The distant of flying's mosquito.

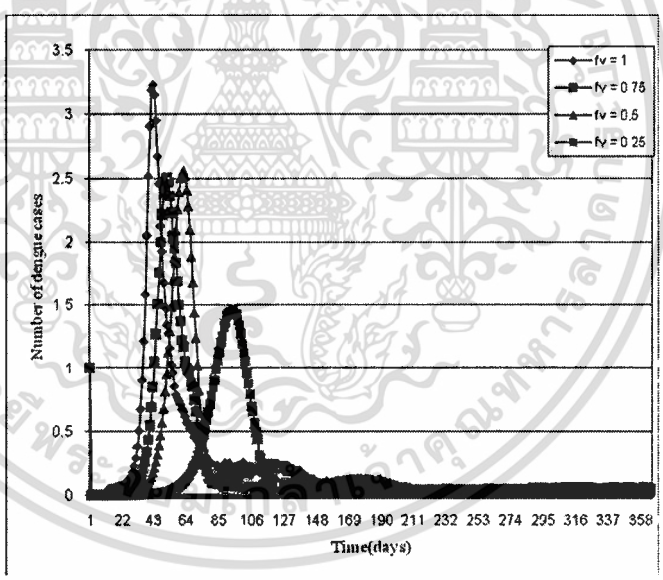


Figure 11.5. The number of dengue case when there is the different Infectious rate of dengue virus from human to vector.

Moreover, we consider when there are the different total human, mosquito populations and the number of houses. The results are shown in Figure6, Figure7 and Figure8.

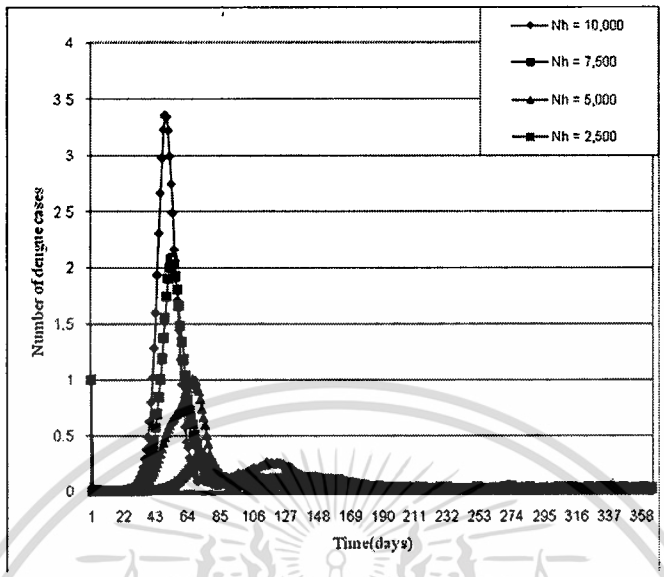


Figure 11.6. The number of dengue case when there is the different total number of human.

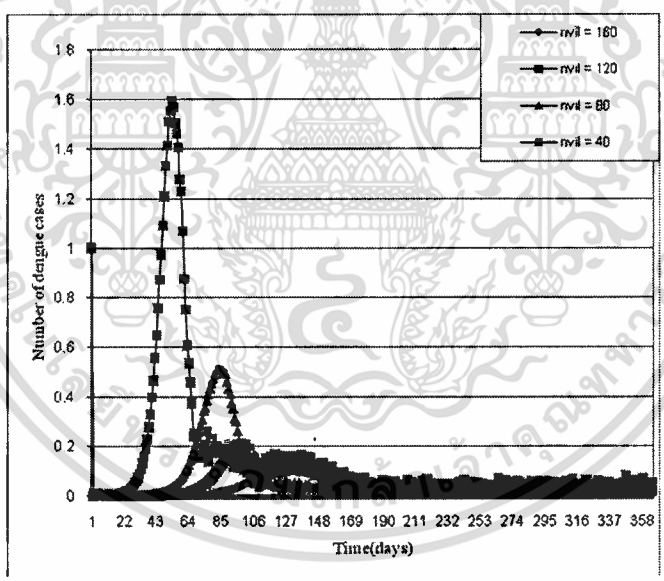


Figure 11.7. The number of dengue case when there is the different total number of human.

In this study, we simulate the different set of parameters to see the factors effect to the transmission of this disease. From our simulations, we found that when percentage of flooding (φ), Infectious rate of dengue virus from vector to human(f_h) are increasing, The distant of flying 's mosquito(r) and the total human population is increasing, the infectious dengue case is increasing and the outburst time of dengue epidemic is longer. But when the number of house is increasing, the number of dengue case is decreasing and the outburst of dengue epidemic is shorter. The preliminary results of this study should suggest the factors influence to dengue transmission.

4.12 แบบจำลองที่ 12 แบบจำลองของโรคไข้เลือดออกเมื่อพิจารณาถึงสิ่งแวดล้อม [67]

We are interested in the effects of environment factors on the spread of DF in Thailand, we have used the SEIRS (host (human) population (the recovered can be susceptible to infection by another serotypes of the DENV) model to describe the transmission of the DF in Thailand. We have taken the mean temperature, and cumulative rainfall to be the values for those southern Thailand. In the flow chart appearing in Figure 12.1, $N_{a(b)}$ is the total human population which will be bitten by an *A. aegypti* mosquito (denoted by the subscript (a)) or by an *A. albopictus* mosquito (now dented by the subscript (b)). The two human populations are each divided into five compartments, $S_i(t)$, $E_i(t)$, $I_i(t)$, $R_i(t)$ and $S_i'(t)$ are the numbers of humans who are susceptible to the dengue virus carried by a specie 'i' mosquito (i is a if the specie is *A. aegypti* and is "b" if the specie is *A. albopictus* the i-th specie of mosquitoes, infected but not infectious, infectious, recovered and susceptible to infection by the second serotype virus, respectively. Denoting the total numbers of *A. aegypti* mosquitoes and *A. albopictus* mosquitoes as N_{va} or N_{vb}. If a second serotype virus is present, then the recovered humans would be susceptible to infection by the second serotype virus. The last group however is immune to further infections by the same serotype of virus. The populations of each species of the mosquitoes are separated into three subclasses, S_{vi} (susceptible 'i' specie mosquito), E_{vi} (infected but not infectious 'i' specie mosquito) and I_{vi} (infectious 'i' specie mosquito). The flow charts for the different classes are shown in Figure12.1.

The dynamical equations for the different population are obtained by inspection and are

$$\frac{dS_a(t)}{dt} = aN_h - (T_{va}\psi_a\gamma_{vah}\frac{I_{va}(t)}{N_h+b} + \delta_h)S_a(t) + \theta_a R_a(t) \quad (12.1)$$

$$\frac{dE_a(t)}{dt} = (T_{va}\psi_a\gamma_{vah}\frac{I_{va}(t)}{N_h+b})S_a(t) - (\delta_h+\alpha_a)E_a(t) \quad (12.2)$$

$$\frac{dI_a(t)}{dt} = \alpha_a E_a(t) - (\delta_h+\beta_a)I_a(t) \quad (12.3)$$

$$\frac{dR_a(t)}{dt} = \beta_a I_a(t) - (\delta_h+\theta_a)R_a(t) \quad (12.4)$$

$$\frac{dS_b(t)}{dt} = (1-a)N_h - (T_{vb}\psi_b\gamma_{vbh}\frac{I_{vb}(t)}{N_h+b} + \delta_h)S_b(t) + \theta_b R_b(t) \quad (12.5)$$

$$\frac{dE_b(t)}{dt} = (T_{vb}\psi_b\gamma_{vbh}\frac{I_{vb}(t)}{N_h+b})S_b(t) - (\delta_h+\alpha_b)E_b(t) \quad (12.6)$$

$$\frac{dI_b(t)}{dt} = \alpha_b E_b(t) - (\delta_h+\beta_b)I_b(t) \quad (12.7)$$

$$\frac{dR_b(t)}{dt} = \beta_b I_b(t) - (\delta_h+\theta_b)R_b(t) \quad (12.8)$$

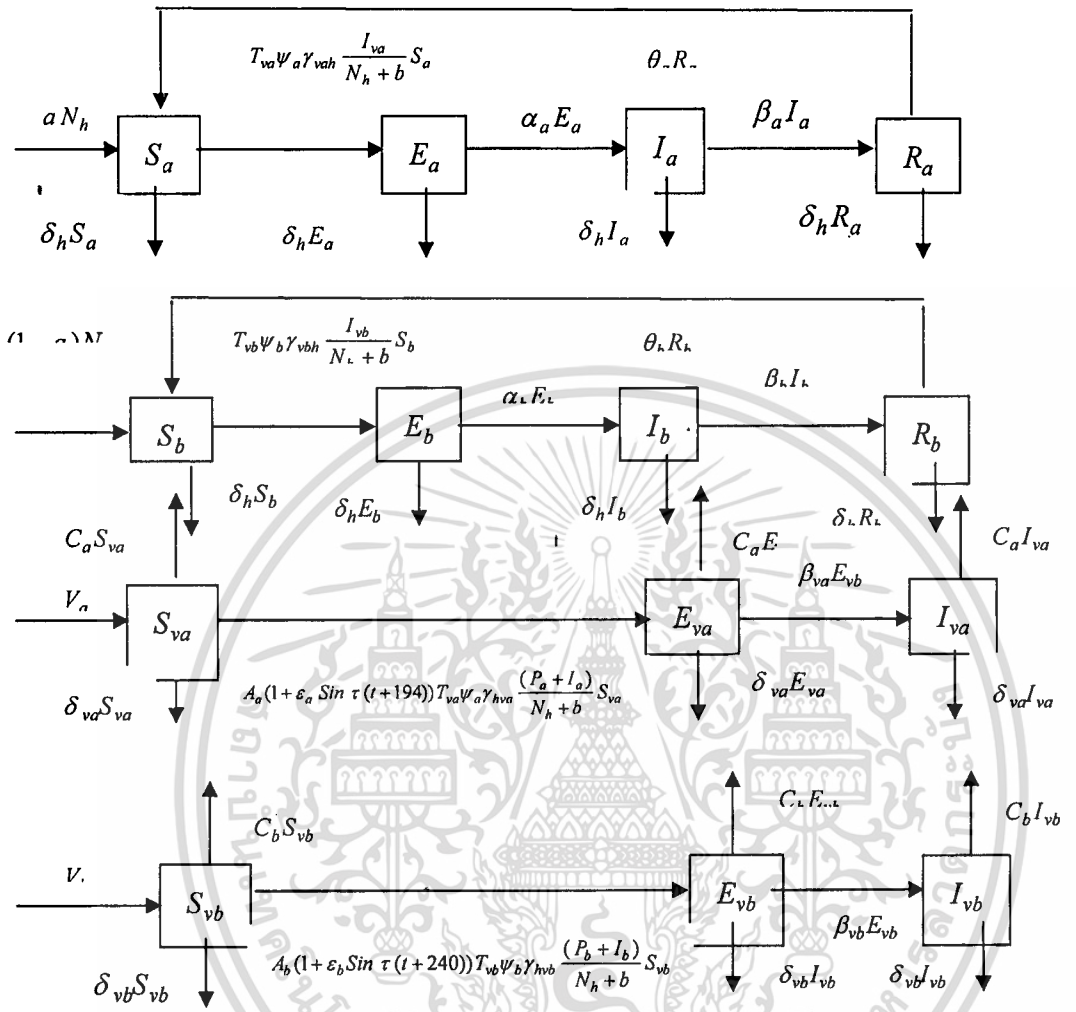


Figure 12.1. Flow Chart of the Model

The dynamical system are described by following equations.

$$\frac{dS_{va}(t)}{dt} = V_a - (A_a(1+\varepsilon_a Sin\tau(t+194))T_{va}\psi_a\gamma_{hva}\frac{(P_a+I_a(t))}{N_h+b} + C_a+\delta_{va})S_{va}(t) \quad (12.9)$$

$$\frac{dE_{va}(t)}{dt} = (A_a(1+\varepsilon_a Sin\tau(t+194))T_{va}\psi_a\gamma_{hva}\frac{(P_a+I_a(t))}{N_h+b})S_{va}(t) - (C_a+\delta_{va}-\beta_{va})E_{va}(t) \quad (12.10)$$

$$\frac{dI_{va}(t)}{dt} = \beta_{va}E_{va}(t) - (C_a+\delta_{va})I_{va}(t) \quad (12.11)$$

$$\frac{dS_{vb}(t)}{dt} = V_b - (A_b(1+\varepsilon_b Sin\tau(t+240))T_{vb}\psi_b\gamma_{hvb}\frac{(P_b+I_b(t))}{N_h+b} + C_b+\delta_{vb})S_{vb}(t) \quad (12.12)$$

$$\frac{dE_{vb}(t)}{dt} = (A_b(1+\varepsilon_b Sin\tau(t+240))T_{vb}\psi_b\gamma_{hvb}\frac{(P_b+I_b(t))}{N_h+b})S_{vb}(t) - (C_b+\delta_{vb}-\beta_{vb})E_{vb}(t) \quad (12.13)$$

$$\frac{dI_{vb}(t)}{dt} = \beta_{vb}E_{vb}(t) - (C_b+\delta_{vb})I_{vb}(t) \quad (12.14)$$

with

$$N_h = S_a(t)+E_a(t)+I_a(t)+R_a(t)+S_b(t)+E_b(t)+I_b(t)+R_b(t)\ , \quad (12.15)$$

$$N_{va} = S_{va}(t) + E_{va}(t) + I_{va}(t)\ , N_{vb} = S_{vb}(t) + E_{vb}(t) + I_{vb}(t) \qquad (12.16)$$

The parameters of our dynamical system are defined in the Table1. Taking the time derivative of N_h and N_{va} (and N_{vb}) and substituting the time derivates of the subpopulations Eqns. (12.1) to (14), we find that

$$\frac{dN_h}{dt} = 0,\ \frac{dN_{va}}{dt} = 0 \text{ and } \frac{dN_{va}}{dt} = 0$$

meaning that N_h, N_{va} and N_{vb} are independent of time, i.e., they are constants. Dividing Eqns. (12.1) – (12.14) by these constants and introducing the new variables.

$$\tilde{S}_a(t) = \frac{S_a(t)}{N_h},\ \tilde{E}_a(t) = \frac{E_a(t)}{N_h},\ \tilde{I}_a(t) = \frac{I_a(t)}{N_h},\ \tilde{R}_a(t) = \frac{R_a(t)}{N_h},\ \tilde{S}_b(t) = \frac{S_b(t)}{N_h},\ \tilde{E}_b(t) = \frac{E_b(t)}{N_h},\ \tilde{I}_b(t) = \frac{I_b(t)}{N_h},$$

$$\tilde{R}_b(t) = \frac{R_b(t)}{N_h},\ \tilde{S}_{va}(t) = \frac{S_{va}(t)}{V_a/(\delta_{va} + C_a)},\ \tilde{E}_{va}(t) = \frac{E_{va}(t)}{V_a/(\delta_{va} + C_a)},\ \tilde{I}_{va}(t) = \frac{I_{va}(t)}{V_a/(\delta_{va} + C_a)},$$

$$\tilde{S}_{vb}(t) = \frac{S_{vb}(t)}{V_b/(\delta_{vb} + C_b)},\ \tilde{E}_{vb}(t) = \frac{E_{vb}(t)}{V_b/(\delta_{vb} + C_b)},\ \tilde{I}_{vb}(t) = \frac{I_{vb}(t)}{V_b/(\delta_{vb} + C_b)}$$

Table 12.1. Definition of variables and parameters in the model.

Parameters	Definition
C_a and C_b	The control effort rates in *Aedes aegypti* and *Aedes albopictus*
δ_a and δ_b	The measure of influence on the transmission
μ_h	The constant recruitment rate of *Aedes aegypti*
Λ_h	The death rate of host population
μ_b	The constant recruitment rate of *Aedes albopictus*
μ_{va}	The development rate of adult female *Aedes aegypti* mosquitoes
μ_{vb}	The development rate of adult female *Aedes albopictus* mosquitoes
β_a	The biting rate of *Aedes aegypti* population
β_b	The biting rate of *Aedes albopictus* population
β_{vah}	The transmission probability (from *Aedes aegypti* to human population)
β_{vbh}	The transmission probability (from *Aedes albopictus* to human population)
β_{hva}	The transmission probability (from human population to *Aedes aegypti*)
β_{hvb}	The transmission probability (from human population to *Aedes albopictus*)
γ_a	The viral development rate of *Aedes aegypti* in human
γ_b	The viral development rate of *Aedes albopictus* in human
γ_{va}	The viral development rate of *Aedes aegypti* bodies
γ_{vb}	The viral development rate of *Aedes albopictus* bodies
α_a	The recovery rate of human population who be infected with *Aedes aegypti*
α_b	The recovery rate of human population who be infected with *Aedes albopictus*
ν_{va}	The death rate of *Aedes aegypti*
ν_{vb}	The death rate of *Aedes albopictus*

we obtain the new set of equations

$$\frac{d\tilde{S}_a(t)}{dt} = a-(T_{va}\psi_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}+\delta_h)\tilde{S}_a(t)+\theta_a\tilde{R}_a(t) \quad (12.17)$$

$$\frac{d\tilde{E}_a(t)}{dt} = (T_{va}\psi_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b})\tilde{S}_a(t)-(\delta_h+\alpha_a)\tilde{E}_a(t) \quad (12.18)$$

$$\frac{d\tilde{I}_a(t)}{dt} = \alpha_a\tilde{E}_a(t)-(\delta_h+\beta_a)\tilde{I}_a(t) \quad (12.19)$$

$$\frac{d\tilde{S}_b(t)}{dt} = (1-a)-(T_{vb}\psi_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}+\delta_h)\tilde{S}_b(t)+\theta_b\tilde{R}_b(t) \quad (12.20)$$

$$\frac{d\tilde{E}_b(t)}{dt} = (T_{vb}\psi_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b})\tilde{S}_b(t)-(\delta_h+\alpha_b)\tilde{E}_b(t) \quad (12.21)$$

$$\frac{d\tilde{I}_b(t)}{dt} = \alpha_b\tilde{E}_b(t)-(\delta_h+\beta_b)\tilde{I}_b(t) \quad (12.22)$$

$$\frac{d\tilde{E}_{va}(t)}{dt} = (A_a(1+\varepsilon_a Sin\pi(t+194))T_{va}\psi_a\gamma_{hva}\frac{(P_a+\tilde{I}_a(t)^*N_h)}{N_h+b})(1-\tilde{E}_{va}(t)-\tilde{I}_{va}(t))-(C_a+\delta_{va}-\beta_{va})\tilde{E}_{va}(t) \quad (12.23)$$

$$\frac{d\tilde{I}_{va}(t)}{dt} = \beta_{va}\tilde{E}_{va}(t)-(C_a+\delta_{va})\tilde{I}_{va}(t) \quad (12.24)$$

$$\frac{d\tilde{E}_{vb}(t)}{dt} = (A_b(1+\varepsilon_b Sin\pi(t+240))T_{vb}\psi_b\gamma_{hvb}\frac{(P_b+\tilde{I}_b(t)^*N_h)}{N_h+b})(1-\tilde{E}_{vb}(t)-\tilde{I}_{vb}(t))-(C_b+\delta_{vb}-\beta_{vb})\tilde{E}_{vb}(t) \quad (12.25)$$

$$\frac{d\tilde{I}_{vb}(t)}{dt} = \beta_{vb}\tilde{E}_{vb}(t)-(C_b+\delta_{vb})\tilde{I}_{vb}(t) \quad (12.26)$$

with $\tilde{S}_a+\tilde{E}_a+\tilde{I}_a+\tilde{R}_a=1$, $\tilde{S}_{va}+\tilde{E}_{va}+\tilde{I}_{va}=1$, $\tilde{S}_{vb}+\tilde{E}_{vb}+\tilde{I}_{vb}=1$. The peak number of mosquito population in a given year are determined by $(A_a(1+\varepsilon_a Sin\,\tau(t+194))$ and $(A_b(1+\varepsilon_b Sin\,\tau(t+240))$, In this paper, we took the period of *A. aegypti* reproduction to be 194 and of the *A. albopictus*, to be 240.

The equilibrium points are obtained by setting the RHS of Eqns. (12.17) – (12.26) to zero. We only consider solutions in the domains

$\Omega_a=\{(\tilde{S}_a,\tilde{E}_a,\tilde{I}_a,\tilde{E}_{va},\tilde{I}_{va}):\tilde{S}_a,\tilde{E}_a,\tilde{I}_a,\tilde{E}_{va},\tilde{I}_{va}\geq 0,\tilde{S}_a+\tilde{E}_a+\tilde{I}_a,\tilde{E}_{va}+\tilde{I}_{va}\leq 1\}$

$\Omega_b=\{(\tilde{S}_b,\tilde{E}_b,\tilde{I}_b,\tilde{E}_{vb},\tilde{I}_{vb}):\tilde{S}_b,\tilde{E}_b,\tilde{I}_b,\tilde{E}_{vb},\tilde{I}_{vb}\geq 0,\tilde{S}_b+\tilde{E}_b+\tilde{I}_b,\tilde{E}_{vb}+\tilde{I}_{vb}\leq 1\}$

since the flow generated by vector field of equation (12.17) – (12.26) in these regions will be positive invariant and the trajectories must not pass into the exterior region of Ω_a and Ω_b.otherwise some of the populations would become negative which is impossible. The equilibrium points in our model are

i) Disease free equilibrium point: $S_{0a}=(1,0,0,0,0)$ if the infecting mosquito is *A. aegypti* and $S_{0b}=(1,0,0,0,0)$ if the infecting mosquito is *A. albopictus*.

ii) Endemic disease equilibrium point: $S^*_{0a}=(S''_a,E''_a,I''_a,E''_{va},I''_{va})$ when the infecting mosquito is *Aedes aegypti* and $S^*_{0b}=(S''_b,E''_b,I''_b,E''_{vb},I''_{vb})$ if the infecting mosquito is *A. albopictus*.

The equilibrium populations are

$$S_a'' = \frac{-a-\theta_a+I_a''\theta_a+\dfrac{A_a(I_a''N_h+P_a)\omega_5(a+\theta_a-I_a''\theta_a)}{\omega_3+A_a(I_a''N_h+P_a)\omega_4}}{\delta_h+\theta_a+\dfrac{(I_a''N_h+P_a)\omega_6}{\omega_7+A_a(I_a''N_h+P_a)\omega_8}} \quad (12.27)$$

$$E_a'' = \frac{A_a(I_a''N_h+P_a)\,\beta_{va}(a+\theta_a-I_a''\theta_a)\omega_1\omega_2}{\omega_3+A_a(I_a''N_h+P_a)\omega_4} \quad (12.28)$$

$$I_a'' = \frac{1}{(2A_aN_h(\alpha_a\beta_a\theta_a\omega_1\omega_2+(\beta_a+\delta_h)\omega_4))}(aA_aN_h\alpha_a\beta_a\omega_1\omega_2+A_aN_h\alpha_a\theta_a\beta_a\omega_1\omega_2-A_aP_a\alpha_a\beta_a\theta_a\omega_1\omega_2-\beta_a\omega_3+\delta_a\omega_3$$
$$A_aP_a\beta_a\omega_4+A_aP_a\delta_h\omega_4+\sqrt{A(A_a^2N_h^2P_a^2\alpha_a^2\beta_a^2(a+\theta_a)^2\omega_1^2\omega_2^2(\alpha_a\beta_a\theta_a\omega_1\omega_2+(\beta_a+\delta_h)\omega_4)^2+(-A_a\alpha_a\beta_a(aN_h^2+(N_h-P_a^2)\theta_a)\omega_1\omega_2+(\beta_a+\delta_h)\omega_3+A_aP_a(\beta_a+\delta_h)\omega_4)^2))} \quad (12.29)$$

$$E_{va}'' = \frac{A_a(I_a''N_h+P_a)\omega_2(-\omega_7+A_a(I_a''N_h+P_a)(\beta_{va}\omega_2-\omega_8))}{\omega_9+A_a(I_a''N_h+P_a)\omega_2)(\omega_7+A_a(I_a''N_h+P_a)\omega_8)} \quad (12.30)$$

$$I_{va}'' = \frac{A_a(I_a''N_h+P_a)\,\beta_{va}\omega_2}{\omega_7+A_a(I_a''N_h+P_a)\omega_8} \quad (12.31)$$

$$S_b'' = \frac{-1+a-\theta_b+I_b''\theta_b+\dfrac{A_b(I_b''N_h+P_b)\beta_{vb}\theta_b(-1+a+(-1+I_b'')\theta_b)\mu_1\mu_2}{\mu_3+A_b(I_b''N_h+P_b)\mu_4}}{\delta_h+\theta_b+\dfrac{A_b(I_b''N_h+P_b)\mu_{10}}{\mu_6+A_b(I_b''N_h+P_b)\mu_7}} \quad (12.32)$$

$$E_b'' = \frac{A_b(I_b''N_h+P_b)\beta_{vb}(-1+a+(-1+I_b'')\theta_b)\mu_1\mu_2}{\mu_3+A_b(I_b''N_h+P_b)\mu_4} \quad (12.33)$$

$$I_b'' = \frac{1}{(2A_bN_h(\alpha_b\beta_b\theta_b\mu_1\mu_2+(\beta_b+\delta_h)\mu_4))}(A_b\alpha_bN_h\alpha_b\beta_b(P_b\theta_b+N_h(1-a+\theta_b))+\mu_1\mu_2+(\beta_b+\delta_h)\mu_3+A_bP_b(\beta_b+\delta_h)\mu_4+$$
$$\sqrt{((\beta_b+\delta_h)^2\mu_3^2+2A_b(\beta_b+\delta_h)\mu_3(\alpha_b\beta_b(N_h-aN_h+N_h\theta_b-P_b\theta_b)\mu_1\mu_2+P_b(\beta_b+\delta_h)\mu_4)+(A_b\alpha_b\beta_b(-1+a)N_h-(N_h+P_b)\theta_b)\mu_1\mu_2+A_bP_b(\beta_b+\delta_h)\mu_4)^2))} \quad (12.34)$$

$$I_{vb}'' = \frac{A_b(I_b''N_h+P_b)\beta_{vb}\mu_2}{\mu_6+A_b(I_b''N_h+P_b)\mu_7} \quad (12.35)$$

$$E_{vb}'' = \frac{A_b(I_b''N_h+P_b)\mu_2(-\mu_6+A_b(I_b''N_h+P_b)\mu_9)}{\mu_8+A_b(I_b''N_h+P_b)\mu_2(\mu_6+A_b(I_b''N_h+P_b)\mu_7)} \quad (12.36)$$

where

$$\omega_1 = \frac{\gamma_{vah}T_{va}V_a\psi_a}{(N_h+b)(\delta_{va}+C_a)}, \omega_2 = \frac{\gamma_{hva}T_{va}\psi_a(1+\varepsilon_a\,Sin\,\tau(t+194))}{N_h+b},$$

$$\omega_3 = (\alpha_a+\delta_h)(\delta_{va}+C_a)(C_a+\beta_{va}+\delta_{va})(\delta_h+\theta_a),$$

$$\omega_4 = ((\alpha_a+\delta_h)(C_a-\beta_{va}+\delta_{va})(\delta_h+\theta_a)+\beta_{va}(\alpha_a+\delta_h+\theta_a)\omega_1)\omega_2,\ \omega_5 = \beta_{va}\theta_a\omega_1\omega_2,\ \omega_6 = A_a\beta_{va}\omega_1\omega_2,$$

$$\omega_7 = (\delta_{va}+C_a)(C_a+\beta_{va}+\delta_{va}),\ \omega_8 = (C_a-\beta_{va}+\delta_{va})\omega_2,\ \omega_9 = C_a+\beta_{va}+\delta_{va}$$

$$\mu_1 = \frac{\gamma_{vbh}T_{vb}V_b\psi_b}{(N_h+b)(\delta_{vb}+C_b)}, \mu_2 = \frac{\gamma_{vbh}T_{vb}\psi_b(1+\varepsilon_b\,Sin\,\tau(t+240))}{N_h+b},$$

$$\mu_3 = (\alpha_b+\delta_h)(\delta_{vb}+C_b)(C_b+\beta_{vb}+\delta_{vb})(\delta_h+\theta_b),$$

$$\mu_4 = ((\alpha_b+\delta_h)(C_b-\beta_{vb}+\delta_{vb})(\delta_h+\theta_b)+\beta_{vb}(\alpha_b+\delta_h-\theta_b)\mu_1)\mu_2,\ \mu_6 = (\delta_{vb}+C_b)(C_b+\beta_{vb}+\delta_{vb}),$$

$$\mu_7 = (C_b-\beta_{vb}+\delta_{vb})\mu_2,\ \mu_8 = C_b+\beta_{vb}+\delta_{vb},\ \mu_9 = \beta_{vb}\mu_2-\mu_7,\ \mu_{10} = \beta_{vb}\mu_1\mu_2.$$

4. Local Stability of SEIRS Model.

The local stability of an equilibrium point is determined from the Jacobian matrix of the system of Eqns. (12.17) – (12.26) evaluated at the equilibrium points. If all the eigenvalues have negative real parts, then the equilibrium point will be locally asymptotically stable. The standard dynamical modeling method [20] is used in this study. From (12.17) – (12.26), the Jacobian matrices are:

$$A_{aa}=\begin{pmatrix} -(T_{va}W_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}+\delta_h) & 0 & 0 & 0 & -(T_{va}W_a\gamma_{vah}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b})\tilde{S}_a(t) \\ (T_{va}W_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}) & -(\delta_h+\alpha_a) & 0 & 0 & (T_{va}W_a\gamma_{vah}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b})\tilde{S}_a(t) \\ 0 & \alpha_a & -(\delta_h+\beta_h) & 0 & 0 \\ 0 & 0 & (A_h(1+\varepsilon_h Sin\pi(t+194)T_{va}W_a\gamma_{hva}\frac{(P_a+N_h)}{N_h+b})(1-\tilde{E}_{va}(t)-\tilde{I}_{va}(t)) & -(C_a+\delta_{va}-\beta_{va}) & 0 \\ 0 & 0 & 0 & \beta_{va} & -(C_a+\delta_{va}) \end{pmatrix} \quad (12.37a)$$

$$A_{bb}=\begin{pmatrix} -(T_{vb}W_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}+\delta_h) & 0 & 0 & 0 & -(T_{vb}W_b\gamma_{vbh}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b})\tilde{S}_b(t) \\ (T_{vb}W_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}) & -(\delta_h+\alpha_b) & 0 & 0 & (T_{vb}W_b\gamma_{vbh}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b})\tilde{S}_b(t) \\ 0 & \alpha_b & -(\delta_h+\beta_h) & 0 & 0 \\ 0 & 0 & (A_h(1+\varepsilon_h Sin\pi(t+24)T_{vb}W_b\gamma_{hvb}\frac{(P_b+N_h)}{N_h+b})(1-\tilde{E}_{vb}(t)-\tilde{I}_{vb}(t)) & -(C_b+\delta_{vb}-\beta_{vb}) & 0 \\ 0 & 0 & 0 & \beta_{vb} & -(C_b+\delta_{vb}) \end{pmatrix} \quad (12.37b)$$

The characteristic equation is determined from

$$|A_{aa}-\lambda I|=\begin{pmatrix} -(T_{va}W_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}+\delta_h)-\lambda & 0 & 0 & 0 & -(T_{va}W_a\gamma_{vah}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b})\tilde{S}_a(t) \\ (T_{va}W_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}) & -(\delta_h+\alpha_a)-\lambda & 0 & 0 & (T_{va}W_a\gamma_{vah}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b})\tilde{S}_a(t) \\ 0 & \alpha_a & -(\delta_h+\beta_h)-\lambda & 0 & 0 \\ 0 & 0 & (A_h(1+\varepsilon_h Sin\pi(t+194)T_{va}W_a\gamma_{hva}\frac{(P_a+N_h)}{N_h+b})(1-\tilde{E}_{va}(t)-\tilde{I}_{va}(t)) & -(C_a+\delta_{va}-\beta_{va})-\lambda & 0 \\ 0 & 0 & 0 & \beta_{va} & -(C_a+\delta_{va})-\lambda \end{pmatrix}=0 \quad (12.38a)$$

when A_{aa} is Jacobian matrix for endemic equilibrium point of *A. aegypti*, λ is the eigenvalue, I is the identity matrix and

$$|A_{bb}-\lambda I|=\begin{pmatrix} -(T_{vb}W_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}+\delta_h)-\lambda & 0 & 0 & 0 & -(T_{vb}W_b\gamma_{vbh}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b})\tilde{S}_b(t) \\ (T_{vb}W_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}) & -(\delta_h+\alpha_b)-\lambda & 0 & 0 & (T_{vb}W_b\gamma_{vbh}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b})\tilde{S}_b(t) \\ 0 & \alpha_b & -(\delta_h+\beta_h)-\lambda & 0 & 0 \\ 0 & 0 & (A_h(1+\varepsilon_h Sin\pi(t+24)T_{vb}W_b\gamma_{hvb}\frac{(P_b+N_h)}{N_h+b})(1-\tilde{E}_{vb}(t)-\tilde{I}_{vb}(t)) & -(C_b+\delta_{vb}-\beta_{vb})-\lambda & 0 \\ 0 & 0 & 0 & \beta_{vb} & -(C_b+\delta_{vb})-\lambda \end{pmatrix}=0 \quad (12.38b)$$

when A_{bb} is the Jacobian matrix for endemic equilibrium point of *A. albopictus* case, λ is the eigenvalue, I is the identity matrix.

The eigenvalues of $|A_{aa}-\lambda I|$ in *A. aegypti* and $|A_{bb}-\lambda I|$ in *A. albopictus* are obtained by solving $\det(A_{aa}-\lambda I_5)=0$ and $\det(A_{bb}-\lambda I_5)=0$, where A_{aa} and A_{bb} are Jacobian matrix for the two species, Eqns. (37a) and (37b) respectively. We are interested in the stabilities of the endemic equilibrium points.

Lemma: If $S_0>1$, the endemic equilibrium S^*_{0a} and S^*_{0b} of Eqns. (17) – (26) is locally asymptotically stable in Ω_a and Ω_b, with the basic reproduction number S_0 is given by [20]

$$S_0 = Max\{S_{0a}, S_{0b}\}$$

where

$$S_{0a}=(\alpha A_h N_h\alpha_a\beta_a\rho_a\varepsilon_a+A_h N_h\alpha_a\beta_a\beta_a\rho_a\varepsilon_a+\delta_a\rho_a+\sqrt{A(A_h^2N_h^2P_a\alpha_a\beta_a(\alpha+\theta_a)\varepsilon_a\varepsilon_a(\alpha_a\beta_a\beta_a\rho_a\varepsilon_a+(\beta_a+\delta_h)\varepsilon_a+(-A_h\alpha_a\beta_a(\alpha)N_h+(N_h-P_a)\theta_a)\varepsilon_a\varepsilon_a+(\beta_a+\delta_h)\alpha_a+A_h^2P_a^2(\beta_a+\delta_h)\alpha_a)^2)))/$$
$$(\beta_a\alpha_a+A_h^2P_a(\alpha_a\beta_a\beta_a\rho_a\varepsilon_a+(\beta_a+\delta_h)\varepsilon_a)) \quad (12.39)$$

$$S_{0b} = \frac{(A_b N_h \alpha_b \beta_{vb} \mu_4 \mu_2 + A_b N_h \alpha_b \beta_{vb} \theta_b \mu_4 \mu_2 + \beta_b \mu_3 + \delta_{vb} \mu_3 + A_b P_b \beta_{vb} \mu_4 + A_b P_b \delta_{vb} \mu_4 + \sqrt{((\beta_b+\delta_h)^2 \mu_3^2 + 2A_b(\beta_b+\delta_h)\mu_3(\alpha_b\beta_{vb}(N_h - aN_h + N_h\theta_b - P_b\theta_b)\mu_4\mu_2 + P_b(\beta_b+\delta_{vb})\mu_4) + (A_b\alpha_b\beta_{vb}((-1+a)N_h - (N_h+P_b)\theta_b)\mu_4\mu_2 + A_b P_b(\beta_b+\delta_h)\mu_4)^2)))}{\alpha(A_b N_h \alpha_b \beta_{vb} \mu_4 \mu_2 + A_b \alpha_b P_b \beta_{vb} \theta_b \mu_4 \mu_2)} \quad (12.40)$$

with $\Omega_a = \{(\tilde{S}_a, \tilde{E}_a, \tilde{I}_a, \tilde{E}_{va}, \tilde{I}_{va}) : \tilde{S}_a, \tilde{E}_a, \tilde{I}_a, \tilde{E}_{va}, \tilde{I}_{va} \geq 0, \tilde{S}_a + \tilde{E}_a + \tilde{I}_a, \tilde{E}_{va} + \tilde{I}_{va} \leq 1\}$.

Proof. After evaluating the eigenvalue equation, Eqn. (38a), i.e., we need to solve $\det(A_a - \lambda I_5) = 0$. Doing this, we obtain

$$(\alpha_a + \delta_h + \lambda)(\beta_a + \delta_h + \lambda)(\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3) = 0 \quad (12.41)$$

where,

$$A_1 = 2C_a + \beta_{va} + \delta_h + 2\delta_{va} + \frac{A_a(I_a'' N_h + P_a)\beta_{va}\omega_1\omega_2}{\omega_7 + A_a(I_a'' N_h + P_a)\omega_8},$$

$$A_2 = C_a^2 + \delta_{va}(2\delta_h + \delta_{va}) + C_a(\beta_{va} + 2\delta_h + 2\delta_{va} + \frac{2A_a(I_a'' N_h + P_a)\beta_{va}\omega_1\omega_2}{\omega_7 + A_a(I_a'' N_h + P_a)\omega_8}) + \beta_{va}(\delta_h + \frac{\delta_{va}(\omega_7 + A_a(I_a'' N_h + P_a)(2\omega_1\omega_2 + \omega_8))}{\omega_7 + A_a(I_a'' N_h + P_a)\omega_8}$$
$$+ (A_a N_h \alpha_a (a + \theta_a - I_a'' \theta_a)\omega_1\omega_2(\omega_3 + A_a(I_a'' N_h + P_a)(\omega_4 - \omega_5))(\omega_7 + A_a(I_a'' N_h + P_a)\omega_8)(2A_a(I_a'' N_h + P_a)\omega_2 + \omega_9))/$$
$$((\omega_3 + A_a(I_a'' N_h + P_a)\omega_4)((\delta_h + \theta_a)\omega_7 + (I_a'' N_h + P_a)(\omega_6 + A_a(\delta_h + \theta_a)\omega_8))(A_a(I_a'' N_h + P_a)\omega_2 + \omega_9))) +$$
$$(A_a(I_a'' N_h + P_a)\beta_{va}^2 \omega_1\omega_2(A_a(I_a'' N_h + P_a)\omega_2\omega_3(I_a'' N_h\omega_6 + P_a\omega_6 + (\delta_h + \theta_a)\omega_7 - 2A_a^4 N_h(I_a'' N_h + P_a)^3 \alpha_a(a + \theta_a - I_a''\theta_a)\omega_2^2$$
$$(\omega_4 - \omega_5)\omega_8 + \omega_3(I_a'' N_h\omega_6 + P_a^2\omega_4\omega_6 + (\delta_h + \theta_a)\omega_7)\omega_9 + A_a(I_a''^2 N_h^2\omega_4\omega_6 + P_a^2\omega_4\omega_6 - N_h\alpha_a(a + \theta_a)\omega_2\omega_3\omega_7 +$$
$$P_a(\delta_h + \theta_a)(\omega_4\omega_7 + \omega_3\omega_8) + I_a'' N_h(2P_a\omega_4\omega_6 + \alpha_a\theta_a\omega_2\omega_3\omega_7 + (\delta_h + \theta_a)(\omega_4\omega_7 + \omega_3\omega_8)))\omega_9 + A_a^2(I_a'' N_h + P_a)$$
$$(I_a''^2 N_h^2\omega_2\omega_4\omega_6 + P_a^2\omega_2\omega_4\omega_6 + P_a(\delta_h + \theta_a)(\omega_2\omega_4\omega_7 + \omega_2\omega_3\omega_8 - \omega_4\omega_8\omega_9) - N_h\alpha_a(a + \theta_a)\omega_2(2\omega_2\omega_3\omega_7 + (\omega_4\omega_7$$
$$- \omega_5\omega_7 + \omega_3\omega_8)\omega_9) + I_a'' N(2P_a\omega_2\omega_4\omega_6 + \alpha_a\theta_a\omega_2(2\omega_2\omega_3\omega_7 + \omega_4\omega_7\omega_9 - \omega_5\omega_7\omega_9 + \omega_3\omega_8\omega_9) + (\delta_h + \theta_a)(\omega_2\omega_4\omega_7 +$$
$$\omega_2\omega_3\omega_8 + \omega_4\omega_8\omega_9))) + A_a^2(I_a'' N_h + P_a)^2\omega_2(P_a(\delta_h + \theta_a)\omega_4\omega_8 + aN_h\alpha_a(-2\omega_2(\omega_4\omega_7 - \omega_5\omega_7 + \omega_3\omega_8) + (-\omega_4 + \omega_5)\omega_8\omega_9)$$
$$+ N_h(I_a''(\delta_h + \theta_a)\omega_4\omega_8 + (-1 + I_a'')\alpha_a\theta_a(2\omega_2(\omega_4\omega_7 - \omega_5\omega_7 + \omega_3\omega_8) + (-\omega_4 + \omega_5)\omega_8\omega_9))))))/$$
$$((\omega_3 + A_a(I_a'' N_h + P_a)\omega_4(\omega_7 + (I_a'' N_h + P_a)\omega_8)((\delta_h + \theta_a)\omega_7 + (I_a'' N_h + P_a)(\omega_6 + (I_a'' N_h + P_a)\omega_8))$$
$$(A_a(I_a'' N_h + P_a)\omega_2 + \omega_9))$$

The first two eigenvalues are $\lambda_1 = -\alpha_a - \delta_h$ and $\lambda_2 = -\beta_a - \delta_h$. They are always negative. The other eigenvalues λ_3, λ_4 and λ_5 which are the solutions to the cubic equation

$$\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3 = 0. \quad (12.42)$$

According the Routh-Hurwitz theory, the three solutions to the characteristic equations in the form of the cubic equations above will all be negative if the coefficients A_1, A_2 and A_3 satisfy the relations

$$A_1 > 0 \ , \ A_3 > 0 \ , \ A_1 A_2 > 0 \quad (12.43)$$

We have plotted the values of A_1, A_2 and A_3 for a set of fixed values appropriate to the *A. aegypti* mosquitoes and a range of viral development rates in this specie of mosquitoes β_{va}. It should be remembered that this rate depends on the temperature of the environment. The fixed values of the other parameters are

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365 * 74.6)\ \text{day}^{-1}$, $a = 0.077$, $N_h = 200{,}000$, $\beta_a = 1/14$, $\alpha_a = 1/6$, $\beta_{va} = 0.11$, $\psi_a = 1/11$, $\gamma_{vah} = 0.0048$, $\gamma_{hva} = 0.0086$, $T_{va} = 0.2$, $A_a = 3000$, $P_a = 0.07$, $C_a = 0.008$, $\theta_a = 1/6$, $b = 6{,}000$, $V_a = 90{,}000$ and $\delta_{va} = 1/3$.

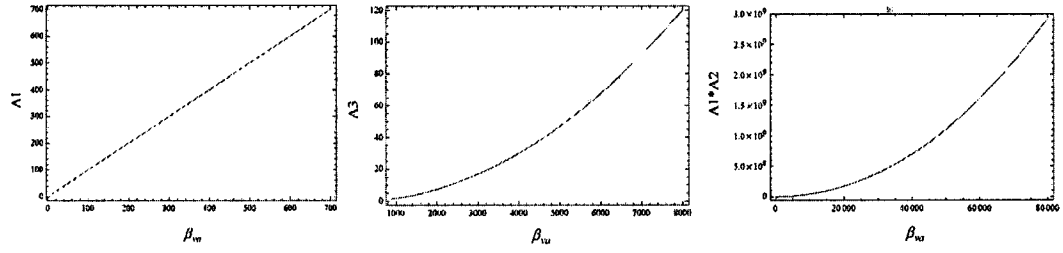


Figure 12.3. The parameters spaces for the endemic equilibrium point which satisfies the Routh – Hurwitz criteria with the value of parameters in S_a'', E_a'', I_a'', E_{va}'' and I_{va}'' for the parameter values listed in the text.

These values will lead to $S_0 > 1$ Looking at the three graphs in Figure 12.3, we see that the conditions stated in Eqn. (40) are satisfied and so the equilibrium state S^*_{0a} is locally asymptotically stable.

To see whether S^*_{0b} is locally asymptotically stable, we evaluate Eqn. (12.38b) to get

$$(\alpha_b + \delta_h + \lambda)(\beta_b + \delta_h + \lambda)(\lambda^3 + B_1\lambda^2 + B_2\lambda + B_3) = 0 \qquad (12.44)$$

where

$$B_1 = 2C_b + \beta_{vb} + \delta_h + 2\delta_{vb} + \frac{A_b(I_b''N_h + P_b)\beta_{vb}\mu_1\mu_2}{\mu_6 + A_b(I_b''N_h + P_b)\mu_7},$$

$$B_2 = C_b^2 + \delta_{vb}(2\delta_h + \delta_{vb}) + C_b(\beta_{vb} + 2\delta_h + 2\delta_{vb} + \frac{2A_b(I_b''N_h + P_b)\beta_{vb}\mu_1\mu_2}{\mu_6 + A_b(I_b''N_h + P_b)\mu_7}) + (A_b^3 N_h(I_b''N_h + P_b)^2$$
$$\alpha_b\beta_{vb}^3\theta_b(-1 + a(-1 + I_b'')\theta_b\mu_1^2\mu_2^3)/((\mu_3 + A_b(I_b''N_h + P_b)\mu_4)((2\delta_h + \theta_b)\mu_6 + A_b(I_b''N_h + P_b)$$
$$(\mu_{10} + (\delta_h + \theta_b)\mu_7))) + \beta_{vb}(\delta_h + \frac{\delta_{vb}(\mu_6 + A_b(I_b''N_h + P_b)(2\mu_1\mu_2 + \mu_7))}{\mu_6 + A_b(I_b''N_h + P_b)\mu_7} - (A_b N_h \alpha_b(-1 + a(-1 + I_b'')\theta_b)$$
$$\mu_1\mu_2(\mu_6\mu_8 + A_b(I_b''N_h + P_b)(2\mu_2\mu_6 + \mu_7\mu_8) + A_b^2(I_b''N_h + P_b)^2\mu_2(\mu_7 - \mu_9)))/(((\delta_h + \theta_b)\mu_6 +$$
$$A_b(I_b''N_h + P_b)(\mu_{10} + (\delta_h + \theta_b)\mu_7))(A_b(I_b''N_h + P_b)\mu_2 + \mu_8))) + (A_b(I_b''N_h + P_b)\beta_{vb}^2\mu_1\mu_2(A_b(I_b''N_h + P_b)$$
$$(\delta_h + \theta_b)\mu_2\mu_3\mu_6 + (\delta_h + \theta_b)\mu_3\mu_6\mu_8 + A_b(N_h\alpha_b(-1 + a - \theta_b)\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6) + P_b(\mu_{10}\mu_3 + (\delta_h + \theta_b)$$
$$(\mu_4\mu_6 + \mu_3\mu_7)) + I_b''N_h(\mu_{10}\mu_3 + \alpha_b\theta_b\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6) + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7)))\mu_8 +$$
$$A_b^2(I_b''N_h + P_b)(P_b\mu_2(\mu_{10}\mu_3 + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7)) + P_b\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7)\mu_8 + N_h\alpha_b$$
$$(-1 + a - \theta_b)\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6) + (\mu_4\mu_6 + (\mu_3 - 2\theta_b\mu_1\mu_6)\mu_7)\mu_8 + I_b''N_h(\mu_{10}(\mu_2\mu_3 + \mu_4\mu_8) + (\delta_h + \theta_b)$$
$$(\mu_2\mu_4\mu_6 + \mu_2\mu_3\mu_7 + \mu_4\mu_7\mu_8) + \alpha_b\theta_b\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6) + (\mu_4\mu_6 + \mu_3\mu_7 - 2\theta_b\mu_1\mu_6\mu_7)\mu_8))) +$$
$$A_b^4N_h(I_b''N_h + P_b)^3\alpha_b(-1 + a + (-1 + I_b'')\theta_b)\mu_2^2\mu_7(\mu_4 + \theta_b\mu_1(-\mu_7 + \mu_9)) + A_b^3(I_b''N_h + P_b)^2\mu_2(P_b\mu_4$$
$$(\mu_{10} + (\delta_h + \theta_b)\mu_7) + N_h\alpha_b(-1 + a - \theta_b)(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8 + \mu_2(\mu_3\mu_7 + \mu_6(\mu_4\mu_2 + \theta_b\mu_1(-3\mu_7 + \mu_9)))) +$$
$$I_b''N_h(\mu_{10}\mu_4 + (\delta_h + \theta_b)\mu_4\mu_7 + \alpha_b\theta_b(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8 + \mu_2(\mu_3\mu_7 + \mu_6(\mu_4\mu_2 + \theta_b\mu_1(-3\mu_7 + \mu_9)))))))))/$$
$$((\mu_3 + A_b(I_b''N_h + P_b)\mu_4)(\mu_6 + A_b(I_b''N_h + P_b)\mu_7)((\delta_h + \theta_b)\mu_6 + A_b(I_b''N_h + P_b)(\mu_{10} + (\delta_h + \theta_b)\mu_7))$$
$$A_b(I_b''N_h + P_b)\mu_2 + \mu_8))$$

$$B_3 = \delta_h\delta_{vb}{}^2 + (C_b{}^2(\delta_h\mu_6 + A_b(I_b^*N_h + P_b)\beta_{vb}\mu_1\mu_2 + \delta_h\mu_7)))/(\mu_6 + A_b(I_b^*N_h + P_b)\mu_7) + (C_b(\beta_{vb} + 2\delta_{vb})\delta_h\mu_6 + A_b(I_b^*N_h + P_b)(\beta_{vb}\mu_1\mu_2 + \delta_h\mu_7)))/(\mu_6 + A_b(I_b^*N_h + P_b)\mu_7) + (A_b{}^3N_h(I_b^*N_h + P_b)^2\alpha_b\beta_{vb}{}^3\delta_h\theta_b(-1 + a(-1 + I_b^*)\theta_b\mu_1{}^2\mu_2{}^3))/((\mu_3 + A_b(I_b^*N_h + P_b)\mu_4)((\delta_h + \theta_b)\mu_6 + A_b(I_b^*N_h + P_b)(\mu_{10} + (\delta_h + \theta_b)\mu_7))) + \beta_{vb}(\frac{A_b(I_b^*N_h + P_b)\delta_{vb}{}^2\mu_1\mu_2}{\mu_6 + A_b(I_b^*N_h + P_b)\mu_7} + (\delta_h(A_b(I_b^*N_h + P_b)\delta_{vb}(\delta_h + \theta_b)\mu_2\mu_6 + \delta_{vb}(\delta_h + \theta_b)\mu_6\mu_8 + A_b(N_h\alpha_b(1 - a + \theta_b)\mu_1\mu_2\mu_6 + P_b\delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7) + I_b^*N_h(-\alpha_b\theta_b\mu_1\mu_2\mu_6 + \delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7))) + \mu_8 + A_b{}^2(I_b^*N_h + P_b)\mu_2(P_b\delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7) - N_h\alpha_b(-1 + a - \theta_b)\mu_1(2\mu_2\mu_6 + \mu_7\mu_8) + I_b^*N_h(\delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7) - \alpha_b\theta_b\mu_1(2\mu_2\mu_6 + \mu_7\mu_8))) - A_b{}^3N_h(I_b^*N_h + P_b)^2\alpha_b(-1 + a(-1 + I_b^*)\theta_b\mu_1\mu_2{}^2(\mu_7 - \mu_9)))/(((\delta_h + \theta_b)\mu_6) + A_b(I_b^*N_h + P_b))((\mu_{10} + (\delta_h + \theta_b)\mu_7))(A_b(I_b^*N_h + P_b)\mu_2 + \mu_8))) + (A_b(I_b^*N_h + P_b)\beta_{vb}{}^2\mu_1\mu_2(A_b(I_b^*N_h + P_b)\delta_{vb}(\delta_h + \theta_b)\mu_2\mu_3\mu_6 + \delta_{vb}(\delta_h + \theta_b)\mu_3\mu_6\mu_8 + A_b(N_h\alpha_b\delta_h(-1 + a - \theta_b)\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6) + P_b\delta_{vb}(\mu_{10}\mu_3 + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7)) + I_b^*N_h(\alpha_b\delta_h\theta_b\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6) + \delta_{vb}(\mu_{10}\mu_3 + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7))))\mu_8 + A_b{}^2(I_b^*N_h + P_b)(N_h\alpha_b\delta_h(-1 + a - \theta_b)\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6) + (\mu_4\mu_6 + \mu_3\mu_7 - 2\theta_b\mu_1\mu_6\mu_7)\mu_8) + P_b\delta_{vb}(\mu_{10}(\mu_2\mu_3 + \mu_4\mu_8) + (\delta_h + \theta_b)(\mu_2\mu_4\mu_6 + \mu_2\mu_3\mu_7 + \mu_4\mu_7\mu_8)) + \delta_{vb}\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7)\mu_8 + \alpha_b\delta_h\theta_b\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6) + (\mu_4\mu_6 + \mu_3\mu_7 - 2\theta_b\mu_1\mu_6\mu_7)\mu_8))) + A_b{}^4N_h(I_b^*N_h + P_b)^3\alpha_b\delta_h(-1 + a + (-1 + I_b^*)\theta_b)\mu_2{}^2\mu_7(\mu_4 + \theta_b\mu_1(-\mu_7 + \mu_9)) + A_b{}^3(I_b^*N_h + P_b)^2\mu_2(P_b\delta_{vb}\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7) + N_h\alpha_b\delta_h(-1 + a - \theta_b)(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8 + \mu_2(\mu_3\mu_7 + \mu_6(\mu_4 + \theta_b\mu_1(-3\mu_7 + \mu_9)))) + I_b^*N_h(\delta_{vb}\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7) + \alpha_b\delta_h\theta_b(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8 + \mu_2(\mu_3\mu_7 + \mu_6(\mu_4 + \theta_b\mu_1(-3\mu_7 + \mu_9))))))))/((\mu_3 + A_b(I_b^*N_h + P_b)\mu_4)(\mu_6 + A_b(I_b^*N_h + P_b)\mu_7)((\delta_h + \theta_b)\mu_6 + A_b(I_b^*N_h + P_b)(\mu_{10} + (\delta_h + \theta_b)\mu_7))A_b(I_b^*N_h + P_b)\mu_2 + \mu_8))).$$

Again we see that the first two eigenvalues $\lambda_1 = -\alpha_b - \delta_h$ and $\lambda_2 = -\beta_b - \delta_h$ are negative. The other three eigenvalues are the solutions of the characteristic equation $(\lambda^3 + B_1\lambda^2 + B_2\lambda + B_3) = 0$ where the B's are given above. Just like before, the three eigenvalues will be negative if i) $B_1 > 0$, ii) $B_3 > 0$, iii) $B_1B_2 > 0$. As before, we have evaluate the values of the B's numerically using the following parameter values

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365*74.6)\,\text{day}^{-1}$, $a = 0.077$, $N_h = 200{,}000$, $\beta_b = 1/19$, $\alpha_b = 1/13$, $\beta_{vb} = 0.8$, $\psi_b = 1/19$, $\gamma_{vbh} = 0.083$, $\gamma_{hvb} = 0.068$, $T_{vb} = 0.6$, $A_b = 35000$, $P_b = 0.97$, $C_b = 0.7$, $\theta_b = 1/9$, $b = 10{,}000$, $V_b = 960{,}000$ and $\delta_{va} = 1/9$.

These values are appropriate for the *A. albopictus* mosquitoes. Looking at Figure 12.4,

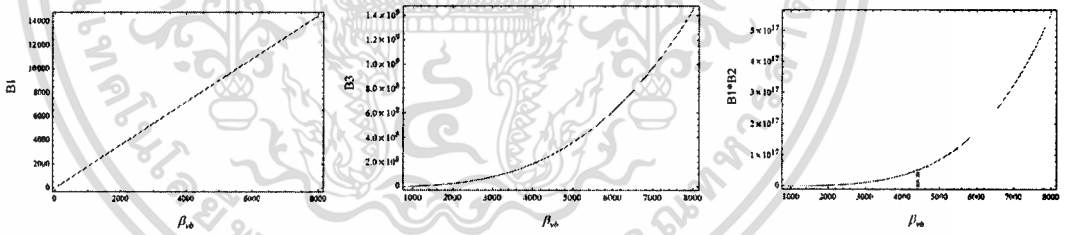


Figure 12.4. The parameters spaces for the endemic equilibrium point which satisfies the Routh – Hurwitz criteria with the value of parameters listed in the text. We see that for the values of the parameters used, the B's satisfy the Routh-Hurwitz criteria and so will be locally asymptotically stable. The expressions for S_b'', E_b'', I_b'', E_{vb}'' and I_{vb}'' are defined by Eqns. (12.32) – (12.36).

After showing that the equilibrium populations during a dengue epidemic in which two species of mosquitoes, *A. aegypti* and *A. albopictus* are co circulating is locally asymptotically stable, we now simulated the trajectories of the epidemic by numerically solving Eqns. (12.17) to (12.26). The values of parameters

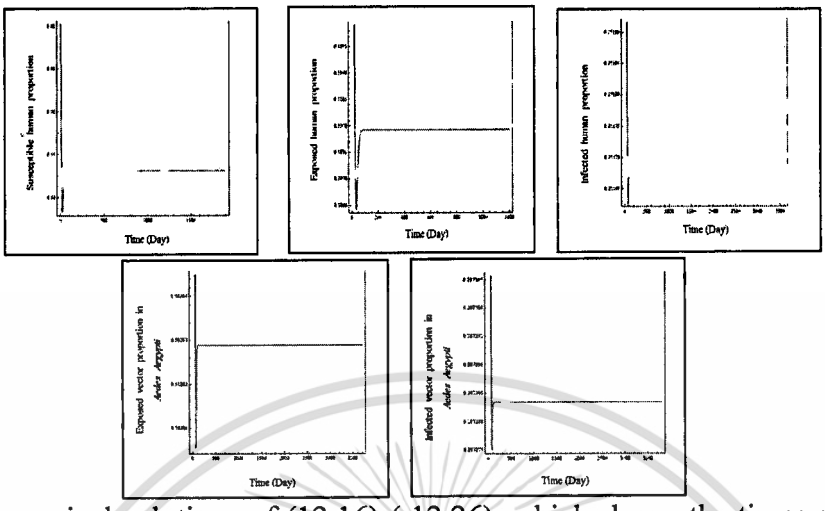


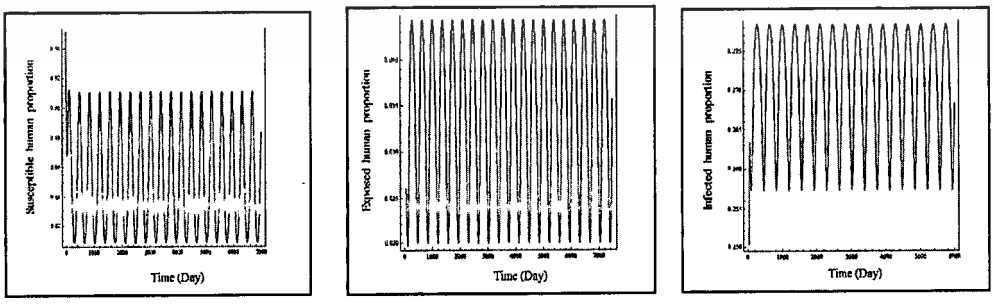
Figure 12.5. Numerical solutions of (12.16)-(12.26), which shows the times series behavior of populations (when $S_0 > 1$) of S_a'', E_a'', I_a'', E_{va}'' and I_{va}''. Used the numerical simulations are $\delta_h = 1/(365*74.6)$ per day, corresponding to a life expectancy of 74.6 years; $\alpha_a = 1/6$ and $\alpha_b = 1/17$, corresponds to the exposed rate of human population; $\beta_a = 1/6$ and $\beta_b = 1/19$, corresponding to the recovery rate of human population due to biting of *A. aegypti* and *A. albopictus*, respectively. The transmission probability of *A. aegypti* (ψ_a) and *A. albopictus* (ψ_b) are arbitrary chosen. We assume that no alternative host. The other parameters were arbitrarily chosen. The numerical solutions of (12.16) – (12.26) are shown in following figures.

For the case of *A. Aegypti* when seasonal change in the total number of this species does not influence the behavior (achieved by setting $\varepsilon_a = 0$) of the populations. To obtain the trajectories, the following numerical values

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365*74.6)\,\text{day}^{-1}$, $a = 0.00077$, $N_h = 200{,}000$, $\beta_a = 1/14$, $\alpha_a = 1/9$, $\beta_{va} = 0.11$, $\psi_a = 1/16$, $\gamma_{vah} = 0.00018$, $\gamma_{hva} = 0.66$, $T_{va} = 0.05$, $A_a = 4000$, $P_a = 0.09$, $C_a = 0.008$, $\theta_a = 1/6$, $b = 3{,}000$, $V_a = 9{,}000{,}000$, $\varepsilon_a = 0$ and $\delta_{va} = 1/3$. $S^*_{0a} = 31.0712$.

These values lead to the following equilibrium state (0.5323, 0.1079, 0.2516, 0.5820, 0.2872).

For the case where the influence when the influence of the seasonal variation is taken into account (case $\varepsilon_a \neq 0$). The numerical values of the parameters have been changed to



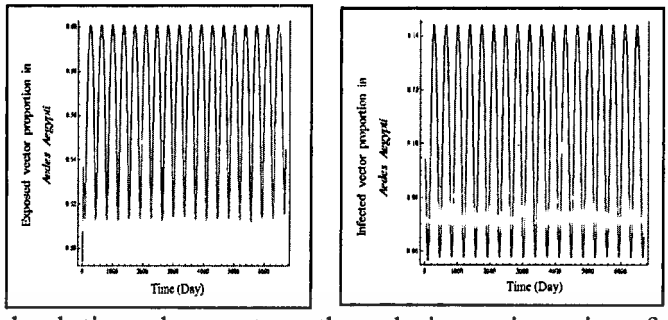


Figure 12.6. Numerical solutions demonstrate the solution trajectories of S_a'', E_a'', I_a'', E_{va}'' and I_{va}''. The values of the parameters are given in the text of the paper.

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365*74.6)\,\text{day}^{-1}$, $a = 0.000007777$, $N_h = 200{,}000$, $\beta_a = 1/14$, $\alpha_a = 1/6$, $\beta_{va} = 0.11$, $\psi_a = 1/18$, $\gamma_{vah} = 0.00018$, $\gamma_{hva} = 0.0026$, $T_{va} = 0.4$, $A_a = 7000$, $P_a = 0.7$, $C_a = 0.08$, $\theta_a = 1/6$, $b = 6{,}000$, $V_a = 90{,}000{,}000$, $\varepsilon_a = 0.5$ and $\delta_{va} = 1/3$.

Plotting the series development of two of the populations on the same figures, we see limit cycle behaviors. The values of the parameters are the same as those used to get Figure12.6. can occur.

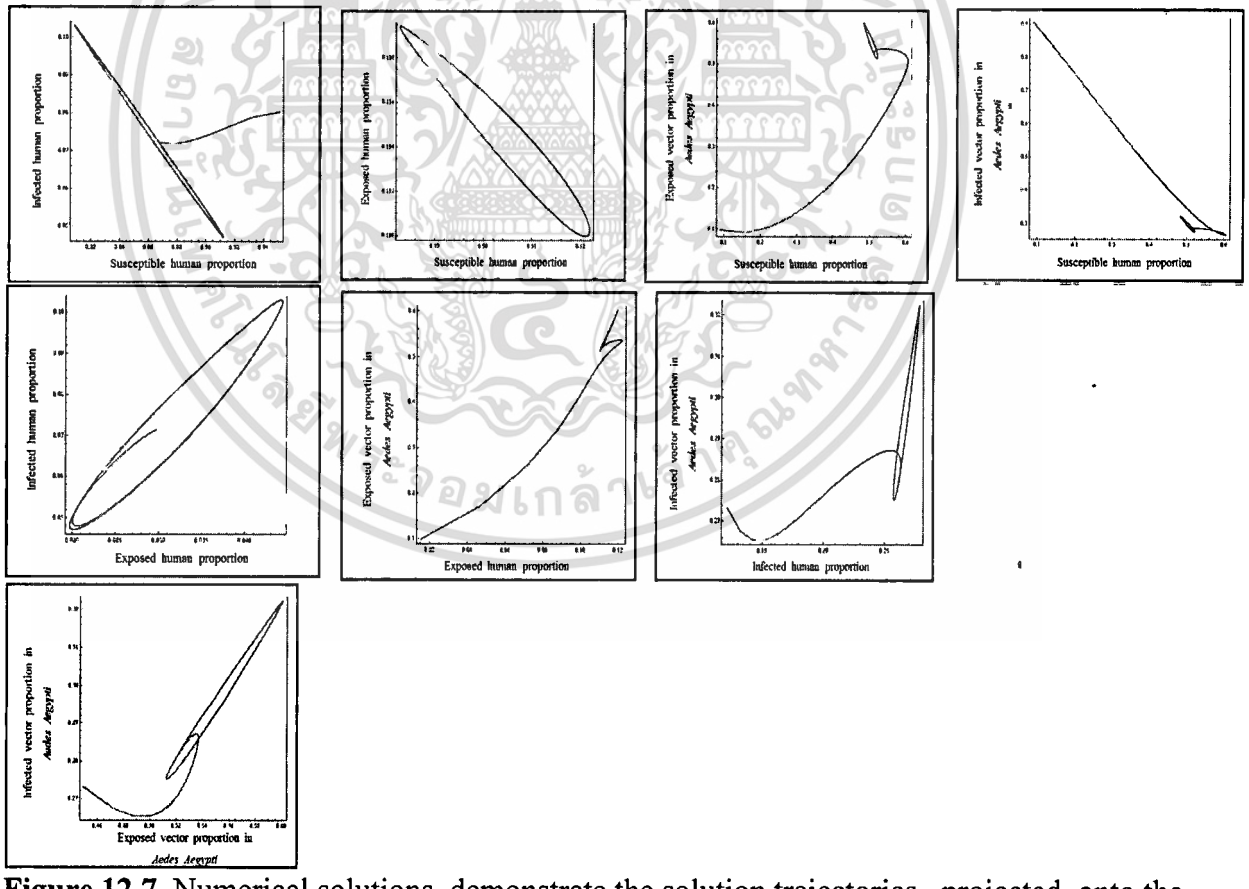


Figure 12.7. Numerical solutions demonstrate the solution trajectories, projected onto the (S_a'', I_a''), (S_a'', E_a''), (S_a'', E_{va}''), (S_a'', I_{va}''), (E_a'', I_a''), (E_a'', E_{va}''), (I_a'', I_{va}'') and (E_{va}'', I_{va}'') space.

Case where the infecting mosquitoes are *A. Albopictus* when the seasonal changes of the mosquitoes population is neglected (achieved by setting $\varepsilon_b = 0$). The numerical values of the parameters used in solving equations are now changed to

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365*74.6)\,\text{day}^{-1}$, $a = 0.00077$, $N_h = 200{,}000$, $\beta_b = 1/19$, $\alpha_b = 1/18$, $\beta_{vb} = 0.8$, $\psi_b = 1/12$, $\gamma_{vbh} = 0.093$, $\gamma_{hvb} = 0.48$, $T_{vb} = 0.8$, $A_b = 45000$, $P_b = 0.00697$, $C_b = 0.00007$, $\theta_b = 1/9$, $b = 100$, $V_b = 660{,}000$, $\varepsilon_b = 0$ and $\delta_{vb} = 1/3$.

These values lead to equilibrium state population of $S_{0b}^{*} = 1.8572$. The time evolutions of the different population are plotted in Figure 12.8. This figure corresponds to Figure 5 for the time evolutions of the different populations when the infecting mosquito is the *A. aegypti* mosquito. The endemic equilibrium point (0.6305, 0.9272, 0.9781, 0.2000, 0.7998).

Case when the influence of the seasonal variation of the number of *A. Albopictus* is taken into account (archived by setting $\varepsilon_b \neq 0$) The values of the parameters are now set to

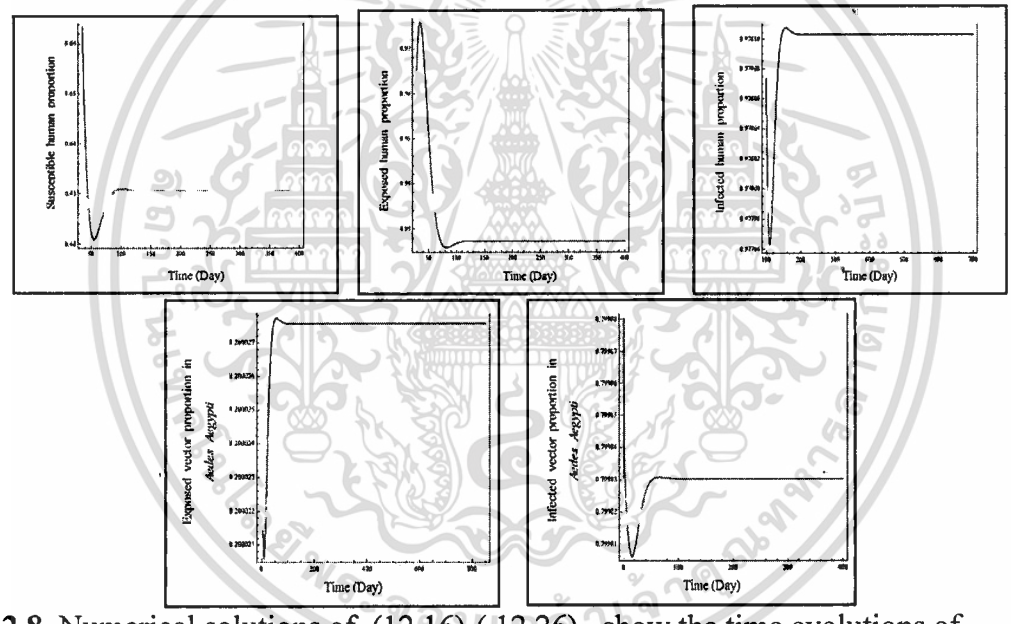


Figure 12.8. Numerical solutions of (12.16)-(12.26) , show the time evolutions of S_b'', E_b'', I_b'', E_{vb}'' and I_{vb}'' when the mosquitoes responsible for the epidemic is *A. albopictus*. The values of the parameters are given in the text.

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365*74.6)\,\text{day}^{-1}$, $a = 0.000007777$, $N_h = 200{,}000$, $\beta_b = 1/19$, $\alpha_b = 1/12$, $\beta_{vb} = 0.8$, $\psi_b = 1/7$, $\gamma_{vbh} = 0.073$, $\gamma_{hvb} = 0.068$, $T_{vb} = 0.04$, $A_b = 25000$, $P_b = 0.03$, $C_b = 0.08$, $\theta_b = 1/9$, $b = 20{,}000$, $V_b = 3{,}000{,}000$, $\varepsilon_b = 0.6$ and $\delta_{vb} = 1/5$.

The time series behaviors of the different populations are show on Figure 12.8. The values of the parameters used to obtain the curves shown in Figure 12.8 are

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365*74.6)\,\text{day}^{-1}$, $a = 0.000007777$, $N_h = 200{,}000$, $\beta_b = 1/19$, $\alpha_b = 1/12$, $\beta_{vb} = 0.8$, $\psi_b = 1/7$, $\gamma_{vbh} = 0.073$, $\gamma_{hvb} = 0.068$, $T_{vb} = 0.04$, $A_b = 25000$, $P_b = 0.03$, $C_b = 0.08$, $\theta_b = 1/9$, $b = 20{,}000$, $V_b = 3{,}000{,}000$, $\varepsilon_b = 0.6$ and $\delta_{vb} = 1/5$.

Pairing up the solutions shown in Figure (12.8) and plotting them on a two plot i.e., (S_b'', E_b''), (S_b'', E_{vb}''), (S_b'', I_b''), (S_b'', I_{vb}''), (I_b'', E_b''), (I_b'', E_{vb}''), (I_b'', I_{vb}''), (E_b'', E_{vb}'') and (E_b'', I_{vb}'') we see the limit cycle behaviors appearing on Figure 9. Similar limit cycle behaviors to those seen in Figs. (7) and (10) will be seen when ε_a is between 0.25 and 0.7 and when ε_b is between 0.3 and 0.65. There appears to be

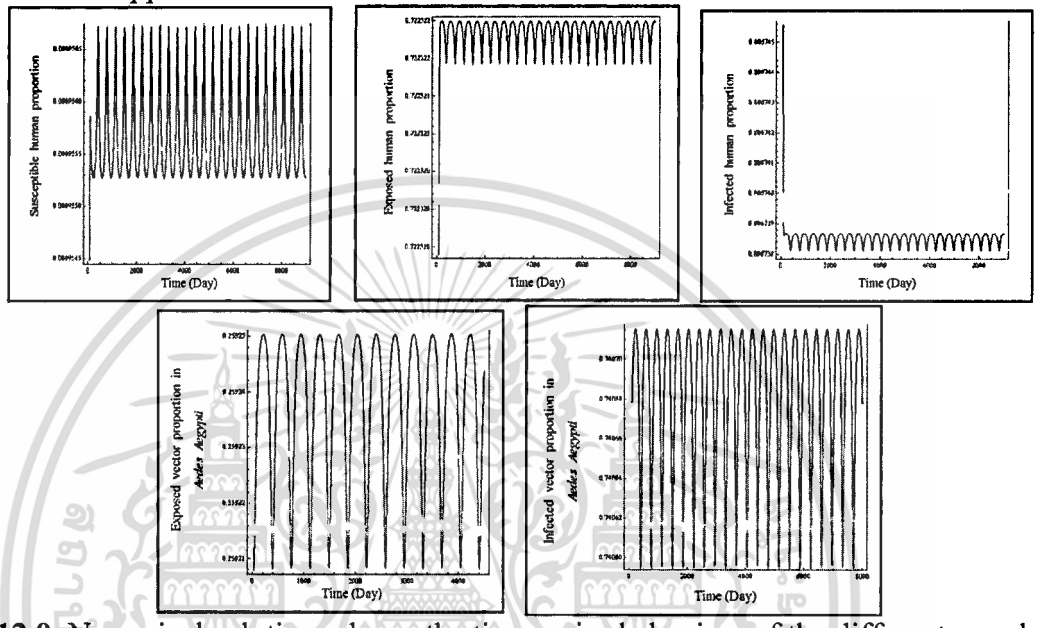
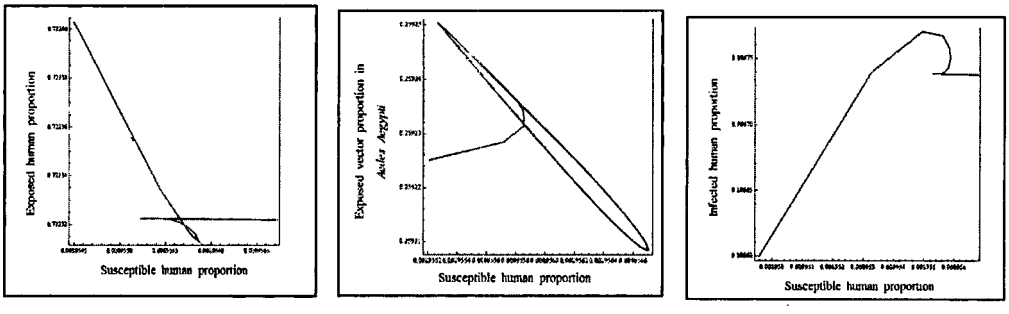


Figure 12.9. Numerical solutions shows the time series behaviors of the different populations S_b'', E_b'', I_b'', E_{vb}'' and I_{vb}''. The values of the parameters are given in the test.

There appears to be a loss of stability when other values are changed especially changes in the biting rates of the two species, ψ_a (biting rate of *A. aegypti* mosquitoes) and ψ_b (biting rate of *A. albopictus* mosquitoes).

We are interested in the transmission of a single serotype of dengue virus when two species of mosquitoes, *A. aegypti* and *A. albopictus* are co circulating. Among a human population. The threshold number or basic reproduction of this model is defined as S_0 where is the maximum of S_{0a} and S_{0b} are defined by Eqs, (39a(and (39b). The square root of this number represents the average number of secondary case that can be produce when one initial infection is produced by a bite of one (either specie) mosquito. If $S_0 < 1$, the number of infections will go to 0 as time progresses. If however $S_0 > 1$, the number of infection will increase as time progress and the dengue virus infection will become endemic.



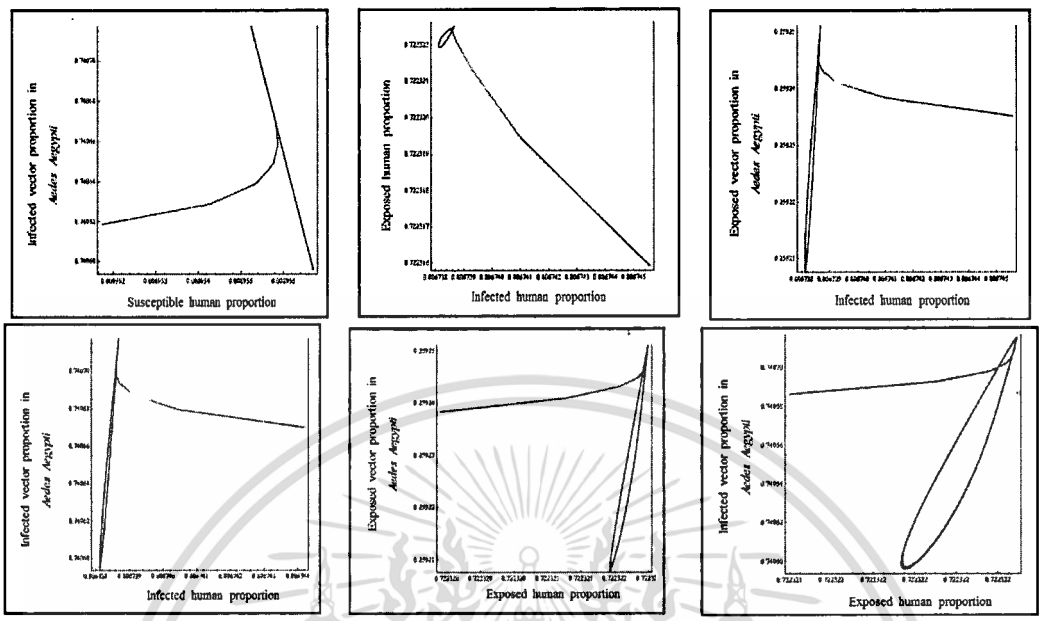


Figure 12.10. Limit Cycle Behavior of the populations in the model of dengue fever when the DENV is plotting transmitted by *A. Albopictus* mosquitoes in different 2D space. The trajectories in the 2D space (S_b'', E_b''), (S_b'', E_{vb}''), (S_b'', I_b''), (S_b'', I_{vb}''), (I_b'', E_b''), (I_b'', E_{vb}''), (I_b'', I_{vb}''), (E_b'', E_{vb}'') and (E_b'', I_{vb}'') exhibit limit cycle behaviors.

The transmission of dengue virus depends on the values of $A_a(1+\varepsilon_a Sin\,\tau(t+194))$ and $A_b(1+\varepsilon_b\, Sin\,\tau(t+240))$ is the virus is being transmitted by the *A. aegypti* and *A. Albopictus* mosquitoes, respectively. The behaviors of our solution depend on the value of ε_a and ε_b .

We have seen that the equilibrium points $S^*{}_{0a} = (S_a'', E_a'', I_a'', E_{va}'', I_{va}'')$ and $S^*{}_{0b} = (S_b'', E_b'', I_b'', E_{vb}'', I_{vb}'')$ when $\varepsilon_a = 0$ and $\varepsilon_b = 0$ are locally asymptotically stable when $S_0 > 1$. . Figure 5 and Figure 8 show the behaviors of human and two species of vectors $(S_a'', E_a'', I_a'', E_{va}'', I_{va}'')$ and $(S_b'', E_b'', I_b'', E_{vb}'', I_{vb}'')$ as time passes. Each of the populations quickly reaches their equilibrium value and remains at the equilibrium values (Lemma 1). When $\varepsilon_a \neq 0$ and $\varepsilon_b \neq 0$,the endemic equilibrium point $S^*{}_{0a} = (S_a'', E_a'', I_a'', E_{va}'', I_{va}'')$ and $S^*{}_{0b} = (S_b'', E_b'', I_b'', E_{vb}'', I_{vb}'')$ are again locally stability when the other parameter values lead t $S_0 > 1$. The two dimensional plots however indicate another type of behavior (see Figs. 6 - 7 and Figs 9 -10). Instead of quickly coming to their equilibrium values, trajectories exhibit limit cycle behaviors (Figs, (12.7) and ((12.10)) Varying the values of ε_a between 0.25 and 0.70.

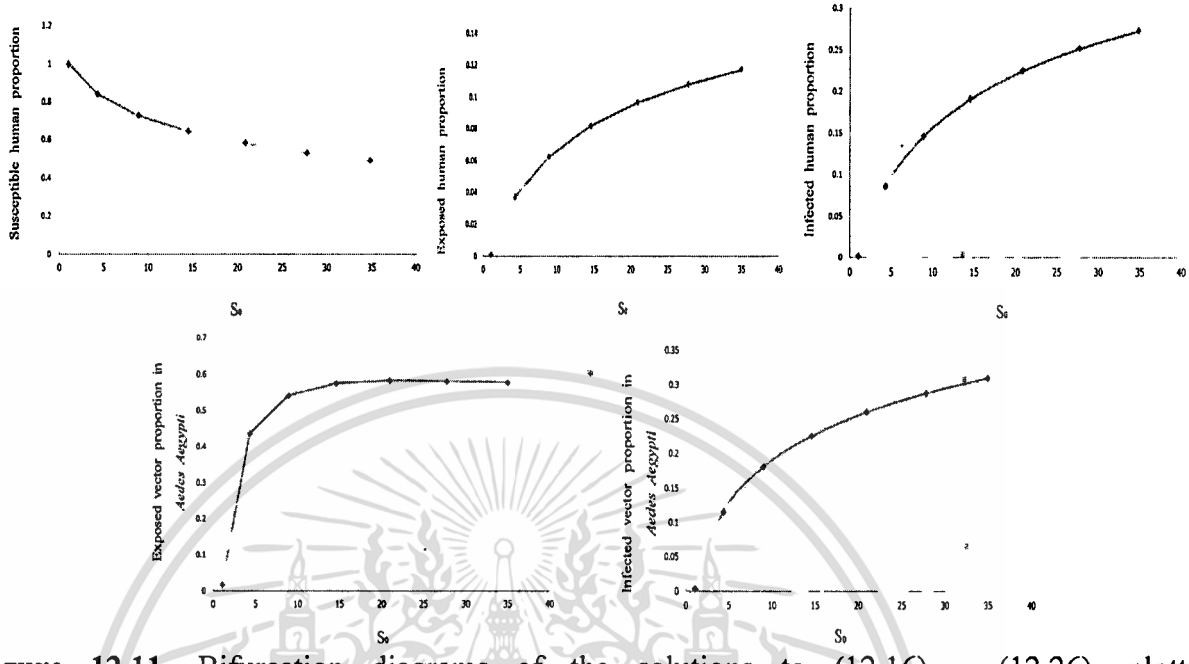


Figure 12.11. Bifurcation diagrams of the solutions to (12.16) – (12.26), plotted onto (S_0, S_a''), (S_0, E_a''), (S_0, I_a''), (S_0, E_{va}'') and (S_0, I_{va}''), respectively for the different values of S_0 —— denote the stable solutions.

and ε_b between 0.3 and 0.65 for the cases of *A. aegypti* and *A. albopictus* vectors, respectively, we get behaviors similar to those of Figs (12.5) and (12.8) and those of Figs. (12.6), (12.7), (12.9) and (12.10) when ε_a and ε_b are greater or less than some critical value (ε_a^* and ε_b^*) which we call the bifurcation values. When its value $\varepsilon_a = 0$ and $\varepsilon_b = 0$ or less than ε_a^* and ε_b^*, the time behaviors do not exhibit any oscillation, but if the values ε_a and ε_b are greater than ε_a^* and ε_b^* oscillations are seen. The bifurcation diagrams of equations (12.17) – (12.26) are shown in the above figures

In this model, we showed that the endemic equilibrium point is local stable, when the threshold number is greater than one. The local stability of all equilibrium states are determined by the threshold numbers S_0. This study shows that by modifying how one reacts to the environment so as to change the values of the parameters, it would be possible to control the spread of dengue fever when two species of mosquitoes, the *A. aegypti* and *A. albopictus* are co circulating.

4.13 แบบจำลองที่ 13 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาความเสถียรภาพแบบวงกว้าง (Global stability) [68]

We use susceptible –infected – recovered (SIR) for human and susceptible – infected (SI) for *Aedes* mosquitoes. Transmission rates of two species (*Aedes aegypti and Aedes albopictus* mosquitoes*)* are considered to be different.

Let N_T, N_{va} and N_{vb} represent the total number of human. In this paper, the total numbers of population are assumed to be constant for each category. The human population of sizes N_T consisted of susceptible human (S), infected human due to *Aedes aegypti* (I_a), *Aedes albopictus* (I_b), and recovered human (R), i.e, $N_T = S + I_a + I_b + R$. For vector population of sizes N_{va}, it represents the total *Aedes aegypti*. It contained the susceptible (S_{va}) and infectious mosquitoes (I_{va}), where $N_{va} = S_{va} + I_{va}$ for *Aedes aegypti*. N_{vb} represents the total *Aedes albopictus*, where, $N_{vb} = S_{vb} + I_{vb}$ and S_{vb} is susceptible mosquito, I_{vb} is infectious mosquito. Note that μ_h and μ_d are the average constant natural death rates of human population and death rate of human population due to the disease, μ_{va} and μ_{vb} are the average constant death rates in *Aedes aegypti* and *Aedes albopictus*, respectively.

The other parameters are defined as follows: κ is the birth rate of human population, ω_a and ω_b are the biting rates of *Aedes aegypti* population and *Aedes albopictus* population, λ_a and λ_b are the measures of influence on the transmission process from human population to *Aedes aegypti* and *Aedes albopictus*, α_{va} and α_{vb} are the recovery rates of human population who be infected with *Aedes aegypti* and *Aedes albopictus*, respectively. For vector population, it is assumed the constant recruitment rates Q_a and Q_b of *Aedes aegypti* and *Aedes albopictus*, λ_{va} and λ_{vb} are the measures of influence on the transmission process from *Aedes aegypti* and *Aedes albopictus*, respectively to human population, β_{va} and β_{vb} are the transmission probabilities of dengue disease from vector populations (*Aedes aegypti* and *Aedes albopictus*) to human population, as well as the number of infectious and susceptible of each species. Our model equations are shown in the next section.

We study the transmission of dengue disease in population by biting of *Aedes aegypti* and *Aedes albopictus* mosquitoes. We study the data of incidence as shown in figure 13.1.

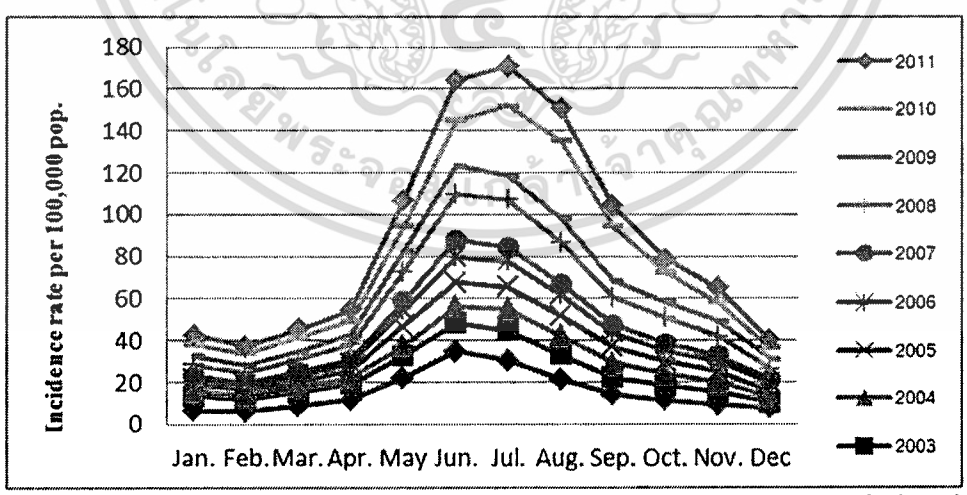


Figure 13.1. Reported cases of Dengue disease per 100,000 population in Thailand during 2002 and 2011 (month - by - month) [Division of Epidemiology, 2002 – 2011].

We can see that the behavior of dengue incidence is shown in the form of Sine function. The transmission diagram of our model is shown in figure 13.2.

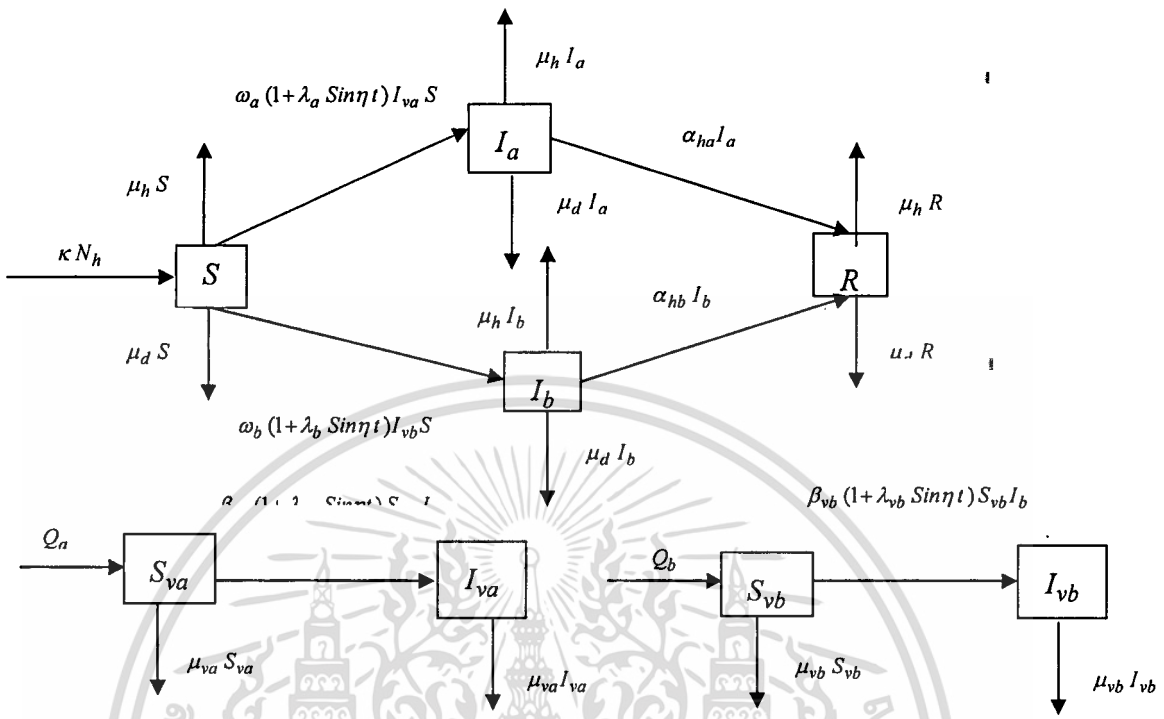


Figure 13.2. Diagram for our model

The model is given by the following system of ordinary differential equations,

$$\frac{dS}{dt} = \kappa N_h - \omega_a(1+\lambda_a \sin\eta t) I_{va} S - \mu_d S - \mu_h S - \omega_b(1+\lambda_b \sin\eta t) I_{vb} S \quad (13.1)$$

$$\frac{dI_a}{dt} = \omega_a(1+\lambda_a \sin\eta t) I_{va} S - \mu_d I_a - \mu_h I_a - \alpha_{ha} I_a \quad (13.2)$$

$$\frac{dI_b}{dt} = \omega_b(1+\lambda_b \sin\eta t) I_{vb} S - \mu_d I_b - \mu_h I_b - \alpha_{hb} I_b \quad (13.3)$$

$$\frac{dR}{dt} = -\mu_d R - \mu_h R - \alpha_{ha} I_a - \alpha_{hb} I_b \quad (13.4)$$

$$\frac{dS_{va}}{dt} = Q_a - \beta_{va}(1+\lambda_{va} \sin\eta t) S_{va} I_a - \mu_{va} S_{va} \quad (13.5)$$

$$\frac{dI_{va}}{dt} = \beta_{va}(1+\lambda_{va} \sin\eta t) S_{va} I_a - \mu_{va} I_{va} \quad (13.6)$$

$$\frac{dS_{vb}}{dt} = Q_b - \beta_{vb}(1+\lambda_{vb} \sin\eta t) S_{vb} I_b - \mu_{vb} S_{vb} \quad (13.7)$$

$$\frac{dI_{vb}}{dt} = \beta_{vb}(1+\lambda_{vb} \sin\eta t) S_{vb} I_b - \mu_{vb} I_{vb} \quad (13.8)$$

All parameters in our model are non- negative. We will show that equations described by (13.1) – v(8), the non – negative octant R_+^8 is positive invariant (where R_+^8 denotes the non – negative region). With respect to system (13.1) – (13.8), we have the following results.

Proposition 13.2.1 Let $(S(t), I_a(t), I_b(t), R(t), S_{va}(t), I_{va}(t), S_{vb}(t), I_{vb}(t))$ be the solution of (1) – (8) with the initial condition $(S(0), I_a(0), I_b(0), R(0), S_{va}(0), I_{va}(0), S_{vb}(0), I_{vb}(0))$ and the compact set

$$\Omega_a = \left\{ (S, I_a, I_b, R, S_{va}, I_{va}, S_{vb}, I_{vb}) \in R_+^8, W_1 \le N_T = \frac{\kappa N_h}{\mu_d + \mu_h}, W_2 \le N_{va} = \frac{Q_a}{\mu_{va}}, W_3 \le N_{vb} = \frac{Q_b}{\mu_{vb}} \right\}.$$

Then, under the flow described by (13.1) – (13.8), Ω_a is a positively invariant set that attracts all solutions in R_+^8 .

Proof. We choose the Lyapunov function

$$W(t) = (W_1(t), W_2(t), W_3(t))$$
$$= (S + I_a + I_b + R,\ S_{va} + I_{va},\ S_{vb} + I_{vb})$$

is positive definite on R_+^8 and we have

$$\frac{dW}{dt} = \left(\frac{dW_1}{dt}, \frac{dW_2}{dt}, \frac{dW_3}{dt}\right)$$
$$= \left(\frac{dS}{dt} + \frac{dI_a}{dt} + \frac{dI_b}{dt} + \frac{dR}{dt}, \frac{dS_{va}}{dt} + \frac{dI_{va}}{dt}, \frac{dS_{vb}}{dt} + \frac{dI_{vb}}{dt}\right)$$
$$= \left(\kappa N_h - (\mu_d + \mu_h)(S + I_a + I_b + R),\ Q_a - \mu_{va}(S_{va} + I_{va}), Q_b - \mu_{vb}(S_{vb} + I_{vb})\right)$$
$$= \left(\kappa N_h - (\mu_d + \mu_h)N_T,\ Q_a - \mu_{va}N_{va}, Q_b - \mu_{vb}N_{vb}\right)$$

We used the fact that $N_T = \frac{\kappa N_h}{\mu_d + \mu_h}$, $N_{va} = \frac{Q_a}{\mu_{va}}$ and $N_{vb} = \frac{Q_b}{\mu_{vb}}$.

With this in mind, it is not hard to prove that

$$\frac{dW_1}{dt} = \kappa N_h - (\mu_d + \mu_h)W_1 \le 0 \text{ , for } W_1 \ge \frac{\kappa N_h}{\mu_d + \mu_h} \tag{13.9}$$

$$\frac{dW_2}{dt} = Q_a - \mu_{va}W_2 \le 0 \quad , \quad \text{for } W_2 \ge \frac{Q_a}{\mu_{va}} \tag{13.10}$$

$$\frac{dW_3}{dt} = Q_b - \mu_{vb}W_3 \le 0 \ , \quad \text{for } W_3 \le \frac{Q_b}{\mu_{vb}} \tag{13.11}$$

From the above equations (13.9) – (13.11) one has that $\frac{dW}{dt} \le 0$ which implies that Ω_a is a positively invariant set. In other words, by solving (13.9) – (13.11), we obtain

$$0 \le (W_1(t), W_2(t), W_3(t)) \le ((\kappa N_h / (\mu_d + \mu_h)) + W_1(0)e^{-(\mu_d + \mu_h)t},$$
$$(Q_a / \mu_{va}) + W_2(0)e^{-\mu_{va}t}, (Q_b / \mu_{vb}) + W(0)e^{-\mu_{vb}t}),$$

where $W_1(0), W_2(0)$ and $W_3(0)$ are respectively, the initial conditions of $W_1(t)$, $W_2(t)$ and $W_3(t)$. Thus, as $t \to \infty$, $0 \le (W_1(t), W_2(t), W_3(t)) \le (\kappa N_h / \mu_d + \mu_h, Q_a / \mu_{va}, Q_b / \mu_{vb}) = (N_T, N_{va}, N_{vb})$ and one can conclude that Ω_a is an attractive set.

From equations (13.1) – (13.8), we set the right hand side of all equations to zero. We obtain two equilibrium points:

I) If $R_0 \le 1$,the only equilibrium is the disease free equilibrium point

$$J_1(S, I_a, I_b, R, S_{va}, I_{va}, S_{vb}, I_{vb})$$
$$= J_1\left(\frac{\kappa N_h}{\mu_d + \mu_h}, 0, 0, 0, \frac{Q_a}{\mu_{va}}, I_{va}, \frac{Q_b}{\mu_{vb}}, 0\right) \in \Omega_a.$$

II) If $R_0 > 1$, there is the endemic equilibrium point

$$J_2(S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^*) \in \Omega_a$$

where $S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^* > 0$ satisfy

$$S^* = \frac{(\mu_{va}(I_a^*\gamma_{AA} + \mu_{va})\mu_{vb}(N_h\gamma_{BB}\kappa + (\alpha_{hb} + \mu_d + \mu_h)\mu_{vb}))}{(\gamma_{BB}\mu_{va}^2(\gamma_{HB}Q_b + (\mu_d + \mu_h)\mu_{vb}) + I_a^*\gamma_{AA}\gamma_{BB}(\gamma_{HB}Q_b\mu_{va} + \gamma_{HA}Q_a\mu_{vb} + (\mu_d + \mu_h)\mu_{va}\mu_{vb}))} \tag{13.12}$$

$$I_b^* = (N_h\gamma_{BB}\gamma_{HB}Q_b\kappa\mu_{va}(I_a^*\gamma_{AA}+\mu_{va})-(\alpha_{hb}+\mu_d+\mu_h)((\mu_d+\mu_h)\mu_{va}^{\ 2}+I_a^*\gamma_{AA}(\gamma_{HA}Q_a+(\mu_d+\mu_h)\mu_{va}))\mu_{vb}^{\ 2})/(\gamma_{BB}(\alpha_{hb}+\mu_d+\mu_h)(\mu_{va}^{\ 2}(\gamma_{HB}Q_b+(\mu_d+\mu_h)\mu_{vb})+I_a^*\gamma_{AA}(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}+(\mu_d+\mu_h)\mu_{va}\mu_{vb})))$$

$$R^* = \{(\alpha_{ha}(-\gamma_{BB}\gamma_{HB}Q_b(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}-\gamma_{BB}(N_h\gamma_{AA}\gamma_{HA}Q_a\kappa+(\mu_d+\mu_h)(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^{\ 2})\mu_{vb}+\gamma_{AA}\gamma_{HA}Q_a(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb}^{\ 2}))/(\gamma_{AA}(\alpha_{ha}+\mu_d+\mu_h)(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}+(\mu_d+\mu_h)\mu_{va}\mu_{vb})+(\alpha_{hb}(N_h\gamma_{BB}\gamma_{HB}Q_b\kappa\mu_{va}(I_a^*\gamma_{AA}+\mu_{va})-(\alpha_{hb}+\mu_d+\mu_h)((\mu_d+\mu_h)\mu_{va}^{\ 2}+I_a^*\gamma_{AA}(\gamma_{HA}Q_a+(\mu_d+\mu_h)\mu_{va}))\mu_{vb}^{\ 2})/((\alpha_{hb}+\mu_d+\mu_h)(\mu_{va}^{\ 2}(\gamma_{HB}Q_b+(\mu_d+\mu_h)\mu_{vb})+I_a^*\gamma_{AA}(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}+(\mu_d+\mu_h)\mu_{va}\mu_{vb})))\}/\{\gamma_{BB}(\mu_d+\mu_h)\} \quad (13.14)$$

$$S_{va}^* = \frac{Q_a}{I_a^*\gamma_{AA}+\mu_{va}} \quad (13.15)$$

$$I_{va}^* = \frac{I_a^*\gamma_{AA}Q_a}{I_a^*\gamma_{AA}\mu_{va}+\mu_{va}^{\ 2}} \quad (13.16)$$

$$S_{vb}^* = ((\alpha_{hb}+\mu_d+\mu_h)(\mu_{va}^{\ 2}(\gamma_{HB}Q_b+(\mu_d+\mu_h)\mu_{vb})+I_a^*\gamma_{AA}(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}(\mu_d+\mu_h)\mu_{va}\mu_{vb})))/(\gamma_{HB}\mu_{va}(I_a^*\gamma_{AA}+\mu_{va})(N_h\gamma_{BB}\kappa+(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb})) \quad (13.17)$$

$$I_{vb}^* = (N_h\gamma_{BB}\gamma_{HB}Q_b\kappa\mu_{va}(I_a^*\gamma_{AA}+\mu_{va})-(\alpha_{hb}+\mu_d+\mu_h)((\mu_d+\mu_h)\mu_{va}^{\ 2}+I_a^*\gamma_{AA}(\gamma_{HA}Q_a+(\mu_d+\mu_h)\mu_{va}))\mu_{vb}^{\ 2})/(\gamma_{HB}\mu_{va}(I_a^*\gamma_{AA}+\mu_{va})\mu_{vb}(N_h\gamma_{BB}\kappa+(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb})) \quad (13.18)$$

$$I_a^* = (-\gamma_{BB}\gamma_{HB}Q_b(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^{\ 2}-\gamma_{BB}(-N_h\gamma_{AA}\gamma_{HA}Q_a\kappa+(\mu_d+\mu_h)(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^{\ 2})\mu_{vb}+\gamma_{AA}\gamma_{HA}Q_a(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb}^{\ 2})/(\gamma_{AA}\gamma_{BB}(\alpha_{ha}+\mu_d+\mu_h)(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}+(\mu_d+\mu_h)\mu_{va})\mu_{vb})) \quad (13.19)$$

and

$$\gamma_{HA} = \omega_a(1+\lambda_a(\sin\eta t)), \qquad \gamma_{HB} = \omega_b(1+\lambda_b(\sin\eta t))$$

$$\gamma_{AA} = \beta_{va}(1+\lambda_{va}(\sin\eta t)), \qquad \gamma_{BB} = \beta_{vb}(1+\lambda_{vb}(\sin\eta t))$$

The basic reproduction number for system (13.1) – (13.8), is defined by,

$$R_0 = \frac{\gamma_{AA}\gamma_{HA}Q_a\mu_{va}(N_h\gamma_{BB}\kappa+(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb})}{\gamma_{BB}(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^{\ 2}(\gamma_{HB}Q_b+(\mu_d+\mu_h)\mu_{vb})}.$$

We study the global behavior of the disease free equilibrium state for equations (13.1) – (13.8).

Theorem 2.1. We assume that

$$\begin{cases} (\mu_{va})(t) = \omega_a(1+\lambda_a sim\eta t)S^*, \\ (\mu_{vb})(t) = \omega_b(1+\lambda_b sim\eta t)S^*, \\ (\mu_d+\mu_h)(t) = \beta_{va}(1+\lambda_{va} sim\eta t)S_{va}^*, \beta_{vb}(1+\lambda_{vb} sim\eta t)S_{vb}^*. \end{cases} \quad (13.20)$$

When $R_0 \le 1$, the disease free equilibrium J_1 is globally asymptotically stable on Ω_a.

Proof. Consider the Lyapunov function on Ω_a,

$$\psi(t) = (S-S^*\ln S)+I_a+I_b+R+(S_{va}-S_{va}^*\ln S_{va})+I_{va}+(S_{vb}-S_{vb}^*\ln S_{vb})+I_{vb}.$$

The derivative with respect to time yields

$$\frac{d\psi(t)}{dt} = \frac{dS}{dt}(1-\frac{S^*}{S})+\frac{dI_a}{dt}+\frac{dI_b}{dt}+\frac{dR}{dt}+\frac{dS_{va}}{dt}(1-\frac{S^*_{va}}{S_{va}})+\frac{dI_{va}}{dt}+\frac{dS_{vb}}{dt}(1-\frac{dS^*_{vb}}{S_{vb}})+\frac{dI_{vb}}{dt}$$

$$\begin{aligned}\frac{d\psi(t)}{dt} = {} & (\kappa N_h - \omega_a(1+\lambda_a \sin\eta t) I_{va} S - \mu_d S - \mu_h S - \omega_b(1+\lambda_b \sin\eta t) I_{vb} S)(1-\frac{S^*}{S}) \\ & +(\omega_a(1+\lambda_a \sin\eta t) I_{va} S - \mu_d I_a - \mu_h I_a - \alpha_{ha} I_a) \\ & +(\omega_b(1+\lambda_b \sin\eta t) I_{vb} S - \mu_d I_b - \mu_h I_b - \alpha_{hb} I_b) \\ & +(-\mu_d R - \mu_h R - \alpha_{ha} I_a - \alpha_{hb} I_b) \\ & +(Q_a - \beta_{va}(1+\lambda_{va}\sin\eta t) S_{va} I_a - \mu_{va} S_{va})(1-\frac{S^*_{va}}{S_{va}}) \\ & +(\beta_{va}(1+\lambda_{va}\sin\eta t) S_{va} I_a - \mu_{va} I_{va}) \\ & +(Q_b - \beta_{vb}(1+\lambda_{vb}\sin\eta t) S_{vb} I_b - \mu_{vb} S_{vb})(1-\frac{S^*_{vb}}{S_{vb}}) \\ & +(\beta_{vb}(1+\lambda_{vb}\sin\eta t) S_{vb} I_b - \mu_{vb} I_{vb})\end{aligned}$$

$$\begin{aligned}\frac{d\psi(t)}{dt} = {} & \kappa N_h(1-\frac{S^*}{S})+Q_a(1-\frac{S^*_{va}}{S_{va}})+Q_b(1-\frac{S^*_{vb}}{S_{vb}}) \\ & +I_{va}(\omega_a(1+\lambda_a\sin\eta t)S^* - \mu_{va})+I_{vb}(\omega_b(1+\lambda_b\sin\eta t)S^* - \mu_{vb}) \\ & +I_a(\beta_{va}(1+\lambda_{va}\sin\eta t)S^*_{va} - (\mu_d+\mu_h))+I_b(\beta_{vb}(1+\lambda_{vb}\sin\eta t)S^*_{vb} - (\mu_d+\mu_h)) \\ & +\mu_h S^*(1-\frac{S}{S^*})+\mu_d S^*(1-\frac{S}{S^*})+\mu_{va}S^*_{va}(1-\frac{S_{va}}{S^*_{va}})+\mu_{vb}S^*_{vb}(1-\frac{S_{vb}}{S^*_{vb}})-\mu_d R-\mu_h R\end{aligned} \quad (13.21)$$

We define

$(\mu_{va})(t) = \omega_a(1+\lambda_a \sin\eta t)S^*$, $(\mu_{vb})(t) = \omega_b(1+\lambda_b \sin\eta t)S^*$,

$(\mu_d+\mu_h)(t) = \beta_{va}(1+\lambda_{va}\sin\eta t)S^*_{va}$ and $(\mu_d+\mu_h)(t) = \beta_{vb}(1+\lambda_{vb}\sin\eta t)S^*_{vb}$.

Note that on Ω_a, we have $S^* = \frac{\kappa N_h}{\mu_d+\mu_h}$, $S^*_{va} = \frac{Q_a}{\mu_{va}}$ and $S^*_{vb} = \frac{Q_b}{\mu_{vb}}$. With this in mind, (13.21) becomes

$$\begin{aligned}\frac{d\psi(t)}{dt} = {} & \kappa N_h(1-\frac{S^*}{S})+Q_a(1-\frac{S^*_{va}}{S_{va}})+Q_b(1-\frac{S^*_{vb}}{S_{vb}}) \\ & +\mu_h S^*(1-\frac{S}{S^*})+\mu_d S^*(1-\frac{S}{S^*})+\mu_{va}(t)S^*_{va}(1-\frac{S_{va}}{S^*_{va}})+\mu_{vb}(t)S^*_{vb}(1-\frac{S_{vb}}{S^*_{vb}})-\mu_d R-\mu_h R\end{aligned} \quad (13.22)$$

$$\frac{d\psi(t)}{dt} = \kappa N_h(2-\frac{S^*}{S}-\frac{S}{S^*})+Q_a(2-\frac{S^*_{va}}{S_{va}}-\frac{S_{va}}{S^*_{va}})+Q_b(2-\frac{S^*_{vb}}{S_{vb}}-\frac{S_{vb}}{S^*_{vb}})-\mu_d R-\mu_h R$$

$$\frac{d\psi(t)}{dt} = -\kappa N_h\frac{(S^*-S)^2}{S^*S}-Q_a\frac{(S^*_{va}-S_{va})^2}{S^*_{va}S_{va}}-Q_b\frac{(S^*_{vb}-S_{vb})^2}{S^*_{vb}S_{vb}}-\mu_d R-\mu_h R. \quad (13.23)$$

We can see that all terms in (23) are always non-positive. By using the LaSelle's extension to Lyapunov's theorem and we have $\frac{d\psi(t)}{dt}\le 0$, then the function $\frac{d\psi(t)}{dt}$ is negative definite. The limit set of each solution is contained in the largest invariant set for which $S=S^*, S_{va}=S^*_{va}, S_{vb}=S^*_{vb}$ and $R^n=0$ which is the singleton $\{J_1\}$. Then, we use the LaSelle's

invariant principle implies that the disease free equilibrium J_1 is globally asymptotically stable on Ω_a.

Next, we consider the global property of the endemic equilibrium of (13.1) – (13.8).

Theorem 2.2. If $R_0 > 1$, there is the endemic equilibrium state

$$J_2(S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^*) \in \Omega_a$$

exists and is globally asymptotically stable on Ω_a if

$$\begin{cases} \mu_{va}(t) = (\omega_a(1+\lambda_a \sin \eta t) N_h) \\ \mu_{vb}(t) = (\omega_b(1+\lambda_b \sin \eta t) N_h) \\ (\mu_d + \mu_h + \alpha_{ha})(t) = Q\beta_{va}(1+\lambda_{va} \sin \eta t) S_{va}^* \\ (\mu_d + \mu_h + \alpha_{hb})(t) = Q\beta_{vb}(1+\lambda_{vb} \sin \eta t) S_{vb}^* \end{cases} \tag{13.24}$$

where

$A_1(t) = \omega_a(1+\lambda_a \sin \eta t)$

$A_2(t) = \omega_b(1+\lambda_b \sin \eta t)$.

Proof. The Lyapunov function is in the form

$$\rho(t) = (S - S^* \ln S) + I_a + I_b + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)(S_{va} - S_{va}^* \ln S_{va}) + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right) I_{va}$$
$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)(S_{vb} - S_{vb}^* \ln S_{vb}) + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right) I_{vb} \tag{13.25}$$

Its derivative along the trajectories of (13.1) – (13.8),

$$\frac{d\rho(t)}{dt} = \frac{dS}{dt}\left(1 - \frac{S^*}{S}\right) + \frac{dI_a}{dt} + \frac{dI_b}{dt} + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)\frac{dS_{va}}{dt}\left(1 - \frac{S_{va}^*}{S_{va}}\right) + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)\frac{dI_{va}}{dt}$$
$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)\frac{dS_{vb}}{dt}\left(1 - \frac{dS_{vb}^*}{S_{vb}}\right) + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)\frac{dI_{vb}}{dt} \tag{13.26}$$

$$\begin{aligned} \frac{d\rho(t)}{dt} &= (\kappa N_h - \omega_a(1+\lambda_a \sin \eta t) I_{va} S - \mu_d S - \mu_h S - \omega_b(1+\lambda_b \sin \eta t) I_{vb} S)\left(1 - \frac{S^*}{S}\right) \\ &+ (\omega_a(1+\lambda_a \sin \eta t) I_{va} S - \mu_d I_a - \mu_h I_a - \alpha_{ha} I_a) \\ &+ (\omega_b(1+\lambda_b \sin \eta t) I_{vb} S - \mu_d I_b - \mu_h I_b - \alpha_{hb} I_b) \\ &+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)(Q_a - \beta_{va}(1+\lambda_{va} \sin \eta t) S_{va} I_a - \mu_{va} S_{va})\left(1 - \frac{S_{va}^*}{S_{va}}\right) \\ &+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)(\beta_{va}(1+\lambda_{va} \sin \eta t) S_{va} I_a - \mu_{va} I_{va}) \\ &+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)(Q_b - \beta_{vb}(1+\lambda_{vb} \sin \eta t) S_{vb} I_b - \mu_{vb} S_{vb})\left(1 - \frac{S_{vb}^*}{S_{vb}}\right) \\ &+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S_{va}^* + A_2 S_{vb}^*}\right)(\beta_{vb}(1+\lambda_{vb} \sin \eta t) S_{vb} I_b - \mu_{vb} I_{vb}) \end{aligned} \tag{13.27}$$

Since we assume that total number of populations are constants, so we have $\kappa N_h = N_T(\mu_d + \mu_h)$, $Q_a = N_{va}\,\mu_{va} = \mu_{va}(S_{va} + I_{va})$ and $Q_b = N_{vb}\,\mu_{vb} = \mu_{vb}(S_{vb} + I_{vb})$. Then above equation become

$$\begin{aligned}\frac{d\rho(t)}{dt} &= (\mu_d + \mu_h)N_T(1-\frac{S^*}{S}) + Q\,\mu_{va}N_{va}(1-\frac{S^*_{va}}{S_{va}}) + Q\mu_{vb}N_{vb}(1-\frac{S^*_{vb}}{S_{vb}})\\ &+ I_{va}(\omega_a(1+\lambda_a\sin\eta t)N_h) - Q\mu_{va}\frac{S_{va}}{S^*_{va}})\\ &+ I_{vb}(\omega_b(1+\lambda_b\sin\eta t)N_h) - Q\mu_{vb}\frac{S_{vb}}{S^*_{vb}})\\ &+ I_a(Q\beta_{va}(1+\lambda_{va}\sin\eta t)S^*_{va} - (\mu_d+\mu_h+\alpha_{ha}))\\ &+ I_b(Q\beta_{vb}(1+\lambda_{vb}\sin\eta t)S^*_{vb} - (\mu_d+\mu_h+\alpha_{hb}))\end{aligned} \tag{13.28}$$

when $Q = (\dfrac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}})$.

Substituting conditions (13.24) into (13.28), we have

$$\begin{aligned}\frac{d\rho(t)}{dt} &= (\mu_d+\mu_h)N_T(1-\frac{S^*}{S}) + Q\mu_{va}S_{va}(1-\frac{S^*_{va}}{S_{va}}) + Q_1(1-\frac{S^*_{va}}{S_{va}}-\frac{S_{va}}{S^*_{va}})\\ &+ QS_{vb}\mu_{vb}(1-\frac{S^*_{vb}}{S_{vb}}) + Q_2(1-\frac{S^*_{vb}}{S_{vb}}-\frac{S_{vb}}{S^*_{vb}})\\ &+ I_{va}((\omega_a(1+\lambda_a\sin\eta t)N_h) - \mu_{va})\\ &+ I_{vb}((\omega_b(1+\lambda_b\sin\eta t)N_h) - \mu_{vb})\\ &+ I_a Q\beta_{va}(1+\lambda_{va}\sin\eta t)S^*_{va} - (\mu_d+\mu_h+\alpha_{ha})I_a\\ &+ I_b Q\beta_{vb}(1+\lambda_{vb}\sin\eta t)S^*_{vb} - (\mu_d+\mu_h+\alpha_{hb})I_b\end{aligned} \tag{13.29}$$

Note that Ω_a, we have $Q_1 = I_{va}Q\mu_{va}$ and $Q_2 = I_{vb}Q\mu_{vb}$. The above equation (13.29) becomes.

$$\begin{aligned}\frac{d\rho(t)}{dt} &= (\mu_d+\mu_h)N_T(1-\frac{S^*}{S}) + Q\mu_{va}(t)S_{va}(1-\frac{S^*_{va}}{S_{va}}) + Q_1(1-\frac{S^*_{va}}{S_{va}}-\frac{S_{va}}{S^*_{va}})\\ &+ QS_{vb}\mu_{vb}(t)(1-\frac{S^*_{vb}}{S_{vb}}) + Q_2(1-\frac{S^*_{vb}}{S_{vb}}-\frac{S_{vb}}{S^*_{vb}})\\ &+ I_{va}((\omega_a(1+\lambda_a\sin\eta t)N_h) - \mu_{va}(t))\\ &+ I_{vb}((\omega_b(1+\lambda_b\sin\eta t)N_h) - \mu_{vb}(t))\\ &+ I_a Q\beta_{va}(1+\lambda_{va}\sin\eta t)S^*_{va} - (\mu_d+\mu_h+\alpha_{ha})(t)I_a\\ &+ I_b Q\beta_{vb}(1+\lambda_{vb}\sin\eta t)S^*_{vb} - (\mu_d+\mu_h+\alpha_{hb})(t)I_b\end{aligned} \tag{13.30}$$

$$\begin{aligned}\frac{d\rho(t)}{dt} &= (\mu_d+\mu_h)N_T(2-\frac{S^*}{S}-\frac{S}{S^*}) + Q\mu_{va}(t)S_{va}(2-\frac{S^*_{va}}{S_{va}}-\frac{S_{va}}{S^*_{va}}) + Q_1(2-\frac{S^*_{va}}{S_{va}}-\frac{S_{va}}{S^*_{va}})\\ &+ QS_{vb}\mu_{vb}(t)(2-\frac{S^*_{vb}}{S_{vb}}-\frac{S_{vb}}{S^*_{vb}}) + Q_2(2-\frac{S^*_{vb}}{S_{vb}}-\frac{S_{vb}}{S^*_{vb}})\end{aligned} \tag{13.32}$$

$$\frac{d\rho(t)}{dt} = -(\mu_d+\mu_h)N_T\frac{(S-S^*)^2}{SS^*} - Q\,\mu_{va}(t)S_{va}\frac{(S_{va}-S_{va}^*)^2}{S_{va}S_{va}^*} - Q_1\frac{(S_{va}-S_{va}^*)^2}{S_{va}S_{va}^*}$$
$$- QS_{vb}\,\mu_{vb}(t)\frac{(S_{vb}-S_{vb}^*)^2}{S_{vb}S_{vb}^*} - Q_2\frac{(S_{vb}-S_{vb}^*)^2}{S_{vb}S_{vb}^*} \qquad (13.31)$$

We use the LaSalle's invariant principle[Salle J. LA. and Lefschetz S.,1961; Keeling Matt J. and Rohani Pejman, 2008] to show that $\frac{d\rho(t)}{dt} \le 0$ for all $(S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^*) \in \Omega_a$, and the strict equality $\frac{d\rho(t)}{dt} = 0$ holds only for $S = S^*, I_a = I_a^*, I_b = I_b^*, R = R^*, S_{va} = S_{va}^*, I_{va} = I_{va}^*, S_{vb} = S_{vb}^*$ and $I_{vb} = I_{vb}^*$. Then, the equilibrium state J_2 is the only invariant set of the equations (13.1) – (13.8) contained entirely in $\{(S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^*), S = S^*, I_a = I_a^*, I_b = I_b^*, R = R^*, S_{va} = S_{va}^*, I_{va} = I_{va}^*, S_{vb} = S_{vb}^*$ and $I_{vb} = I_{vb}^*\}$ and hence the asymptotic stability theorem, the positive endemic equilibrium state J_2 is global asymptotic stability in Ω_a.

Let

$$R_0 = \frac{\gamma_{AA}\gamma_{HA}Q_a\mu_{va}(N_h\gamma_{BB}\kappa+(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb})}{\gamma_{BB}(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^{\,2}(\gamma_{HB}Q_b+(\mu_d+\mu_h)\mu_{vb})}$$

be the threshold parameters. Then, we define $R_0 = \sqrt{R_0}$ as the basic reproductive number of disease. Also, it represents the average number of secondary cases produced from susceptible population. We consider human and vector (*Aedes aegypti* and *Aedes albopictus*) populations. It depends on the transmission rate of dengue virus.

We study the mathematical model of dengue disease considering the global stability of our model by the Lyapunov functions. The global stability of transmission of dengue disease in human and vector (*Aedes aegypti* and *Aedes albopictus*) population has been studied by using Lyapunov functions. If $R_0 \le 1$, then the disease – free equilibrium state is globally asymptotically stable. In the feasible region and the disease dies out of population. If $R_0 > 1$, then there is the unique endemic equilibrium state is globally asymptotically stable in the interior of feasible region and the disease is present. If the disease is present in the population,then it will persist.

บทที่ 5
สรุป วิจารณ์ และเสนอแนะงานวิจัยในอนาคต

ในงานวิจัยฉบับนี้ได้ศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์ โดยพิจารณาแบบจำลองต่างๆดังนี้

- แบบจำลองที่ 1 แบบจำลองของโรคไข้เลือดออกโดยที่ไม่ได้คำนึงถึงสภาพแวดล้อมแต่พิจารณาถึงยุงที่ติดเชื้อมาตั้งแต่เกิด
- แบบจำลองที่ 2 แบบจำลองของโรคไข้เลือดออกโดยที่ไม่ได้คำนึงถึงสภาพแวดล้อมแต่พิจารณาถึงยุงที่ติดเชื้อมาตั้งแต่เกิด และพิจารณาถึงการฟักตัวของเชื้อ
- แบบจำลองที่ 3 แบบจำลองของโรคไข้เลือดออกโดยคำนึงถึงปริมาณน้ำฝนที่มีผลต่อยุงที่เกิดใหม่
- แบบจำลองที่ 4 แบบจำลองของโรคไข้เลือดออกที่พิจารณาความแตกต่างระหว่างพื้นที่ที่มีน้ำท่วมกับพื้นที่ที่ไม่มีน้ำท่วม
- แบบจำลองที่ 5 แบบจำลองของโรคมาลาเรียเมื่อพิจารณาการเกิดน้ำท่วมในประเทศไทย
- แบบจำลองที่ 6 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงชนิดของยุงลาย
- แบบจำลองที่ 7 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงชนิดของยุงลายและฤดูกาล
- แบบจำลองที่ 8 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงประเภทของการเกิดโรคไข้เลือดออก
- แบบจำลองที่ 9 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงอุณหภูมิของสิ่งแวดล้อม
- แบบจำลองที่ 10 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาถึงชนิดของยุงลายและปริมาณน้ำฝน
- แบบจำลองที่ 11 แบบจำลองของโรคไข้เลือดออกเมื่อประชากรมีการเดินทางโดยพิจารณาพื้นที่ที่มีน้ำท่วมในประเทศไทย
- แบบจำลองที่ 12 แบบจำลองของโรคไข้เลือดออกเมื่อพิจารณาถึงสิ่งแวดล้อม
- แบบจำลองที่ 13 แบบจำลองของโรคไข้เลือดออกโดยพิจารณาความเสถียรภาพแบบวงกว้าง (Global stability)

โดยที่แบบจำลองแต่ละแบบได้ศึกษาถึงพฤติกรรมของประชากรคนและประชากรยุงโดยประยุกต์วิธีการของการจำลองเชิงพลวัตมาตรฐาน ซึ่งทำให้ได้ เงื่อนไขที่จำเป็นสำหรับตัวแปรที่ทำให้เกิดความเสถียรภายในของจุดสมดุล โดยการใช้เงื่อนไข Routh-Hurwitz ตรวจสอบความเสถียรของจุดสมดุล ผลที่ได้จากทฤษฎี ทำให้ได้ชุดของค่าพารามิเตอร์ที่สามารถลดการระบาดของโรคได้ ซึ่ง

แสดงในรูปของเงื่อนไข ความเสถียร และค่าสืบพันธุ์พื้นฐาน (basic reproductive number) ซึ่งชุดของพารามิเตอร์แต่ละชุดที่ได้นั้นจะมีผลทำให้ลดการระบาดของโรคนี้ ผลเฉลยเชิงตัวเลขได้นำมาพิจารณาในกรณีแบบต่างๆ ดังแสดงไว้ในบทที่ 4 ทฤษฎีบทเกี่ยวกับการลดการระบาดของโรคได้นำมาแสดงไว้ในแบบจำลองที่ 13 ผลที่ได้แสดงให้เห็นว่า ภัยพิบัติทางธรรมชาติอันได้แก่ ฝนตก น้ำท่วม และอุณหภูมิ มีผลต่อการระบาดของโรคไข้เลือดออกและโรคมาลาเรีย

อย่างไรก็ตาม ในงานวิจัยชิ้นนี้ยังไม่ได้คำนึงถึงการเกิดโรคในเด็กทารกที่คลอดมาจากสตรีมีครรภ์ที่เป็นโรคทั้งสองนี้ งานวิจัยในอนาคตนั้นควรมีการคำนึงถึงอิทธิพลนี้

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การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่น โรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

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ภาคผนวก ก

นิยามและทฤษฎีบทที่เกี่ยวข้อง

A1. Theoretical Background

Many biological problems can be explained mathematically by a set of differential equation, which may be nonlinear. In many situations, it is possible to replace the nonlinear differential equation by a set of related linear differential equation that approximates the real nonlinear equation close enough to give useful effects. The method of "linearization" may not always be appropriated. Then the original nonlinear differential equation must be considered. The study of nonlinear differential equation is usually confined to a variety of special cases and we have to use various approximation methods. In this part, we shall give an introduction to the method which we use in this research.

Definition A.1 A point $X_e \in \Re^n$ is an equilibrium point (or stationary point, singular point, critical point or rest point) of

$$\frac{dX}{dt} = f(t, X) \qquad (A.1)$$

if $f(t, X_e) = 0$ for all $t \geq t^*$.

If X_e is an equilibrium point of (A.1) at t^*, then it is an equilibrium point for all $\tau \geq t^*$.

Definition A.2 The equilibrium point $X = 0$ of (A.1) is stable if for every $\delta > 0$ and any $t_0 \in \Re^+$ there is a $\omega(\delta, t_0) > 0$ such that

$|u(t, t_0, \gamma)| < \delta$ for every $t \geq t_0$

whenever $|\gamma| < \omega(\delta, t_0)$ where $u(t, \gamma)$ is the solution of (A.1).

Definition A.3 The equilibrium point $X = 0$ of (A.1) is asymptotically stable if

1) it is stable and
2) for every $t_0 \geq 0$ there is an $\varepsilon(t_0) > 0$ such that

$$\lim_{t \to \infty} u(t, t_0, \gamma) = 0 \text{ whenever } |\gamma| < \varepsilon \text{ [10]} \qquad (A.2)$$

Definition A.4 The equilibrium point $X = 0$ of (A.1) is unstable if it is not stable. In this case there is a $t_0 \geq 0$ and a sequence $\gamma_n \to 0$ of initial points and a sequence t_m such that $|u(t_0 + t_m, t_0, \gamma_m)| \geq \gamma$ for every m, $t_m \geq 0$.

For more general setting, consider a system of two autonomous first-order differential equations :

$$\frac{dX}{dt} = g_1(X, Y) \qquad (A.3)$$

$$\frac{dY}{dt} = g_2(X, Y) \qquad (A.4)$$

where g_1 and g_2 are nonlinear functions. We let $(\bar{X}, \bar{Y})$ is the equilibrium point, then

$$g_1(\bar{X}, \bar{Y}) = g_2(\bar{X}, \bar{Y}) = 0. \qquad (A.5)$$

Setting the solution at any time in the form

$$X(t) = \bar{X} + x(t) \qquad (A.6)$$

and

$$Y(t) = \bar{Y} + y(t). \qquad (A.7)$$

This method is called perturbation of the equilibrium point. We substitute X(t) and Y(t) from (A.6) and (A.7) into (A.3) and (A.4),

$$\frac{d}{dt}(\bar{X} + x) = g_1(\bar{X} + x, \bar{Y} + y) \qquad (A.8)$$

$$\frac{d}{dt}(\bar{Y} + y) = g_2(\bar{X} + x, \bar{Y} + y) \qquad (A.9)$$

On the left hand side, we expand the derivatives and on the right hand side, we expand g_1 and g_2 in a Taylor series about the equilibrium point $(\bar{X}, \bar{Y})$. Then we obtain

$$\frac{d\bar{X}}{dt} + \frac{dx}{dt} = g_1(\bar{X}, \bar{Y}) + g_{1_x}(\bar{X}, \bar{Y})x + g_{1_y}(\bar{X}, \bar{Y})y$$

$$+ \text{ terms of order } x^2, y^2, xy \text{ and higher,} \qquad (A.10)$$

$$\frac{d\bar{Y}}{dt} + \frac{dy}{dt} = g_2(\bar{X}, \bar{Y}) + g_{2_x}(\bar{X}, \bar{Y})x + g_{2_y}(\bar{X}, \bar{Y})y$$

$$+ \text{ terms of order } x^2, y^2, xy \text{ and higher,} \qquad (A.11)$$

where $g_{1_x}(\bar{X}, \bar{Y})$ is $\frac{\partial g_1}{\partial x}$ calculated at $(\bar{X}, \bar{Y})$ and similarly for $g_{1_y}(\bar{X}, \bar{Y})$, $g_{2_x}(\bar{X}, \bar{Y})$, $g_{2_y}(\bar{X}, \bar{Y})$ and other terms.

By the definition of the equilibrium point, we have $\frac{d\bar{X}}{dt} = 0$, $\frac{d\bar{Y}}{dt} = 0$, $g_1(\bar{X}, \bar{Y}) = 0$ and $g_2(\bar{X}, \bar{Y}) = 0$. We consider only linear term. Thus from (A.10) and (A.11), we obtain

$$\frac{dx}{dt} = a_{11}x + a_{12}y,$$

$$\frac{dy}{dt} = a_{21}x + g_{22}y.$$

We denote J as the Jacobian matrix of equations (A.3) and (A.4) and is given by

$$J(\bar{X}, \bar{Y}) = \begin{bmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{bmatrix} = \begin{bmatrix} \frac{\partial g_1}{\partial x} & \frac{\partial g_1}{\partial y} \\ \frac{\partial g_2}{\partial x} & \frac{\partial g_2}{\partial y} \end{bmatrix}_{(\bar{X}, \bar{Y})}.$$

Letting $\alpha = a_{11} + a_{22}$

$\beta = a_{11}a_{22} - a_{12}a_{21}$

and $\gamma = \alpha^2 - 4\beta$ is called the discriminant.

Then the characteristic equation is $\lambda^2 - \alpha\lambda + \beta = 0$

The eigenvalues are obtained from:

$$\lambda_{1,2} = \frac{\alpha \pm \sqrt{\gamma}}{2}$$

A linear system can have at most one equilibrium point, (0,0) if $\beta = \det J \neq 0$.

Theorem A.1 The equilibrium point X = 0 of (A.1) is stable if all eigenvalues of J have negative real parts and every eigenvalues of J which has a zero real part is a simple zero of the characteristic polynomial of J.

The behavior of the equilibrium points of the system of equations (A.3) and (A.4) can be determined by considering the different kinds of eigenvalues of the Jacobian matrix.

The different behavior of equilibrium points are determined from the characteristics of eigenvalues of J.

i) The eigenvalues of J are real and distinct.

ii) The eigenvalues of J are real and repeated.

iii) The eigenvalues of J are complex.

The behaviors of the equilibrium points for all three cases are described as follows.

Case I The eigenvalues of J are real and distinct. There are three possible behaviors.

a. If both eigenvalues of J are negative, the equilibrium point will be a stable-two tangent node (Figure A.1).

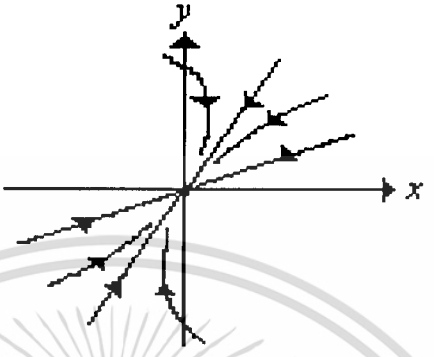


Figure A.1 A stable two-tangent node.

b. If both eigenvalues of J are positive, the equilibrium point will be an unstable two - tangent node(Figure A.2).

Figure A.2 An unstable two-tangent node.

c. If the eigenvalues of J have opposite signs, the critical point will be a saddle point (Figure A.3).

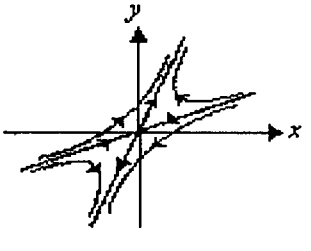


Figure A.3 A saddle point.

ii) The eigenvalues of J are real and repeated. There are two possible behaviors.

a. If J is diagonal and J is similar to the matrix as $J = \begin{bmatrix} \lambda & 0 \\ 0 & \lambda \end{bmatrix}$, then the critical point is called a stellar node which be stable if $\lambda < 0$ and unstable if $\lambda > 0$ (Figure A.4).

(a) Stable (b) Unstable

Figure A.4 A stellar node.

b. If J is not diagonal, then it is not similar to a diagonal matrix. The critical point is called a stable one-tangent node if $\lambda < 0$, and an unstable one-tangent node if $\lambda > 0$ (Figure A.5).

(a) Stable (b) Unstable

Figure A.5 The one-tangent node.

iii) The eigenvalues of J are complex.

It is necessary and sufficient that $\gamma = \alpha^2 - 4\beta$ is negative and then

$$\lambda_{1,2} = \frac{\alpha \pm i\sqrt{-\gamma}}{2}$$

There are six possible behaviors as follows.

a. If $\alpha > 0$ and $\beta > 0$, then the equilibrium point will be unstable node.

b. If $\alpha < 0$ and $\beta > 0$, then the equilibrium point will be stable node.

c. If $\alpha < 0$ then the equilibrium point will be a saddle point.

d. If $\alpha^2 < 4\beta$ and $\alpha > 0$, then the equilibrium point will be an unstable spiral node (Figure A.6).

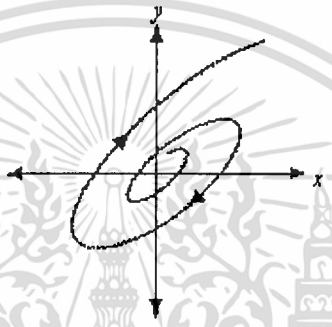
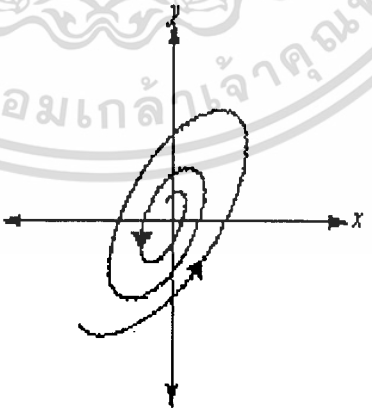


Figure A.6 An unstable spiral node.

e. If $\alpha^2 < 4\beta$ and $\alpha < 0$, then the equilibrium point will be a stable spiral node

Figure A.7 A stable spiral node.

f. If $\alpha^2 < 4\beta$ and $\alpha = 0$ mean that the eigenvalues of J are purely imaginary, then the



critical point will be a center (Figure A.8).

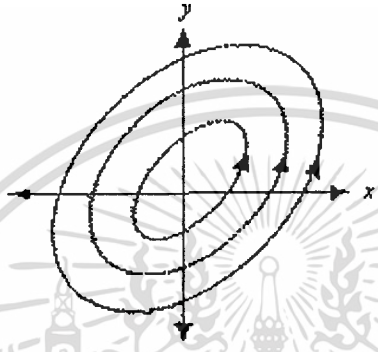


Figure A.8 A center.

In this section, we use the above ideas to apply for systems of $n > 2$ equations.

Consider

$$\frac{dX}{dt} = f_j(X_1, X_2, \ldots, X_k) \quad \text{where } j = 1,2,\ldots,k \qquad (A.12)$$

or in the form of vector notation

$$\frac{dX}{dt} = F(X) \qquad (A.13)$$

for $X = (X_1, X_2, \ldots, X_k)$ and $F = (f_1, f_2, \ldots, f_k)$ where each function f_j depend on all or some $Y_1, Y_2, \ldots, Y_k$. The equilibrium point $\overline{Y}$ is obtained by solving $F(Y) = 0$. The next step is to determine stability properties of this equilibrium point.

When we linearlize equation (A.13), the Jacobian is obtained by setting

$$J = \frac{\partial}{\partial X} F(\overline{Y}) \qquad (A.14)$$

where J is a $k \times k$ matrix. The eigenvalues λ of the matrix satisfy $\det(J - \lambda I) = 0$. We obtain a characteristic equation in the form

$$\lambda^k + b_1\lambda^{k-1} + \cdots + b_k = 0 \quad . \qquad (A.15)$$

The stability of the equilibrium point can be determined without solving the actual values of eigenvalues by using the Routh-Hurwitz criteria.

Definition A.5 (Routh-Hurwitz criteria for local asymptotical stability)

Take the characteristic equation (A.15), define k matrices as follows:

$H_1 = [b_1]$,

$$H_2 = \begin{bmatrix} b_1 & 1 \\ b_3 & b_2 \end{bmatrix},$$

$$H_3 = \begin{bmatrix} b_1 & 1 & 0 \\ b_3 & b_2 & b_1 \\ b_5 & b_4 & b_3 \end{bmatrix},\ldots$$

$$Hj = \begin{bmatrix} b_1 & 1 & 0 & 0 & \cdots & 0 \\ b_3 & b_2 & b_1 & 1 & \cdots & 0 \\ b_5 & b_4 & b_3 & b_2 & \cdots & 0 \\ b_{2j-1} & b_{2j-2} & b_{2j-3} & b_{2j-4} & \cdots & b_j \end{bmatrix},\ldots$$

$$H_k = \begin{bmatrix} b_1 & 1 & 0 & \cdots & 0 \\ b_3 & b_2 & b_1 & \cdots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & \cdots & & b_k \end{bmatrix}.$$

where the (l,m) term in the matrix H_j is

b_{2l-m} for $0 < 2l-m < k$

1 for $2l = m$

0 for $2l < m$ or $2l > k+m$.

Then all eigenvalues have negative real part. This means that the equilibrium point $\bar{X}$ is stable if and only if the determination of all Hurwitz matrices are positive which is

$\text{Det } H_j > 0$ for $j = 1, 2, 3, \ldots, k$.

Next, we show conditions of Routh-Hurwitz criteria for case k = 3 and 5 which are appeared in the thesis.

For k = 3;

We need to show that $\text{Det } H_j > 0$ for $j = 1, 2$ and 3.

$H_1 = [b_1]$; $\text{Det } H_1 = b_1$,

$$H_2 = \begin{bmatrix} b_1 & 1 \\ b_3 & b_2 \end{bmatrix}; \quad \text{Det } H_2 = b_1 b_2 - b_3,$$

$$H_3 = \begin{bmatrix} b_1 & 1 & 0 \\ b_3 & b_2 & b_1 \\ b_5 & b_4 & b_3 \end{bmatrix}; \quad \text{Det } H_3 = b_1 b_2 b_3 - b_3^2 - b_1^2 b_4 + b_1 b_5.$$

Since coefficients b_4 and b_5 in 3^{rd} order characteristic polynomial equation equal to zero then we have

$\text{Det}\, H_1 = b_1$,

$\text{Det}\, H_2 = b_1b_2 - b_3$ and

$\text{Det}\, H_3 = b_1b_2b_3 - b_3^2 = b_3(b_1b_2 - b_3)$.

So the three conditions which correspond to $\text{Det}\, H_j > 0$ for $j = 1, 2$ and 3 are $b_1 > 0$, $b_3 > 0$ and $b_1b_2 > b_3$.

Therefore the three conditions of Routh-Hurwitz criteria for local asymptotical stability in 3^{rd} order characteristic polynomial equation are

i) $b_1 > 0$,

ii) $b_3 > 0$ and

iii) $b_1b_2 > b_3$.

For $k = 5$

We need to show that $\text{Det}\, H_j > 0$ for $j = 1, 2, 3, 4$ and 5.

$H_1 = [b_1]$; $\text{Det}\, H_1 = b_1$,

$$H_2 = \begin{bmatrix} b_1 & 1 \\ b_3 & b_2 \end{bmatrix}; \quad \text{Det}\, H_2 = b_1b_2 - b_3,$$

$$H_3 = \begin{bmatrix} b_1 & 1 & 0 \\ b_3 & b_2 & b_1 \\ b_5 & b_4 & b_3 \end{bmatrix}; \quad \text{Det}\, H_3 = b_1b_2b_3 - b_3^2 - b_1^2b_4 + b_1b_5,$$

$$H_4 = \begin{bmatrix} b_1 & 1 & 0 & 0 \\ b_3 & b_2 & b_1 & 1 \\ b_5 & b_4 & b_3 & b_2 \\ b_7 & b_6 & b_5 & b_4 \end{bmatrix};$$

$$\text{Det}\, H_4 = b_1b_2b_3b_4 - b_3^2b_4 - b_1^2b_4^2 - b_1b_2^2b_5 + b_2b_3b_5 + 2b_1b_4b_5 - b_5^2 + b_1^2b_2b_6 - b_1b_3b_6 - b_1b_2b_7 + b_3b_7,$$

$$H_5 = \begin{bmatrix} b_1 & 1 & 0 & 0 & 0 \\ b_3 & b_2 & b_1 & 1 & 0 \\ b_5 & b_4 & b_3 & b_2 & b_1 \\ b_7 & b_6 & b_5 & b_4 & b_3 \\ b_9 & b_8 & b_7 & b_6 & b_5 \end{bmatrix}$$

$$\begin{aligned}\text{Det } H_5 = {} & b_1b_2b_3b_4b_5 - b_3^2b_4b_5 - b_1^2b_4^2b_5 - b_1b_2^2b_5^2 + b_2b_3b_5^2 + 2b_1b_4b_5^2 - b_5^3 - b_1b_2b_3^2b_6 \\ & + b_3^2b_6 + b_1^2b_3b_4b_6 + 2b_1^2b_2b_5b_6 - 3b_1b_3b_5b_6 - b_1^3b_6^2 + b_1b_2^2b_3b_7 - b_2b_3^2b_7 \\ & - b_1^2b_2b_4b_7 - b_1b_2b_5b_7 + 2b_3b_5b_7 + 2b_1^2b_6b_7 - b_1b_7^2 - b_1^2b_2b_3b_8 + b_1b_3^2b_8 \\ & + b_1^3b_4b_8 - b_1^2b_5b_8 + b_1b_2b_3b_9 - b_3^2b_9 - b_1^2b_4b_9 + b_1b_5b_9.\end{aligned}$$

Since the coefficients b_6, b_7, b_8 and b_9 in 5^{th} order characteristic polynomial equation equal to zero then we have

$$\text{Det } H_1 = b_1,$$

$$\text{Det } H_2 = b_1b_2 - b_3,$$

$$\begin{aligned}\text{Det } H_3 &= b_1b_2b_3 - b_3^2 - b_1^2b_4 + b_1b_5 \\ &= b_3(b_1b_2 - b_3) - b_1(b_1b_4 - b_5),\end{aligned}$$

$$\begin{aligned}\text{Det } H_4 &= b_1b_2b_3b_4 - b_3^2b_4 - b_1^2b_4^2 - b_1b_2^2b_5 + b_2b_3b_5 + 2b_1b_4b_5 - b_5^2 \\ &= b_4(b_1b_2b_3 - b_3^2 - b_1^2b_4) - b_5(b_1b_2^2 - b_2b_3 - 2b_1b_4 + b_5),\end{aligned}$$

$$\begin{aligned}\text{Det } H_5 &= b_1b_2b_3b_4b_5 - b_3^2b_4b_5 - b_1^2b_4^2b_5 - b_1b_2^2b_5^2 + b_2b_3b_5^2 + 2b_1b_4b_5^2 - b_5^3 \\ &= b_5(b_4(b_1b_2b_3 - b_3^2 - b_1^2b_4) - b_5(b_1b_2^2 - b_2b_3 - 2b_1b_4 + b_5))\end{aligned}$$

So the conditions which correspond to $\text{Det } H_j > 0$ for $j = 1, 2, 3, 4$ and 5.

are $b_1 > 0$,

$b_1b_2 - b_3 > 0$,

$b_3(b_1b_2 - b_3) - b_1(b_1b_4 - b_5) > 0$,

$b_4(b_1b_2b_3 - b_3^2 - b_1^2b_4) - b_5(b_1b_2^2 - b_2b_3 - 2b_1b_4 + b_5) > 0.$

After we rearrange all above inequalities, we get the conditions of Routh-Hurwitz criteria for local asymptotical stability in 5^{th} order characteristic polynomial equation

i) $b_i > 0 \ (i = 1, 2, 3, 4, 5)$

ii) $b_1b_2b_3 > b_3^2 + b_1^2b_4$ and

iii) $(b_1b_4 - b_5)(b_1b_2b_3 - b_3^2 - b_1^2b_4) > b_5(b_1b_2 - b_3)^2 + b_1b_5^2.$

A2. Numerical Solutions of Differential Equations

In this research, we use Runge-Kutta-Fehlberg's method which is one of the most widely used methods, and is particularly suitable in cases when the computation of higher derivatives is complicated. It can be used for equations of arbitrary order by means of a transformation to a

system of first-order equations. We shall discuss the solution of three first-order equations. Let this system be

$$\frac{dx}{dt} = f(x, y, z, t)$$
$$\frac{dy}{dt} = g(x, y, z, t)$$
$$\frac{dz}{dt} = h(x, y, z, t)$$

with initial point (x_0, y_0, z_0, t_0) and interval length h.

Runge-Kutta-Fehlberg's method for finding approximate values of x,y and z at each step is

$$x_{n+1} = x_n + \frac{(2375k_1 + 11264k_3 + 10985k_4 - 4104k_5}{20520},$$
$$y_{n+1} = y_n + \frac{(2375r_1 + 11264r_3 + 10985r_4 - 4104k_5}{20520}$$
$$z_{n+1} = z_n + \frac{(2375s_1 + 11264s_3 + 10985s_4 - 4104s_5}{20520}$$

where

$$k_1 = hf(x_n, y_n, z_n, t_n),$$
$$k_2 = hf(x_n + \frac{k_1}{4}, y_n + \frac{r_1}{4}, z_n + \frac{s_1}{4}, t_n + \frac{h}{4}),$$
$$k_3 = hf(x_n + \frac{(3k_1 + 9k_2)}{32}, y_n + \frac{(3r_1 + 9r_2)}{32}, z_n + \frac{(3s_1 + 9s_2)}{32}, t_n + \frac{3h}{8}),$$
$$k_4 = hf(x_n + \frac{(1932k_1 - 7200k_2 + 7296k_3)}{2197},$$
$$y_n + \frac{(1922r_1 - 7200r_2 + 7296r_3)}{2197},$$
$$z_n + \frac{(1932s_1 - 7200s_2 + 7296s_3)}{2197}, t_n + \frac{12h}{13}),$$

$$k_5 = hf(x_n + \frac{(8341k_1 - 32832k_2 + 29440k_3 - 845k_4)}{4104},$$
$$y_n + \frac{(8341r_1 - 32832r_2 + 29440r_3 - 854r_4)}{4104},$$
$$z_n + \frac{(8341s_1 - 32832s_2 + 29440s_3 - 854s_4)}{4104}, t_n + h),$$

$$k_6 = hf(x_n + \frac{(-6080k_1 + 41040k_2 - 28352k_3 + 9295k_4 - 5643k_5)}{20520},$$

$$y_n + \frac{(-6080r_1 + 41040r_2 - 28352r_3 + 9295r_4 - 5643r_5)}{20520},$$

$$z_n + \frac{(-6080s_1 + 41040s_2 - 28352s_3 + 9295s_4 - 5643s_5)}{20520}, t_n + \frac{h}{2}),$$

and the error for each step will be

$$\text{Error} = \frac{k_1}{360} - \frac{128k_3}{4275} - \frac{2197k_4}{75240} + \frac{k_5}{50}.$$

$r_1, r_2, ..., r_6$ and the error of y value can be evaluated from the above equations. $s_1, s_2, ..., s_6$ and the error of z value can be evaluated from the above equations. $k_1, k_2, ..., k_6$ and error of x by replacing function f with function g and function h.

Runge-Kutta-Fehlberge's method can be applied directly to a system of n first-order differential equations

Definition A3. A probability space (Ω, F, P), a stochastic process (or random process) with state space X is a collection of X-valued random variables indexed by a set T ("time"). That is,

a stochastic process F is a collection

$$\{F_t : t \in T\}$$

where each F_t is an X-valued random variable.

ทฤษฎีบท A4. ทฤษฎีบท Hopf - Bifurcation [9,10,11]

กำหนดให้ระบบสมการไม่เชิงเส้น n สมการ n ตัวแปร ซึ่งมีพารามิเตอร์ υ มีรูปแบบดังนี้

$$\frac{dX}{dt} = f(X, \upsilon); X \in R^n \qquad (6)$$

โดยที่ X เป็นจุดสมดุลของระบบสมการ(6) และ υ เป็นพารามิเตอร์ค่าจริงบนช่วง J จาโคเบียนเมทริกซ์นิยามโดย

$$A(\upsilon) = D_x f(X^*(\upsilon),\upsilon) = \frac{\partial f_i}{\partial X_j}(X^*(\upsilon),\upsilon); \quad i,j = 1,2,\ldots,m \tag{7}$$

สมมติให้ 1) $A(\upsilon)$ มีค่าลักษณะเฉพาะเป็นจำนวนเชิงซ้อนสังยุค λ_1 และ λ_2 ที่ทำให้

$$\lambda_1(\upsilon) = \lambda_2(\upsilon) = \alpha(\upsilon) \pm i\omega(\upsilon) \tag{8}$$

ที่ทำให้สำหรับบางค่า $\upsilon = \upsilon_c \in J$ โดยที่ υ_c เรียกว่าค่าวิกฤติของ υ

$$\omega(\upsilon_c) = \omega_0 > 0, \ \alpha(\upsilon_c) = 0 \text{ และ } \alpha'(\upsilon_c) \neq 0 \tag{9}$$

2) ถ้าค่าลักษณะเฉพาะดังกล่าวมีส่วนจริงที่เป็นลบ แล้วสมการ (9) จะมีกลุ่มของผลเฉลยที่เป็นคาบ หมายความว่าความเสถียรภาพเชิงเส้นของจุดวิกฤติ $X^*(\upsilon)$ จะหายไป ที่ υ ตัดกับ υ_c ระบบจะมีกลุ่มของผลเฉลยเป็นคาบ $X = P_\upsilon(t)$ โดยที่ $0 < \upsilon < \upsilon_0$ และ υ เป็นค่าแอมพลิจูด $\max_t \left\| P_\varepsilon(t) - X^*(\upsilon_c) \right\|$.

และ ε_0 มีขนาดเล็กที่เพียงพอ ผลเฉลยที่เป็นคาบที่ออกมาจากจุดสมดุลจะเรียกว่า **โฮปไบเฟอร์เคชัน** และจะได้คาบ $T(\varepsilon) = \frac{2\pi}{\omega}$ ผลเฉลยที่เป็นคาบซึ่งเป็นผลมาจากโฮปไบเฟอร์เคชัน จากจุดวิกฤต $X^*(\upsilon)$ ซึ่งสัมพันธ์กับแนววิถีบนเส้นโค้งปิดหรือ orbit รอบจุดวิกฤติในระนาบเฟส (phase plane) สำหรับแนววิถีปิด (closed trajectory) ในย่านใกล้เคียง (neighborhood) โดยที่ทุก ๆ แนววิถี (trajectory) มีลักษณะเป็น limit cycle

ทฤษฎีบท A5. ทฤษฎีบท ของ Lyapunov [12-14]

ให้ $x = 0$ เป็นจุดสมดุลของระบบสมการ $\frac{dx}{dt} = f(x)$ และ $D \subset \mathbb{R}^n$ กำหนดให้ V เป็นฟังก์ชันต่อเนื่อง

โดยที่ 1. $V(0) = 0$ และ $V(x) > 0$; $\forall x \in D \setminus \{0\}$

2. $V'(x) \leq 0$; $\forall x \in D$ แล้ว $x = 0$ มีความเสถียรภาพ

นอกจากนั้นถ้า $V'(x) < 0$; $\forall x \in D \setminus \{0\}$ แล้ว $x = 0$ มีความเป็นเสถียรภาพเชิงเส้นกำกับ (Asymptotically stable)

บทนิยาม A6. มิติความน่าจะเป็น (Ω, F, P) , กระบวนการสโตคาสติก หรือกระบวนการสุ่ม เกิดจากการที่ชุดของตัวแปรสุ่ม X ดำเนินการ ภายใต้กระบวนการที่เกิดจากการดำเนินการของปัญหานั้นๆ ภายใต้ดัชนีเวลา T ซึ่งคือ

$$\{F_t : t \in T\}$$

โดยที่ F_t คือตัวแปรสุ่มที่เกิดจากกระบวนการดำเนินงานแบบสุ่มของตัวแปร X [15].

บทนิยาม A7. ระบบสารสนเทศภูมิศาสตร์ หรือ Geographic Information System (GIS) คือ กระบวนการทำงานเกี่ยวกับข้อมูลในเชิงพื้นที่ด้วยระบบคอมพิวเตอร์ที่ใช้กำหนดข้อมูลและสารสนเทศ ที่มีความสัมพันธ์กับตำแหน่งในเชิงพื้นที่ เช่น ที่อยู่ บ้านเลขที่ สัมพันธ์กับตำแหน่งในแผนที่ ตำแหน่ง เส้นรุ้ง เส้นแวง ข้อมูลและแผนที่ใน GIS เป็นระบบข้อมูลสารสนเทศที่อยู่ในรูปของตารางข้อมูล และฐานข้อมูลที่มีส่วนสัมพันธ์กับข้อมูลเชิงพื้นที่ (Spatial Data) ซึ่งรูปแบบและความสัมพันธ์ของข้อมูลเชิงพื้นที่ทั้งหลาย จะสามารถนำมาวิเคราะห์ด้วย GIS และทำให้สื่อความหมายในเรื่องการเปลี่ยนแปลงที่สัมพันธ์กับเวลาได้ เช่น การแพร่ขยายของโรคระบาด การเคลื่อนย้าย ถิ่นฐาน การบุกรุกทำลาย การเปลี่ยนแปลงของการใช้พื้นที่ ฯลฯ ข้อมูลเหล่านี้ เมื่อปรากฏบนแผนที่ทำให้สามารถแปลและสื่อความหมายได้ง่าย [16,17]

ภาคผนวก ข

ผลงานการวิจัย

ผลงานตีพิมพ์และนำเสนอที่ประชุมวิชาการระดับนานาชาติมีดังนี้

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The transmission dynamics of SIR modeling for dengue fever with vector-born infection

Pratchaya Chanprasopchai[a], Puntani Pongsumpun[b]
Department of Mathematics, Faculty of Science,
King Mongkut's Institute of Technology Ladkrabang,
Chalongkrung road, Ladkrabang, Bangkok, 10520, Thailand
Email: [a]: pchanprasopcai@gmail.com, [b]: kppuntan@kmitl.ac.th

ABSTRACT

This paper describes the mathematical model for transmission dynamics of dengue fever, which is transmitted between human by biting of infectious mosquitoes. The Susceptible – Infected – Recovery (SIR) model is a tool to investigate the disease. The infected vectors, which are caused by both biting of infected human and vector-born infection are proposed. We apply standard dynamic modeling method to analysis our mathematical model. The stability of the model is analyzed by Routh – Hurwitz criteria. The numerical solutions show that the dynamical behaviors converge to the endemic equilibrium state. The relation between each individual variable with the biting rate of mosquito are presented.

Keywords: dengue fever, mathematical model, SIR model, Routh – Hurwitz criteria,

INTRODUCTION

Dengue fever is a fastest emerging arboviral infection spread by *Aedes* mosquitos with major public health consequences in over 100 tropical and sub-tropical countries in South-East Asia, the Western Pacific and Latin and Central America which around 2.5 billion people, globally live under the threat of dengue fever (WHO, 2011). The rising level of dengue infections around the world has become seriously an international concern that has increased with increasing geographic expansion distribution as shown in Figure 1.

In Thailand, dengue fever was reported cases about 64,374 and 74,250 in 2011 and 2012 respectively. Last year, the numbers of cases are remarkable rate, which were reported 150,934 cases (BVBD, 2013). The danger of dengue fever is no antibiotic treatment and actually everyone can be affected by the transmission of dengue fever since the growths of mosquitoes are wide spreading. It can be available in any places that have stagnant water which can be found anywhere and anytime in your home.

Dengue fever is transmitted to human by infected female *Aedes* mosquitoes and caused by infection with one of four different viruses known as DEN-1, DEN-2, DEN-3 and DEN-4. When mosquitoes are biting of infected human, the dengue virus will transmit to mosquito and will be the infected vector. There are many researches to concentrate in this area. Estava

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Burapha University, Thailand
July 3-4, 2014

and Vargus (1998) was proposed dengue fever model in 1998. Pongsumpun (2006, 2007) proposed mathematical model of dengue fever with incubation period. Naowarat et al. proposed and analyzed dynamical model for determining human susceptibility to dengue fever. In this paper, we are considered infected vector caused by both biting of infected human and vector-born infection. The vector-born infection is caused by infected egg and will be the infected vector.

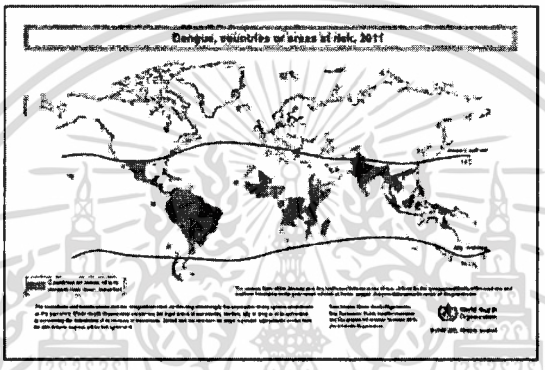

Fig. 1: Dengue, the countries at risk 2011 (WHO, 2011)

MATERIALS AND METHODS

Mathematical model

We formulate the mathematical model by considering infected vector by both biting of infected human and vector-born infection. The human and vector population are related in this study, which human populations are separated into three classes, susceptible, infected and recovered human while the vector populations are separated into two classes, susceptible and infected vector populations. The transmission of dengue fever is shown in Figure 2.

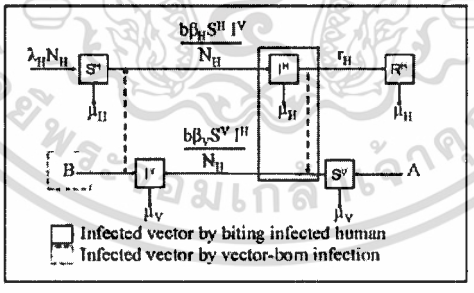

Fig. 2: The transmission flow chart of dengue fever

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Burapha University, Thailand
July 3-4, 2014

Let:

$S^H(t)$ = Number of susceptible humans at time t,
$I^H(t)$ = Number of infected humans at time t,
$R^H(t)$ = Number of recovered humans at time t,
$S^V(t)$ = Number of susceptible vector population at time t,
$I^V(t)$ = Number of infected vector population at time t,
A = Recruitment rate of vector population,
B = Vector-born rate of vector population.

The dengue fever transmission model with vector-born infection can be explained by the following equation:

$$\frac{dS^H}{dt} = \lambda_H N_H - \frac{b\beta_H}{N_H} S^H I^V - \mu_H S^H \quad (1)$$

$$\frac{dI^H}{dt} = \frac{b\beta_H}{N_H} S^H I^V - (\mu_H + r_H) I^H \quad (2)$$

$$\frac{dR^H}{dt} = \mu_H I^H - \mu_H R^H \quad (3)$$

$$\frac{dS^V}{dt} = A - \frac{b\beta_V}{N_H} S^V I^H - \mu_V S^V \quad (4)$$

$$\frac{dI^V}{dt} = B + \frac{b\beta_V}{N_H} S^V I^H - \mu_V I^V \quad (5)$$

with the conditions:

$$N_H = S^H + I^H + R^H \quad (6)$$

$$N_V = S^V + I^V \quad (7)$$

where:

N_H = Total number the human population,
λ_H = Birth rate of the human population,
b = Biting rate of the vector population,
β_H = Transmission probability of dengue virus from vector population to human population,
β_V = Transmission probability of dengue virus from human population to vector population,
μ_H = Death rate of the human population,
μ_V = Death rate of the vector population,
r_H = Recovery rate of the human population.

The total number of human and vector are assumed to be constant. It means that the rate of change of vector and human population are zero. It can be expressed as following:

$$\frac{dS^H}{dt} + \frac{dI^H}{dt} + \frac{dR^H}{dt} = 0 \quad (8)$$

$$\frac{dS^V}{dt} + \frac{dI^V}{dt} = 0 \quad (9)$$

So, we can obtain the following equations:

$$N_V = (A+B)/\mu_V \quad (10)$$

$$\lambda_H = \mu_H \quad (11)$$

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Burapha University, Thailand
July 3-4, 2014

In order to analyze the model, it should be normalized equation (1) – (5). Let

$$S_H = \frac{S^H}{N_H}, I_V = \frac{S^H}{N_H}, R_V = \frac{R^H}{N_H}, S_V = \frac{S^V}{N_V}, I_V = \frac{S^V}{N_V} \quad (12)$$

The mathematical model can be reduced as following:

$$\frac{dS_H}{dt} = \mu_H(1 - S_H) - \frac{b\beta_H S_H I_V N_V}{N_H} \quad (13)$$

$$\frac{dI_H}{dt} = \frac{b\beta_H S_H I_V N_V}{N_H} - (\mu_H + r_H) I_H \quad (14)$$

$$\frac{dI_V}{dt} = \frac{B}{N_V} + b\beta_V S_V I_H - \mu_V I_V \quad (15)$$

Analysis our model

The equilibrium points of equations (13) – (15) are investigated. The solution can be found by setting the right hand side equal to zero. So, we can get the two equilibrium points E_1 and E_2. The E_1 and E_2 are shown as following:

$$E_1 = (S_H^*, I_H^*, I_V^*) \quad (16)$$

$$E_2 = (S_H^{**}, I_H^{**}, I_V^{**}) \quad (17)$$

$$S_H^* = \frac{N_H \mu_H}{bd_1 N_V \mu_H + N_H \mu_H} \quad (18)$$

$$S_H^{**} = \frac{N_H \mu_H}{bd_2 N_V \mu_H + N_H \mu_H} \quad (19)$$

$$I_H^* = \frac{bd_1 \beta_H N_V \mu_H}{(\mu_H + r_H)(bd_1 N_V \beta_H + N_H \mu_H)} \quad (20)$$

$$I_H^{**} = \frac{bd_2 \beta_H N_V \mu_H}{(\mu_H + r_H)(bd_2 N_V \beta_H + N_H \mu_H)} \quad (21)$$

$$I_V^* = d_1 \quad (22)$$

$$I_V^{**} = d_2 \quad (23)$$

where:

$$d_1 = \frac{M + R_0 M}{N}$$

$$d_2 = \frac{M - R_0 M}{N}$$

$$M = b^2 N_V^2 \beta_H \beta_V \mu_H + N_V(\mu_H + r_H)(b\beta_H \beta_V - N_H \mu_H \mu_V)$$

$$N = 2bN_V^2 \beta_H (b\beta_V \mu_H + (\mu_H + r_H)\mu_V)$$

$$R_0 = \frac{\sqrt{N_V^2(4bN_H \beta_H \beta_V \mu_H(\mu_H + r_H)(b\beta_H \beta_V \mu_H) + (\mu_H + r_H)\mu_V) + (b\beta_H \beta_V(r_H + \mu_H + bN_V \mu_V) - N_H \mu_H(\mu_H + r_H)\mu_V)^2}}{b^2 N_V^2 \beta_H \beta_V \mu_H + N_V(\mu_H + r_H)(b\beta_H \beta_V - N_H \mu_H \mu_V)}$$

The local stability of the equilibrium point is calculated by Jacobian matrix of equations (13) – (15). The eigenvalues will indicate the local stability. The equilibrium solution is local stability when all eigenvalues are negative real parts. The eigenvalues of Jacobian matrix are determined by solving:

$$\det(J - \lambda I) = 0 \quad (24)$$

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Burapha University International Conference 2014
Burapha University, Thailand
July 3-4, 2014

where:
J = The Jacobian matrix of the equilibrium point,
λ = The eigenvalue,
I = The identity matrix.
All eigenvalues are determined by following:

$$(\lambda^3 + e_0\lambda^2 + e_1\lambda + e_2) = 0 \quad (25)$$

Routh-Hurwitz criteria is used to analyze the local stability of equilibrium point. The solution is local stability when the conditions are satisfied by following:

$$(e_0 > 0), (e_1 > 0) \text{ and } (e_0 e_1 > e_2) \quad (26)$$

By solving equation (13) – (15) and (24) – (25), it can be found that all conditions are complied with equation (26). Thus, we can conclude that equilibrium point E_1 is local stable.

RESULTS

Numerical results

The basic reproductive number of the dengue fever in this study is $\sqrt{R_0}$. It is the average number of secondary case that one case can produce into a susceptible human. In case of R_0 value more than one, the endemic equilibrium is stable. Numerical solutions of equations (13) – (15) are presented the dengue fever situation. The computer software package is used to analyze in this investigated. The values of parameters are as following:

A = 400,
B = 200,
N_H = 10,000,
b = 1/3 day^{-1},
β_H = 0.75,
β_V = 1.00,
μ_H = 0.0000391 day^{-1},
μ_V = 0.075 day^{-1},
r_H = 0.1428 day^{-1}.

All eigenvalues of Jacobian matrix from equations (13) – (15) are determined by equation (24) and we obtained the characteristic equation as below:

$$(-\lambda^3 - 0.21457\lambda^2 - 0.0603873\lambda - 6.3884*10^{-6}) = 0 \quad (27)$$

The results of calculated values are: $\lambda_1 = -0.181491$, $\lambda_2 = -0.0319781$, $\lambda_3 = -0.00110074$ and $R_0 = 1.07768$. All eigenvalues are negative that leads to the equilibrium state. R_0 is more than 1 that leads to be the endemic state. The solutions oscillate to the endemic equilibrium points (S_H^{1*}, I_H^{1*}, I_V^{1*}).

Where
$S_H^{1*} = 0.060569$,
$I_H^{1*} = 0.000257$,
$I_V^{1*} = 0.002870$.

Graphical results

The time series solutions of susceptible human, infected human and infected vector populations are shown in Fig. 3.

Burapha University International Conference 2014
Burapha University, Thailand
July 3-4, 2014

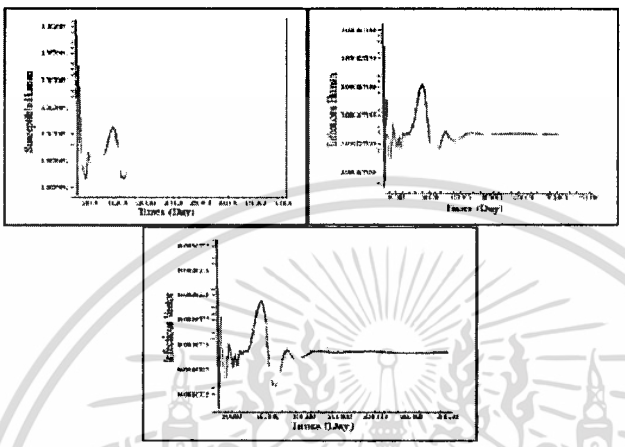

Fig. 3: Numerical solutions of (13) – (15) yield the time series of S_H, I_H and I_V

The relationship between mosquito biting and R_0, susceptible human, infected human and infected vector populations are shown in Fig. 4. If the mosquito biting is increased, the values of R_0 and S_H will increase while I_H and I_V will increase as below.

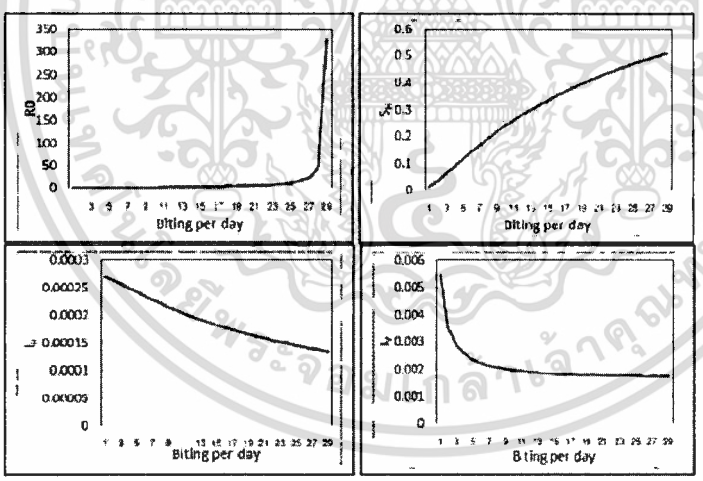

Fig. 4: Relationship of mosquito biting and R_0, S_H, I_H and I_V

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Burapha University, Thailand
July 3-4, 2014

DISCUSSION AND CONCLUSION

The values of parameters are satisfied with Routh – Hurwitz criteria and the numerical solutions converge to the endemic equilibrium point E_1 (0.060569, 0.000257, 0.002870). Figure 3 shows time series solution of S_H, I_H and I_V. The simulations of the biting rate of mosquitoes are investigated and the results show in Figure 4. The value of R_0 can control by decreasing the mosquitoes biting. The basic reproductive numbers are used to control the transmission of dengue fever. The effective way to control the dengue fever is decreased the carry capacity of the environment of mosquitoes such as mosquitoes breeding sites and decreased the mosquitoes biting.

In this paper, we propose and analyze the transmission dynamics of SIR modelling for dengue with vector – born infection. We consider vector population both the recruitment rate of mosquitoes and mosquitoes-born infection. We found the endemic equilibrium state and we can reduce the human susceptibility to the dengue fever that can reduce the outbreak of dengue fever.

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O-018

The SEIR Dynamical Model of Dengue Disease with The Effect of New Infected Vectors

Pratchaya Chanprasopchai*, Puntani Pongsumpun

Department of Mathematics, Faculty of Science, King Mongkut's Institute of Technology Lakrabang, Bangkok 10520, Thailand

Abstract

In this research, we propose a mathematical model in order to analyze the transmission dynamic of dengue disease, which is caused by 2 behaviors, biting infected human and vector born infection. The mathematical model is used as a tool to describe and explain transmission of dengue disease. The SEIR model, Susceptible-Exposed-Infected-Recovered, is applied to investigate the system mechanism. We applied standard dynamical modeling method to analyze the stability of the model by using Routh – Hurwitz criteria. The numerical solutions show that the basic reproductive number more than 1, R0 >1. It indicates that the dynamical system behavior converges to the endemic equilibrium state. The numerical solutions of our model are presented.

Keywords: Basic reproductive number, dengue disease, endemic equilibrium state, Routh – Hurwitz criteria, SEIR model, vector born infection.

***Corresponding author. Email:** pchanprasopcai@gmail.com, kppuntan@kmitl.ac.th

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Transmission Model of Dengue Disease with the Effect of Raining in Thailand

Puntani Pongsumpun
Department of Mathematics, Faculty of Science, King Mongkut's institute of Technology Ladkrabang, Chalongkrung road, Ladkrabang, Bangkok 10520, Thailand

*corresponding author: puntani_p@yahoo.com, kppuntan@kmitl.ac.th

ABSTRACT

Dengue disease is transmitted to the human by biting of the infected vector. This disease is occurred in the tropical countries, especially Thailand. In this paper, we describe the transmission of dengue disease with the effect of raining in Thailand by using mathematical modeling. The models consider two groups of populations such as human and vector populations. The standard dynamical modeling method is applied to analyze our model. The numerical simulations aré shown to describe our analytical results. The different parameters are simulated to see the behavior of solutions.

Keyword: Dengue disease, Mosquito, Simulation, Transmission model

1. Introduction

Dengue disease is the most important arboviral disease occurred in Thailand more than 200 years. Three forms of dengue disease: Dengue Fever(DF), Dengue Hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS) have the different symptoms. This disease is occurred by biting of infected *Aedes Aegypti* mosquitoes [1]. Dengue virus has three types denoted as DEN-1, DEN-2, DEN-3 and DEN-4. Infection by any single type of dengue virus apparently produces permanent immunity to it, but only temporary cross immunity to the others. In Thailand, dengue cases are reported every year. In 2011, there are about 64,374 cases. After that in year 2012, 74,250 cases. Recently (2013), the numbers of cases are remarkable rate, which were reported 150,934 cases [2]. Because mosquitoes are wide spreading, therefore everybody can be affected by the transmission of dengue virus. The appropriated temperature for the transmission of dengue virus is above 20^0 C, but it can not be transmitted at 16 ^{0}C. In countries where seasonal changes in temperature are affected, the transmission of dengue virus is decreased with the lower of temperature. For example, the epidemic of dengue virus in Australia ceased as the temperature dropped to 14-15 ^{0}C at the beginning of winter. The maturation of mosquitoes are depend on the temperature, higher temperature produces smaller females mosquitoes which are forced to take more blood meals to obtain the protein needed for egg production. This has the effect of increasing the number of individuals infected by a single female and thus the capacity of the mosquitoes [3-4]. The temperature and humidity are

thought to influence the extrinsic incubation period of the mosquitoes and are important variables in causing epidemic transmission. In Thailand, dengue cases are occurred every month as shown in fig.1 [2]. We can see that most cases are found in rainy season.

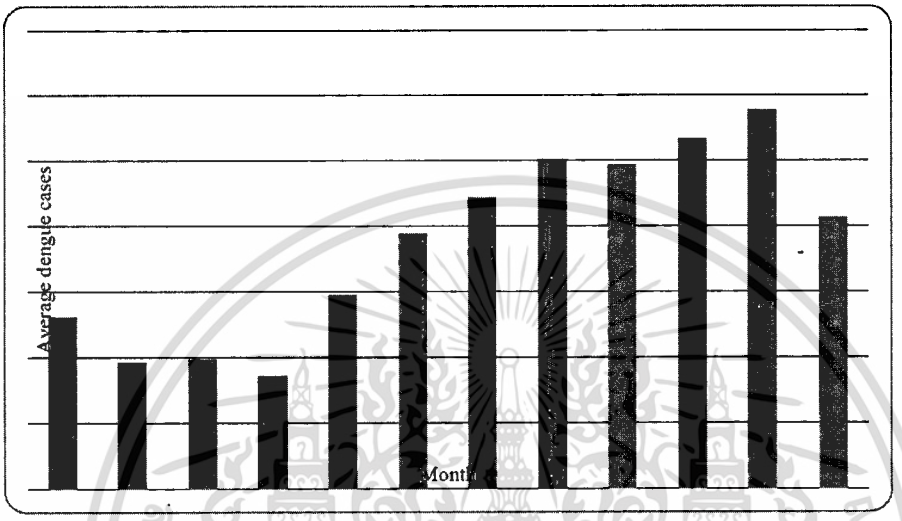


Fig. 1 Average dengue cases in Thailand, year 2011-2013. [2]

There are many research papers studied on the transmission model of dengue disease. In 1998, Esteva and Vargas [5] proposed their first mathematical model for the transmission of dengue virus infection. They assume that there is the constant number of human and mosquito populations. After that, they constructed many transmission models of dengue disease with the different situations [6]-[8]. We [9] proposed mathematical model with the effect of incubation of dengue virus. Recently[10], we formulated the transmission model of dengue disease considered infected vector caused by both biting of infected human and vector-born infection. In this study, we consider the transmission of dengue virus with the effect of raining in Thailand. The transmission model is formulated to describe the dengue transmission. The numerical simulations are shown to see the dengue transmission behaviors.

2. Mathematical Model

In this study, we use the knowledge of mathematical model to formulate our model. The variables and parameters in our model are defined in the following table:

Table 1: Definitions of variables and parameters in our model.

Variable/Parameter	Definition
S_h	The number of susceptible human population
I_h	The number of infectious human population
R_h	The number of recovered human population
O_v	The number of mosquitoes' eggs
S_v	The number of susceptible mosquitoes
I_v	The number of infectious mosquitoes
b	The biting rate of mosquitoes
β_h	The transmission probability of dengue virus from mosquitoes to human population
β_v	The transmission probability of dengue virus from human to mosquitoes
N_h	The size of human population
N_v	The size of mosquitoes
a_h	The birth rate of human population
μ_h	The death rate of human population
μ_v	The death rate of vector population
e_h	The recovery rate of human population
α	The percentage of mosquitoes' eggs which can be susceptible mosquitoes
b_{ov}	The rate of new mosquitoes' eggs per 1 volume of raining
n_r	The volume of raining

The diagram of our dynamical equations can be described by following figure:

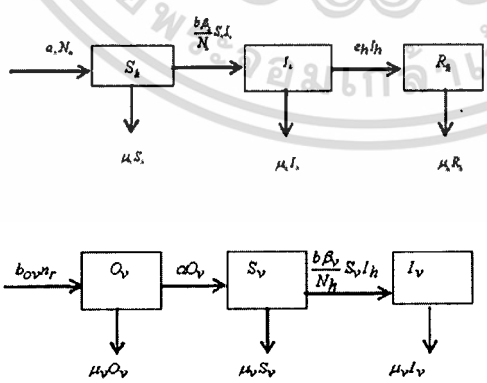


Fig. 2 Diagram of our equations.

The system of differential equations for describing dengue disease is given by following equations.

For human population:

$$\frac{dS_h}{dt} = a_h N_h - \frac{b\beta_h}{N_h} S_h I_v - \mu_h S_h \quad (1)$$

$$\frac{dI_h}{dt} = \frac{b\beta_h}{N_h} S_h I_v - (e_h + \mu_h) I_h \quad (2)$$

$$\frac{dR_h}{dt} = e_h I_h - \mu_h R_h \quad (3)$$

with a condition $S_h + I_h + R_h = N_h$.

For vector population:

$$\frac{dO_v}{dt} = b_{ov} n_r - (\alpha + \mu_v) O_v, \quad (4)$$

$$\frac{dS_v}{dt} = \alpha O_v - \frac{b\beta_v}{N_h} S_v I_h - \mu_v S_v, \quad (5)$$

$$\frac{dI_v}{dt} = \frac{b\beta_v}{N_h} S_v I_h - \mu_v I_v, \quad (6)$$

with a condition $O_v + S_v + I_v = N_v$.

We reduced our equations by letting

$$s_h = \frac{S_h}{N_h}, i_h = \frac{I_h}{N_h}, r_h = \frac{R_h}{N_h}. \quad (7)$$

$$o_v = \frac{O_v}{N_v}, s_v = \frac{S_v}{N_v}, i_v = \frac{I_v}{N_v}. \quad (8)$$

The normalized equations become

$$\frac{ds_h}{dt} = \mu_h (1 - s_h) - \frac{b\beta_h}{N_h} \left(\frac{b_{ov} n_r}{\mu_v} \right) i_v s_h, \quad (9)$$

$$\frac{di_h}{dt} = \frac{b\beta_h}{N_h} \left(\frac{b_{ov} n_r}{\mu_v} \right) i_v s_h - i_h (e_h + \mu_h), \quad (10)$$

$$\frac{ds_v}{dt} = -(b\beta_v i_h + \mu_v) s_v + \alpha (1 - s_v - i_v), \quad (11)$$

$$\frac{di_v}{dt} = b\beta_v i_h s_v - \mu_v i_v \quad (12)$$

where $s_h + i_h + r_h = 1, o_v + s_v + i_v = 1$.

Our assumption is the total human and total vector populations have constant sizes. This means that rates of change for human and vector populations equal to zero. Thus, we have the following equations:

$$\frac{dN_h}{dt} = 0 \text{ and } \frac{dN_v}{dt} = 0. \quad (13)$$

Then we obtain the relations:

$$a_{lh} = \mu_h \quad \text{and} \quad N_v = \frac{b_{ov} n_r}{\mu_v} . \tag{14}$$

3. Analysis of model

To analyze our model, we use standard dynamical modeling method to find steady states and their local stabilities.

3.1 Steady states:

The steady states are obtained by setting (9)-(12) equal to zero. We obtain two steady states:

i) Disease free steady state: $(1,0, \frac{\alpha}{\alpha+\mu_v},0)$

ii) Endemic disease state: $(s_h^*, i_h^*, s_v^*, i_v^*)$

where

$$s_h^* = \frac{\mu_v(\alpha+\mu_v)(b\beta_v\mu_h + (e_h+\mu_h)\mu_v)N_h}{b\beta_v(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\beta_h b_{ov} n_r)}, \tag{15}$$

$$i_h^* = \frac{-\mu_h(e_h+\mu_h)\mu_v^2(\alpha+\mu_v)N_h + \alpha b^2\beta_h b_{ov}\beta_v\mu_h n_r}{b\beta_v(e_h+\mu_h)(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\beta_h b_{ov} n_r)}, \tag{16}$$

$$s_v^* = \frac{(e_h+\mu_h)\mu_v(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\ b\beta_h b_{ov}\beta_v n_r)}{b\beta_h(e_h+\mu_h)(\mu_h\mu_v(\alpha+\mu_v)N_h + \alpha b\beta_h b_{ov} n_r)}, \tag{17}$$

$$i_v^* = \frac{-\mu_h(e_h+\mu_h)\mu_v^2(\alpha+\mu_v)N_h + \alpha b^2\beta_h b_{ov}\beta_v\mu_h n_r}{b\beta_h b_{ov}(\alpha+\mu_v)(b\beta_v\mu_h + (e_h+\mu_h)\mu_v)n_r}. \tag{18}$$

We let

$$G_1(s_h, i_h, s_v, i_v) = \mu_h(1-s_h) - \frac{b\beta_h}{N_h}\left(\frac{b_{ov} n_r}{\mu_v}\right) i_v s_h, \tag{19}$$

$$G_2(s_h, i_h, s_v, i_v) = \frac{b\beta_h}{N_h}\left(\frac{b_{ov} n_r}{\mu_v}\right) i_v s_h - i_h(e_h+\mu_h), \tag{20}$$

$$G_3(s_h, i_h, s_v, i_v) = -(b\beta_v i_h + \mu_v)s_v + \alpha(1-s_v-i_v), \tag{21}$$

$$G_4(s_h, i_h, s_v, i_v) = b\beta_v i_h s_v - \mu_v i_v. \tag{22}$$

The local stability of each steady state is determined by the sign of all real parts of eigenvalues for each steady state. If the sign of real parts give the negative, then that steady state is local stability [11]. The eigenvalues (θ) are produced from the solutions of the following characteristic equation:

$$\det(J - \theta I) = 0$$

where $J=\begin{pmatrix} \frac{\partial G_1}{\partial s_h} & \frac{\partial G_1}{\partial i_h} & \frac{\partial G_1}{\partial s_v} & \frac{\partial G_1}{\partial i_v} \\ \frac{\partial G_2}{\partial s_h} & \frac{\partial G_2}{\partial i_h} & \frac{\partial G_2}{\partial s_v} & \frac{\partial G_2}{\partial s_v} \\ \frac{\partial G_3}{\partial s_h} & \frac{\partial G_3}{\partial i_h} & \frac{\partial G_3}{\partial s_v} & \frac{\partial G_3}{\partial i_v} \\ \frac{\partial G_4}{\partial s_h} & \frac{\partial G_4}{\partial i_h} & \frac{\partial G_4}{\partial s_v} & \frac{\partial G_4}{\partial i_v} \end{pmatrix}$ and 1 is the identity matrix. (23)

After calculating our equations(19)-(22), the Jacobian matrix(J) is defined by

$$J=\begin{pmatrix} -\mu_h N_h+\frac{b\beta_h b_{ov} i_v n_r}{\mu_v N_h} & 0 & 0 & -\frac{b\beta_h b_{ov} s_h n_r}{\mu_v N_h} \\ \frac{b\beta_h b_{ov} i_v n_r}{\mu_v N_h} & -e_h-\mu_h & 0 & \frac{b\beta_h b_{ov} s_h n_r}{\mu_v N_h} \\ 0 & -b\beta_v s_v & -\alpha-b\beta_v i_h-\mu_v & -\alpha \\ 0 & b\beta_v s_v & b\beta_v i_h & -\mu_v \end{pmatrix}.$$

We consider two cases:

Case I: Disease free steady state: the characteristic equation is

$$(\theta+\mu_h)(\theta+\alpha+\mu_v)(\theta^2+B_1\theta+B_0)=0 \quad (24)$$

where

$B_1=e_h+\mu_h+\mu_v$,

$B_0=(e_h+\mu_h)\mu_v-\frac{\alpha b^2\beta_h\beta_v b_{ov} n_r}{\alpha\mu_v N_h+\mu_v^2 N_h}$.

From evaluating all eigenvalues, the real parts of all eigenvalues have negative signs when $R_0<1$

where $R_0=\frac{\alpha b^2\beta_h\beta_v b_{ov} n_r}{(e_h+\mu_h)\mu_v^2(\alpha+\mu_v)N_h}$. (25)

Case II: Endemic disease state: the characteristic equation is calculated in the same method as the disease free state. The real parts of all eigenvalues have negative signs when $R_0>1$, where R_0 is defined in (25). To explain the local stability of the steady states clearly, we use the numerical simulations on the next section.

3.2 Numerical Solutions:

In this section, we use numerical solution to confirm our analytical results [11-12]. We simulate our equations(9)-(12) by using the conditions of endemic disease steady state. The parameters are follows: $\mu_h=1/(365\times 65)$ corresponds to the life cycle 65 years of human. $b=1/3$ corresponds to the 3 times per day of biting for the vector. $\mu_v=1/14$ satisfy to the life cycle 14 days of vectors. $e_h=1/7$ corresponds to the 7 days of recovering for human. The other parameters are arbitrary chosen: $\beta_h=0.75$, $\beta_v=1.0$, $b_{ov}=500$, $n_r=100$, $\alpha=0.8$, $N_h=100.000$ and $R_0=52.47$.

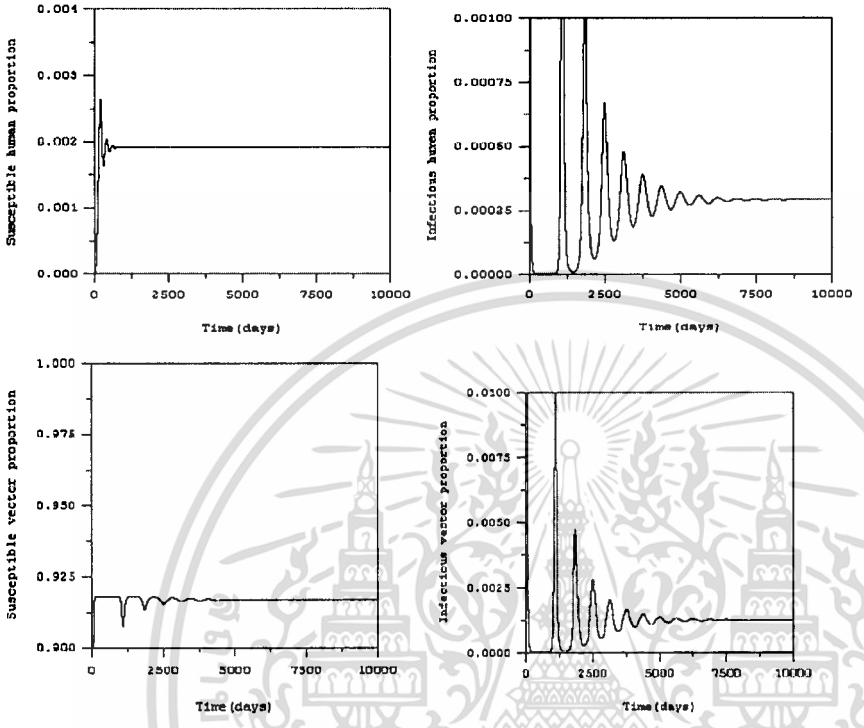
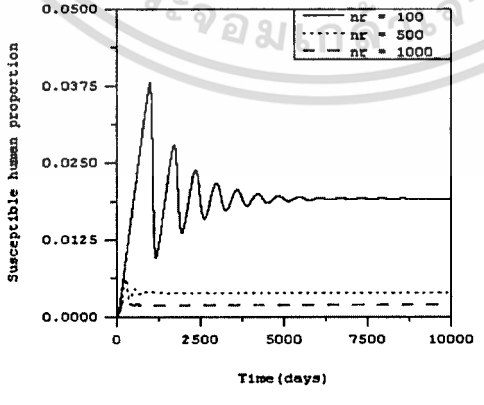


Fig. 3 Numerical solutions of our equations(9)-(12). The conditions of parameters are satisfied to the endemic disease state. The solution converges to the endemic steady state(0.0019, 0.00029, 0.91677, 0.00126).

We can see that the solutions converge to the endemic steady state when $R_0 > 1$.

Furthermore, we analyze the parameter n_r (the volume of raining) as shown in fig.4.



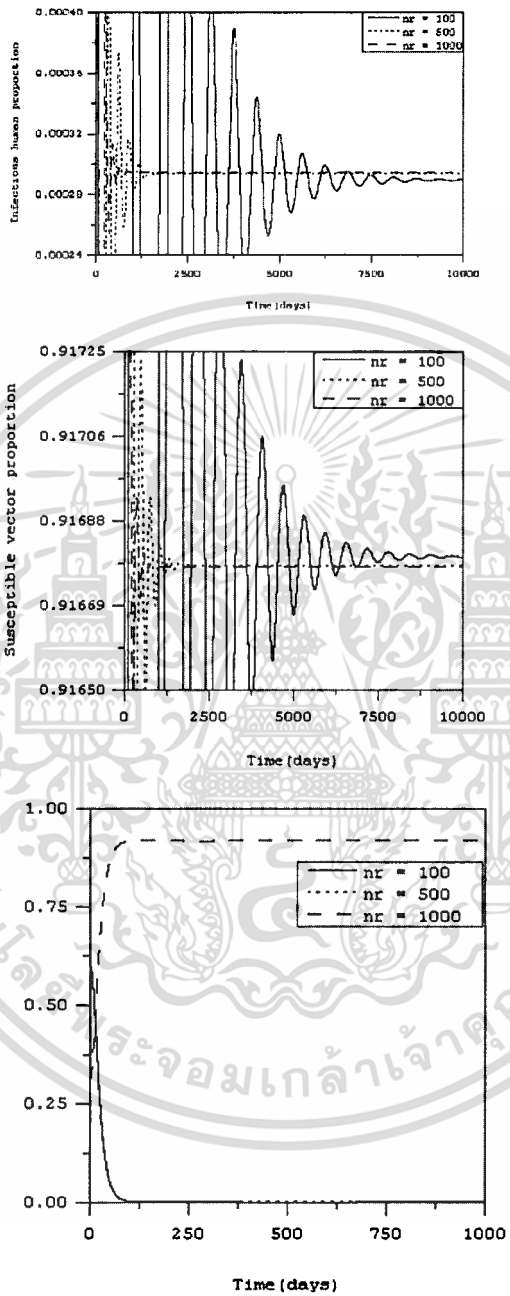


Fig. 4 Numerical solutions of susceptible human, infectious human, susceptible vector and infectious vector populations when there are the different volumes of raining.

4. Conclusion

We analyze the model of dengue disease with the volume of raining in this study. The basic reproductive number is defined in the form of R_0 is given by

$$R_0 = \frac{\alpha b^2 \beta_h \beta_v b_{ov} n_r}{(e_h + \mu_h)\mu_v^2(\alpha + \mu_v)N_h}. \qquad (26)$$

From (26), we can see that the three effects α (percentage of mosquitoes' eggs which can be susceptible mosquitoes), b_{ov} (The rate of new mosquitoes' eggs per 1 volume of raining) and n_r (volume of raining) are proportional to the basic reproductive number as shown in fig.5 to fig.7.

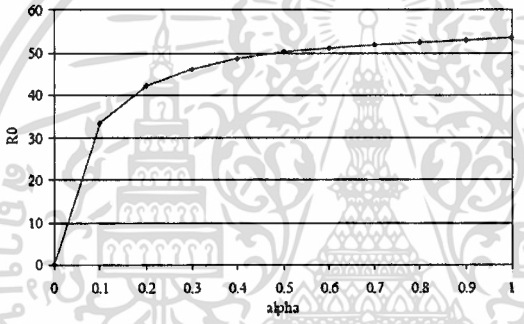


Fig. 5 Numerical solutions of R_0 versus α. The other parameters are same as fig.3.

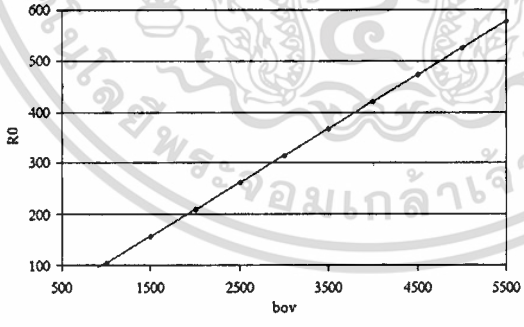


Fig. 6 Numerical solutions of R_0 versus b_{ov}. The other parameters are same as fig.3.

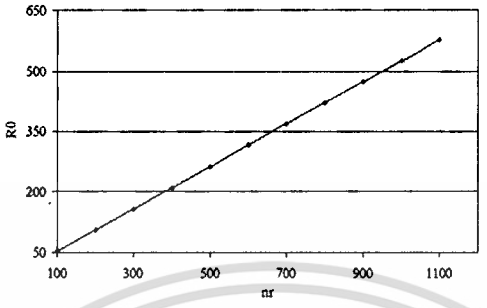


Fig. 7 Numerical solutions of R_0 versus n_r. The other parameters are same as fig.3.

We can see that the infectious human and vector proportions are higher and the smaller proportions of susceptible human and susceptible vector proportions when there is the higher volume of raining as shown in fig.4. This is fact because when there is the higher volume of raining, the temperature and humidity are appropriated for growth of dengue virus.

Acknowledgment

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Dengue model in the flooding area

Puntani Pongsumpun

Department of Mathematics, Faculty of Science,
King Mongkut's institute of Technology Ladkrabang,
Chalongkrung road, Ladkrabang, Bangkok 10520, Thailand
corresponding author: kppuntan@kmitl.ac.th

Abstract

Dengue transmission is found around the world. Dengue fever, Dengue hemorrhagic fever and dengue shock syndrome are three types of this disease. This disease is transmitted between human by biting of infected female *Aedes aegypti* vector. The endemic of this disease is depending on many factors. Mosquitoes are usually found in the flooding area. We describe the transmission of this disease by formulating the mathematical model and then we analyze this model by standard dynamical modeling method. The factor of flooding areas is considered in this study. We simulate the transmission of dengue virus with the different transmission rates in the different areas to see the behaviors of each population group.

Keywords: states dengue; flooding area; model; stability; equilibrium.

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1. Introduction

Dengue virus can transmit to human by biting of infected female *Aedes aegypti* and *Aedes albopictus*. Dengue disease was occurred around 200 years. Three form of this disease such as dengue fever (DF), dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). Each form of this disease has the different characteristics. The symptoms of DF patients are headaches, bone or joint pains, rash and leukopenia. A more virulent manifestation of this disease is Dengue hemorrhagic fever (DHF). DHF is characterized by four major clinical manifestations: high fever, hemorrhagic phenomena, often with hepatomegaly and, in severe cases, signs of circulatory failure. These cases may develop hypovolaemic shock resulting from the plasma leakage. This is called dengue shock syndrome (DSS) and can be fatal [1]. Four serotypes of dengue virus are called as DEN-1, DEN-2, DEN-3 and DEN-4. DHF appears in person who has had a previous infection with a heterologous serotype. *Aedes aegypti* is a tropical and subtropical species of mosquito. *Aedes aegypti* is found in tropical and subtropical areas of South-East Asia, and is found in most urban area. The female *Aedes aegypti* can transmit dengue virus but the male *Aedes aegypti* mosquito does not take a blood meal, but may feed on plant nectar. He lives for only a short time after mating [2]. The cycle of dengue transmission by the *Aedes aegypti* starts with a dengue infectious person. Most cases have virus circulating in the blood (viremia) that lasts for about five days but may last up to 12 days [3]. During the period of viremic, an uninfected female *Aedes aegypti* mosquito bites the person and ingests blood that contains dengue virus. There is some evidence of transovarial transmission of dengue virus in *Aedes aegypti*, usually mosquitoes are only infected by biting a viremic person. Then, within the vector, the viruses replicate during an extrinsic incubation period of eight to twelve days. After an extrinsic incubation period of vector, its salivary glands become infected and the virus is transmitted when the infectious vector bites and injects the salivary fluid into the wound of the human. The vector can bite a susceptible person and could transmit the virus to him or her, as well as to every other susceptible persons the mosquito bites for the rest of its lifetime. The virus then replicates in the person during an intrinsic incubation period of four to seven days and produces infection [4,5]. This disease is usually found in tropical and subtropical countries around the world. In Thailand, dengue cases are usually found every year since 1949. In Thailand, flooding in 2011 is considered to be the worst evidence from the past. There are many flooding areas around Thailand, especially in the north and central of Thailand. Dengue cases in 2011 are greater than in 2010. Flooding influence to the number of dengue cases. Mathematical model is used for describing the dengue transmission since 1998. Esteva and Vargas [6] proposed their mathematical model for the transmission of dengue virus infection in a constant human population They supposed that the populaion can be infected only one time. In 2008, we incorporated the influence of incubation to our model [7]. In 2011, we studied the monthly distribution of dengue disease in the highest epidemic year between 2001 and 2009 , the corresponding fitted curves were found. The basic reproductive number by season of this disease was found and analyzed [8]. From the previous studies, we can see that there is no model considering the influence of flooding in Thailand. In this study, we consider the flooding and non flooding areas. The transmission rates of dengue virus for two areas are different. The numerical simulations are used to see the behaviours of each population group.

2. Mathematical model

In this study, we formulate the mathematical model for describing the transmission of this disease by using SIR(Susceptible-Infectious-Recovered) model for human and SI(Susceptible-Infectious) model for vector population. We assume SIR model for human and SI for vector population because vector can not recover from infection. We suppose that there are the different transmission rates for the different areas. The transmission diagram of dengue disease is given as follows:

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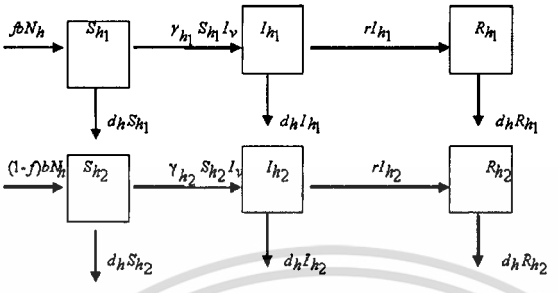

Figure1. Transmission diagram for human population.

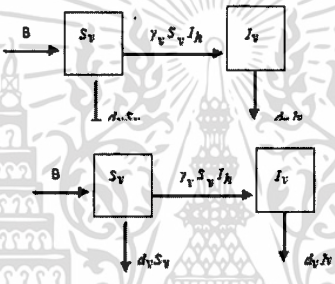

Figure2. Transmission diagram for vector population.

From the above figures, the dynamical transmission model can be written as

$$
\begin{aligned}
\frac{d}{dt}S_{h1} &= fbN_h - \gamma_{h1} S_{h1} I_v - d_h S_{h1} \\
\frac{d}{dt}I_{h1} &= \gamma_{h1} S_{h1} I_v - (r+d_h) I_{h1} \\
\frac{d}{dt}R_{h1} &= rI_{h1} - d_h R_{h1} \\
\frac{d}{dt}S_{h2} &= (1-f)bN_h - \gamma_{h2} S_{h2} I_v - d_h S_{h2} \\
\frac{d}{dt}I_{h2} &= \gamma_{h2} S_{h2} I_v - (r+d_h) I_{h2} \\
\frac{d}{dt}R_{h2} &= rI_{h2} - d_h R_{h2}
\end{aligned}
\qquad (1)
$$

Proceedings of the Burapha University International Conference 2015, 10-12 July 2015, Bangsaen, Chonburi, Thailand

$$\frac{d}{dt}S_v = B - \gamma_v S_v I_h - d_v S_v$$
$$\frac{d}{dt}I_v = \gamma_v S_v I_h - d_v I_v$$

where $I_h = I_{h_1} + I_{h_2}$,
$N_h = S_{h_1} + I_{h_1} + R_{h_1} + S_{h_2} + I_{h_2} + R_{h_2}$,
$N_v = S_v + I_v$. (2)

The variables and parameters are described in the following table.

2.1 List of Nomenclature

The variables and parameters in our model are defined in the following table:

Table1: Definitions of variables and parameters for our model.

variable/parameter	definition
S_{h_1}	Number of susceptible human in the flooding area
I_{h_1}	Number of infectious human in the flooding area
R_{h_1}	Number of recovered human in the flooding area
S_{h_2}	Number of susceptible human in the non flooding area
I_{h_2}	Number of infectious human in the non flooding area
R_{h_2}	Number of recovered human in the non flooding area
I_h	Total infectious human
S_v	Number of susceptible vector
I_v	Number of infectious vector
f	Probability of human who stay in flooding area
b	Birth rate of human population
d_h	Death rate of human population
N_h	Total number of human population
N_v	Total vector population
γ_{h_1}	Transmission rate of dengue virus from vector to human population in flooding area
γ_{h_2}	Transmission rate of dengue virus from vector to human population in non flooding area
r	Recovery rate
B	Constant recruitment rate of vector population
γ_v	Transmission rate of dengue virus from human to vector population
d_v	Death rate of vector population

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We suppose that the total human and vector population have constant sizes. Then rates of change for human and vector population are zero. Thus $\frac{d}{dt}N_h = 0$ and, then we have $b = d_h$ and $N_v = \frac{B}{d_v}$. This means that birth and death rate is equivalent for human population. The number of vector population is ratio between constant recruitment rate of vector and death rate of vector population.

To simplify our model, we introduce new variables by letting

$$s_{h_1} = \frac{S_{h_1}}{N_T},\ i_{h_1} = \frac{I_{h_1}}{N_T},\ r_{h_1} = \frac{R_{h_1}}{N_T}\ s_{h_2} = \frac{S_{h_2}}{N_T},\ i_{h_2} = \frac{I_{h_2}}{N_T},\ r_{h_2} = \frac{R_{h_2}}{N_T} \qquad (2)$$

and $s_v = \frac{S_v}{N_v},\ i_v = \frac{I_v}{N_v}$, then we obtain the following equations:

$$\begin{aligned}
\frac{d}{dt}s_{h_1} &= bf - (b+\gamma_{h_1} i_v (B/d_v))s_{h_1} \\
\frac{d}{dt}i_{h_1} &= -i_{h_1}(b+r) + \gamma_{h_1} i_v (B/d_v)s_{h_1} \\
\frac{d}{dt}r_{h_1} &= ri_{h_1} - brh_1 \\
\frac{d}{dt}s_{h_2} &= -\gamma_{h_2} i_v (B/d_v)s_{h_2} + b(1-f-s_{h_2}) \\
\frac{d}{dt}i_{h_2} &= -i_{h_2}(b+r) + \gamma_{h_2} i_v (B/d_v)s_{h_2} \\
\frac{d}{dt}i_v &= \gamma_v (i_{h_1} + i_{h_2})N_h (1-i_v) - d_v i_v
\end{aligned} \qquad (3)$$

After setting (3) to zero. we obtain steady states. The steady states of our equations are follows:

i) Disease free state: $e_1 = (f,0,0,1-f,0,0)$ (4)

ii) Endemic disease state: $e_2 = (s\tilde{h}_1, i\tilde{h}_1, r\tilde{h}_1, s\tilde{h}_2, i\tilde{h}_2, i\tilde{v})$ (5)

where

$$i\tilde{v} = \frac{b(BM - bd_v^2(B(\gamma_{h_1}+\gamma_{h_2}) + d_v(b+r)R_0)) + \sqrt{\begin{aligned} &b^2B^2(4d_v^3\gamma_{h_1}\gamma_{h_2}(b+r)(b(d_v+\gamma_v N_h)+d_v r)(R_0-1) \\ &+(-M+bd_v^2(\gamma_{h_1}+\gamma_{h_2}+\frac{d_v(b+r)R_0}{B}))^2)\end{aligned}}}{2B^2\gamma_{h_1}\gamma_{h_2}(b(d_v+\gamma_v N_h)+d_v r)},$$

$$s\tilde{h}_1 = \frac{bd_v f}{bd_v + B\gamma_{h_1} i\tilde{v}},\ i\tilde{h}_1 = \frac{B\gamma_{h_1} i\tilde{v}\, s\tilde{h}_1}{d_v(b+r)},\ r\tilde{h}_1 = \frac{r}{b} i\tilde{h}_1,\ s\tilde{h}_2 = \frac{d_v b(1-f)}{bd_v + B\gamma_{h_2} i\tilde{v}},\ i\tilde{h}_2 = \frac{B\gamma_{h_2} i\tilde{v}\, s\tilde{h}_2}{d_v(b+r)}.$$

To determine the local stability of our equations, we check the sign of eigenvalues. The eigenvalues are the solutions of characteristic equations: $\det(J-\lambda I)=0$; where J is the jacobian matrix of (3) , I is the identity matrix. If all eigenvalues have negative real parts, then that steady state will be local stability[9-11].

For disease free steady state: Jacobian matrix is defined by

$$J_0 = \begin{pmatrix} -b & 0 & 0 & 0 & -\frac{Bf\gamma_{h_1}}{d_v} \\ 0 & -b-r & 0 & 0 & \frac{Bf\gamma_{h_1}}{d_v} \\ 0 & 0 & -b & 0 & -\frac{B(1-f)\gamma_{h_2}}{d_v} \\ 0 & 0 & 0 & -b-r & \frac{B(1-f)\gamma_{h_2}}{d_v} \\ 0 & \gamma_v N_h & 0 & \gamma_v N_h & -d_v \end{pmatrix}. \quad (6)$$

Jacobian matrix for endemic steady state is given by

$$J = \begin{pmatrix} -b-\frac{B\gamma_{h_1}}{d_v}\tilde{i_v} & 0 & 0 & 0 & -\frac{B\gamma_{h_1}}{d_v}\tilde{s_{h_1}} \\ \frac{B\gamma_{h_1}}{d_v}\tilde{i_v} & -b-r & 0 & 0 & \frac{B\gamma_{h_1}}{d_v}\tilde{s_{h_1}} \\ 0 & 0 & -b-\frac{B\gamma_{h_2}}{d_v}\tilde{i_v} & 0 & -\frac{B\gamma_{h_2}}{d_v}\tilde{s_{h_2}} \\ 0 & 0 & \frac{B\gamma_{h_2}}{d_v}\tilde{i_v} & -b-r & \frac{B\gamma_{h_2}}{d_v}\tilde{s_{h_2}} \\ 0 & \gamma_v(1-\tilde{i_v})N_h & 0 & \gamma_v(1-\tilde{i_v})N_h & -d_v-\gamma_v(\tilde{i_{h_1}}+\tilde{i_{h_2}})N_h \end{pmatrix} \quad (7)$$

We check the sign of all eigenvalues for disease free steady state and endemic steady state, then we conclude that the disease free steady state is local stability for $R_0 < 1$ and endemic steady state is local stability for $R_0 > 1$; where $R_0 = \frac{B(f(\gamma_{h_1}-\gamma_{h_2})+\gamma_{h_2})\gamma_v N_h}{d_v^2(b+r)}$.

3.Results and discussion

We show our analytical results by numerical solutions for endemic disease state. We simulate our equations by using parameters as shown in fig.3.

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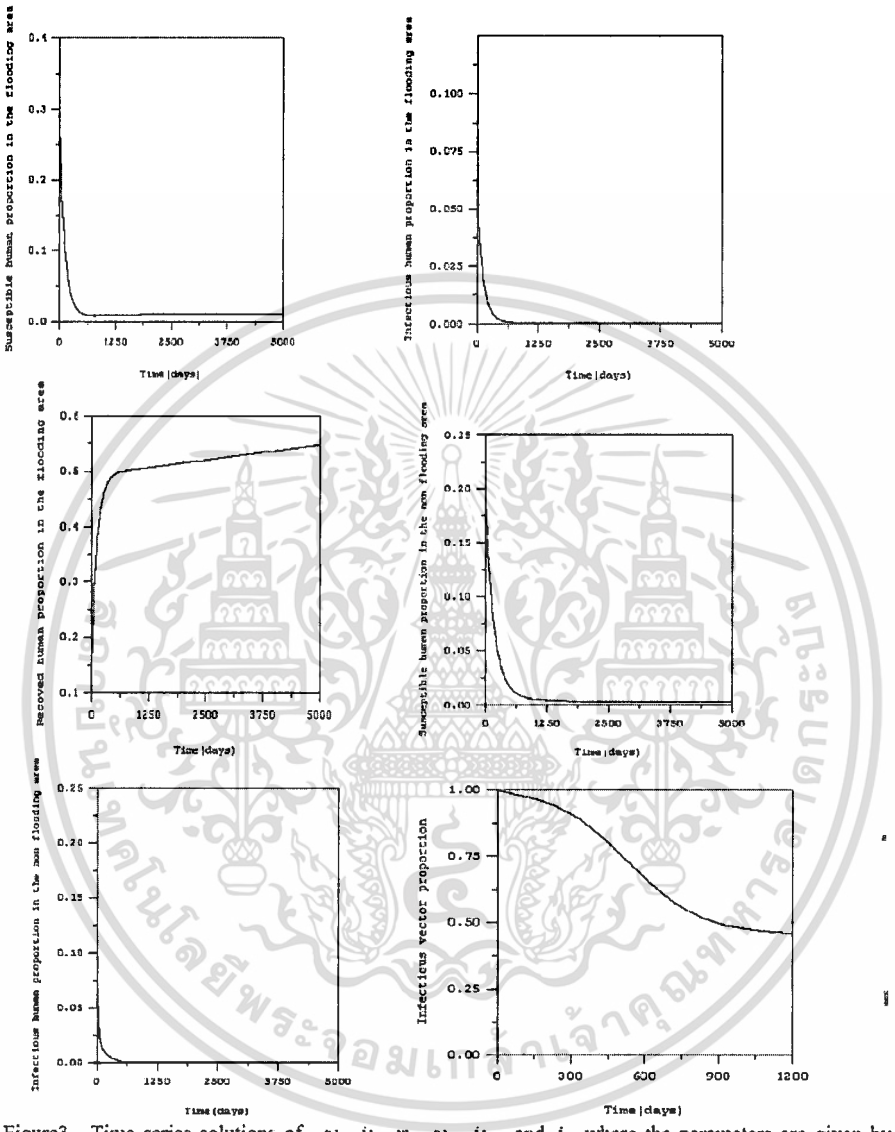

Figure3 . Time series solutions of $s_{h_1}, i_{h_1}, r_{h_1}, s_{h_2}, i_{h_2}$ and i_v where the parameters are given by f = 0.8.b=1/(365*65). N_h =100. γ_{h_1} = 0.0000006 , γ_{h_2} = 0.0000004 , r = 1/20, B = 1,000, γ_v =0.7, d_v =1/14 and

$R_0 = 137$. The solutions converge to the endemic disease state(0.009, 0.0007, 0.55, 0.003, 0.00016. 0.45). We can see that the solutions converge to the endemic disease state.

In this study. we consider the transmission of dengue disease in flooding and non flooding areas. Standard dynamical modeling method is used in this paper. We found equilibrium states and determine the conditions for local stability. The basic reproductive number is used for reduce the transmission of many diseases [6-8,11-12]. The basic reproductive number of this disease is defined by

$$R_0 = \frac{B(f(\gamma_{h_1} - \gamma_{h_2}) + \gamma_{h_2})\gamma_v N_h}{d_v^2(b+r)}.$$

We can see that the transmission rate of dengue disease in flooding area, probability of people who stay in flooding area, the constant recruitment rate of vector and the transmission rate of dengue disease from human to vector effect to the basic reproductive number. If the transmission rate of dengue disease is high, the basic reproductive number is high too. Moreover, we simulate our model by input the different values of probabilities of people who stay in flooding area. The results are shown in fig.4.

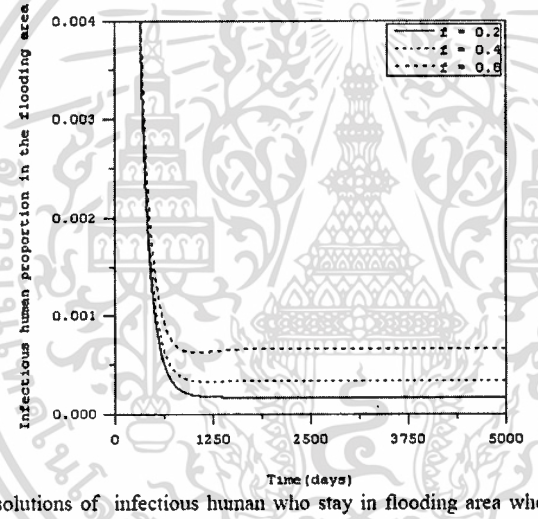

Figure4 . Time series solutions of infectious human who stay in flooding area when there is the different probabilities of people who stay in flooding areas.

From fig.4, we can see that the infectious human proportion who stay in the area where there is the more probability of flooding will be greater than the infectious human proportion who stay in the area where there is the less probability of flooding. The results correspond to the real life situation. The results of this study suggest the way for controlling this disease.

Acknowledgements

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2015 International Conference on Data Mining, Electronics and Information Technology (DMEIT'15) August 10-11, 2015 Pattaya, Thailand

Mathematical model of Malaria with flooding in Thailand

Puntani Pongsumpun
Department of Mathematics, Faculty of Science,
King Mongkut's institute of Technology Ladkrabang,
Chalongkrung road, Ladkrabang, Bangkok 10520, Thailand
puntani_p@yahoo.com, kppuntan@kmitl.ac.th

Abstract: *Malaria is occurred by biting of infected Anopheles mosquitoes. Four species of Plasmodium are Plasmodium falciparum, Plasmodium vivax, Plasmodium ovale and Plasmodium malariae .This disease is found in tropical countries, especially Thailand. We consider the effect of flooding in Thailand with the transmission of Malaria disease. Mathematical model is formulated by using theory of modeling. The variables and parameters are defined corresponding to the characteristic of this disease. Our model is analyzed by using dynamical modeling method. Numerical simulations are shown comparing with the analytical solutions.*

Keywords: *Anopheles mosquito, Malaria disease, Mathematical model, Plasmodium*

1. Introduction

Anopheles mosquitoes is the epidemic vector of this disease. This disease is caused by the multiplication of protozoa parasite of the genus Plasmodium. P.falciparum, P.vivax, P.malariae and P.ovale are four species of Plasmodiums. Greater than three hundred million Malaria cases are reported per year [1]. Each species are discovered in the different areas. Plasmodium falciparum is found on the tropic and subtropics such as Africa, South America and Asia. Plasmodium vivax is found in the widest area. It can be found in many temperate zones, subtropics and tropic such as China, Turkey, Latin America and Asia. Plasmodium malariae is found in the same area as Plasmodium falciparum but is much less common in areas such as Central America. Plasmodium ovale is found predominantly in tropic Africa, but many occur in the West Pacific. Blood transfusion can receive this disease accidentally. This is one of the reasons why people who have been infected with disease can never donate blood. Infection of a newborn from an infected mother also happens, but it is comparatively rare [2]. In the first two months of life, children may not contact malaria or their manifestations may be mild with low-grade parasitemia[2]. Host, agent and environment are three factors which influence to the transmission of Malaria. The most important environmental factors are temperature and humidity. When the temperature is under 16, Malaria parasites stop developing in the mosquitoes. The best temperature for the development of this disease is between 20 – 30 C. The average relative humidity is at least 60% [3]. There are 4 cycles of this mosquito: egg, larva, pupa and adult. The male Anopheles feeds on nectar and fruit juices while the female takes both these plant products and blood [4]. The female may lay several batches of eggs during her lifetime. The eggs hatch within 2 – 3 days, releasing the larvae into water, the larvae transform into the non-feeding pupae. Within the pupae, over a period of 2 – 4 days, metamorphosis takes place, terminating in the materialization of the adults [5]. Sick due to this disease causes significant economic loss. Situations of global temperatures increase the life cycle of a mosquito vector[3]-[5]. The period of mosquito eggs and larvae molt growth as a mosquito can take 7-10 days. The average life expectancy of the mosquito is 45 days. In Thailand, Malaria is found along the border with Burma, Cambodia, and Malaysia. The original Malaria model is usually described by the RossMacDonald (RM) model [6].In 2001, Kammanee A et al.[7] formulated the mathematical model for Malaria transmission and basic reproductive number is found to reduce the outbreak of the disease. To describe the flooding in Thailand with the transmission of Malaria, we incorporate the flooding parameters to our model. Analytical result and numerical simulations are used in our study to suggest the way for reducing the disease outbreak.

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2. Mathematical Model

We study the transmission of Malaria with flooding in Thailand by formulating the differential equations. We use the knowledge of mathematical model to describe the transmission of this disease. We consider the dynamical equations of human and mosquitoes. The differential equations for describing the transmission of this disease is

$$S_n'(t) = hN_n - \gamma_n S_n I_v - dS_n \tag{1}$$

$$E_n'(t) = \gamma_n S_n I_v - \frac{1}{\Pi_n} E_n - dE_n \tag{2}$$

$$I_n'(t) = \frac{1}{\Pi_n} E_n - (\gamma + d) I_n \tag{3}$$

$$R_n'(t) = \gamma I_n - dR_n \tag{4}$$

$$S_{vf}'(t) = A_f - \gamma_{vf} S_{vf} I_n - d_v S_{vf} \tag{5}$$

$$I_{vf}'(t) = \gamma_{vf} S_{vf} I_n - d_v I_{vf} \tag{6}$$

$$S_{vnf}'(t) = A_{nf} - \gamma_{vnf} S_{vnf} I_n - d_v S_{vnf} \tag{7}$$

$$I_{vnf}'(t) = \gamma_{vnf} S_{vnf} I_n - d_v I_{vnf} \tag{8}$$

where $N_n = S_n + E_n + I_n + R_n$, $N_{vf} = S_{vf} + I_{vf}$ and $N_{vnf} = S_{vnf} + I_{vnf}$.

The variables and parameters in our equations are described as follows:

$S_n(t)$ is the size of susceptible human population at time t.

$E_n(t)$ is the size of exposed human population at time t.

$I_n(t)$ is the size of infectious human population at time t.

$R_n(t)$ is the size of recovered human population at time t.

$S_{vf}(t)$ is the size of susceptible mosquito during the flood at time t.

$I_{vf}(t)$ is the size of infectious mosquito during the flood at time t.

$S_{vnf}(t)$ is the size of susceptible mosquito during the non-flood at time t.

$I_{vf}(t)$ is the size of infectious mosquito during the non-flood at time t.

h is the birth rate of human population.

d is the death rate of human population.

γ_n is the transmission rate of *Plasmodium malaria* from mosquito to human.

Π_n is the incubation period of *Plasmodium malaria* in human.

N_n is the size of human population.

N_{vf} is the size of mosquitoes during flooding time.

N_{vnf} is the size of mosquitoes during non-flooding time.

γ is the recovery rate of human population.

A_f is the constant recruitment rate of mosquitoes during flooding time.

A_{nf} is the constant recruitment rate of mosquitoes during non-flooding time.

γ_{vf} is the transmission rate of *Plasmodium malaria* from human to mosquitoes during flooding time.

γ_{vnf} is the transmission rate of *Plasmodium malaria* from human to mosquitoes during non-flooding time.

d_v is the death rate of mosquitoes.

Suppose that the size of human and mosquitoes are constant, then $N_n' = S_n' + E_n' + I_n' + R_n' = 0$, $N_{vf}' = S_{vf}' + I_{vf}' = 0$ and $N_{vnf}' = S_{vnf}' + I_{vnf}' = 0$. From the above equations, we get h = d, $N_{vf} = A_f / d_v$ and $N_{vnf} = A_{nf} / d_v$.

2015 International Conference on Data Mining, Electronics and Information Technology (DMEIT'15) August 10-11, 2015 Pattaya, Thailand

Normalizing the above equations by letting $s_n = S_n / N_n$, $e_n = E_n / N_n$, $i_n = I_n / N_n$, $r_n = R_n / N_n$, $s_{v_f} = S_{v_f} / N_v$, $i_{v_f} = I_{v_f} / N_v$, $s_{v_{nf}} = S_{v_{nf}} / N_{v_{nf}}$, $i_{v_{nf}} = I_{v_{nf}} / N_{v_{nf}}$, $s_{v_f} = S_{v_f} / N_{v_f}$, $i_{v_f} = I_{v_f} / N_{v_f}$.

Thus, the reduced equations become:

$$s_n'(t) = h - (d + \gamma_n i_v) s_h \tag{9}$$

$$e_n'(t) = \gamma_n s_n i_v - \frac{1}{\Pi_n} e_n - d e_n \tag{10}$$

$$i_n'(t) = \frac{1}{\Pi_n} e_n - (\gamma + d) i_n \tag{11}$$

$$i_{v_f}'(t) = \gamma_{v_f} s_{v_f} i_n N_n - d_v i_{v_f} \tag{12}$$

$$i_{v_{nf}}'(t) = \gamma_{v_{nf}} s_{v_{nf}} i_n N_n - d_v i_{v_{nf}} \tag{13}$$

3. Analysis of Mathematical Model

3.1 Analytical Solutions

The standard dynamical method is used for analysis our model. Steady states of our equations are found by setting (9)-(13) to zero, then we obtain the steady states:

i) Disease free steady state: (1,0,0,0,0) and

ii) Endemic steady state: $(s_n, e_n, i_n, i_{v_f}, i_{v_{nf}})$ where

$$s_n^* = \frac{h}{h + \gamma_n (i_{v_f}^* + i_{v_{nf}}^*)}, \quad e_n^* = \frac{\gamma_n \Pi_n i_v^* s_h^*}{1 + d\Pi_n},$$

$$i_{v_f}^* = \frac{\gamma_{v_f} \mathrm{N_h}}{(h+\gamma)\Pi_n (d_v + \gamma_{v_f} i_n^* \mathrm{N_h})} e_n^* \text{ and } i_{v_{nf}}^* = \frac{\gamma_{v_f} \mathrm{N_h}}{(h+\gamma)\Pi_n d_v + e_n^* \gamma_{v_{nf}} \mathrm{N_h}} e_n^*$$

where

$$i_n^* = \frac{1}{2(d+\gamma)(d+2\gamma_n)\gamma_{v_f}\gamma_{v_{nf}}(1+d\Pi_n)\mathrm{N_h}^2} \Big(-d_v(d+\gamma)(d+\gamma_n)(\gamma_{v_f}+\gamma_{v_{nf}})(1+d\Pi_n)\mathrm{N_h}$$
$$+ 2\gamma_n\gamma_{v_f}\gamma_{v_{nf}}\mathrm{N_h}^2 + \sqrt{\begin{array}{l}(\mathrm{N_h}^2((d_v(d+\gamma)(d+\gamma_n)(\gamma_{v_f}+\gamma_{v_{nf}})(1+d\Pi_n) - 2\gamma_n\gamma_{v_f}\gamma_{v_{nf}}\mathrm{N_h})^2 \\ -4d_v(d+\gamma)(d+2\gamma_n)\gamma_{v_f}\gamma_{v_{nf}}(1+d\Pi_n)(dd_v(d+\gamma)(1+d\Pi_n) \\ -\gamma_n(\gamma_{v_f}+\gamma_{v_{nf}})h\mathrm{N_h}))\end{array}} \Big) \tag{14}$$

By using Standard dynamical modeling method, the local stability of each steady state is determined by considering the signs of eigenvalues. If the signs of all eigenvalues give negative, then we can conclude that that steady state is local stability [8-10]. The characteristic equation is defined by following equation:

$$|\mathrm{J} - \kappa \mathrm{I}| = 0$$

where $|\mathrm{A}|$ means determinant of A, J is the Jacobian matrix, κ is the eigenvalues and I is the identity matrix .

2015 International Conference on Data Mining, Electronics and Information Technology (DMEIT'15) August 10-11, 2015 Pattaya, Thailand

After evaluating our model, the condition for negative real parts of eigenvalues is $R_0 > 1$, where

$$R_0 = \frac{\gamma_n N_n(\gamma_{v_f} + \gamma_{v_{n_f}})}{d_v(d+\gamma)(1+d\Pi_n)}.$$

Therefore, we can conclude that the disease free steady state is local stability for $R_0 < 1$ and the endemic steady state is local stability for $R_0 > 1$.

3.2 Numerical Solutions:

Numerical method is used for solving numerical solutions of (9)-(13). We simulate our equations for disease free and endemic regions.

For disease free region:

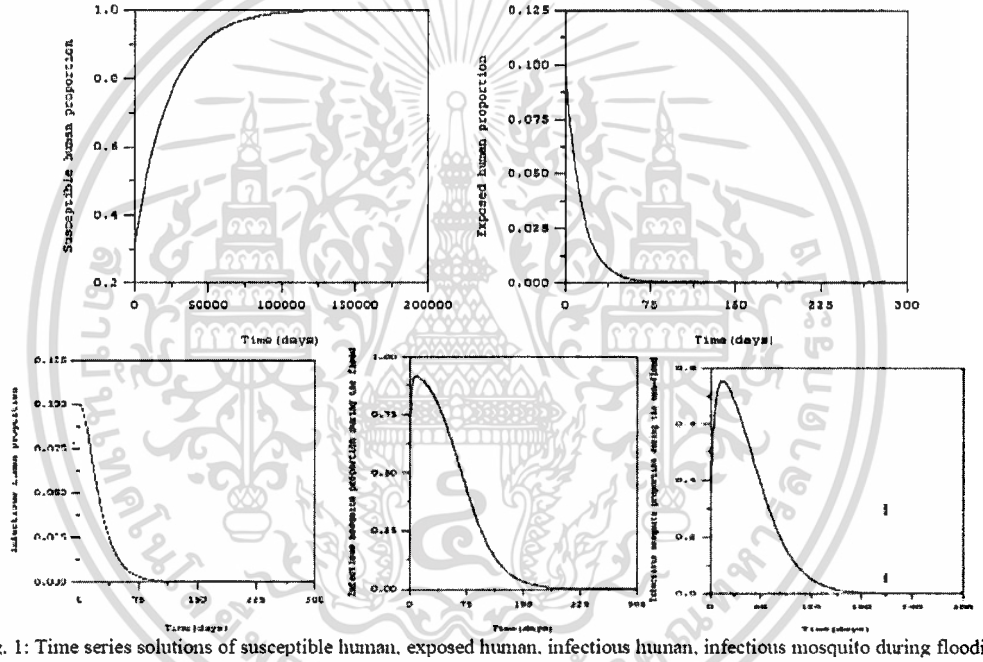

Fig. 1: Time series solutions of susceptible human, exposed human, infectious human, infectious mosquito during flooding time and infectious mosquito during non-flooding time on disease free region. The solutions converge to (1.0,0,0,0)

For endemic region:

The parameters are follows:

$h = 1/(365 \times 65)$ corresponds to the life cycle 65 years of human. $\gamma_n = 0.006$, $\gamma_{v_f} = 0.008$, $\gamma_{v_{n_f}} = 0.002$ and $N_h = 10{,}000$ are arbitrary chosen parameters. $d_v = 1/45$ corresponds to 45 days life time of *Anopheles* mosquitoes. Π_n = 14 corresponds to 14 days of incubation period of *Plasmodium malaria* in human. $\gamma = 1/14$ corresponds to the 14 days of recovering of human and $R_0 = 493$.

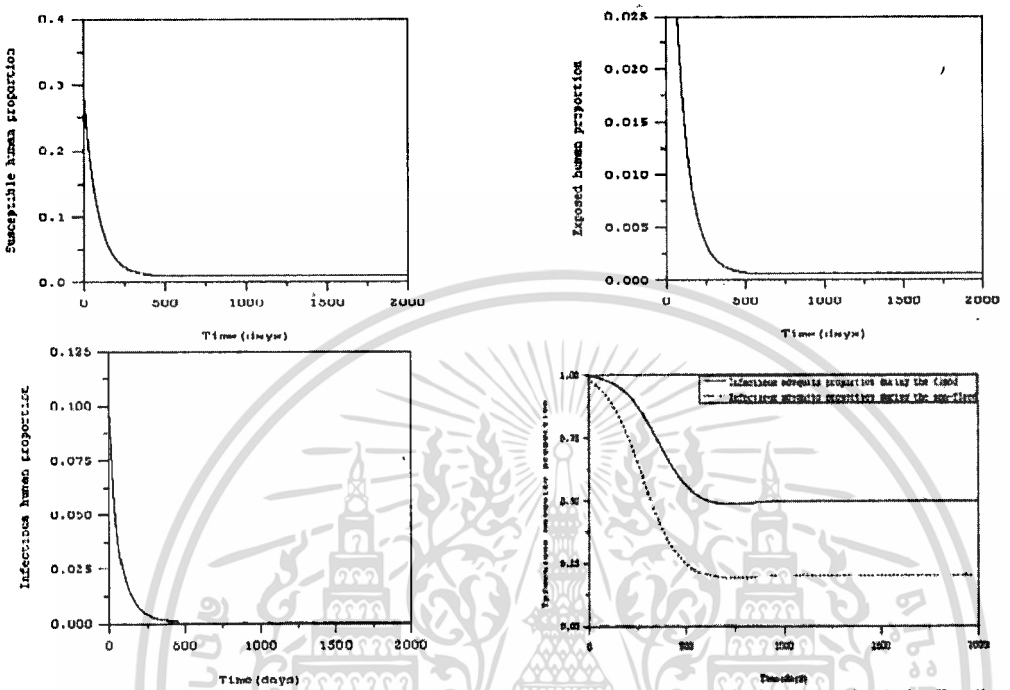

Fig. 2: Time series solutions of susceptible human, exposed human, infectious human, infectious mosquito during flooding time and infectious mosquito during non-flooding time on endemic region. The solutions converge to (0.01.0.0006,0.0006,0.5,0.2)

From the above figures, we can see that the solutions converge to the disease free steady state for $R_0 < 1$. For $R_0 > 1$, the solutions converge to the endemic steady state.

4. Conclusions

In this study, we formulate the model of Malaria transmission with the influence of flooding in Thailand. Condition for local stabilities of disease free steady state and endemic steady state is defined by R_0, where

$$R_0 = \frac{\gamma_n N_n(\gamma_{v_f} + \gamma_{v_{n_f}})}{d_v(d+\gamma)(1+d\Pi_n)}. \quad (15)$$

The basic reproductive number is given as $R_0' = \sqrt{R_0}$, defined as the average number of secondary cases produced from primary cases [8]. From (15), we can see that the transmission rates of *Plasmodium* Malaria (γ_n, γ_{v_f} and $\gamma_{v_{n_f}}$) effect to the basic reproductive number. If we can reduce the transmission rate of this disease, then we can reduce the outbreak of the disease. Next, we simulate our solutions for different values of transmission rates.

การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

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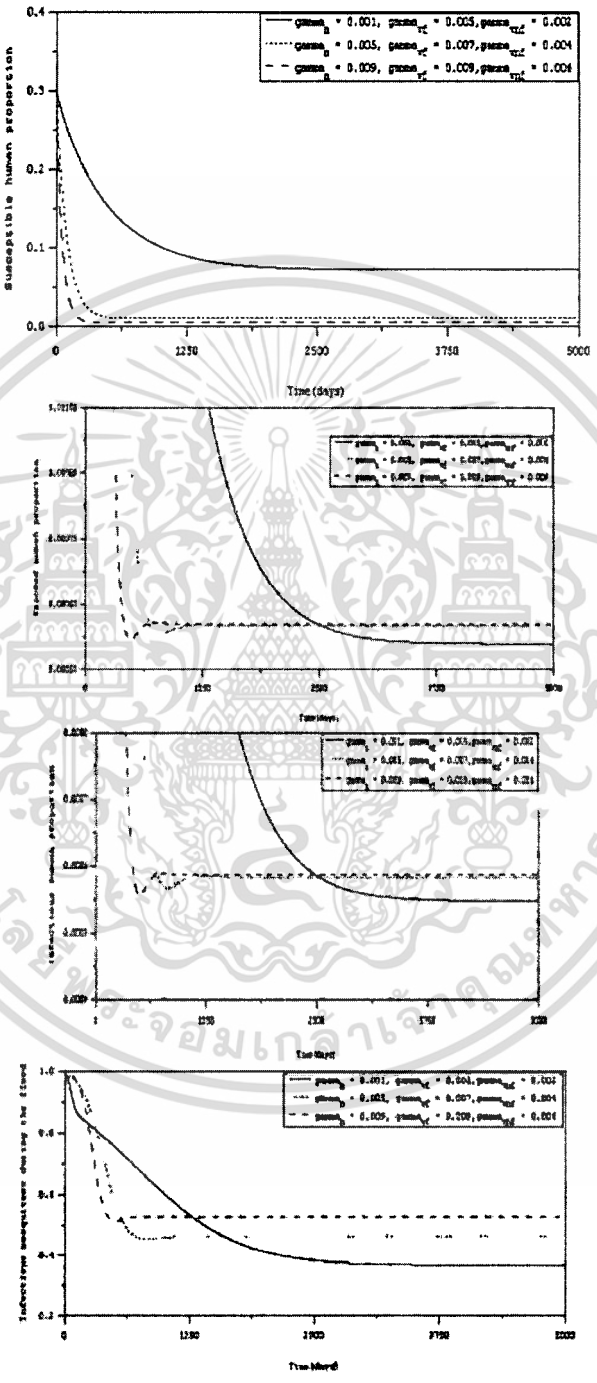

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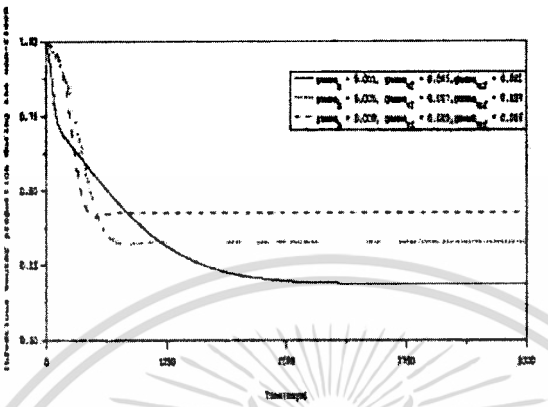

Fig.3: Time series solutions of susceptible human, exposed human, infectious human, infectious mosquito during flooding time and infectious mosquito during non-flooding time for the different sets of transmission rates.

We can see that when the transmission rates are higher, the steady state solutions of exposed and infectious groups are increasing but the steady state solutions of susceptible group is decreasing. From our simulations, we can see that the infectious proportion during flooding time is higher than the infectious proportion during non-flooding time. This is true because mosquitoes in the flooding time can grow faster than mosquitoes in the non-flooding time.

5. Acknowledgements

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American Journal of Applied Sciences

Original Research Paper

SIR Transmission Model of Dengue Virus Taking Into Account Two Species of Mosquitoes and an Age Structure in the Human Population

[1]R. Sungchasit, [1]P. Pongsumpun and [2,3]I.M. Tang

[1]*Department of Mathematics, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Chalongkrung Road, Ladkrabang, Bangkok, 10520, Thailand*
[2]*Department of Materials Science, Faculty of Science, Kasetsart University, 50 Ngam Wong Wan Road, Lat Yao Chatuchak, Bangkok 10900, Thailand*
[3]*Department of Physics, Faculty of Science, Mahidol University, Rama 6 road, Bangkok 10400, Thailand*

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Corresponding Author:
P. Pongsumpun
Department of Mathematics, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Chalongkrung Road, Ladkrabang, Bangkok, 10520, Thailand
Email: kppuntan@kmitl.ac.th

Abstract: Dengue is a vector-borne disease. It is transmitted to humans by the bites of the *Aedes aegypti* and *Aedes albopictus* mosquitoes. The human population is separated into two classes, a child class and an adult class, each class being described by a SIR model. The transmission rates of the two mosquito species are different and depend on what class the humans belong to. We develop a single model taking into account the presence of two type of mosquitoes and two age classes and apply it to dengue fever. The model shows how it is possible for the maximum level of infected human to be reached in a short time. The nature of stability of the equilibrium state and the trajectories of the individual classes in the model are determined by the values of the basic reproduction number by setting the values of the parameters in the model to different values which reflect the environment in which the epidemic is occurring in the model.

Keywords: *Aedes Aegypti*, *Aedes Albopictus*, Dengue Disease, Endemic Disease State, Equilibrium State, SIR Model

Introduction

Dengue fever is regarded as a serious infectious disease that risks about 2.5 billion people around the world, especially in tropical countries. It is a major epidemic disease occurred in Southeast Asia. Such epidemic arises due to climate change, knowledge of people and awareness on dengue fever so as to the dengue fever possibly become an endemic for a long time. Moreover, World Health Organization (WHO) (WHO, 2009) estimated 50 to 100 million cases worldwide. About 500,000 people are estimated to be infected by dengue hemorrhagic fever each year.

Dengue fever is caused by four serotypes and they are closely related as a family of dengue virus 1 (DEN 1), virus 2 (DEN2), virus 3 (DEN3) and virus 4 (DEN4). There are viruses carried by two kinds of mosquitoes such as Aedes aegypti and Aedes albopictus. This disease is transmitted to the human though biting of mosquitoes. Recently, It was detected in Asia. However, *Aedes aegypti* is still the principal vector of dengue fever transmission. Another interesting fact is the shift of patients' phenomena where dengue fever previously attacks children of primary school age, but now everybody is vulnerable to fever (Pongsumpun and Tang, 2001; Syafruddin and Noorani, 2012).

Dengue virus is transmitted between the human by biting of an infected Aedes mosquito. When a vector bites someone who be infected with dengue virus, the virus is transferred to mosquitoes and it become infected mosquito. After the infected vector bites the susceptible human, then the virus move into the human bloodstream and it spreads throughout the body. Usually, the mosquitoes bite susceptible people during the day time. Dengue fever is the most common disease in urban areas. The outbreaks commonly occur during the rainy season when the mosquitoes heavily breed in standing water. The dengue fever cases are increasing worldwide. The complications of the disease are leading cases of serious illness and most death in children (Kerpaninch *et al*., 2001; Kabilan *et al*., 2003; Malhotra *et al*., 2006; Wiwanitkit, 2006; Pongsumpun, 2011; Joshi *et al*., 2002; Koenraadt *et al*., 2007). One of the major public health problems in many tropical and subtropical regions where *Aedes aegypti* and *Aedes albopictus* are present.

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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It is noted that *Aedes albopictus* was the principal vector in the 1940 s outbreaks in Japan (Hotta, 1998), whereas, *Aedes aegypti* is commonly the principal dengue vector in the tropical and subtropical regions. *Aedes aegypti* is highly domesticated and exhibits strong anthropophilia.

Traditional modeling in epidemiology focus on stability equilibria, since this characterizes if a disease will become endemic and this is a major concern for public health officers. The concept of a basic reproductive number (R_0) was introduced and became a modeling paradigm (Smith *et al.*, 2012) for a very recent review on the works by Ross and Macdonald from a medical modeling point of view. In a fairly large class of models, we can define R_0 unambiguously and it can be shown that if $R_0<1$, the disease is extinct while if $R_0>1$ it becomes endemic (Diekmann and Heesterbeek, 2000).

Hence, in this study, we analyze the SIR (Susceptible-Infected-Recovered) equations for human and SI (Susceptible-Infected) equations for mosquitoes. The model will apply empirically on data of dengue patients reports by Ministry of Public Health, Thailand (2002-2012) as shown in Fig. 1. The purpose of this paper is to study the age structural model of dengue disease incorporated the influence of *Aedes aegypti* and *Aedes albopictus*.

Mathematical Model

The SIR and SI simulates the spread of dengue virus between host and vector populations. The model is based on the Susceptible, Infected and Recovered (SIR) model of infected disease epidemiology, which was adopted by (Nuraini *et al.*, 2007; Yaacob, 2007). The age structure is introduced into a model, i.e., children and adults, then we modify it by incorporating the different behaviors of *Aedes aegypti* and *Aedes albopictus*. In Fig. 1, we show the age distribution of the incidence rates in one province in Thailand during 2002-2012 epidemic. As we see, most cases occur in children under the age of 15. However, a small number of cases do occur in older people. Similar distributions are seen in the other provinces in the country.

This model with age structure, the dynamics of each component of the human is given by:

$$\frac{dS_c}{dt} = P_c N_{tc} - \beta_{ac}(1+\alpha_a \sin \varepsilon t) I_{va1} S_c - \beta_{bc}(1+\alpha_b \sin \varepsilon t) I_{vb1} S_c - \mu_d S_c \quad (1a)$$

$$\frac{dI_{c1}}{dt} = \beta_{ac}(1+\alpha_a \sin \varepsilon t) I_{va1} S_c - \kappa_{c1} I_{c1} - \mu_d I_{c1} \quad (1b)$$

$$\frac{dI_{c2}}{dt} = \beta_{bc}(1+\alpha_b \sin \varepsilon t) I_{vb1} S_c - \kappa_{c2} I_{c2} - \mu_d I_{c2} \quad (1c)$$

$$\frac{dR_c}{dt} = \kappa_{c1} I_{c1} + \kappa_{c2} I_{c2} - \mu_d R_c \quad (1d)$$

$$\frac{dS_a}{dt} = P_a N_{ta} - \beta_{aa}(1+\alpha_a \sin \varepsilon t) I_{va2} S_a - \beta_{ba}(1+\alpha_b \sin \varepsilon t) I_{vb2} S_a - \mu_d S_a \quad (1e)$$

$$\frac{dI_{a1}}{dt} = \beta_{aa}(1+\alpha_a \sin \varepsilon t) I_{va2} S_a - \kappa_{a1} I_{a1} - \mu_d I_{a1} \quad (1f)$$

$$\frac{dI_{a2}}{dt} = \beta_{ba}(1+\alpha_b \sin \varepsilon t) I_{vb2} S_a - \kappa_{a2} I_{a2} - \mu_d I_{a2} \quad (1g)$$

$$\frac{dR_a}{dt} = \kappa_{a1} I_{a1} + \kappa_{a2} I_{a2} - \mu_d R_a \quad (1h)$$

where the variables and parameters are defined in Table 1.

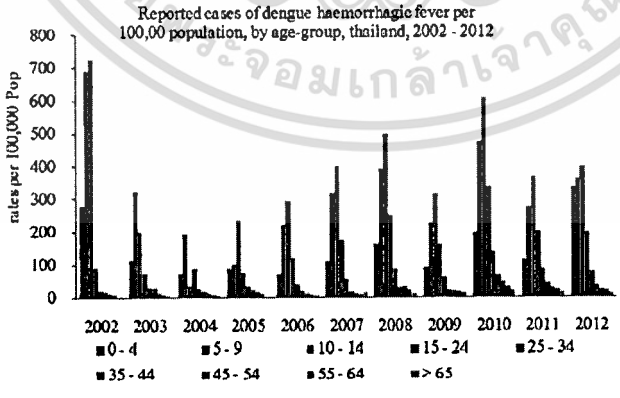

Fig. 1. Age distribution of the 2002-2012 Dengue fever incidence rates in Thailand

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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Table 1. Parameters for equations (1a)-(1h) and their definitions

Variable/parameter	Definition
S_c, I_{c1}, I_{c2}, R_c	The numbers of susceptible children, infected from *Aedes aegypti* and *Aedes albopictus* in children and recovered children
S_a, I_{a1}, I_{a2}, R_a	The numbers of susceptible adult, infected from *Aedes aegypti* and *Aedes albopictus* in adult and recovered adult
N_t	The total population
N_{tc} and N_{ta}	The total population in children and the total population in adult they are constant variables
P_c and P_a	The birth rate of children and adult human
β_{ac}	The transmission probability of dengue virus from *Aedes aegypti* to children
β_{bc}	The transmission probability of dengue virus from *Aedes albopictus* to children
β_{aa}	The transmission probability of dengue virus from *Aedes aegypti* to adult
β_{ba}	The transmission probability of dengue virus from *Aedes albopictus* to adult
κ_{c1}	The rate at which the infected children from *Aedes aegypti* can recover
κ_{c2}	The rate at which the infected children from *Aedes albopictus* can recover
κ_{a1}	The rate at which the infected adult from *Aedes aegypti* can recover
κ_{a2}	The rate at which the infected adult from *Aedes albopictus* can recover
μ_d	The natural death rate of human
a_a	The measure of influence on the transmission process from *Aedes aegypti* mosquito to human
a_b	The measure of influence on the transmission process from *Aedes albopictus* to human
ρ_{va}	The measure of influence on the transmission process from *Aedes aegypti* to human
ρ_{vb}	The measure of influence on the transmission process from *Aedes albopictus* to human

It we add Equation (1a) – (1h) together, we get:

$$\frac{dN_t}{dt} = \frac{dN_{tc}}{dt} + \frac{dN_{ta}}{dt}$$
$$= (S_c + I_{c1} + I_{c2} + R_c) + (S_a + I_{a1} + I_{a2} + R_a)$$

The total children and adult populations are supposed to have constant sizes, i.e., $\frac{dN_{tc}}{dt} = 0$ and $\frac{dN_{ta}}{dt} = 0$, the birth rate would have to be equivalent to the death rate, $P_c = P_a = \mu_d$ in children and adult, respectively.

where, N_{tc} is the total number of children and is equivalent to $S_c + I_{c1} + I_{c2} + R_c$, N_{ta} the total population in adult and is equal to $S_a + I_{a1} + I_{a2} + R_a$.

The dynamics of mosquitoes is described by:

$$\frac{dS_{va1}}{dt} = A_{v_a} - \lambda_{va1}(1 + \rho_{va}\sin\varepsilon t) I_{c1} S_{va1} - \mu_{v_a} S_{va1} \quad (2a)$$

$$\frac{dI_{va1}}{dt} = \lambda_{va1}(1 + \rho_{va}\sin\varepsilon t) I_{c1} S_{va1} - \mu_{v_a} I_{va1} \quad (2b)$$

$$\frac{dS_{va2}}{dt} = A_{v_a} - \lambda_{va2}(1 + \rho_{va}\sin\varepsilon t) I_{a1} S_{va2} - \mu_{v_a} S_{va2} \quad (2c)$$

$$\frac{dI_{va2}}{dt} = \lambda_{va2}(1 + \rho_{va}\sin\varepsilon t) I_{a1} S_{va2} - \mu_{v_a} I_{va2} \quad (2d)$$

$$\frac{dS_{vb1}}{dt} = A_{v_b} - \lambda_{vb1}(1 + \rho_{vb}\sin\varepsilon t) I_{c2} S_{vb1} - \mu_{v_b} S_{vb1} \quad (2e)$$

$$\frac{dI_{vb1}}{dt} = \lambda_{vb1}(1 + \rho_{vb}\sin\varepsilon t) I_{c2} S_{vb1} - \mu_{v_b} I_{vb1} \quad (2f)$$

$$\frac{dS_{vb2}}{dt} = A_{v_b} - \lambda_{vb2}(1 + \rho_{vb}\sin\varepsilon t) I_{a2} S_{vb2} - \mu_{v_b} S_{vb2} \quad (2g)$$

$$\frac{dI_{vb2}}{dt} = \lambda_{vb2}(1 + \rho_{vb}\sin\varepsilon t) I_{a2} S_{vb2} - \mu_{v_b} I_{vb2} \quad (2h)$$

where, the variable and parameters are given in Table 2.

If we add Equation (2a)-(2h) together, we get:

$$\frac{d(S_{va1} + I_{va1})}{dt} = A_{v_a} - \mu_{v_a} N_{va1} \quad (3a)$$

$$\frac{d(S_{va2} + I_{va2})}{dt} = A_{v_a} - \mu_{v_a} N_{va2} \quad (3b)$$

$$\frac{d(S_{vb1} + I_{vb1})}{dt} = A_{v_b} - \mu_{v_b} N_{vb1} \quad (3c)$$

$$\frac{d(S_{vb2} + I_{vb2})}{dt} = A_{v_b} - \mu_{v_b} N_{vb2} \quad (3d)$$

where, N_{va1} and N_{va2} are the numbers of *Aedes aegypti* in children and adult respectively, which is equal to $S_{va1}+I_{va1}$ and $S_{va2} + I_{va2}$. N_{vb1} and N_{vb2} are the numbers of *Aedes albopictus* in children and adult respectively, which is equal to $S_{vb1} + I_{vb1}$ and $S_{vb2} + I_{vb2}$. If the numbers of mosquitoes are also constant each other (3a)-(3d) gives $N_{va1} = A_{v_a} / \mu_{v_a}$, $N_{va2} = A_{v_a} / \mu_{v_a}$, $N_{vb1} = A_{v_b} / \mu_{v_b}$ and $N_{vb2} = A_{v_b} / \mu_{v_b}$.

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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Table 2. Parameters for equations (2a)-(2g) and their definitions

Variable/ parameter	Definition
S_{va1} and I_{va1}	The number of susceptible and infected *Aedes aegypti* mosquitoes who be infected from children
μ_{v_a}	The death rate of *Aedes aegypti* mosquito
A_{v_a}	The carrying capacity of the environment for *Aedes aegypit*
λ_{va1}	The probability that a dengue virus transmitted to the *Aedes aegypti* from an infected children
S_{va2} and I_{va2}	The number of susceptible and infected *Aedes aegypti* mosquitoes who be infected from adult
μ_{v_a}	The death rate of *Aedes aegypti* mosquito
A_{v_a}	The carrying capacity of the environment for *Aedes aegypit* mosquito
λ_{va2}	The probability that a dengue virus transmitted to the *Aedes aegypti* from an infected adult human
S_{vb1} and I_{vb1}	The number of susceptible and infected *Aedes albopictus* mosquitoes who be infected from children
μ_{v_b}	The death rate of *Aedes albopictus* mosquito
A_{v_b}	The carrying capacity of the environment for *Aedes albopictus* mosquito
λ_{vb1}	The probability that a dengue virus transmitted to the *Aedes albopictus* from an infected human in children
S_{vb2} and I_{vb2}	The number of susceptible and infected *Aedes albopictus* mosquitoes who be infected from adult human
μ_{v_b}	The death rate of *Aedes albopictus* mosquito
A_{v_b}	The carrying capacity of the environment for *Aedes albopictus* mosquito
λ_{vb2}	The probability that a dengue virus transmitted to the *Aedes albopictus* from an infected adult

We normalize parameter (1a)-(1h) and (2a)-(2h) by writing $S'_c=\frac{S_c}{N_{hc}}$, $I'_{c1}=\frac{I_{c1}}{N_{hc}}$, $I'_{c2}=\frac{I_{c2}}{N_{hc}}$, $R'_c=\frac{R_c}{N_{hc}}$ in children and $S'_a=\frac{S_a}{N_{ha}}$, $I'_{a1}=\frac{I_{a1}}{N_{ha}}$, $I'_{a2}=\frac{I_{a2}}{N_{ha}}$, $R'_a=\frac{R_a}{N_{ha}}$ in adult. $S'_{va1}=\frac{S_{va1}}{N_{va1}}$, $I'_{va1}=\frac{I_{va1}}{N_{va1}}$, $S'_{va2}=\frac{S_{va2}}{N_{va2}}$, $I'_{va2}=\frac{I_{va2}}{N_{va2}}$, $S'_{vb1}=\frac{S_{vb1}}{N_{vb1}}$, $I'_{vb1}=\frac{I_{vb1}}{N_{vb1}}$, $S'_{vb2}=\frac{S_{vb2}}{N_{vb2}}$ and $I'_{vb2}=\frac{I_{vb2}}{N_{vb2}}$, then the reduced equations become:

$$\frac{d}{dt}S'_c = \mu_d - \beta_{ac}\ (1+\alpha_a \sin \varepsilon t)\ I'_{va1}\ N_{va1}\ S'_c - \beta_{bc}\ (1+\alpha_b \sin \varepsilon t)\ I'_{vb1}\ N_{vb1}\ S'_c - \mu_d\ S'_c \quad (4a)$$

$$\frac{d}{dt}I'_{c1} = \beta_{ac}(1+\alpha_a \sin \varepsilon t)\ I'_{va1} N_{va1}\ S'_c - \kappa_{c1} I'_{c1} - \mu_d I'_{c1} \quad (4b)$$

$$\frac{d}{dt}I'_{c2} = \beta_{bc}(1+\alpha_b \sin \varepsilon t) I'_{vb1} N_{vb1}\ S'_c - \kappa_{c2} I'_{c2} - \mu_d I'_{c2} \quad (4c)$$

$$\frac{d}{dt}S'_a = \mu_d - \beta_{aa}(1+\alpha_a \sin \varepsilon t)\ I'_{va2}\ N_{va2} S'_a - \beta_{ba}(1+\alpha_b \sin \varepsilon t) I'_{vb2}\ N_{vb2} S'_a - \mu_d\ S'_a \quad (4d)$$

$$\frac{d}{dt}I'_{a1} = \beta_{aa}(1+\alpha_a \sin \varepsilon t)\ I'_{va2} N_{va2} S'_a - \kappa_{a1} I'_{a1} - \mu_d I'_{a1} \quad (4e)$$

$$\frac{d}{dt}I'_{a2} = \beta_{ba}(1+\alpha_b \sin \varepsilon t) I'_{vb2} N_{vb2} S'_a - \kappa_{a1} I'_{a2} - \mu_d I'_{a2} \quad (4f)$$

$$\frac{d}{dt}I'_{va1} = \lambda_{va1}(1+\rho_{va} \sin \varepsilon t) I'_{c1} N_{hc} S'_{va1} - \mu_{v_a} I'_{va1} \quad (4g)$$

$$\frac{d}{dt}I'_{va2} = \lambda_{va2}(1+\rho_{va} \sin \varepsilon t) I'_{a1} N_{ha} S'_{va2} - \mu_{v_a} I'_{va2} \quad (4h)$$

$$\frac{d}{dt}I'_{vb1} = \lambda_{vb1}(1+\rho_{vb} \sin \varepsilon t) I'_{c2} N_{hc} S'_{vb1} - \mu_{v_b} I'_{vb1} \quad (4i)$$

$$\frac{d}{dt}I'_{vb2} = \lambda_{vb2}(1+\rho_{vb} \sin \varepsilon t) I'_{a2} N_{ha} S'_{vb2} - \mu_{v_b} I'_{vb2} \quad (4j)$$

Where:

$S'_c + I'_{c1} + I'_{c2} + R'_c = 1$, $S'_a + I'_{a1} + I'_{a2} + R'_a = 1$,
$S_{va1} + I_{va1} = 1$, $S'_{va2} + I'_{va2} = 1$, $S'_{vb1} + I'_{vb1} = 1$ *and* $S'_{vb2} + I'_{vb2} = 1$

Mathematical Analysis

Equilibrium States

The equilibrium states $(S'_c, I'_{c1}, I'_{c2}, S'_a, I'_{a1}, I'_{a2}, I'_{va1}, I'_{vb1}, I'_{va2}, I'_{vb2})$ are obtained by setting the right hand side of (4a)-(4j) to zero. Therefore we obtain $(S'_c, I'_{c1}, I'_{c2}, I'_{va1}, I'_{vb1})$ and $(S'_a, I'_{a1}, I'_{a2}, I'_{va2}, I'_{vb2})$. Doing this, we get four equilibrium states.

A. The two group disease free equilibrium state:

$$E_0 = (1,0,0,1,0,0,0,0,0,0)$$

A1.the disease free equilibrium state:

$$E_{ac} = (S'_c, I'_{c1}, I'_{c2}, I'_{va1}, I'_{vb1}) = (1,0,0,0,0) \text{ in children}$$

A2.the disease free equilibrium state:

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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$$E_{0a} = (S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*) = (1,0,0,0,0) \text{ in adult}$$

B. The two group endemic equilibrium state:

$$\hat{E} = (S_c^*, I_{c1}^*, I_{c2}^*, I_{va1}^*, I_{vb1}^*, S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*)$$

B1.the endemic state:

$$E_{1c} = (S_c^*, I_{c1}^*, I_{c2}^*, I_{va1}^*, I_{vb1}^*) \text{ in children}$$

Where:

$$S_c^* = \frac{(N_{tc}\mu_d\lambda_{vb1} + (\kappa_{c2}+\mu_d)\mu_{vb1} + N_{tc}\mu_d\lambda_{vb1}\rho_{vb}\sin\varepsilon t)}{(N_{tc}\lambda_{vb1}(I_{va1}^* N_{va1}\beta_{ac} + N_{vb1}\beta_{bc} + \mu_d + (I_{va1}^* N_{va1}\alpha_a\beta_{ac} + N_{vb1}\alpha_b\beta_{bc})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t)))} \quad (5a)$$

$$I_{c1}^* = \frac{I_{va1}^* N_{va1}\beta_{ac}(1+\alpha_a\sin\varepsilon t)(N_{tc}\mu_d\lambda_{vb1} + (\kappa_{c2}+\mu_d)\mu_{v_b} + N_{tc}\mu_d\lambda_{vb1}\rho_{vb}\sin\varepsilon t))}{(N_{tc}\lambda_{vb1}(\kappa_{c1}+\mu_d)(I_{va1}^* N_{va1}\beta_{ac} + N_{vb1}\beta_{bc} + \mu_d + (I_{va1}^* N_{va1}\alpha_a\beta_{ac} + N_{vb1}\alpha_b\beta_{bc})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))} \quad (5b)$$

$$I_{c2}^* = \frac{(I_{vb1}^* N_{vb1}\beta_{bc}(1+\alpha_b\sin\varepsilon t)(N_{tc}\lambda_{vb1}\mu_d + (\kappa_{c2}+\mu_d)\mu_{v_b} + N_{tc}\lambda_{vb1}\mu_d\rho_{vb}\sin\varepsilon t))}{(N_{tc}\lambda_{vb1}(\kappa_{c2}+\mu_d)(I_{va1}^* N_{va1}\beta_{ac} + I_{vb1}^* N_{vb1}\beta_{bc} + \mu_d + (I_{va1}^* N_{va1}\alpha_a\beta_{ac} + N_{vb1}\alpha_b\beta_{bc})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))} \quad (5c)$$

$$\begin{aligned}
I_{va1}^* = {} & [(2(-2\lambda_{vb1}\mu_d(\kappa_{c1}+\mu_d)\mu_{v_a} \\
& + 2N_{va1}\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{v_b} \\
& + N_{va1}\alpha_a\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d) \\
& \mu_{v_b}\rho_{va} - N_{vb1}\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}(2+\alpha_b\rho_{vb}) \\
& + N_{tc}N_{va1}\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d(2+\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb}))) \\
& - 2(N_{va1}\alpha_a\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{v_b}\rho_{va} \\
& - N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}\rho_{vb} \\
& + N_{tc}N_{va1}\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d(\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb})))\cos \\
& 2\varepsilon t + (4(N_{va1}\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{v_b}(\alpha_a+\rho_{va}) \\
& - \lambda_{vb1}\mu_d(\kappa_{c1}+\mu_d)\mu_{v_a} - N_{vb1}\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}(\alpha_b+\rho_{vb})) \\
& + N_{tc}N_{va1}\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d(4(\rho_{va}+\rho_{vb}) \\
& + \alpha_a(4+3\rho_{va}\rho_{vb})))\sin\varepsilon t \\
& - N_{tc}N_{va1}\alpha_a\beta_{ac}\lambda_{va1}\lambda_{vb1}\mu_d\rho_{va}\rho_{vb}\sin\varepsilon t)] \\
& /[(2N_{va1}\beta_{ac}(1+\alpha_a\sin\varepsilon t)(2\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a} \\
& + 2\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{v_b}(\kappa_{c2}+\mu_d)\mu_{v_b} \\
& + N_{tc}\mu_d\lambda_{va1}\lambda_{vb1}(2+\rho_{va}\rho_{vb}) - N_{tc}\mu_d\lambda_{va1}\lambda_{vb1}\rho_{va}\rho_{vb}\cos 2\varepsilon t \\
& + 2(\lambda_{va1}(\kappa_{c2}+\mu_d)\mu_{v_b}\rho_{va} + \lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_b}\rho_{vb} \\
& + N_{tc}\mu_d\lambda_{va1}\lambda_{vb1}(\rho_{va}+\rho_{vb}))\sin\varepsilon t))] \quad (5d)
\end{aligned}$$

$$\begin{aligned}
I_{vb1}^* = {} & [(N_{tc}N_{vb1}\beta_{ac}\lambda_{vb1}\mu_d - (I_{va1}^* N_{va1}\beta_{ac} + \mu_d)(\kappa_{c2}+\mu_d)\mu_{v_b} \\
& + \sin\varepsilon t(-I_{va1}^* N_{va1}\alpha_a\beta_{ac}(\kappa_{c2}+\mu_d)\mu_{v_b} \\
& + N_{tc}N_{vb1}\beta_{bc}\lambda_{vb1}\mu_d(\alpha_b+\rho_{vb}) \\
& + N_{tc}N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}\mu_d\rho_{vb}\sin\varepsilon t))] \\
& /[N_{vb1}\beta_{bc}(1+\alpha_b\sin\varepsilon t)(N_{tc}\lambda_{vb1}\mu_d \\
& + (\kappa_{c2}+\mu_d)\mu_{v_b} + N_{tc}\lambda_{vb1}\mu_d\rho_{vb}\sin\varepsilon t))]
\end{aligned} \quad (5e)$$

B2. The endemic state:

$$E_{1a} = (S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*) \text{ in adult}$$

Where:

$$S_a^* = \frac{(N_{ta}\mu_d\lambda_{vb2} + (\kappa_{a2}+\mu_d)\mu_{v_b} + N_{ta}\mu_d\lambda_{vb2}\rho_{vb}\sin\varepsilon t)}{(N_{ta}\lambda_{vb2}(I_{va2}^* N_{va2}\beta_{aa} + N_{vb2}\beta_{ba} + \mu_d + (I_{va2}^* N_{va2}\alpha_a\beta_{aa} + N_{vb2}\alpha_b\beta_{ba})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t)))} \quad (6a)$$

$$I_{a1}^* = \frac{I_{va2}^* N_{va2}\beta_{aa}(1+\alpha_a\sin\varepsilon t)(N_{ta}\mu_d\lambda_{vb2} + (\kappa_{a2}+\mu_d)\mu_{v_b} + N_{ta}\mu_d\lambda_{vb2}\rho_{vb}\sin\varepsilon t))}{(N_{ta}\lambda_{vb2}(\kappa_{a1}+\mu_d)(I_{va2}^* N_{va2}\beta_{aa} + N_{vb2}\beta_{ba} + \mu_d + (I_{va2}^* N_{va2}\alpha_a\beta_{aa} + N_{vb2}\alpha_b\beta_{ba})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))} \quad (6b)$$

$$\begin{aligned}
I_{a2}^* = {} & [(I_{vb2}^* N_{vb2}\beta_{ba}(1+\alpha_b\sin\varepsilon t)(N_{ta}\lambda_{vb2}\mu_d \\
& + (\kappa_{a2}+\mu_d)\mu_{v_b} + N_{ta}\lambda_{vb2}\mu_d\rho_{vb}\sin\varepsilon t)) \\
& / N_{ta}\lambda_{vb2}(\kappa_{a2}+\mu_d)(I_{va2}^* N_{va2}\beta_{aa} \\
& + I_{vb2}^* N_{vb2}\beta_{ba} + \mu_d + (I_{va2}^* N_{va2}\alpha_a\beta_{aa} \\
& + N_{vb2}\alpha_b\beta_{ba})\sin\varepsilon t)(1+\rho_{vb}\sin\varepsilon t))]
\end{aligned} \quad (6c)$$

$$\begin{aligned}
I_{va2}^* = {} & [(2(-2\lambda_{vb2}\mu_d(\kappa_{a1}+\mu_d)\mu_{v_a} + 2N_{va2}\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{v_b} \\
& + N_{va2}\alpha_a\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{v_b}\rho_{va} \\
& - N_{vb2}\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}(2+\alpha_b\rho_{vb}) \\
& + N_{ta}N_{va2}\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d(2+\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb}))) \\
& - 2(N_{va2}\alpha_a\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{v_b}\rho_{va} \\
& - N_{vb2}\alpha_b\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}\rho_{vb} \\
& + N_{ta}N_{va2}\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d(\rho_{va}\rho_{vb}+\alpha_a(\rho_{va}+\rho_{vb})))\cos 2\varepsilon t \\
& + (4(N_{va2}\beta_{aa}\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{v_b}(\alpha_a+\rho_{va}) \\
& - \lambda_{vb2}\mu_d(\kappa_{a1}+\mu_d)\mu_{v_a} - N_{vb2}\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}(\alpha_b+\rho_{vb})) \\
& + N_{ta}N_{va2}\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d(4(\rho_{va}+\rho_{vb}) \\
& + \alpha_a(4+3\rho_{va}\rho_{vb})))\sin\varepsilon t \\
& - N_{ta}N_{va2}\alpha_a\beta_{aa}\lambda_{va2}\lambda_{vb2}\mu_d\rho_{va}\rho_{vb}\sin\varepsilon t)] \\
& /[(2N_{va2}\beta_{aa}(1+\alpha_a\sin\varepsilon t)(2\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a} \\
& + 2\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{v_b}(\kappa_{a2}+\mu_d)\mu_{v_b} + N_{ta}\mu_d\lambda_{va2}\lambda_{vb2}(2+\rho_{va}\rho_{vb}) \\
& - N_{ta}\mu_d\lambda_{va2}\lambda_{vb2}\rho_{va}\rho_{vb}\cos 2\varepsilon t + 2(\lambda_{va2}(\kappa_{a2}+\mu_d)\mu_{v_b}\rho_{va} \\
& + \lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}\rho_{vb} + N_{ta}\mu_d\lambda_{va2}\lambda_{vb2}(\rho_{va}+\rho_{vb}))\sin\varepsilon t))]
\end{aligned} \quad (6d)$$

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R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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$$
\begin{aligned}
I^{*}_{vb2} = {} & [(N_{ia} N_{vb2} \beta_{aa} \lambda_{vb2} \mu_d - (I^{*}_{va2} N_{va2} \beta_{aa} + \mu_d)(\kappa_{a2} + \mu_d)\mu_{v_a} \\
& + \sin \varepsilon t(-I^{*}_{va2} N_{va2} \alpha_a \beta_{aa} (\kappa_{a2} + \mu_d)\mu_{v_a} \\
& + N_{ia} N_{vb2} \beta_{ba} \lambda_{vb2} \mu_d (\alpha_b + \rho_{vb}) \\
& + N_{ia} N_{vb2} \alpha_b \beta_{ba} \lambda_{vb2} \mu_d \rho_{vb} \sin \varepsilon t))]/ \\
& [N_{vb2} \beta_{ba}(1 + \alpha_b \sin \varepsilon t)(N_{ia} \lambda_{vb2} \mu_d + (\kappa_{a2} + \mu_d)\mu_{v_a} \\
& + N_{ia} \lambda_{vb2} \mu_d \rho_{vb} \sin \varepsilon t))]
\end{aligned} \tag{6e}
$$

Local Asymptotically Stability

The local stability of each equilibrium state is determined from Jacobian matrix of right hand side of the above set of differential equations evaluated at the equilibrium state.

Proposition A. If $S_0<1$, $S_{0c}<1$ and $S_{0a}<1$ when $\varepsilon = 0$, then the disease free equilibrium state E_{0c} in children and E_{0a} in adult are locally asymptotically stable, where:

$$
S_0 = \max \left\{ \begin{array}{l}
\dfrac{\begin{array}{l} 2N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}\rho_{vb} + \\ N_{va1}\beta_{ac}\lambda_{va1}(2(N_{ic}\lambda_{vb1}\mu_d + (\kappa_{c2}+\mu_d)\mu_{v_b}) \\ (2+\alpha_a\rho_{va}) + 2N_{ic}\lambda_{vb1}\mu_d(\alpha_a+\rho_{va})) \end{array}}{\begin{array}{l} (2\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}(2\mu_d + N_{vb1}\beta_{bc}(2+\alpha_b\rho_{vb})) \\ +2N_{va1}\beta_{ac}\lambda_{va1}(\alpha_a(\kappa_{c2}+\mu_d)\mu_{v_b}\rho_{va} \\ +N_{ic}\lambda_{vb1}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb}))) \end{array}} \\
\dfrac{\begin{array}{l} 2N_{vb2}\alpha_b\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}\rho_{vb} \\ +N_{va2}\beta_{aa}\lambda_{va2}(2(N_{ia}\lambda_{vb2}\mu_d + (\kappa_{a2}+\mu_d)\mu_{v_b}) \\ (2+\alpha_a\rho_{va}) + 2N_{ia}\lambda_{vb2}\mu_d(\alpha_a+\rho_{va})) \end{array}}{\begin{array}{l} (2\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}(2\mu_d + N_{vb2}\beta_{ba} \\ (2+\alpha_b\rho_{vb})) + 2N_{va2}\beta_{aa}\lambda_{va2}(\alpha_a(\kappa_{a2}+\mu_d) \\ \mu_{v_b}\rho_{va} + N_{ia}\lambda_{vb2}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb}))) \end{array}}
\end{array} \right. \tag{6f}
$$

$$
S_{0c} = \frac{\begin{array}{l} 2N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}\rho_{vb} \\ +N_{va1}\beta_{ac}\lambda_{va1}(2(N_{ic}\lambda_{vb1}\mu_d + (\kappa_{c2}+\mu_d)\mu_{v_b}) \\ (2+\alpha_a\rho_{va}) + 2N_{ic}\lambda_{vb1}\mu_d(\alpha_a+\rho_{va})) \end{array}}{\begin{array}{l} (2\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}(2\mu_d + N_{vb1}\beta_{bc}(2+\alpha_b\rho_{vb})) \\ +2N_{va1}\beta_{ac}\lambda_{va1}(\alpha_a(\kappa_{c2}+\mu_d)\mu_{v_b}\rho_{va} \\ +N_{ic}\lambda_{vb1}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb}))) \end{array}} \text{ in children} \tag{6g}
$$

$$
S_{0a} = \frac{\begin{array}{l} 2N_{vb2}\alpha_b\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}\rho_{vb} \\ +N_{va2}\beta_{aa}\lambda_{va2}(2(N_{ia}\lambda_{vb2}\mu_d + (\kappa_{a2} \\ +\mu_d)\mu_{v_b})(2+\alpha_a\rho_{va}) + 2N_{ia}\lambda_{vb2}\mu_d(\alpha_a+\rho_{va})) \end{array}}{\begin{array}{l} (2\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}(2\mu_d + N_{vb2}\beta_{ba}(2+\alpha_b\rho_{vb})) \\ +2N_{va2}\beta_{aa}\lambda_{va2}(\alpha_a(\kappa_{a2}+\mu_d)\mu_{v_b}\rho_{va} \\ +N_{ia}\lambda_{vb2}\mu_d(\alpha_a\rho_{va} + (\alpha_a+\rho_{va})\rho_{vb}))) \end{array}} \text{ in adult} \tag{6h}
$$

Proof.

For the disease free equilibrium state in children $E_{0c} = (1, 0, 0, 0, 0, 0)$ and in adult $E_{0a} = (1, 0, 0, 0, 0, 0)$.

The system defined by Equation (4a) - (4j), the Jacobian matrix evaluated at E_{0c} and E_{0a} respectively, given by:

$$
J_c = \begin{bmatrix}
-(\mu_d) & 0 & 0 & -\beta_{ac}(1+\alpha_a \sin(\varepsilon t)) \\
N_{va1} - \beta_{bc}(1+\alpha_b \sin(\varepsilon t)) N_{vb1} & & & \\
0 & -(\kappa_{c1}+\mu_d) & 0 & \beta_{ac}(1+\alpha_a \sin(\varepsilon t)) N_{va1} \\
0 & 0 & -(\kappa_{c2}+\mu_d) & 0 \beta_{bc}(1+\alpha_b \sin(\varepsilon t)) N_{vb1} \\
0 & \lambda_{va1}(1+\rho_{va} \sin(\varepsilon t)) & 0 & -\mu_{va1} \quad 0 \\
0 & 0 & \lambda_{vb1}(1+\rho_{vb} \sin(\varepsilon t)) & 0 -\mu_{vb1}
\end{bmatrix} \tag{7a}
$$

$$
J_a = \begin{bmatrix}
-(\mu_d) & 0 & 0 & -\beta_{aa}(1+\alpha_a \sin(\varepsilon t)) N_{va2} \\
-\beta_{ba}(1+\alpha_b \sin(\varepsilon t)) N_{vb2} & & & \\
0 & -(\kappa_{a1}+\mu_d) & 0 & \beta_{aa}(1+\alpha_a \sin(\varepsilon t)) N_{va2} \; 0 \\
0 & 0 & -(\kappa_{a2}+\mu_d) & 0 \beta_{ba}(1+\alpha_b \sin(\varepsilon t)) N_{vb2} \\
0 & \lambda_{va2}(1+\rho_{va} \sin(\varepsilon t)) & 0 & -\mu_{va2} \; 0 \\
0 & 0 & \lambda_{vb2}(1+\rho_{vb} \sin(\varepsilon t)) & 0 -\mu_{vb2}
\end{bmatrix} \tag{7b}
$$

The eigenvalues are obtained by solving the characteristic equations, $\det |\eta I_5 - J_i| = 0$. Where I_5 is the 5×5 identity matrix and $J_i(J_i;\ i = c,a)$ is the Jacobian matrix matrix for (7a) and (7b), respectively. To evaluate the determinant, we get the following characteristic equations:

$$
(\eta + \mu_d)(\eta^4 + W_1\eta^3 + W_2\eta^2 + W_3\eta + W_4) = 0 \tag{8a}
$$

$$
(\eta + \mu_d)(\eta^4 + F_1\eta^3 + F_2\eta^2 + F_3\eta + F_4) = 0 \tag{8b}
$$

Where:

$$
W_1 = \kappa_{c1} + \kappa_{c2} + 2\mu_d + \mu_{v_a} + \mu_{v_b} \tag{9a}
$$

$$
\begin{aligned}
W_2 = {} & -N_{va1}\beta_{ac}\lambda_{va1} - N_{vb1}\beta_{bc}\lambda_{vb1}) \\
& + \mu_d^2 + 2\mu_d\mu_{v_a} + 2\mu_d\mu_{v_b} + \mu_{v_a}\mu_{v_b} \\
& + \kappa_{c2}(\mu_d + \mu_{v_a} + \mu_{v_b}) + \kappa_{c1}(\kappa_{c2} + \mu_d + \mu_{v_a} + \mu_{v_b})
\end{aligned} \tag{9b}
$$

$$
\begin{aligned}
W_3 = {} & (\kappa_{c1}+\mu_d)(\kappa_{c2}+\mu_d)\mu_{v_a} - N_{vb1}\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d+\mu_{v_a}) \\
& + ((\kappa_{c1}+\mu_d)(\kappa_{c2}+\mu_d) + (\kappa_{c1}+\kappa_{c2}+2\mu_d)\mu_{v_a}) \\
& \mu_{v_b} - N_{va1}\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d+\mu_{v_b}) + (\beta_{ac}\lambda_{va1}(\kappa_{c2}+\mu_d+\mu_{v_b}))
\end{aligned} \tag{9c}
$$

$$
\begin{aligned}
W_4 = {} & (N_{va1}\beta_{ac}\lambda_{va1} - (\kappa_{c1}+\mu_d)\mu_{v_a}) \\
& (N_{vb1}\beta_{bc}\lambda_{vb1} + (\kappa_{c2}+\mu_d)\mu_{v_b})
\end{aligned} \tag{9d}
$$

$$
F_1 = \kappa_{a1} + \kappa_{a2} + 2\mu_d + \mu_{v_a} + \mu_{v_b} \tag{9e}
$$

$$
\begin{aligned}
F_2 = {} & -N_{va2}\beta_{aa}\lambda_{va2} - N_{vb2}\beta_{ba}\lambda_{vb2}) + \mu_d^2 + 2\mu_d\mu_{v_a} + 2\mu_d\mu_{v_b} \\
& + \mu_{v_a}\mu_{v_b} + \kappa_{a2}(\mu_d + \mu_{v_a} + \mu_{v_b}) + \kappa_{a1}(\kappa_{a2} + \mu_d + \mu_{v_a} + \mu_{v_b})
\end{aligned} \tag{9f}
$$

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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$$F_3=(\kappa_{a1}+\mu_d)(\kappa_{a2}+\mu_d)\mu_{v_a}-N_{vb2}\beta_{bu}\lambda_{vb2}(\kappa_{a1}+\mu_d+\mu_{v_a})$$
$$+((\kappa_{a1}+\mu_d)(\kappa_{a2}+\mu_d)+(\kappa_{a1}+\kappa_{a2}+2\mu_d)\mu_{v_a})\mu_{v_b} \quad (9g)$$
$$-N_{va2}\beta_{au}\lambda_{va2}(\kappa_{a2}+\mu_d+\mu_{v_b})+(\beta_{au}\lambda_{va2}(\kappa_{a2}+\mu_d+\mu_{v_b}))$$

$$F_4=(N_{va2}\beta_{au}\lambda_{va2}-(\kappa_{a1}+\mu_d)\mu_{v_b})(N_{vb2}\beta_{bu}\lambda_{vb2}+(\kappa_{a2}+\mu_d)\mu_{v_b}) \quad (9h)$$

From the characteristic equation, Equation (8a)-(8b), we see that eigenvalues are $\eta_c=-\mu_d$ and $\eta_a=-\mu_d$, all of these eigenvalues are negative, for $S_0<1$. The sign of other four eigenvalues can be ascertained by solving equation $(\eta^4+W_1\eta^3+W_2\eta^2+W_3\eta+W_4)=0$ and $(\eta^4+F_1\eta^3+F_2\eta^2+F_3\eta+F_4)=0$. The remaining four eigenvalues have negative real parts if they satisfy Routh-Hurwitz criteria (10a) - (10d) (Esteva and Vargas, 1998), each equilibrium state is locally asymptotically stable if the following conditions are satisfied:

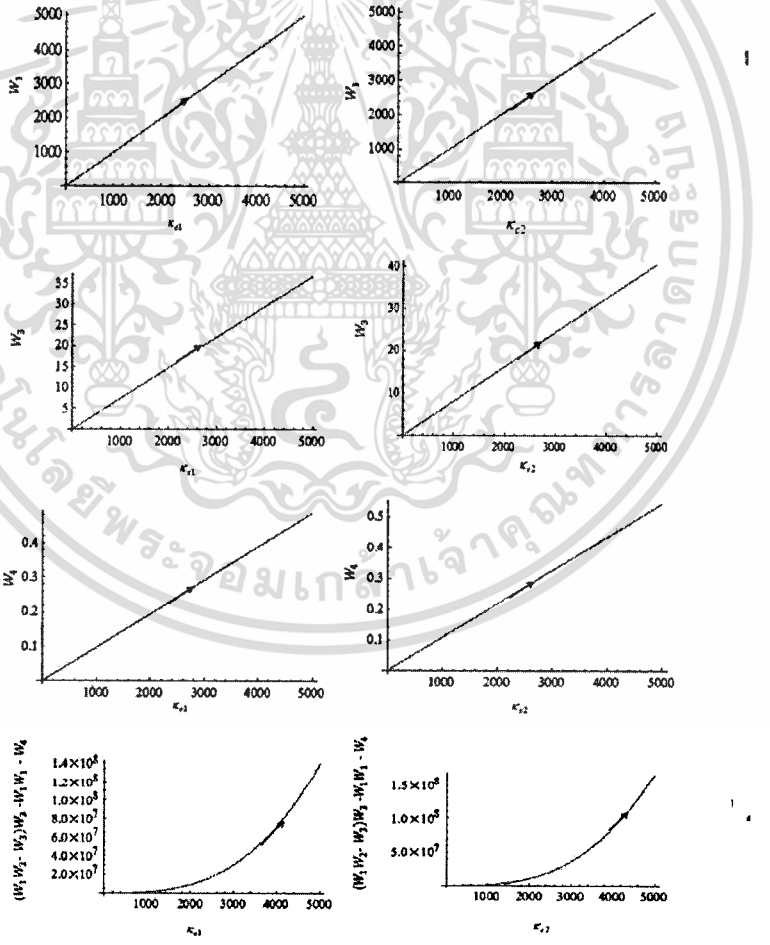
$$W_1 \text{ and } F_1>0 \quad (10a)$$

$$W_3 \text{ and } F_3>0 \quad (10b)$$

$$W_4 \text{ and } F_4>0 \quad (10c)$$

$$(W_1W_2-W_3)W_3+W_1^2W_4>0 \text{ and } (F_1F_2-F_3)F_3+F_1^2F_4>0 \quad (10d)$$

After we use *Mathematica* to show the conditions of locally asymptotically stable, we can see that W_1 and F_1 are always positive. For the equations given by (10b)-(10d), we show these conditions by using the following Fig. 2.



R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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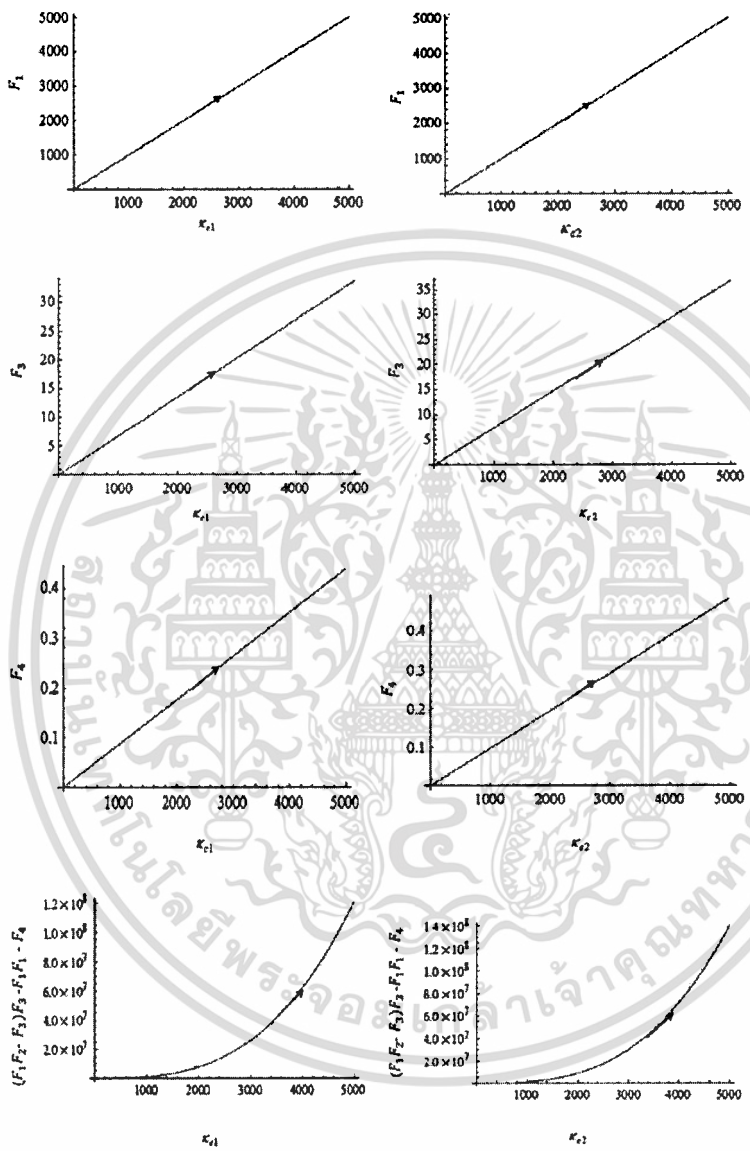

Fig. 2. The parameter spaces for the disease free equilibrium state, which satisfies the Routh-Hurwitz conditions, show onto (κ_{c1}, W_3), (κ_{c2}, W_3), (κ_{a1}, F_3), (κ_{a2}, F_3), (κ_{c1}, W_4), (κ_{c2}, W_4), (κ_{a1}, F_4), (κ_{a2}, F_4), $(\kappa_{c1}, ((W_1W_2 - W_3)W_3 - W_1^2W_4))$, $(\kappa_{c1}, ((W_1W_2 - W_3)W_3 - W_1^2W_4))$, $(\kappa_{a1}, ((F_1F_2 - F_3)F_3 - F_1^2F_4))$, $(\kappa_{a2}, ((F_1F_2 - F_3)F_3 - F_1^2F_4))$, respectively. The values of parameter are follows: $\kappa_{c1}=1/(17/2)$, $\kappa_{c2}=1/(19/2)$, $\mu_d=1/(365*74.6)$ day^{-1}, $N_\kappa=9000$, $N_{va1}=4000$, $N_{vb1}=5500$, $\beta_{ac}=0.00769$, $\beta_{bc}=0.000246$, $\lambda_{va1}=0.00000576$, $\lambda_{vb1}=0.00000335$, $\alpha_a=0.07$, $\alpha_b=0.067$ and $N_t=100000$, $\kappa_{a1}=1/(19/2)$, $\kappa_{a2}=1/(21/2)$, $\mu_d=1/(365*74.6)$ day^{-1}, $N_{ta}=6000$, $N_{va2}=3000$, $N_{vb2}=4100$, $\beta_{aa}=0.000045$, $\beta_{ba}=0.000067$, $\lambda_{va2}=0.0066$, $\lambda_{vb2}=0.00235$, $\alpha_a=0.07$, $\alpha_b=0.067$ and $N_t=100000$. From the above figures, the Routh-Hurwitz conditions are satisfied for $S_0>1$

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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Endemic Disease State

Proposition B. If $S_0>1$, when $\varepsilon = 0$, then the equilibrium state $\hat{S}=(S_c^*, I_{c1}^*, I_{c2}^*, I_{vo1}^*, I_{vb1}^*, S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*)$ is locally asymptotically stable.

Proof.

For the endemic disease equilibrium state $E_{1c} = (S_c^*, I_{c1}^*, I_{c2}^*, I_{vo1}^*, I_{vb1}^*)$ in children and $E_{1a} = (S_a^*, I_{a1}^*, I_{a2}^*, I_{va2}^*, I_{vb2}^*)$ in adult, we obtain the characteristic equation:

$$(\eta^5 + D_1\eta^4 + D_2\eta^3 + D_3\eta^2 + D_4\eta + D_5) = 0 \text{ in children} \quad (11a)$$

$$(\eta^5 + G_1\eta^4 + G_2\eta^3 + G_3\eta^2 + G_4\eta + G_5) = 0 \text{ in adult} \quad (11b)$$

Where:

$$D_1 = N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \kappa_{c1} + \kappa_{c2} + 3\mu_d + \mu_{v_a} + \mu_{v_b} \quad (12a)$$

$$\begin{aligned} D_2 = {} & \kappa_{c1}\kappa_{c2} + 2\kappa_{c1}\mu_d + 2\kappa_{c2}\mu_d + 3\mu_d^2 + \kappa_{c1}\mu_{v_a} + \kappa_{c2}\mu_{v_a} \\ & + 3\mu_d\mu_{v_a} + (\kappa_{c1} + \kappa_{c2} + 3\mu_d + \mu_{v_a})\mu_{v_b} + N_{vo1}\beta_{ac} \\ & (-(\lambda_{vo1}\mu_d / N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2\mu_d) + \theta_1(\kappa_{c1} + \kappa_{c2} + 2\mu_d \\ & + (\lambda_{vo1}\mu_d / N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2\mu_d) + \mu_{v_a} + \mu_{v_b})) \\ & + N_{vb1}\beta_{bc}(-(\lambda_{vb1}\mu_d / N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2\mu_d) + \theta_2(\kappa_{c1} \\ & + \kappa_{c2} + 2\mu_d + (\lambda_{vb1}\mu_d / N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2\mu_d)\mu_{v_a} + \mu_{v_b})) \end{aligned} \quad (12b)$$

$$\begin{aligned} D_3 = {} & \frac{1}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d}(N_{vo1}^2\beta_{ac}^2\theta_1^2(\mu_d^2 + 2\mu_d\mu_{vo1} \\ & + 2\mu_d\mu_{v_b} + \mu_{v_a}\mu_{v_b} + \kappa_{c2}(\mu_d + \mu_{v_a} + \mu_{v_b}) + \kappa_{c1}(\kappa_{c2} + \mu_d \\ & + \mu_{v_a} + \mu_{v_b})) + N_{vb1}^2\beta_{bc}^2\theta_2^2 \\ & (\mu_d^2 + 2\mu_d\mu_{v_a} + 2\mu_d\mu_{v_b} \\ & + \mu_{v_a}\mu_{v_b} + \kappa_{c2}(\mu_d + \mu_{v_a} + \mu_{v_b}) + \kappa_{c1}(\kappa_{c2} + \mu_d + \mu_{v_a} \\ & + \mu_{v_b})) + \mu_d(\kappa_{c2}(\mu_d^2 + \mu_{v_a}\mu_{v_b} + 2\mu_d(\mu_{v_a} + \mu_{v_b})) \\ & + \mu_d(\mu_d^2 + 3\mu_{v_a}\mu_{v_b} + 3\mu_d(\mu_{v_a} + \mu_{v_b})) + \kappa_{c1}(\mu_d^2 + \mu_{v_a}\mu_{v_b} \\ & + 2\mu_d(\mu_{v_a} + \mu_{v_b}) + \kappa_{c2}(\mu_d + \mu_{v_a} + \mu_{v_b}))) + N_{vb1}\beta_{bc} \\ & (-\lambda_{vb1}\mu_d(\kappa_{c1} + 2\mu_d + \mu_{v_a}) + \theta_2(\mu_d(2\mu_d(\kappa_{c2} + \lambda_{vb1} \\ & + \mu_d) + (3\kappa_{c2} + \lambda_{vb1} + 5\mu_d)\mu_{v_a}) + (\kappa_{c2}(3\mu_d + \mu_{v_a}) \\ & + \mu_d(5\mu_d + 4\mu_{v_a}))\mu_{v_b} + \kappa_{c2}(2\mu_d + \mu_{v_a} + \mu_{v_b})))) \\ & + N_{vo1}\beta_{ac}(-\lambda_{vo1}\mu_d \\ & (\kappa_{c2} + 2\mu_d + \mu_{v_b}) + \theta_1(\kappa_{c2}\mu_d(\lambda_{vo1} \\ & + 2\mu_d + 3\mu_{v_b}) + \kappa_{c2}(3\mu_d + \mu_{v_a})\mu_{v_b} \\ & + \mu_d(2\mu_d(\lambda_{vo1} + \mu_d) \\ & + 5\mu_d\mu_{v_b} + (\lambda_{vo1} + 5\mu_d + 4\mu_{v_a})\mu_{v_b}) + \kappa_{c1}(2\mu_d^2 + \mu_{v_a}\mu_{v_b} \\ & + 3\mu_d(\mu_{v_a} + \mu_{v_b}) + \kappa_{c2}(2\mu_d + \mu_{v_a} + \mu_{v_b}))) \\ & + N_{vb1}\beta_{bc}(-\theta_2\lambda_{vo1}\mu_d + \theta_1(-\lambda_{vb1}\mu_d + \theta_2(\mu_d(\lambda_{vo1} + \lambda_{vb1} \\ & + 2\mu_d + 4\mu_{v_a}) + 2(2\mu_d + \mu_{v_b})\mu_{v_b} \\ & + 2\kappa_{c2}(\mu_d + \mu_{v_a} + \mu_{v_b}) \\ & + 2\kappa_{c1}(\kappa_{c2} + \mu_d + \mu_{v_a} + \mu_{v_b}))))) \end{aligned} \quad (12c)$$

$$\begin{aligned} D_4 = {} & \kappa_{c1}\kappa_{c2}\mu_d\mu_{v_a} + \kappa_{c1}\mu_d^2\mu_{v_a} + \kappa_{c2}\mu_d^2\mu_{v_a} + \mu_d^3\mu_{v_a} + \kappa_{c1}\kappa_{c2}\mu_d\mu_{v_b} \\ & + \kappa_{c1}\mu_d^2\mu_{v_b} + \kappa_{c2}\mu_d^2\mu_{v_b} + \mu_d^3\mu_{v_b} + \kappa_{c1}\kappa_{c2}\mu_{v_a}\mu_{v_b} + 2\kappa_{c1}\mu_d\mu_{v_a}\mu_{v_b} \\ & + 2\kappa_{c2}\mu_d\mu_{v_a}\mu_{v_b} + 3\mu_d^2\mu_{v_a}\mu_{v_b} + \frac{1}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} \\ & N_{vb1}\beta_{bc}((-1+\theta_2)\lambda_{vb1}\mu_d^2(\mu_d + 2\mu_{v_a}) + \theta_2(N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d) \\ & (\mu_d(\kappa_{c2} + \mu_d)\mu_{v_a} + (\mu_d(\kappa_{c2} + \mu_d) + (\kappa_{c2} + 2\mu_d)\mu_{v_a})\mu_{v_b}) \\ & + \kappa_{c1}((-1+\theta_2)\lambda_{vb1}\mu_d(\mu_d + 2\mu_{v_a}) + \theta_2(N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d)((\kappa_{c2} + \mu_d)\mu_{v_a} \\ & + (\kappa_{c2} + \mu_d + \mu_{v_a})\mu_{v_b}))) + N_{vo1}\beta_{ac}(-\frac{\kappa_{c2}\lambda_{vo1}\mu_d^2}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \frac{\theta_1\kappa_{c2}\lambda_{vo1}\mu_d^2}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} \\ & - \frac{\lambda_{vo1}\mu_d^3}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \frac{\theta_1\lambda_{vo1}\mu^3{}_d}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \theta_1\kappa_{c1}\kappa_{c2}\mu_{v_a} + \theta_1\kappa_{c1}\mu_d\mu_{v_a} \\ & + \theta_1\kappa_{c2}\mu_d\mu_{v_a} + \theta_1\mu_d^2\mu_{v_a} + \theta_1\kappa_{c1}\kappa_{c2}\mu_{v_b} + \theta_1\kappa_{c1}\mu_d\mu_{v_b} + \theta_1\kappa_{c2}\mu_d\mu_{v_b} + \theta_1\mu_d^2\mu_{v_b} \\ & - \frac{\kappa_{c2}\lambda_{vo1}\mu_d\mu_{v_b}}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \frac{\theta_1\kappa_{c2}\lambda_{vo1}\mu_d\mu_{v_b}}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} - \frac{2\lambda_{vo1}\mu_d^2\mu_{v_b}}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} + \frac{2\theta_1\lambda_{vo1}\mu_d^2\mu_{v_b}}{N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d} \\ & + \theta_1\kappa_{c1}\mu_{v_a}\mu_{v_b} + \theta_1\kappa_{c2}\mu_{v_a}\mu_{v_b} + 2\theta_1\mu_d\mu_{v_a}\mu_{v_b} + \frac{1}{(N_{vo1}\beta_{ac}\theta_1 + N_{vb1}\beta_{bc}\theta_2 + \mu_d)^2}N_{vb1}\beta_{bc}\mu_d(N_{vo1}\beta_{ac}\theta_1 \\ & (-\theta_1\lambda_{vb1}(\kappa_{c1} + \mu_d + \mu_{v_a}) + \theta_2((-1+\theta_1)\kappa_{c2}\lambda_{vo1} - \lambda_{vo1}(\mu_d + \mu_{v_a}) + \theta_1(\lambda_{vb1}(\kappa_{c1} + \mu_d + \mu_{v_a}) + \lambda_{vo1}(\mu_d + \mu_{v_b})))) \\ & + N_{vb1}\beta_{bc}\theta_2(-\theta_1\lambda_{vb1}(\kappa_{c1} + \mu_d + \mu_{v_a}) + \theta_2((-1+\theta_1)\kappa_{c2}\lambda_{vo1} - \lambda_{vo1}(\mu_d + \mu_{vb1}) + \theta_1(\lambda_{vb1}(\kappa_{c1} + \mu_d + \mu_{v_a}) \\ & + \lambda_{vo1}(\mu_d + \mu_{v_b})))) + \mu_d(-\lambda_{vb1}(-\lambda_{vo1} + \theta_1(\kappa_{c1} + \lambda_{vo1} + \mu_d + \mu_{v_a})) + \theta_2((-1+\theta_1)\kappa_{c2}\lambda_{vo1} - \lambda_{vo1}(\lambda_{vb1} + \mu_d + \mu_{v_b}) + \\ & \theta_1(\kappa_{c1}\lambda_{vb1} + \lambda_{vb1}(\mu_d + \mu_{v_b}) + \lambda_{vo1}(\lambda_{vb1} + \mu_d + \mu_{v_b}))))) \end{aligned} \quad (12d)$$

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R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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$$D_3=\frac{1}{(N_{va1}\beta_{ac}\theta_1+N_{vb1}\beta_{bc}\theta_2+\mu_d)^2}(N_{va1}^3\beta_{ac}^3\theta_1^3(\kappa_{c1}+\mu_d)(\kappa_{c2}+\mu_d)\mu_{va1}\mu_{v_b}$$
$$+(N_{vb1}\beta_{bc}\theta_2+\mu_d)(\kappa_{c1}+\mu_d)\mu_{v_a}(N_{vb1}\beta_{bc}(-1+\theta_2)\lambda_{vb1}\mu_d^2+(N_{vb1}\beta_{bc}\theta_2+\mu_d)^2(\kappa_{c2}+\mu_d)\mu_{v_b})$$
$$+N_{va1}^2\beta_{ac}^2\theta_1(N_{vb1}\beta_{bc}\theta_1(-1+\theta_2)\lambda_{vb1}\mu_d(\kappa_{c1}+\mu_d)\mu_{v_a}+(N_{vb1}\beta_{bc}\theta_2+\mu_d)(\kappa_{c2}+\mu_d) \quad (12e)$$
$$((-1+\theta_1)\lambda_{va1}\mu_d+3\theta_1(\kappa_{c1}+\mu_d)\mu_{v_a})\mu_{v_b})+N_{va1}\beta_{ac}(\mu_d^2(\kappa_{c1}+\mu_d)((-1+\theta_1)\lambda_{va1}\mu_d$$
$$+3\theta_1(\kappa_{c1}+\mu_d)\mu_{v_a})\mu_{v_b})+N_{vb1}^2\beta_{bc}^2\theta_2(\theta_1(-1+\theta_2)\lambda_{vb1}\mu_d(\kappa_{c1}+\mu_d)\mu_{v_a}+\theta_2(\kappa_{c2}+\mu_d)((-1+\theta_1)\lambda_{va1}\mu_d+3\theta_1(\kappa_{c1}+\mu_d)\mu_{v_a})\mu_{v_b})$$
$$+N_{vb1}\beta_{bc}\mu_d((-1+\theta_2)\lambda_{vb1}\mu_d+2\theta_1(\kappa_{c1}+\mu_d)\mu_{v_a})+2\theta_2(\kappa_{c2}+\mu_d)((-1+\theta_1)\lambda_{va1}\mu_d+3\theta_1(\kappa_{c1}+\mu_d)\mu_{v_a})\mu_{v_b})))$$

$$G_1=N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\kappa_{a1}+\kappa_{a2}+3\mu_d+\mu_{v_a}+\mu_{v_b} \quad (12f)$$

$$G_2=\kappa_{a1}\kappa_{a2}+2\kappa_{a1}\mu_d+2\kappa_{a2}\mu_d+3\mu_d^2+\kappa_{a1}\mu_{v_a}+\kappa_{a2}\mu_{v_a}+3\mu_d\mu_{v_a}+$$
$$(\kappa_{a1}+\kappa_{a2}+3\mu_d+\mu_{v_a})\mu_{v_b}+N_{va2}\beta_{aa}(-(\lambda_{va2}\mu_d/N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4\mu_d) \quad (12g)$$
$$+\theta_3(\kappa_{a1}+\kappa_{a2}+2\mu_d+(\lambda_{va2}\mu_d/N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4\mu_d)+\mu_{v_a}+\mu_{v_b}))+N_{vb2}\beta_{ba}$$
$$(-(\lambda_{vb2}\mu_d/N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4\mu_d)+\theta_4(\kappa_{a1}+\kappa_{a2}+2\mu_d+(\lambda_{vb2}\mu_d/N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4\mu_d)\mu_{v_a}+\mu_{v_b}))$$

$$G_3=\frac{1}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}(N_{va2}^2\beta_{aa}^2\theta_3^2(\mu_d^2+2\mu_d\mu_{v_a}+2\mu_d\mu_{v_b}$$
$$+\mu_{va2}\mu_{v_b}+\kappa_{a2}(\mu_d+\mu_{v_a}+\mu_{v_b})+\kappa_{a1}(\kappa_{a2}+\mu_d+\mu_{v_a}+\mu_{v_b}))+N_{vb2}^2\beta_{ba}^2\theta_4^2(\mu_d^2+2\mu_d\mu_{v_a}$$
$$+2\mu_d\mu_{v_b}+\mu_{v_a}\mu_{v_b}+\kappa_{a2}(\mu_d+\mu_{v_a}+\mu_{v_b})+\kappa_{a1}(\kappa_{a2}+\mu_d+\mu_{v_a}+\mu_{v_b}))+\mu_d(\kappa_{a2}(\mu_d^2+\mu_{v_a}\mu_{v_b}$$
$$+2\mu_d(\mu_{v_a}+\mu_{v_b}))+\mu_d(\mu_d^2+3\mu_{v_a}\mu_{v_b}+3\mu_d(\mu_{v_a}+\mu_{v_b}))+\kappa_{a1}(\mu_d^2+\mu_{v_a}\mu_{v_b} \quad (12h)$$
$$+2\mu_d(\mu_{v_a}+\mu_{v_b})+\kappa_{a2}(\mu_d+\mu_{v_a}+\mu_{v_b})))+N_{vb2}\beta_{ba}(-\lambda_{vb2}\mu_d(\kappa_{a1}+2\mu_d+\mu_{v_a})$$
$$+\theta_4(\mu_d(2\mu_d(\kappa_{a2}+\lambda_{vb2}+\mu_d)+(3\kappa_{a2}+\lambda_{vb2}+5\mu_d)\mu_{v_a})+(\kappa_{a2}(3\mu_d+\mu_{v_a})+\mu_d(5\mu_d+4\mu_{v_a}))\mu_{v_b}$$
$$+\kappa_{a2}(2\mu_d+\mu_{v_a}+\mu_{v_b})))+N_{va2}\beta_{aa}(-\lambda_{va2}\mu_d(\kappa_{a2}+2\mu_d+\mu_{v_b})+\theta_3(\kappa_{a2}\mu_d(\lambda_{va2}$$
$$+2\mu_d+3\mu_{v_a})+\kappa_{a2}(3\mu_d+\mu_{v_a})\mu_{vb2}+\mu_d(2\mu_d(\lambda_{va2}+\mu_d)+5\mu_d\mu_{v_a}+(\lambda_{va2}+5\mu_d+4\mu_{v_a})\mu_{v_b})$$
$$+\kappa_{a1}(2\mu_d^2+\mu_{v_a}\mu_{v_b}+3\mu_d(\mu_{v_a}+\mu_{v_b})+\kappa_{a2}(2\mu_d+\mu_{v_a}+\mu_{v_b})))+N_{vb2}\beta_{ba}(-\theta_4\lambda_{va2}\mu_d$$
$$+\theta_3(-\lambda_{vb2}\mu_d+\theta_4(\mu_d(\lambda_{va2}+\lambda_{vb2}+2\mu_d+4\mu_{v_a})+2(2\mu_d+\mu_{v_b})\mu_{v_a}+2\kappa_{a2}(\mu_d+\mu_{v_a}+\mu_{v_b})+2\kappa_{a1}(\kappa_{a2}+\mu_d+\mu_{va2}+\mu_{v_b})))))$$

$$G_4=\kappa_{a1}\kappa_{a2}\mu_d\mu_{v_a}+\kappa_{a1}\mu_d^2\mu_{v_a}+\kappa_{a2}\mu_d^2\mu_{v_a}+\mu_d^3\mu_{v_a}+\kappa_{a1}\kappa_{a2}\mu_d\mu_{v_b}$$
$$+\kappa_{a1}\mu_d^2\mu_{v_b}+\kappa_{a2}\mu_d^2\mu_{v_b}+\mu_d^3\mu_{v_b}+\kappa_{a1}\kappa_{a2}\mu_{v_a}\mu_{v_b}+2\kappa_{a1}\mu_d\mu_{v_a}\mu_{v_b}$$
$$+2\kappa_{a2}\mu_d\mu_{v_a}\mu_{v_b}+3\mu_d^2\mu_{v_a}\mu_{v_b}+\frac{1}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}N_{vb2}\beta_{ba}((-1+\theta_4)$$
$$\lambda_{vb2}\mu_d^2(\mu_d+2\mu_{v_a})+\theta_4(N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d)(\mu_d(\kappa_{a2}+\mu_d)\mu_{v_a}+(\mu_d(\kappa_{a2}+\mu_d)$$
$$+(\kappa_{a2}+2\mu_d)\mu_{v_a})\mu_{v_b})+\kappa_{a1}((-1+\theta_4)\lambda_{vb2}\mu_d(\mu_d+2\mu_{v_a})+\theta_4(N_{va2}\beta_{aa}\theta_3$$
$$+N_{vb2}\beta_{ba}\theta_4+\mu_d)((\kappa_{a2}+\mu_d)\mu_{v_a}+(\kappa_{a2}+\mu_d+\mu_{v_a})\mu_{v_b})))+N_{va2}\beta_{aa}$$
$$(-\frac{\kappa_{a2}\lambda_{va2}\mu_d^2}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}+\frac{\theta_3\kappa_{a2}\lambda_{va2}\mu_d^2}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}-\frac{\lambda_{va2}\mu_d^3}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}+\frac{\theta_3\lambda_{va2}\mu_d^3}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}$$
$$+\theta_3\kappa_{a1}\kappa_{a2}\mu_{v_a}+\theta_3\kappa_{a1}\mu_d\mu_{v_a}+\theta_3\kappa_{a2}\mu_d\mu_{v_a}+\theta_3\mu_d^2\mu_{v_a}+\theta_3\kappa_{a1}\kappa_{a2}\mu_{v_b}\theta_2\kappa_{a1}\mu_d\mu_{vb}+\theta_3\kappa_{a2}\mu_d\mu_{vb}+\theta_3\mu_d^2\mu_{v_b}$$
$$-\frac{\kappa_{a1}\lambda_{va2}\mu_d\mu_{v_b}}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}+\frac{\theta_3\kappa_{a1}\lambda_{va2}\mu_d\mu_{v_b}}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}-\frac{2\lambda_{va2}\mu_d^2\mu_{v_b}}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}+\frac{2\theta_3\lambda_{va2}\mu_d^2\mu_{v_b}}{N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d}$$
$$+\theta_3\kappa_{a1}\mu_{v_a}\mu_{v_b}+\theta_3\kappa_{a2}\mu_{v_a}\mu_{v_b}+2\theta_3\mu_d\mu_{v_a}\mu_{v_b}+\frac{1}{(N_{va2}\beta_{aa}\theta_3+N_{vb2}\beta_{ba}\theta_4+\mu_d)^2}$$
$$N_{vb2}\beta_{ba}\mu_d(N_{va2}\beta_{aa}\theta_3(-\theta_3\lambda_{va2}(\kappa_{a1}+\mu_d+\mu_{v_a})+\theta_4((-1+\theta_3)\kappa_{a2}\lambda_{va2}-\lambda_{va2}(\mu_d+\mu_{v_b})$$
$$+\theta_3(\lambda_{vb2}(\kappa_{a1}+\mu_d+\mu_{v_a})+\lambda_{va2}(\mu_d+\mu_{v_b}))))+N_{vb2}\beta_{ba}\theta_4(-\theta_3\lambda_{vb1}(\kappa_{a1}+\mu_d+\mu_{v_a})+\theta_4((-1+\theta_3)\kappa_{a2}\lambda_{va2}$$
$$-\lambda_{va2}(\mu_d+\mu_{v_b})+\theta_3(\lambda_{vb2}(\kappa_{a1}+\mu_d+\mu_{v_a})+\lambda_{va2}(\mu_d+\mu_{v_b}))))+\mu_d(-\lambda_{vb2}(-\lambda_{va2}+\theta_3(\kappa_{a1}+\lambda_{va2} \quad (12i)$$
$$+\mu_d+\mu_{v_a}))+\theta_4((-1+\theta_3)\kappa_{a2}\lambda_{va2}-\lambda_{va2}(\lambda_{vb2}+\mu_d+\mu_{v_b})+\theta_3(\kappa_{a1}\lambda_{vb2}+\lambda_{vb2}(\mu_d+\mu_{v_a})+\lambda_{va2}(\lambda_{vb2}+\mu_d+\mu_{v_b}))))))$$

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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$$G_5 = \frac{1}{(N_{va2}\,\beta_{aa}\theta_3 + N_{vb2}\,\beta_{ba}\,\theta_4 + \mu_d)^2}(\lambda^3_{vb2}\,\beta^2_{aa}\theta^2_3(\kappa_{a1}+\mu_d)(\kappa_{a2}+\mu_d)$$
$$\mu_{v_a}\mu_{v_b} + (N_{vb2}\,\beta_{ba}\,\theta_4+\mu_d)(\kappa_{a1}+\mu_d)\,\mu_{v_a}(N_{vb2}\,\beta_{ba}(-1+\theta_4)\,\lambda_{vb2}\mu^2_d + (N_{vb2}\,\beta_{ba}\,\theta_4+\mu_d)^2$$
$$(\kappa_{a2}+\mu_d)\,\mu_{v_b}) + N^2_{va2}\,\beta^2_{aa}\,\theta_3\,(N_{vb2}\,\beta_{ba}\,\theta_3(-1+\theta_4)\lambda_{vb2}\,\mu_d(\kappa_{a1}+\mu_d)\mu_{v_a} + (N_{vb2}\,\beta_{ba}\,\theta_4+\mu_d)$$
$$(\kappa_{a2}+\mu_d)((-1+\theta_3)\,\lambda_{va2}\,\mu_d + 3\,\theta_3(\kappa_{a1}+\mu_d)\mu_{v_a})\,\mu_{v_b}) + N_{va2}\,\beta_{aa}(\mu^2_d(\kappa_{a2}+\mu_d)((-1+\theta_3)\lambda_{va2}\,\mu_d$$
$$+ 3\,\theta_3(\kappa_{a1}+\mu_d)\,\mu_{v_a})\,\mu_{v_b}) + N^2_{vb2}\beta^2_{ba}\,\theta_4(\theta_3(-1+\theta_4)\,\lambda_{vb2}\,\mu_d\,(\kappa_{a1}+\mu_d)\,\mu_{v_a} + \theta_4(\kappa_{a2}+\mu_d)$$
$$((-1+\theta_3)\,\lambda_{va2}\,\mu_d + 3\,\theta_3(\kappa_{a1}+\mu_d)\,\mu_{v_a})\mu_{v_b}) + N_{vb2}\,\beta_{ba}\mu_d((-1+\theta_4)\,\lambda_{vb2}\,\mu_d + 2\,\theta_3(\kappa_{a1}+\mu_d)\mu_{v_a})$$
$$+ 2\theta_4(\kappa_{a2}+\mu_d)\,((-1+\theta_3)\,\lambda_{va2}\mu_d + 3\theta_3\,(\kappa_{a1}+\mu_d)\,\mu_{v_a})\,\mu_{v_b})) \qquad (12\,j)$$

Where:

$$\theta_1 = \frac{(N_{rc}\,N_{va1}\,\beta_{ac}\,\lambda_{va1}\,\lambda_{vb1}\,\mu_d - \lambda_{vb1}(N_{vb1}\,\beta_{bc}+\mu_d)}{(\kappa_{c1}+\mu_d)\,\mu_{v_a} + N_{va1}\,\beta_{ac}\,\lambda_{va1}(\kappa_{c2}+\mu_d)\,\mu_{v_b})} \qquad (13a)$$
$$(N_{va1}\,\beta_{ac}(N_{rc}\,\lambda_{va1}\,\lambda_{vb1}\,\mu_d + \lambda_{vb1}$$
$$(\kappa_{c1}+\mu_d)\,\mu_{v_a} + \lambda_{va1}(\kappa_{c2}+\mu_d)\,\mu_{v_b}))$$

$$\theta_2 = \frac{N_{rc}\,N_{vb1}\,\beta_{bc}\,\lambda_{vb1}\,\mu_d - (N_{va1}\,\beta_{ac}\,\theta_1+\mu_d)(\kappa_{c2}+\mu_d)\,\mu_{v_b}}{N_{vb1}\,\beta_{bc}(N_{rc}\,\lambda_{vb1}\,\mu_d + (\kappa_{c2}+\mu_d)\,\mu_{v_b})} \qquad (13b)$$

$$\theta_3 = \frac{(N_{ra}\,N_{va2}\,\beta_{aa}\,\lambda_{va2}\,\lambda_{vb2}\,\mu_d - \lambda_{vb2}(N_{vb2}\,\beta_{ba}+\mu_d)}{(\kappa_{a1}+\mu_d)\,\mu_{v_a} + N_{va2}\,\beta_{aa}\,\lambda_{va2}(\kappa_{a2}+\mu_d)\,\mu_{v_b})} \qquad (13c)$$
$$(N_{va2}\,\beta_{aa}(N_{ra}\,\lambda_{va2}\,\lambda_{vb2}\,\mu_d$$
$$+ \lambda_{vb2}(\kappa_{a1}+\mu_d)\,\mu_{v_a} + \lambda_{va2}(\kappa_{a2}+\mu_d)\,\mu_{v_b}))$$

$$\theta_4 = \frac{N_{ra}\,N_{vb2}\,\beta_{ba}\,\lambda_{vb2}\,\mu_d - (N_{va2}\,\beta_{aa}\,\theta_3+\mu_d)(\kappa_{a2}+\mu_d)\,\mu_{v_b}}{N_{vb2}\,\beta_{ba}(N_{ra}\,\lambda_{vb2}\,\mu_d + (\kappa_{a2}+\mu_d)\,\mu_{v_b})} \qquad (13d)$$

From the characteristic Equation (11a)-(11b), the eigenvalues are found by solving $(\eta^5 + D_1\eta^4 + D_2\eta^3 + D_3\eta^2 + D_4\eta + D_5) = 0$ in children and in adult $(\eta^5 + G_1\eta^4 + G_2\eta^3 + G_3\eta^2 + G_4\eta + G_5) = 0$, when $T_1 = D_1$ and G_1 for children and adult, $T_2 = D_2$ *and* G_2, for children and adult, $T_3 = D_3$ and G_3 for children and adult $T_4 = D_4$ and G_4 for children and adult, $T_5 = D_5$ and G_5 for children and adult. The five eigenvalues have negative real parts if they satisfy Routh-Hurwitz criteria (14b)-(14e) (Edelstein-Keshet, 1988). each equilibrium state is locally asymptotically stable, when it satisfies the following conditions:

$$\det H_1 = T_1 > 0 \qquad (14a)$$

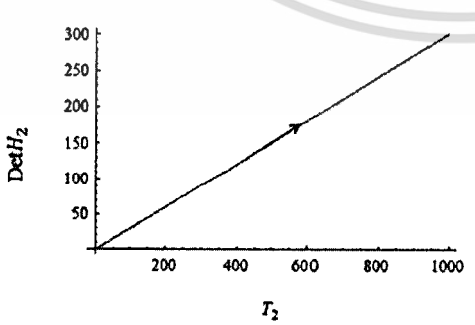
$$\det H_2 = T_1T_2 - T_3 > 0 \qquad (14b)$$

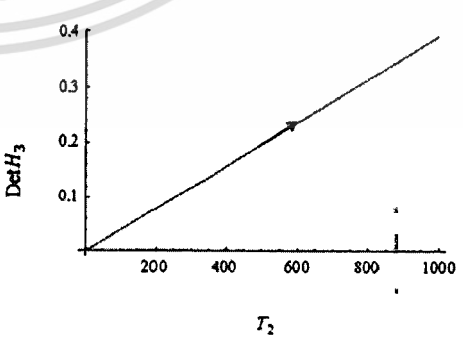
$$\det H_3 = T_1T_2T_3 - T_3^2 - T_1^2T_4 > 0 \qquad (14c)$$

$$\det H_4 = T_1T_2T_3T_4 - T_3^2T_4 - T_1^2T_4^2 > 0 \qquad (14d)$$

$$\det H_5 = T_1T_2T_3T_4T_5 - T_3^2T_4^2T_5 - T_1^2T_5^2 + T_1T_4T_5^2 - T_2^2T_5^3 + T_2T_3T_5^2 + 2T_1T_4T_5^2 - T_5^3 > 0 \qquad (14e)$$

We check the stability of endemic equilibrium state by using the Routh-Hurwitz conditions (14a)-(14e), the results are given in Fig. 3.





R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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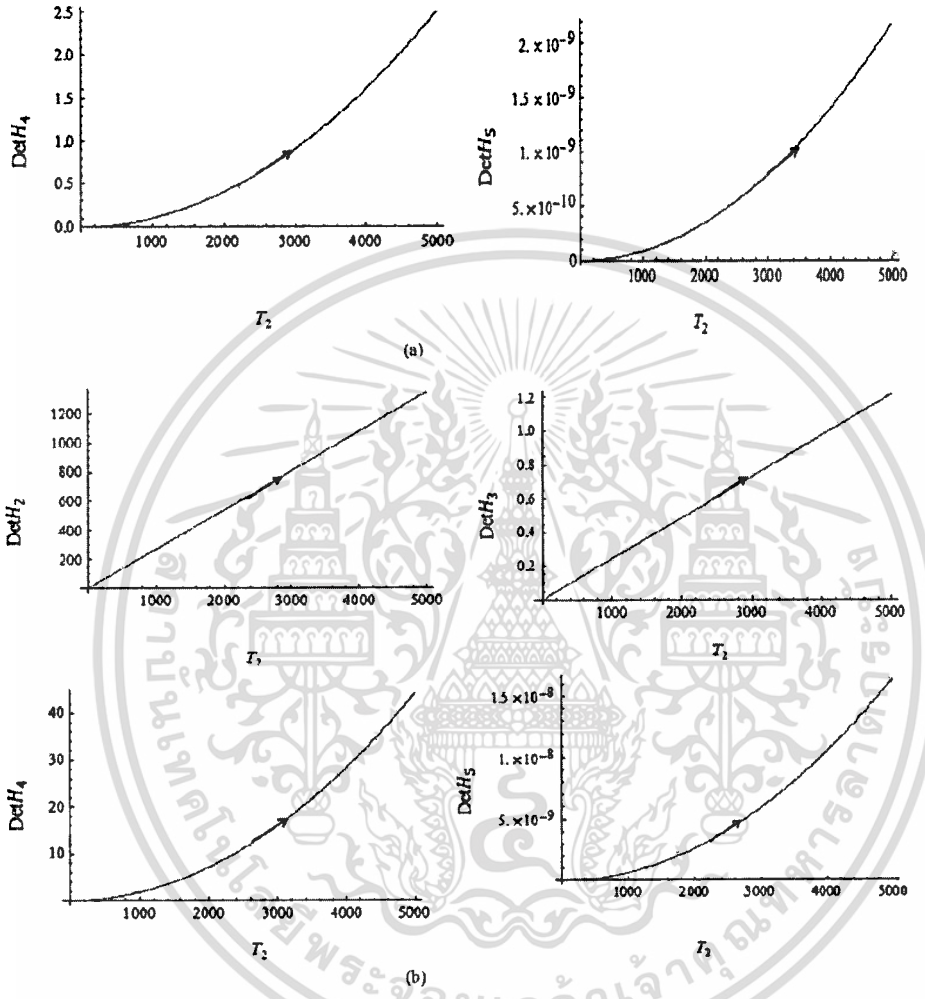


Fig. 3. The parameter spaces for endemic disease equilibrium state. which satisfies the Routh-Hurwitz conditions, plotted onto $(\kappa_{c1}, \det H_2)$, $(\kappa_{c1}, \det H_3)$, $(\kappa_{c1}, \det H_4)$, $(\kappa_{c1}, \det H_5)$, $(\kappa_{a1}, \det H_2)$, $(\kappa_{a1}, \det H_3)$, $(\kappa_{a1}, \det H_4)$ and $(\kappa_{a1}, \det H_5)$, respectively. The values of parameter are follows: (a) $\kappa_{c1}=1/(17/2)$, $\kappa_{c2}=1/(19/2)$, $\mu_d=1/(365*74.6)$ day^{-1}, $N_h=6000$, $N_{va1}=5000$, $N_{vb1}=2500$, $\beta_{ac}=0.2$, $\beta_{bc}=0.0714$, $\lambda_{va1}=0.00000000576$, $\lambda_{vb1}=0.00000435$, $\alpha_a=0.08$, $\alpha_b=0.047$ and $N_t=100{,}000$, (b) $\kappa_{a1}=1/(19/2)$, $\kappa_{a2}=1/(21/2)$, $\mu_d=1/(365*746)$ day^{-1}, $N_{ha}=4000$, $N_{va2}=7000$, $N_{vb2}=4300$, $\beta_{au}=0.1667$, $\beta_{ba}=0.125$, $\lambda_{va2}=0.00000000176$, $\lambda_{vb2}=0.000000835$, $\alpha_a=0.07$, $\alpha_b=0.027$ and $N_t=100000$. From the above figures, the Routh-Hurwitz conditions are satisfies for $S_0>1$

Numerical Results

We consider the numerical solutions for dengue virus transmission. The main effect of introducing an age structure into the model is to change the definition of the basic reproductive rate. The parameters in this study are determined by the real life observations. The values of the parameters are as follows: $\mu_d=1/(365*74.6)$ day^{-1}, corresponding to life expectancy of 74.6 years for human: $\kappa_{c1}=1/(8.5)$ and $\kappa_{c2}=1/(9.5)$ corresponding to the 8.5 days and 9.5 days of recovering due to biting of *Aedes aegypti* and *Aedes albopictus*, respectively. The death rate of mosquitoes are 1/28 per day and

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6). 426.443
DOI: 10.3844/ajassp.2015.426.443

1/35 per day satisfies to the life time of 28 days for *Aedes aegypti* and the life time of 35 days for *Aedes albopictus*, respectively $\kappa_{a1} = 1/(9.5)$ and $\kappa_{a1} = 1/(10.5)$ corresponding to the 9.5 days and 10.5 days of recovering of adult human population due to biting of *Aedes aegypti* and *Aedes albopictus*, respectively. The other parameters are arbitrary chosen. Numerical solutions of (4a)-(4j) are shown in Fig. 4-9.

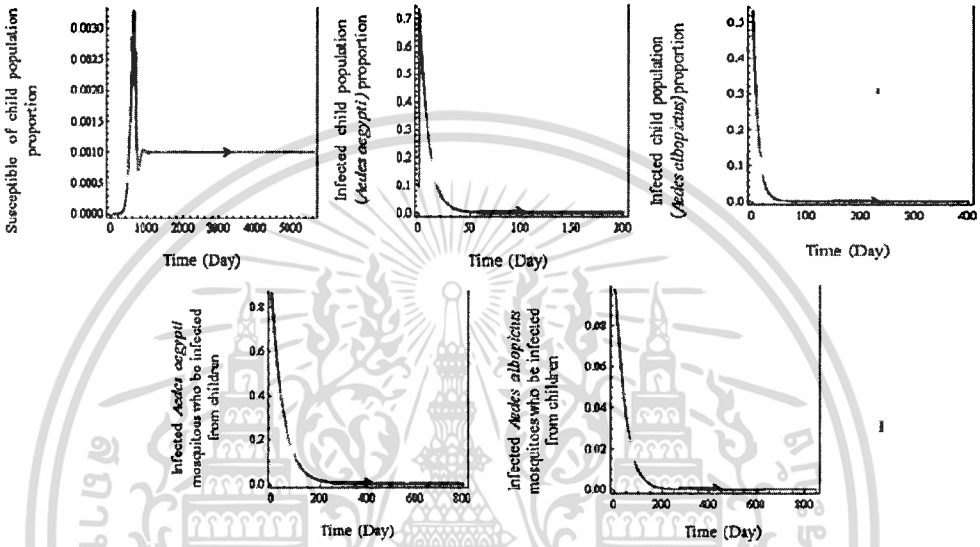
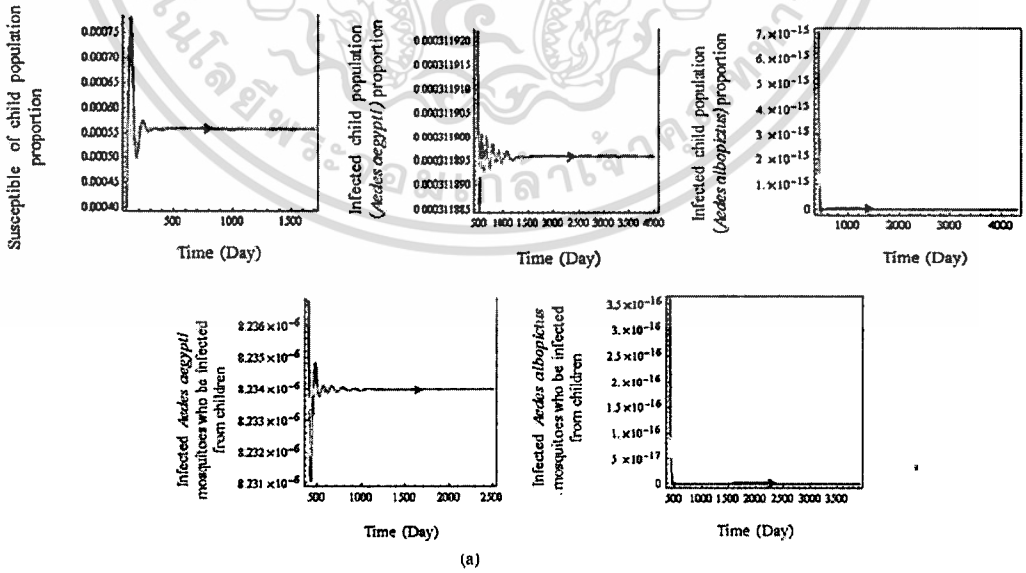
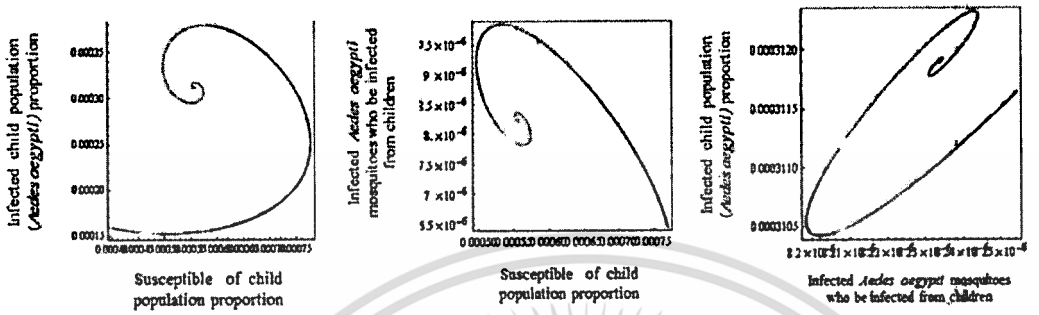


Fig. 4. Time series solutions of $S_c, I_{c1}, I_{c2}, I_{wa1}$ and I_{vb1} respectively. For $S_0 < 1$ and $S_{0c} = 0.000023944$ with parameters are following: $\mu_{wa1} = 1/49$, $\mu_{vb1} = 1/39$, $N_w = 71000$, $N_{wa1} = 5800$, $N_{vb1} = 10000$, $\beta_{ac} = 0.0239$, $\beta_{bc} = 0.0333$, $\lambda_{wa1} = 0.00000000000347$, $\lambda_{vb1} = 0.0000000675$, $\alpha_a = 0.07$, $\alpha_b = 0.027$ and $N_t = 100,000$. The proportions of populations $(S_c', I_{c1}', I_{c2}', I_{wa1}', I_{vb1}')$ approach to the disease free equilibrium state (1.0,0,0,0)



(a)

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
DOI: 10.3844/ajassp.2015.426.443



(b)

Fig. 5. (a) Time series solutions of $S_c, I_{c1}, I_{c2}, I_{vol}, I_{vb1}$. Values of parameters in the model are following: $\mu_{vol}=1/7$, $\mu_{vb1}=1/14$, $N_c=50000$, $N_{vol}=32000$, $N_{vb1}=17000$, $\beta_{ca}=0.2$, $\beta_{bc}=0.125$, $\lambda_{vol}=0.0000000058$, $\lambda_{vb1}=0.00000000465$, $\alpha_a=0.026$, $\alpha_b=0.009$ and $N_t=100,000$, when $S_{0c}=174.473$. (b) Numerical solutions projected onto (S_c, I_{c1}), (S_c, I_{vol}), (I_{vol}, I_{c1}). The solutions oscillate to the endemic equilibrium state $(S_c^*, I_{c1}^*, I_{c2}^*, I_{vol}^*, I_{vb1}^*)$ where $S_c^*=0.000556913$, $I_{c1}^*=0.0003$, $I_{c2}^*=1.6622\times10^{-14}$, $I_{vol}^*=8.23484\times10^{-6}$ and $I_{vb1}^*=7.38289\times10^{-17}$, respectively

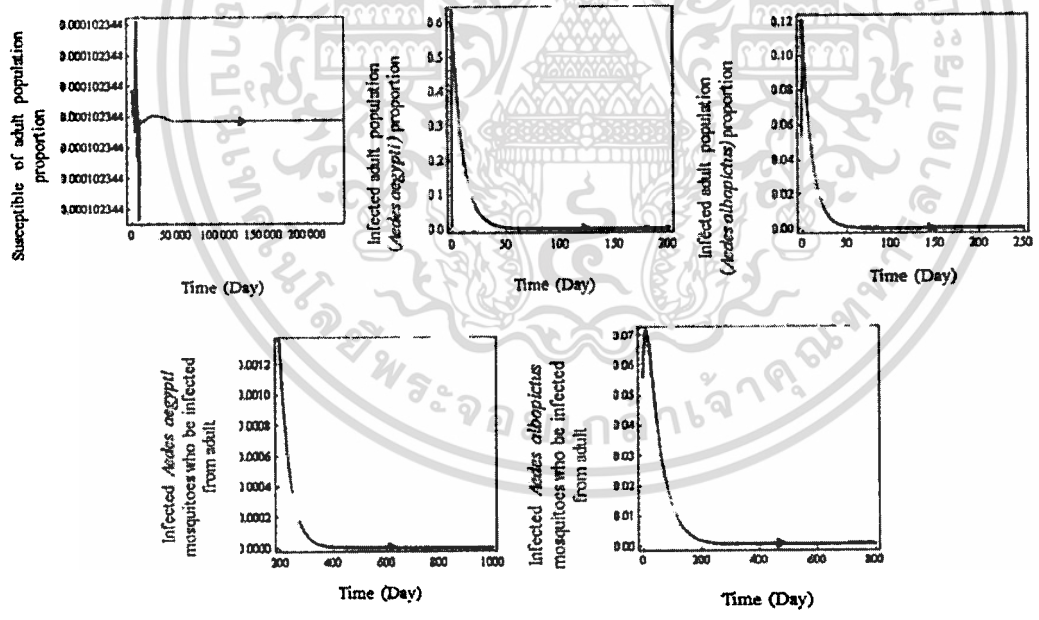


Fig. 6. Time series solution of $S_a, I_{a1}, I_{a2}, I_{va2}$ and I_{vb2} respectively. For $S_0<1$ and $S_{0a}=0.0307919$ with parameters are following: $\mu_{va2}=1/36$, $\mu_{vb2}=1/46$, $N_{ta}=61000$, $N_{va2}=4800$, $N_{vb2}=10000$, $\beta_{aa}=0.03225$, $\beta_{ba}=0.02941$, $\lambda_{va2}=0.000000000076$, $\lambda_{vb2}=0.0000000000664$, $\alpha_a=0.04$, $\alpha_b=0.06$ and $N_t=100,000$. The proportions of populations $(S_a, I_{a1}, I_{a2}, I_{va2}, I_{vb2})$ approach to the disease free equilibrium state (1,0,0,0,0)

รองศาสตราจารย์ ดร.พันธนี พงศ์สัมพันธ์

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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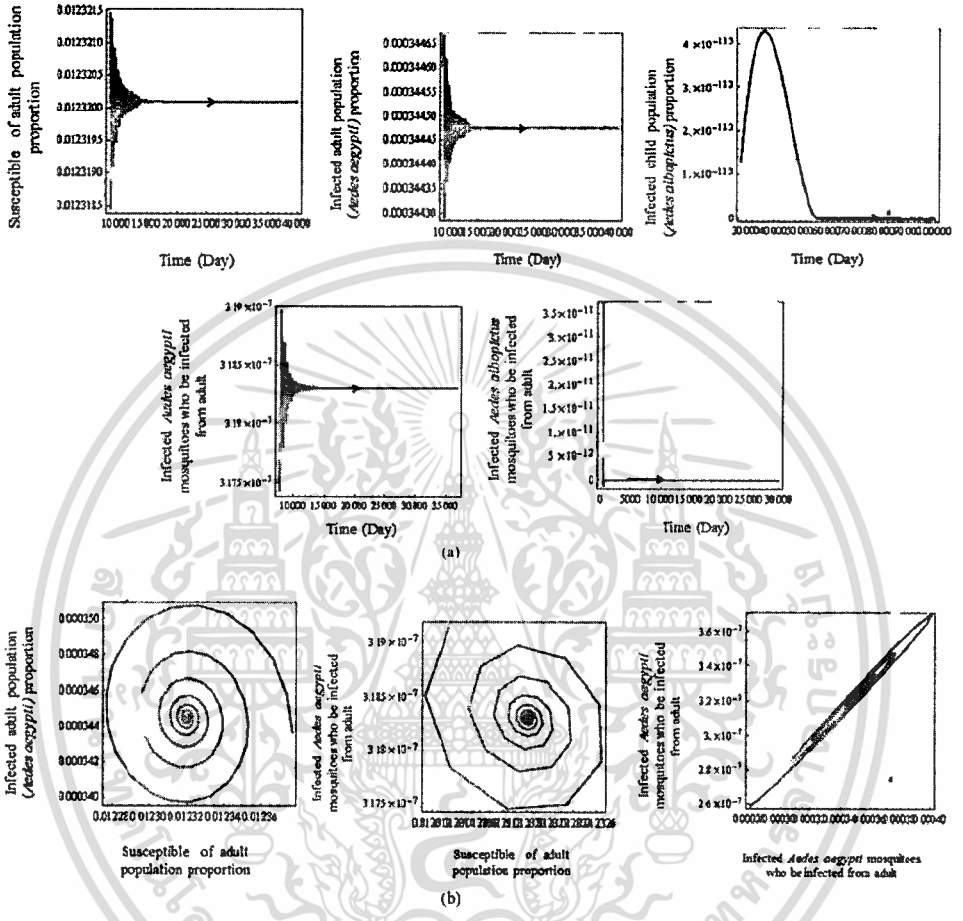

Fig. 7. (a) Time series solutions of $S_a, I_{a1}, I_{a2}, I_{wa2}, I_{vb2}$. Values of parameters in the model are following: $\mu_{wa2}=1/7$, $\mu_{vb2}=1/13$, $N_{ta}=30000$, $N_{wa2}=37000$, $N_{vb2}=19000$, $\beta_{aa}=0.25$, $\beta_{ba}=0.1428$, $\lambda_{wa2}=0.00000000044$, $\lambda_{vb2}=0.000000000335$, $\alpha_a=0.02$, $\alpha_b=0.07$ and $N_t=100,000$, where $S_{0a}=21.7785$ in adult. (b) Numerical solutions projected onto (S_a^*, I_{a1}^*), (S_a^*, I_{wa2}^*), (I_{wa2}^*, I_{a1}^*). The solutions oscillate to the endemic equilibrium state $(S_a^*, I_{a1}^*, I_{a2}^*, I_{wa2}^*, I_{vb2}^*)$ where $S_c^*=0.0123201$, $I_{a1}^*=0.000344474$, $I_{a2}^*=6.9961\times10^{-14}$, $I_{wa2}^*=3.18294\times10^{-7}$ and $I_{vb1}^*=1.40069\times10^{-16}$, respectively

Case A.1, in children, we consider the locally asymptotically stable of disease free equilibrium state, when ε 0 as shown in Fig. 4.

Case A.2, in children, we consider the locally asymptotically stable of endemic equilibrium state, when ε = 0 as shown in Fig. 5.

Case B.1, in adult, we consider the locally asymptotically stable of disease free equilibrium state, when ε = 0 as shown in Fig. 6.

Case B.2, in adult, we consider the locally asymptotically stable of endemic equilibrium state, when ε = 0 as shown in Fig. 7.

Case C, in children, when ε ≠ 0 as shown in Fig. 8.

Case D, in adult, when ε ≠ 0 as shown in Fig. 9.

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
DOI: 10.3844/ajassp.2015.426.443

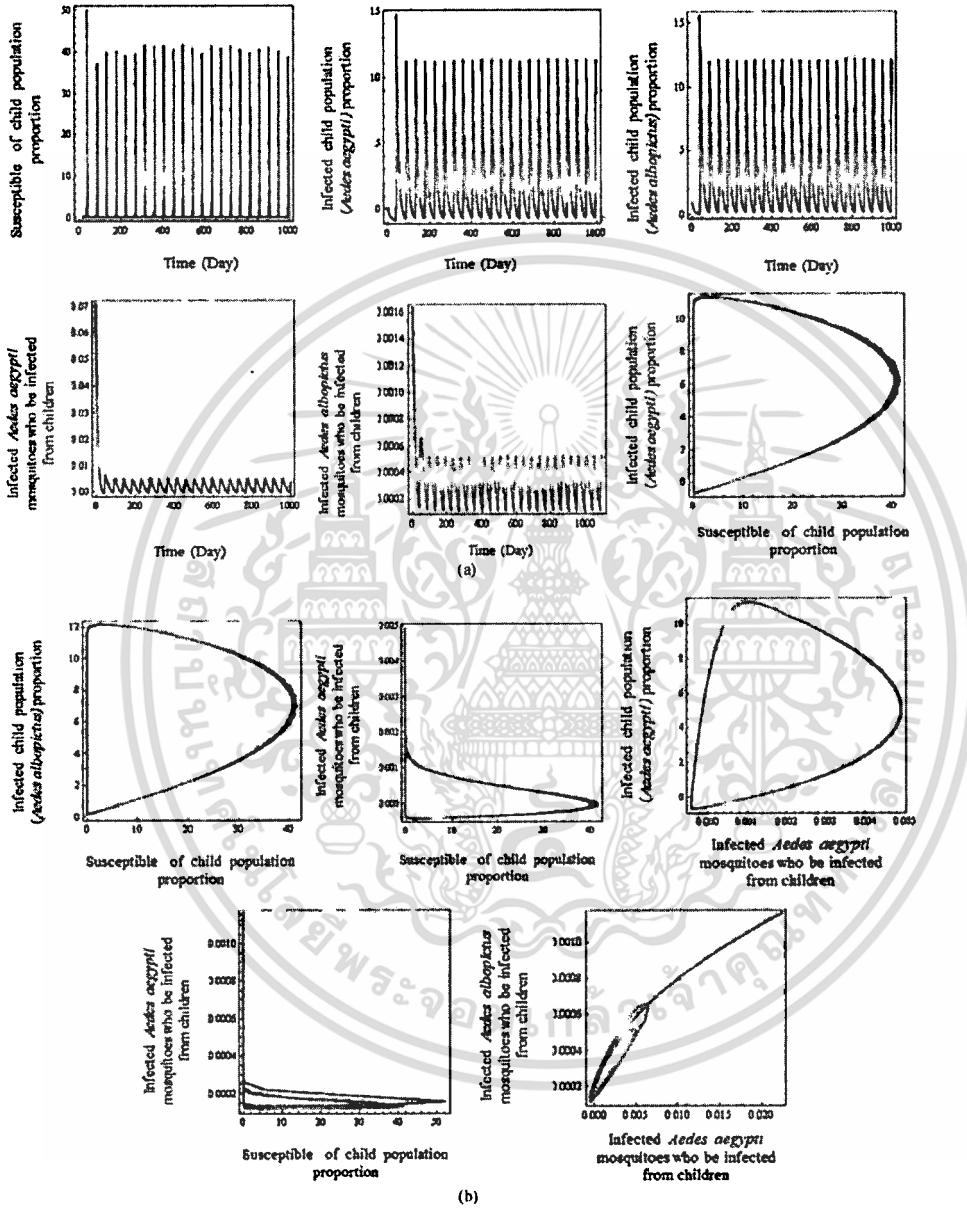

Fig. 8. (a) Time series solutions of $S_c, I_{c1}, I_{c2}, I_{wl}, I_{vbl}$. Values of parameters in the model are following: N_{hc} =50000, N_{wl} =32000, N_{vbl} =17000, β_{ac} =0.2, β_{hc} = 0.125, λ_{wl} = 0.0000000028, λ_{vbl} = 0.000000000165, α_a=0.005, α_h=0.004 and N_t = 100.000 and S_{0c} = 22.8627. (b) Numerical solutions projected onto (S_c', I_{c1}'), (S_c', I_{c2}'), (S_c', I_{wl}'), (S_c', I_{vbl}'), (I_{wl}', I_{c1}'), (I_{wl}', I_{vbl}'). Limit cycles are produced in this case

รองศาสตราจารย์ ดร.พันธนี พงศ์สัมพันธ์

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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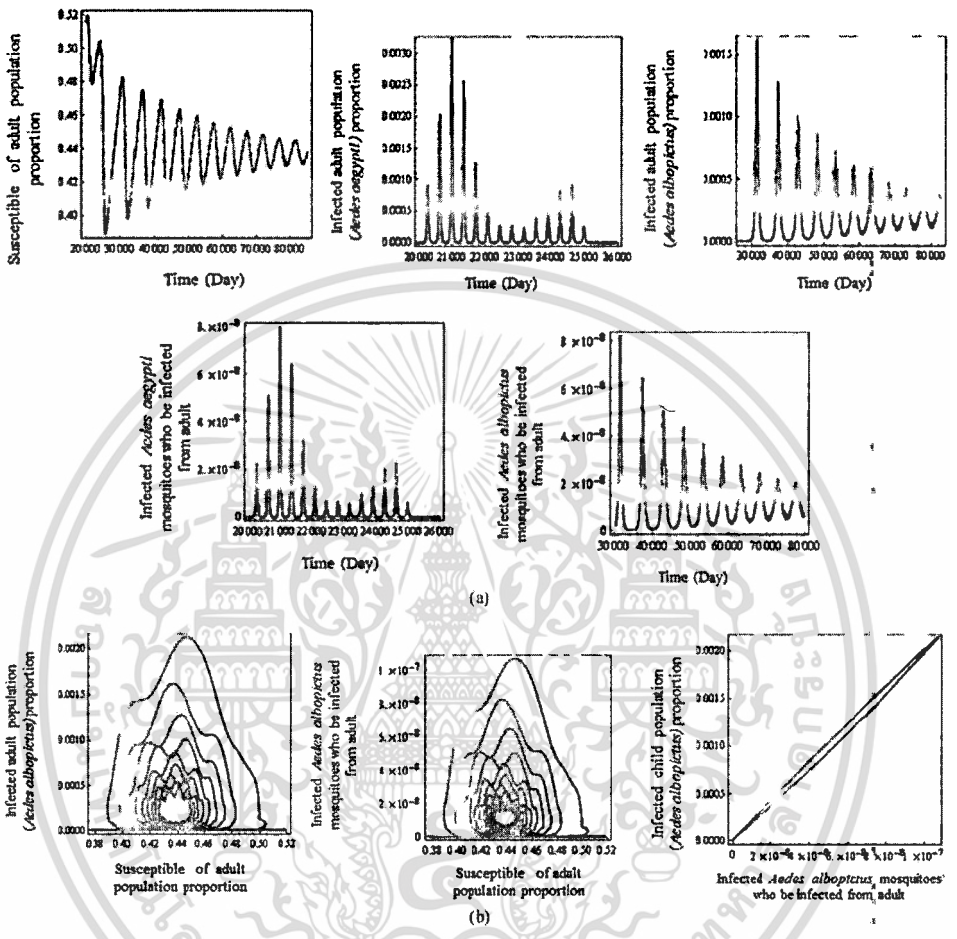

Fig. 9. (a) Time series solutions of $S_a, I_{a1}, I_{a2}, I_{w2}, I_{vb2}$. Values of parameters in the model are following: $N_w = 50000$. $N_{w2} = 34000$. $N_{vb2} = 30000$. $\beta_{ab} = 0.25$, $\beta_{ba} = 0.1428$. $\lambda_{w2} = 0.0000000075$. $\lambda_{vb2} = 0.000000000625$. $\alpha_a = 0.02$. $\alpha_b = 0.07$ and $N_t = 100,000$. when $S_{0a} = 9.26764$. (b) Numerical solutions projected onto (S_a^*, I_{a2}^*). (S_a^*, I_{vb2}^*). (I_{vb2}^*, I_{a2}^*). The solutions oscillate to the endemic equilibrium state $(S_a^*, I_{a1}^*, I_{a2}^*, I_{w2}^*, I_{vb2}^*)$ are limit cycles

Discussion

Several investigations have been conducted using the SIR and SI models. The SIR and SI models which provide suitable for the states of children and adult in two species are used in this study. (*Aedes aegypti* and *Aedes albopictus*).

The basic reproductive number of equations (4a)-(4j) is defined as follows (Chong *et al*., 2013):

$$2N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}\rho_{vb}$$
$$+N_{w1}\beta_{ac}\lambda_{w1}(2(N_{ic}\lambda_{vb1}\mu_d+(\kappa_{c1}+\mu_d)\mu_{v_b})$$

$$S_0 = \max\left\{\frac{(2+\alpha_a\rho_{va})+2N_{ic}\lambda_{vb1}\mu_d(\alpha_a+\rho_{va}))}{(2\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}(2\mu_d+N_{vb1}\beta_{bc}}\right.$$
$$(2+\alpha_b\rho_{vb}))+2N_{w1}\beta_{ac}\lambda_{w1}(\alpha_a(\kappa_{c2}+\mu_d)$$
$$\mu_{v_b}\rho_{va}+N_{ic}\lambda_{vb1}\mu_d(\alpha_a\rho_{va}+(\alpha_a+\rho_{va})\rho_{vb})))$$
$$2N_{vb2}\alpha_b\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}\rho_{vb}$$
$$+N_{w2}\beta_{ac}\lambda_{w2}(2(N_{ic}\lambda_{vb2}\mu_d+(\kappa_{a2}+\mu_d)\mu_{v_b})$$
$$\left.\frac{(2+\alpha_a\rho_{va})+2N_{ic}\lambda_{vb2}\mu_d(\alpha_a+\rho_{va}))}{(2\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}(2\mu_d+N_{vb2}\beta_{ba}(2+\alpha_b\rho_{vb}))}\right\}$$
$$+2N_{w2}\beta_{ac}\lambda_{va2}(\alpha_a(\kappa_{a2}+\mu_d)\mu_{v_b}\rho_{va}$$
$$+N_{ic}\lambda_{vb2}\mu_d(\alpha_a\rho_{va}+(\alpha_a+\rho_{va})\rho_{vb})))$$

รองศาสตราจารย์ ดร.พันธนี พงศ์สัมพันธ์

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6): 426.443
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Table 3. Determination of the values S_0 of infected mosquitoes

I_{va1} value	I_{vb1} value	I_{va2} value	I_{va2} value	S_0 value
		2.3860×10-18	6.44744×10-7	0.00310
2.5687×10-26	0.000065	-	-	0.00732
0	0.00036	-	-	0.06795
-	-	4.9155×10-23	0.0007175	0.68842
-	-	7.3376×10-14	1.07169×10-8	3.61291
8.234×10-6	7.982×10-17	-	-	38.6066
3.16331×10-5	1.118×10-6	-	-	80.3505
-	-	9.933×10-8	2.822×10-17	89.3077

S_0 describes the number of infectious human produced from primary infection of children and adult. Using the initial values and parameter values from data, the obtained result of threshold parameter value S_0 for S_{0c} and S_{0a} can be rewritten in mathematical form as follows:

$$S_{0c} = \frac{\begin{array}{l}2N_{vb1}\alpha_b\beta_{bc}\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}\rho_{vb} \\ +N_{va1}\beta_{ac}\lambda_{va1}(2(N_{tc}\lambda_{vb1}\mu_d+(\kappa_{c2}+\mu_d) \\ \mu_{v_b})(2+\alpha_a\rho_{va})+2N_{tc}\lambda_{vb1}\mu_d(\alpha_a+\rho_{va})) \\ (2\lambda_{vb1}(\kappa_{c1}+\mu_d)\mu_{v_a}(2\mu_d+N_{vb1}\beta_{bc} \\ (2+\alpha_b\rho_{vb}))+2N_{va1}\beta_{ac}\lambda_{va1}(\alpha_a(\kappa_{c2}+\mu_d) \\ \mu_{v_b}\rho_{va}+N_{tc}\lambda_{vb1}\mu_d(\alpha_a\rho_{va}+(\alpha_a+\rho_{va})\rho_{vb})))\end{array}}{}$$ in children

$$S_{0a} = \frac{\begin{array}{l}2N_{vb2}\alpha_b\beta_{ba}\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}\rho_{vb}+ \\ N_{va2}\beta_{aa}\lambda_{va2}(2(N_{ta}\lambda_{vb2}\mu_d+(\kappa_{a2}+\mu_d)\mu_{v_b}) \\ (2+\alpha_a\rho_{va})+2N_{ta}\lambda_{vb2}\mu_d(\alpha_a+\rho_{va})) \\ (2\lambda_{vb2}(\kappa_{a1}+\mu_d)\mu_{v_a}(2\mu_d+N_{vb2}\beta_{ba} \\ (2+\alpha_b\rho_{vb}))+2N_{va2}\beta_{aa}\lambda_{va2}(\alpha_a(\kappa_{a2}+\mu_d) \\ \mu_{v_b}\rho_{va}+N_{ta}\lambda_{vb2}\mu_d(\alpha_a\rho_{va}+(\alpha_a+\rho_{va})\rho_{vb})))\end{array}}{}$$ in adult

The reproductive rate is depend on the number of infected mosquitoes I_{va1}, I_{vb1} in children and I_{va2}, I_{vb2} in adult.

From the above table (Table 3), we will see that if the number of infected mosquitoes is increased, the basic reproductive rate is also increased.

Moreover, we consider the effect of sinusoidal variation (ε), we will see that if ε 0, then the solutions oscillation to the steady state. The limit cycle occurs for $\varepsilon \neq 0$. Thus the limit cycles occurs while there is the seasonal variation of mosquitoes (*Aedes aegypti* and *Aedes albopictus*). It can be seen that the dynamical behavior of the endemic state change while there is the influence of season.

Conclusion

The basic reproductive number of disease is defined by $\tilde{S}_0 = \sqrt{S_0}$. This value is the threshold condition for the existence of the endemic state. When $S_0 \leq 1$, the solutions oscillate to disease free equilibrium state, whereas $S_0 > 1$, the solutions oscillate to the endemic state. The behaviors of the proportion of susceptible, infective human into two classes (a child class and an adult class) and infective vectors of the two species (*Aedes aegypti* and *Aedes albopictus*) are initially positive. If this can be seen as follow; the infective human are introduced into the susceptible is bitten during each period, by the fraction $\frac{bN_h}{(N_h+m)}\left(\frac{1}{\mu_v}\right)$ (that the biting rate b of mosquitoes is the average number of bites per mosquito per day. μ_v is the per capita mortality rate of mosquito, of these bites becomes new infective in the human population) (Esteva and Vargas, 1998). The parameters β_{ac}, β_{bc}, β_{aa}, β_{ba}, β_{ac}, λ_{va1}, λ_{va2}, λ_{vb1} and λ_{vb2} are effects to the basic reproductive number of this disease as we see in (6f)-(6h). If the basic reproductive number is less or equal than one, then the infective replaces less than one, then disease dies. On the other hand, if this number is greater than one and when the susceptible fraction get large enough to birth of new susceptible, then there are secondary infections and endemic equilibrium state is occurred. As we can see in this study, the seasonal parameters such as ε, ρ_{va} and ρ_{vb} which are the measure of influence on the transmission process reflect the environment.

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Author's Contributions

The work preseted here was carried out in collaboration between all authors. R. Sungchasit, P. Pongsumpun and I.M. Tang. Designed and analyzed the model. All authors have contributed to, seen and approved the manuscript.

Ethics

The authors confirm that this work is original and contains has not published elsewhere.

R. Sungchasit *et al.* / American Journal of Applied Sciences 2015, 12 (6). 426.443
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787 - 798

Effect of season on the transmission model of dengue disease

Rattiya Sungchasit and Puntani Pongsumpun*

Department of Mathematics , Faculty of Science ,
King Mongkut's Institute of Technology Ladkrabang ,
Bangkok 10520 ,Thailand

puntani_p@yahoo.com

ABSTRACT

The transmission of dengue disease in the mathematical model is analyzed. We used SIRS model to describe the transmission of dengue disease in mosquito due to the different of dengue transmission rate in each season. *Aedes aegypti* and *Aedes albopictus* are primary vectors for the disease. The human population is separated into three population such as human in winter season, human in summer season and vector population. The infection rate of dengue disease depends on difference of the season and the number of the mosquito infected in season. We use standard dynamic analysis method for analyzing mathematical model. The conditions for the disease free equilibrium state and the endemic state are determined from the value of the reproductive number for the disease.

Keywords : Dengue, equilibrium state, mathematical model, SIRS model.

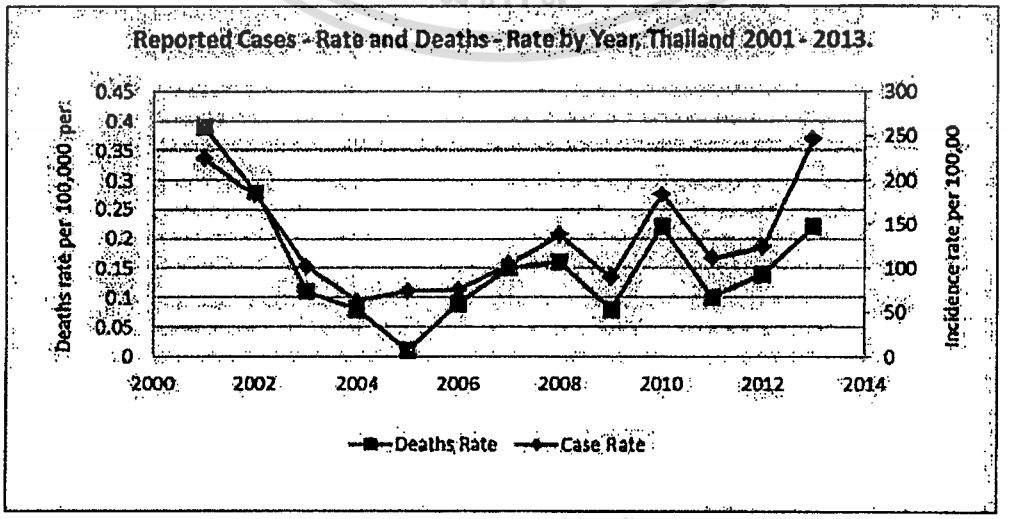
การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรค ไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

1. Introduction

Dengue fever is transmitted to human by bitting of the female mosquitoes infected with a dengue virus. When the female mosquitoes bites the human with dengue virus in their blood, thus the human are exposed and infected. It can't be spread directly from human to another human. In a human, the virus incubates for 3 to 14 days before symptoms appear, with an average symptom onset at 4 to 7 days. The exactly symptoms depend on age. In older children, teenage and adults, the most common symptoms of dengue disease are a fever that comes on quickly and lasts two to seven days, a headache, muscle and joint pain (dengue fever is also known as "breakbone fever"), a red rash that starts on chest, pain behind eyes and feeling sick and vomiting. Dengue fever (DF), Dengue Haemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS) are three types of dengue disease. There are four serotypes of dengue virus, namely DEN-1, DEN-2, DEN-3 and DEN-4[1,2,3]. Infection from one serotype grants life-long immunity to that strain, and also appears to temporarily grant the host a degree of cross – protection. Dengue fever is caused by a type of virus called a *flavivirus*, which is transmitted by infected female *Aedes* mosquitoes. *Aedes* mosquitoes are commonly found in tropical and subtropical countries. Each year, an estimated 100 million cases of dengue fever occur worldwide. Most of these cases are in tropical areas of the world, with the greatest risk occurring in the Indian subcontinent, Southeast Asia, Southern China, Taiwan, Mexico, Africa and India. There are about 2.5 billion people—nearly 40 percent of the world's population live in areas where the disease can be acquired from local mosquitoes. According to the WHO, many dengue cases were reported in Southeast Asian and South Asian countries during the first to eight months of 2010, with 60,000 cases recorded in Indonesia, 58,000 in Thailand and 27,000 in Sri Lanka[7,8,9,10,11].

In recent decades, mathematical models were developed to investigate the infectious epidemiology. Most of the models incorporate several factors of the disease to predict the possible magnitude of the outbreaks. The moisture content, temperature, season and rainfall are influence to the mosquito development. Dengue infection is endemic in Thailand. From the data of Dengue cases rate and deaths rate in 2001 – 2013, we can see that most dengue patients are occurred in rainy season. We can see as shown in figure 1.

Figure1 : The reports cases rate and deaths rate of dengue disease in Thailand by year during 2001 – 2013.[4]



Esteva and Vargas developed a model for dengue disease transmission and included the dynamics of the *Aedes aegypti* mosquito into standard SIR (susceptible – infective-recovered) epidemic model [5]. This disease is occurred by biting of infected *Aedes aegypti* and *Aedes albopictus* mosquitoes. Dengue outbreak is found during the rainy season. Each Aedes mosquito has the different dengue outbreaks and they are depend on the temperature and areas[3]. Dengue outbreak is found in the rainy, winter and summer seasons. Each season has the different dengue outbreaks and they are depend on the temperature of the environment[6]. In this paper, we develop the transmission of dengue disease by formulating the mathematical models. We used SIRS model for analyzing and finding the method to decrease the outbreak of this disease. We analyze dengue model of seasonality compartment (rainy season, winter season and summer season).

2. Methodology

The model consists of the standard SIRS model, where S, I ,R denote the number of susceptible, infectious, and recovered hosts, respectively. The mathematical modeling for dengue disease describes the relevance of human and mosquito population. In this study, we assume that the total human and mosquito population have constant sizes. Hence, the set of ordinary differential equations (ODEs) representing the *SIRS* model is given by:

The dynamics of human population are given by

$$\frac{d\bar{S}_r}{dt} = RN_T - \tau\frac{b_{v\to hr}}{N_{Tr}+g}\bar{I}_v\bar{S}_r - \eta_d\bar{S}_r + \theta\bar{R}_r \quad (1a)$$

$$\frac{d\bar{I}_r}{dt} = \tau\frac{b_{v\to hr}}{N_{Tr}+g}\bar{I}_v\bar{S}_r - \eta_d\bar{I}_r - \gamma\bar{I}_r \quad (1b)$$

$$\frac{d\bar{R}_r}{dt} = \gamma\bar{I}_r - \eta_d\bar{R}_r - \theta\bar{R}_r \quad (1c)$$

$$\frac{d\bar{S}_w}{dt} = WN_T - \tau\frac{b_{v\to hw}}{N_{Tw}+g}\bar{I}_v\bar{S}_w - \eta_d\bar{S}_w + \theta\bar{R}_w \quad (1d)$$

$$\frac{d\bar{I}_w}{dt} = \tau\frac{b_{v\to hw}}{N_{Tw}+g}\bar{I}_v\bar{S}_w - \eta_d\bar{I}_w - \gamma\bar{I}_w \quad (1e)$$

$$\frac{d\bar{R}_w}{dt} = \gamma\bar{I}_w - \eta_d\bar{R}_w - \theta\bar{R}_w \quad (1f)$$

$$\frac{d\bar{S}_s}{dt} = SN_T - \tau\frac{b_{v\to hs}}{N_{Ts}+g}\bar{I}_v\bar{S}_s - \eta_d\bar{S}_s + \theta\bar{R}_s \quad (1g)$$

$$\frac{d\bar{I}_s}{dt} = \tau\frac{b_{v\to hs}}{N_{Ts}+g}\bar{I}_v\bar{S}_s - \eta_d\bar{I}_s - \gamma\bar{I}_s \quad (1h)$$

$$\frac{d\bar{R}_s}{dt} = \gamma\bar{I}_s - \eta_d\bar{R}_s - \theta\bar{R}_s \quad (1i)$$

The variables are defined as follows: $\bar{S}_r$ is the number of susceptible human population in rainy season, $\bar{I}_r$ is the number of infectious human population in rainy season, $\bar{R}_r$ is the number of recovered human population in rainy season, $\bar{S}_w$ is the number of susceptible human population in winter season, $\bar{I}_w$ is the number of infectious human population in winter season, $\bar{R}_w$ is the number of recovered human population in winter season, $\bar{S}_s$ is the number of susceptible human population in summer season, $\bar{I}_s$ is the number of infectious human population in summer season, $\bar{R}_s$ is the number of recovered human population in summer season.

The dynamics of the mosquito population are given by:

$$\frac{d\bar{S}_v}{dt} = V - (\tau(\frac{b_{hr\to v}}{N_{Tr}+g}\bar{I}_r)+\tau(\frac{b_{hw\to v}}{N_{Tw}+g}\bar{I}_w)+\tau(\frac{b_{hs\to v}}{N_{Ts}+g}\bar{I}_s))\bar{S}_v - \eta_d\bar{S}_v \qquad (2a)$$

$$\frac{d\bar{I}_v}{dt} = (\tau(\frac{b_{hr\to v}}{N_{Tr}+g}\bar{I}_r)+\tau(\frac{b_{hw\to v}}{N_{Tw}+g}\bar{I}_w)+\tau(\frac{b_{hs\to v}}{N_{Ts}+g}\bar{I}_s))\bar{S}_v - \eta_d\bar{I}_v \qquad (2b)$$

We define

Table1 : Definitions of variables and parameters for our model.

variable/parameter	definition
$\bar{S}_v$	the number of susceptible mosquito population
$\bar{I}_v$	the number of infectious mosquito population
N_T	the total human population
N_{Tr}	the total human population in rainy season
N_{Tw}	the total human population in winter season
N_{Ts}	the total human population in summer season
N_v	the total mosquito population
η_d	the natural death rate of human population
R	the birth rate of human population in rainy season
W	the birth rate of human population in winter season
S	the birth rate of human population in summer season
$b_{v\to hr}$	the transmission probability of dengue disease from mosquito to human in rainy season
$b_{v\to hw}$	the transmission probability of dengue disease from mosquito to human in winter season
$b_{v\to hs}$	the transmission probability of dengue disease from mosquito to human in summer season
$b_{v\to hs}$	the transmission probability of dengue disease from mosquito to human in summer season
$b_{hr\to v}$	the transmission probability of dengue disease from human to mosquito in rainy season
$b_{hw\to v}$	the transmission probability of dengue disease from human to mosquito in winter season
$b_{hs\to v}$	the transmission probability of dengue disease from human to mosquito in summer season
γ	the recovery rate of human population
τ	the biting rate of mosquito population
θ	the infection rate of human population
g	the number of other animals available as blood sources

We suppose that $N_r=\bar{S}_r+\bar{I}_r+\bar{R}_r$, $N_w=\bar{S}_w+\bar{I}_w+\bar{R}_w$, $N_s=\bar{S}_s+\bar{I}_s+\bar{R}_s$ and $N_v=\bar{S}_v+\bar{I}_v$.

We assume the total human and mosquito populations have constant sizes $\frac{dN_{Tr}}{dt}=0$ in rainy season, $\frac{dN_{Tw}}{dt}=0$ in winter season, $\frac{dN_{Ts}}{dt}=0$ in summer season and $\frac{dN_v}{dt}=0$.

$S_r=\frac{\bar{S}_r}{N_{Tr}}$, $I_r=\frac{\bar{I}_r}{N_{Tr}}$, $R_r=\frac{\bar{R}_r}{N_{Tr}}$, $S_w=\frac{\bar{S}_w}{N_{Tw}}$, $I_w=\frac{\bar{I}_w}{N_{Tw}}$, $R_w=\frac{\bar{R}_w}{N_{Tw}}$, $S_s=\frac{\bar{S}_s}{N_{Ts}}$, $I_s=\frac{\bar{I}_s}{N_{Ts}}$, $R_s=\frac{\bar{R}_s}{N_{Ts}}$,

$S_v=\frac{\bar{S}_v}{N_v}$, $I_v=\frac{\bar{I}_v}{N_w}$

The total human and mosquito populations have constant sizes. Thus rates of change for human and mosquito populations equal to zero. Thus, the birth and death rates are equivalent for human populations , the total mosquito equal to $\frac{V}{\eta_v}$.

The reduced equations become:

$$\frac{dS_r}{dt} = R - \tau \frac{b_{v\to hr}}{N_{Tr}+g} I_v \left(\frac{V}{\eta_v}\right) S_r - \eta_d S_r + \theta(1 - S_r - I_r) \quad (3a)$$

$$\frac{dI_r}{dt} = \tau \frac{b_{v\to hr}}{N_{Tr}+g} I_v \left(\frac{V}{\eta_v}\right) S_r - \eta_d I_r - \gamma I_r \quad (3b)$$

$$\frac{dS_w}{dt} = W - \tau \frac{b_{v\to hw}}{N_{Tw}+g} I_v \left(\frac{V}{\eta_v}\right) S_w - \eta_d S_w + \theta(1 - S_w - I_w) \quad (3c)$$

$$\frac{dI_w}{dt} = \tau \frac{b_{v\to hw}}{N_{Tw}+g} I_v \left(\frac{V}{\eta_v}\right) S_w - \eta_d I_w - \gamma I_w \quad (3d)$$

$$\frac{dS_s}{dt} = S - \tau \frac{b_{v\to hs}}{N_{Ts}+g} I_v \left(\frac{V}{\eta_v}\right) S_s - \eta_d S_s + \theta(1 - S_s - I_s) \quad (3e)$$

$$\frac{dI_s}{dt} = \tau \frac{b_{v\to hs}}{N_{Ts}+g} I_v \left(\frac{V}{\eta_v}\right) S_s - \eta_d I_s - \gamma I_s \quad (3f)$$

$$\frac{dI_v}{dt} = \left(\tau\left(\frac{b_{hr\to v}}{N_{Tr}+g} I_r N_{Tr}\right) + \tau\left(\frac{b_{hw\to v}}{N_{Tw}+g} I_w N_{Tw}\right) + \tau\left(\frac{b_{hs\to v}}{N_{Ts}+g} I_s N_{Ts}\right)\right) S_v - \eta_d I_v \quad (3g)$$

from conditions $S_r + I_r + R_r = 1$, $S_w + I_w + R_w = 1$, $S_s + I_s + R_s = 1$ and $S_v + I_v = 1$.

3. Analysis of the Mathematical Model

From the above equations, we find two equilibrium states; the disease free equilibrium state $A_0 = (1,0,1,0,1,0,0)$ and the endemic disease equilibrium state $A_1 = (S_r', I_r', S_w', I_w', S_s', I_s', I_v')$ where

$$S_r' = \frac{(\gamma+\eta_d)\eta_v (R+\theta)}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_1}$$

$$I_r' = \frac{I_v' V(R+\theta)\tau\varpi_1}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_1}$$

$$S_w' = \frac{(\gamma+\eta_d)\eta_v (W+\theta)}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_2}$$

$$I_w' = \frac{I_v' V(W+\theta)\tau\varpi_2}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_2}$$

$$S_s' = \frac{(\gamma+\eta_d)\eta_v (S+\theta)}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_3}$$

$$I_s' = \frac{I_v' V(R+\theta)\tau\varpi_3}{(\gamma+\eta_d)\eta_v(\eta_d+\theta) + I_v' V(\gamma+\eta_d+\theta)\tau\varpi_3} \quad \text{and}$$

$$I_v' = 1 - \frac{\eta_v}{\eta_v I_r' N_{Tr}\eta_1\tau + \eta_v I_w' N_{Tw}\eta_2\tau + \eta_v I_s' N_{Ts}\eta_3\tau}$$

with

$$\varpi_1 = \frac{b_{v\to hr}}{N_{Tr}+g}, \quad \varpi_2 = \frac{b_{v\to hw}}{N_{Tw}+g}, \quad \varpi_3 = \frac{b_{v\to hs}}{N_{Ts}+g},$$

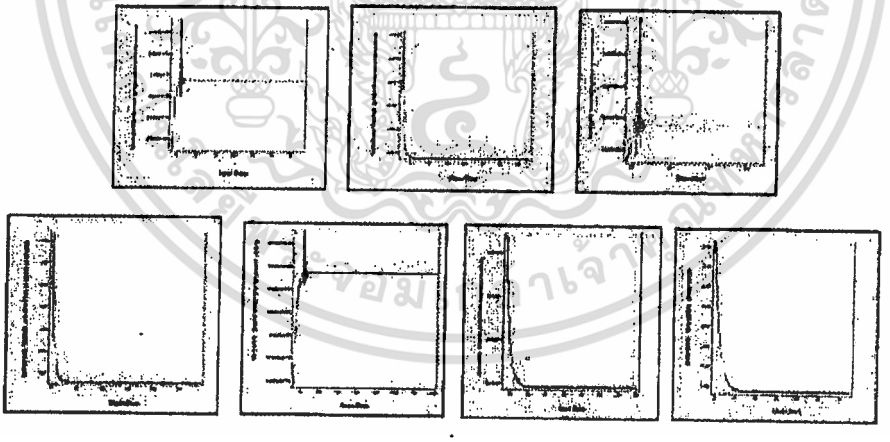
$$\eta_1 = \frac{b_{hr\to v}}{N_{Tr}+g}, \quad \eta_2 = \frac{b_{hw\to v}}{N_{Tw}+g}, \quad \eta_3 = \frac{b_{hs\to v}}{N_{Ts}+g}$$

The reproductive number, E_0 is defined by $E_0 = \frac{\sum_{i=1}^{a} \eta_i \varpi_i N_{\eta_i}}{N_T}$. The parameters are defined as follows: $\eta_d = 1/(365*74.61), \gamma = 1/4.5, \theta = 1/((180+365)/2)$. WE suppose that $\gamma_1 = <N_T><\eta_i><\varpi_i>\tau^2$. Thus, we obtain $E_0 = \frac{3.961x10^{25}\gamma_1}{8.8083x10^{22}}$. $<N_T>$ the weighted average defined as $<N_T> = N_{T\gamma} + N_{Tw} + N_{Ts}$, $<\eta_i>$ when $i=1,2,3$ and $<\varpi_i>$ when $i=1,2,3$. Which is η_i the efficiency of the transmission of the dengue virus to the mosquito from human in each season (rainy, winter, summer).

4. Numerical Simulation

In this paper, we are interested in transmission of dengue disease with the season. The values of the parameter used in this study are as follows: $\eta_d = 1/(365*74.61)$ per day corresponds to a life expectancy of 74.61 years in human. The other parameters are arbitrarily chosen. We presented the numerical solutions of (3a) – (3g) for endemic equilibrium state on the follows figures.

Figure 2 : Numerical solutions of (3a)-(3g), demonstrate the times series of each human population, for $E_0 > 1$ in rainy season, in winter and in summer. $N_{hr} = 190{,}000$, $N_{hw} = 95{,}000$, $N_{ts} = 30{,}000$, $N_v = 20{,}000$, $\eta_d = 1/(365*74.61)$, $\gamma = 1/4.5$, $\tau = 35$, $\eta_v = 1/4$, $\theta = 1/((180+365)/2)$, $g = 3{,}800$ and $R_0 = 2.13674$.

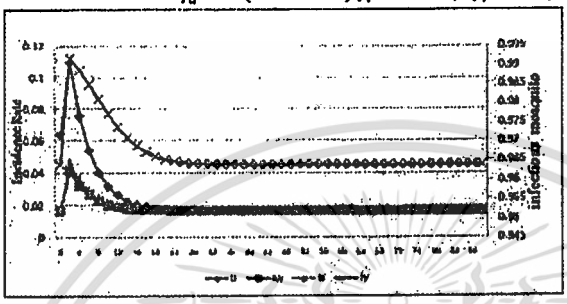


From the above figures we can see that the solutions converge to the disease free state for $E_0 < 1$. If $E_0 > 1$ the solutions oscillate to the disease endemic state [12, 13, 14, 15].

5. Results, Discussion and Conclusion

When the value of E_0 is lowered such as lowering the weighted average efficacy $<\varpi_i>$ or changing the transmission probability of dengue disease from mosquito to human $<\eta_i>$ or changing the transmission probability of dengue disease from human to mosquito in the difference season. The incidence rate at the equilibrium state A_0, can be determined by setting the time rate of change of the different season (by using equations 3a – 3g) and the equivalent equations for the infected and recovered to zero.

Figure 3 : The value of solutions of each human population, for in infective rainy season, winter season and summer season. $\eta_d = 1/(365*74.61), \gamma = 1/4.5, \eta_v = 1/4, \theta = 1/((180+365)/2)$.



From fig.3, the variables are $\bar{I}_r, \bar{I}_w, \bar{I}_s$ and $\bar{I}_v$. The number of infectious mosquito population affect the value of $\bar{I}_r, \bar{I}_w$ and $\bar{I}_s$. When are the number of infectious mosquito population increase will do the number of infectious population of different season.

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รองศาสตราจารย์ ดร.พันธนี พงศ์สัมพันธ์

Analyzing of model for Dengue with its characteristics

Rattiya Sungchasit and Puntani Pongsumpun*

Department of Mathematics , Faculty of Science ,
King Mongkut's Institute of Technology Ladkrabang ,
Bangkok 10520 ,Thailand

puntani_p@yahoo.com

ABSTRACT

Model of dengue epidemics are parametrized on disease incidence data and therefore high – quality data are essential. Dengue disease is occurred by biting of the infected *Aedes* mosquitoes. When infected mosquito bites the human, thus the human are exposed and infected. Dengue fever (DF), Dengue Haemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS) are three types of dengue disease. dengue virus is separated into DEN-1, DEN-2, DEN-3 and DEN-4. The Symptom of each dengue case is depending on type of dengue disease (DF,DHF,DSS) that each person is infected. In this model, we studied the yearly distribution of dengue cases between 2000 and 2012.The curves are fitted with data. Mathematical model is formulated by type of dengue disease. Numerical simulations of the model are shown by solving a system of differential equations. It shows that the local stability of endemic and disease free equilibrium states are depend on the basic reproductive rate of the disease.

Keywords; DF,DHF,DSS, transmission model, SIR model, *Aedes aegypti* .

1. Introduction

Transmission of dengue discase is occurred by biting of the female *Aedes* mosquito. The development of virus and mosquito are affected by the climatic factors. When infected mosquito bites the human, thus the human are exposed and then infected. Dengue fever (DF), Dengue Haemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS) are three types of dengue disease. There are four serotypes of dengue virus, namely DEN-1, DEN-2, DEN-3 and DEN-4. Infection from one serotype gives life-long immunity to that strain, and also appears temporarily immune with the other strains. Dengue fever is caused by a type of virus called a *flavivirus*, which is transmitted by infected female *Aedes* mosquitoes. We can catch the virus if we get be bitten by an infected mosquito. Mosquito become infected when it bites an infected person and pass on the virus for the rest of its life. *Aedes aegypti* mosquitoes carry the virus that causes dengue disease. There are 50 million cases a year, including 500,000 serious cases requiring hospitalization[1,2,3,4].

Dengue fever (DF), a viral mosquito – borne infection is a major international public health concern with about 3 billion people at risk of acquiring the infection [5]. It is estimated that every year, there are 70–500 million dengue infections, 36 million cases of DF and 2.1 million cases of DHF/DSS. There are more than 20,000 deaths per year [5,6]. Infection by dengue virus causes a wide range of clinical manifestations and its classification into DF and DHF/DSS are given according to World Health Organization (WHO) guidelines. DF is an acute febrile viral disease frequently presenting with headaches, bone or joint and muscular pains, rash and leukopenia as symptoms. DHF is characterized by four major clinical manifestations: high fever, haemorrhagic phenomena, often with hepatomegaly and, in severe cases, signs of circulatory failure. Infected patients may develop hypovolaemic shock resulting from plasma leakage. This is designated DSS and can be fatal [7].If DF cases are often benign or asymptomatic, DHF cases may evolve towards a group of symptoms with haemorrhagic fever leading to shock or DSS. In Thailand, the annual estimations of dengue fever cases are depend on the season. *Aedes aegypti* is the principal transmitter of Dengue fever in Thailand but it also transmits Chikungunya fever, yellow fever and Filariasis among other diseases. *Aedes aegypti* prefers feed during daylight hours. They adapt very easily to human surroundings and lay their eggs where there is water, including plastic containers, bins, plant pots, etc.This disease is occurred by biting of infected *Aedes aegypti* and *Aedes albopictus* mosquitoes. Dengue outbreak is found during the rainy season. Each *Aedes* mosquito has the different dengue outbreaks and they are depend on the temperature and areas [7]. The symptom of each dengue patient is depend on the type of dengue disease that each person is infected[8]. Dengue infection is endemic in Thailand. From the data of Dengue cases in 2000 – 2012, we can see that most dengue patients are occurred in rainy season [9]. Models keep track of an individual's infection-age for particular diseases, for instance tubercolosis[10]. Esteva and Vargas developed a model for dengue disease transmission and included the dynamics of the *Aedes aegypti* mosquito into standard SIR (susceptible – infective-recovered) epidemic model [11] and each season has the different dengue outbreaks and they are depend on the temperature of the environment. The standard dynamical modeling method is used in this study. The SEIR (S = susceptible , E= exposed , I = infected and R = recovered) model is used[12].

In this paper, we study the yearly distribution of dengue cases (DF,DHF,DSS) in Thailand (2000 -2012) by finding the analytical approximated equations. We used SIR model for analyzing and finding the method to decrease the outbreak of this disease.

2. Methodology

We analyze the data of dengue cases in Thailand [13] , between 1992 and 2012 by fitting curves.

We denote x_i as the i^{th} year and $f(x_i)$ as the number of dengue cases (DF, DHF,DSS) of i^{th} year .Here, we use the polynomial curve fitting to find the best analytical approximated equations.

Consider the general form of Polynomial order j

$$f(x_i) = a+b_1x_i+b_2x_i^2+b_3x_i^3+\ldots+b_jx_i^j = a+\sum_{k=1}^{j}b_kx_i^k \qquad (1)$$

where a, $b_1,b_2,\ldots,$bj are some coefficients; i = 1,2,3,…,n and n is the total data sets. Error-Least squares approach is the method to find the general form of the Error -Least squares approach. We define

$$err = \sum_{i=1}^{n}(d_i)^2 \qquad (2)$$

where $d_i = y_i - f(x_i)$; i = 1,2,3,…,n; y_i is the real data of dengue cases in each year and $f(x_i)$ is the approximated number of dengue cases from fitting curves.

Thus,

$$err = \sum_{i=1}^{n}(y_i - f(x_i))^2 \qquad (3)$$

then we obtain;

$$err = \sum_{i=1}^{n}(y_i - (a+\sum_{k=1}^{j}b_kx_i^k))^2 \qquad (4)$$

Coefficient of determination is the proportion of variability in a data set. The value of R^2 is always positive and it is between 0 and 1. If this value is closed to 1, then the model is appropriated. We define

$$R^2 = \frac{\sum_{i=1}^{n}(f(x_i)-\bar{y})^2}{\sum_{i=1}^{n}(y_i-\bar{y})^2} \qquad (5)$$

where $\bar{y}$ is the average of real data. From the data of dengue cases (DF, DHF,DSS), we found the polynomial equations and coefficient of determination (R^2) as follows:

Table 1 : Polynomial equations and R^2 of DF cases by year (2000 – 2012)

Polynomial equations	R^2
$0.2497x^2 - 0.2908x + 27.197$	0.3871
$0.0033x^3 + 0.1797x^2 + 0.1159x + 26.637$	0.3872
$-0.0776x^4 + 2.1759x^3 - 19.895x^2 + 68.243x - 36.679$	0.6209
$0.0208x^5 - 0..8073x^4 + 11.453x^3 - 71.702x^2 + 188.68x + 121.74$	0.7743
$-0.0011.x^6 + 0.068x^5 - 1.15714x^4 + 17.452x^3 - 95.067x^2 + 229.68x - 145.46$	0.778

Table 2 : Polynomial equations and R^2 of DHF cases by year (2000 – 2012)

Polynomial equations	R^2
$0.468x^2 - 9.0354x + 105.69$	0.0834
$0.1337x^3 - 2.3393x^2 + 7.2739x + 83.235$	0.1031
$-0.1925x^4 + 5.5232x^3 - 52.138x^2 + 176.27x - 73.831$	0.4993
$0.056x^5 - 2.1508x^4 + 30.422x^3 - 191.18x^2 + 499.5x + 302.12$	0.8036
$-0.0115x^6 + 0.5402x^5 - 10.001x^4 + 92.048x^3 - 431.21x^2 + 920.72x + 545.86$	0.9117

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Table 3 : Polynomial equations and R^2 of DSS cases by year (2000 – 2012)

Polynomial equations	R^2
$0.0213x^2 - 0.3056x + 3.1742$	0.0402
$0.0032x^3 - 0.046x^2 + 0.0851x + 2.6362$	0.0495
$-0.0077x^4 + 0.22x^3 - 2.0495x^2 + 6.8846x - 3.6831$	0.5755
$0.0013x^5 - 0.053x^4 + 0.7956x^3 - 5.2638x^2 + 14.357x - 8.9605$	0.7089
$-0.0002x^6 + 0.0106x^5 - 0.2032x^4 + 1.9749x^3 - 9.8569x^2 + 22.417x - 13.625$	0.7414

Table 4 : Polynomial equations and R^2 of DF deaths by year (2000 – 2012)

Polynomial equations	R^2
$-0.000004x^2 + 0.0006x - 0.0013$	0.0013
$-0.0000008x^3 + 0.0002x^2 - 0.0006x0.0004$	0.4
$-0.0000002x^4 - 0.000006x^3 + 0.0007x^2 - 0.0025x + 0.0023$	0.4712
$0.00000009x^5 - 0.000003x^4 + 0.0004x^3 - 0.002x^2 + 0.0041x - 0.0026$	0.6631
$-0.000000002x^6 + 0.0000002x^5 - 0.000005x^4 + 0.0005x^3 - 0.0026x^2 + 0.0052x - 0.0032$	0.6642

Table 5 : Polynomial equations and R^2 of DHF deaths by year (2000 – 2012)

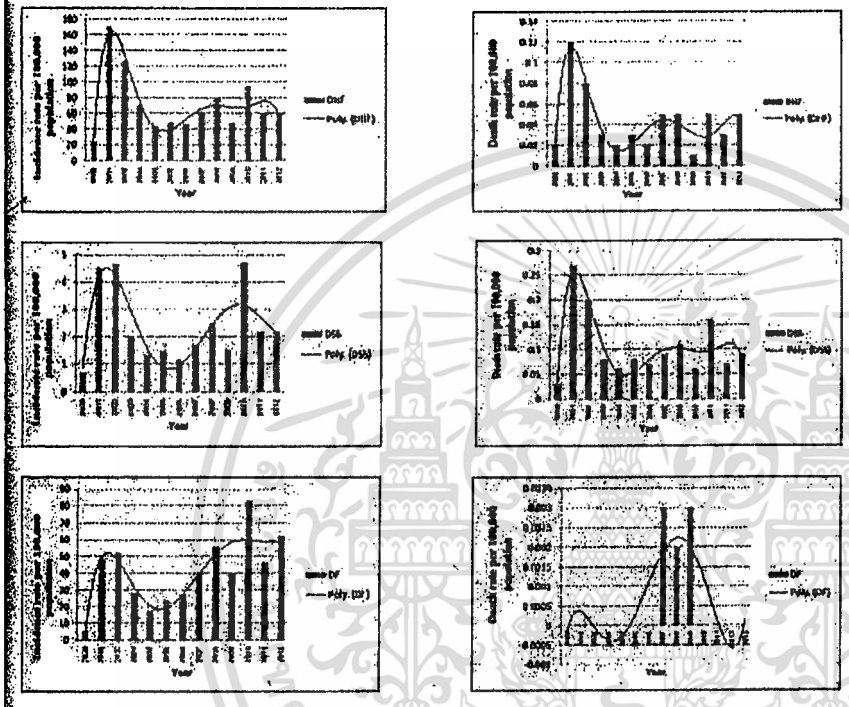
Polynomial equations	R^2
$0.0006x^2 - 0.0106x + 0.0788$	0.1412
$0.0001x^3 - 0.0017x^2 + 0.0029x + 0.0602$	0.1649
$-0.000009x^4 + 0.0025x^3 - 0.024x^2 + 0.0784x - 0.01$	0.3036
$0.000005x^5 - 0.0018x^4 + 0.024x^3 - 0.1441x^2 + 0.3578x - 0.2073$	0.7019
$-0.000001x^6 + 0.0005x^5 - 0.0088x^4 + 0.0798x^3 - 0.3595x^2 + 0.7356x - 0.4259$	0.8544

Table 6 : Polynomial equations and R^2 of DSS deaths by year (2000 – 2012)

Polynomial equations	R^2
$0.0008x^2 - 0.0147x + 0.1606$	0.0796
$0.0002x^3 - 0.0033x^2 + 0.0091x + 0.1278$	0.0944
$-0.0003x^4 + 0.0084x^3 - 0.0788x^2 + 0.2653x - 0.1103$	0.415
$0.000009x^5 - 0.0036x^4 + 0.05x^3 - 0.3112x^2 + 0.8056x - 0.4918$	0.7144
$-0.000002x^6 + 0.001x^5 - 0.0176x^4 + 0.1605x^3 - 0..7418x^2 + 1.5612x - 0.9291$	0.837

From the above tables, the appropriated equations are 6 th order polynomial equations because R^2 converges to 1.

Figure 1 : The real data and the corresponding fitted curves.of dengue disease (DHF,DSS ,DF) in Thailand (a)Cases and (b) Deaths by Year).



a) b)

3.Mathematical model

In this study, we assume that the total human and mosquito populations have constant sizes. The human population is divided into susceptible, infected and recovered classes. The model considers transmission of dengue virus in human and mosquito population:

The dynamics of human population are given by

$$\frac{d}{dt}Ds(t) = \gamma P_h - \tau_h Ds(t) - \alpha_1 \frac{\theta \varpi_{FH}}{P_h + c} Ds(t) Ai(t) - (1-\alpha_1)\frac{\theta \varpi_{HH}}{P_h + c} Ds(t) Ai(t) \quad (6.1)$$

$$\frac{d}{dt}Fi(t) = \alpha_1 \frac{\theta \varpi_{FH}}{P_h + c} Ds(t) Ai(t) - \tau_h Fi(t) - \delta_1 Fi(t) \quad (6.2)$$

$$\frac{d}{dt}Hi(t) = (1-\alpha_1)\frac{\theta \varpi_{HH}}{P_h + c} Ds(t) Ai(t) - \tau_h Hi(t) - \beta Hi(t) - (1-\beta) Hi(t) \quad (6.3)$$

$$\frac{d}{dt}HFi(t) = \beta Hi(t) - \tau_h HFi(t) - \delta_2 HFi(t) \quad (6.4)$$

$$\frac{d}{dt}Si(t) = (1-\beta) Hi(t) - \tau_d Si(t) - \tau_h Si(t) - \delta_3 Si(t) \quad (6.5)$$

$$\frac{d}{dt}Dr(t) = \delta_1 Fi(t) + \delta_2 Hi(t) + \delta_3 Si(t) - \tau_h Dr(t) \quad (6.6)$$

We define

$Ds(t)$ is the number of susceptible human population at time t,

$Fi(t)$ is the number of DF infectious human at time t,

$Hi(t)$ is the number of infectious human who be suspected with DHF infection,
$HFi(t)$ is the number of DHF infectious human at time t,
$Si(t)$ is the number of DSS infectious human at time t,
$Dr(t)$ is the number of recovered human population at time t.

The dynamics of the mosquito population are given by :

$$\frac{d}{dt}As(t) = P_v - \frac{\theta \varpi_{FV}}{P_h + c} Fi(t)\,As(t) + \frac{\theta \varpi_{HV}}{P_h + c} Hi(t)\,As(t) - \tau_v As(t) \quad (7.1)$$

$$\frac{d}{dt}Ai(t) = \frac{\theta \varpi_{FV}}{P_h + c} Fi(t)\,As(t) + \frac{\theta \varpi_{HV}}{P_h + c} Hi(t)\,As(t) - \tau_v Ai(t) \quad (7.2)$$

We define

$As(t)$ is the number of susceptible mosquito population at time t,
$Ai(t)$ is the number of infectious mosquito population at time t.

The parameters of our equations are defined as follows:

P_h is the total human population,
P_v is the constant recruitment rate of mosquito population,
γ is the birth rate of human population,
θ is the biting rate of mosquito population,
α_1 is the probability of infection with DF,
$1-\alpha_1$ is the probability of infection with DHF,
β is the probability of patient with type DHF plasma leakage is not in shock,
$1-\beta$ is the probability of patient with type DHF plasma leakage in shock,
c is the number of other animals available as blood sources,
τ_h is the natural death rate of human population,
τ_d is the death rate of human population due to the disease,
τ_v is the death rate of mosquito population,
ϖ_{FH} is the transmission probability of DF from mosquito to human ,
ϖ_{HH} is the transmission probability of DHF from mosquito to human,
ϖ_{FV} is the transmission probability of DF from human to mosquito,
ϖ_{HV} is the transmission probability of DHF from human to mosquito,
δ_1 is the recovery rate of human population from DF infection,
δ_2 is the recovery rate of human population from DHF infection,
δ_3 is the recovery rate of human population from DSS infection.

We suppose that $P_h = Ds + Fi + Hi + HFi + Si + Dr$ and $N_v = As + Ai$,we assume the total human and mosquito populations have constant sizes $\frac{d}{dt}P_h = 0$ and $\frac{d}{dt}P_v = 0$

4. Analysis of the mathematical model

Equilibrium Points:

The equilibrium points $(Ds^*, Fi^*, Hi^*, HFi^*, Si^*, Dr^*, As^*, Ai^*)$ are found by setting the right hand side of (1.1) – (1.6) and (2.1) – (2.2) equal to zero. The system has two possible equilibrium points: disease free equilibrium point and endemic disease equilibrium point. This gives

1) Disease free equilibrium point: $S_0 = (\frac{P_h \gamma}{\tau_h}, 0, 0, 0, 0, 0, \frac{P_v}{\tau_v}, 0)$

2) Endemic disease equilibrium point: $S_1 = (Ds^*, Fi^*, Hi^*, HFi^*, Si^*, Dr^*, As^*, Ai^*)$ where

$$Ds^* = \frac{P_h\gamma}{Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h} \tag{8.1}$$

$$Fi^* = \frac{Ai\,P_h\alpha_1\gamma\varepsilon_1}{(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_1+\tau_h)} \tag{8.2}$$

$$Hi^* = \frac{Ai\,P_h(-1+\alpha_1)\gamma\varepsilon_2}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)} \tag{8.3}$$

$$HFi^* = \frac{Ai\,P_h(-1+\alpha_1)\beta\gamma\varepsilon_2}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_2+\tau_h)} \tag{8.4}$$

$$Si^* = \frac{Ai\,P_h(-1+\alpha_1)(-1+\beta)\gamma\varepsilon_2}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_2+\tau_h+\tau_d)} \tag{8.5}$$

$$Dr^* = \frac{Ai\,P_h\gamma\left(-\frac{\alpha_1\varepsilon_1\delta_1}{\delta_1+\tau_h}-\frac{(-1+\alpha_1)\beta\varepsilon_2\delta_2}{(1+\tau_h)(\delta_2+\tau_h)}-\frac{(-1+\alpha_1)\beta\varepsilon_2\delta_3}{(1+\tau_h)(\delta_3+\tau_h+\tau_d)}\right)}{\tau_h(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)} \tag{8.6}$$

$$As^* = \frac{P_v}{\frac{Ai\,P_h\gamma(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1+(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4)\tau_h)}{(1+\tau_h)(Ai(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)+\tau_h)(\delta_1+\tau_h)}+\tau_v} \tag{8.7}$$

$$Ai^* = \frac{P_vP_h\gamma(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1+(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4)\tau_h)-\tau_h(1+\tau_h)(\delta_1+\tau_h)\tau_v^2)}{(\tau_v(P_h\gamma(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1+(\alpha_1\varepsilon_1\varepsilon_3+(-1+\alpha_1)\varepsilon_2\varepsilon_4)\tau_h)+(\alpha_1(\varepsilon_1-\varepsilon_2)+\varepsilon_2)(1+\tau_h)(\delta_1+\tau_h)\tau_v))} \tag{8.8}$$

with $\varepsilon_1 = \frac{(\theta\varpi_{FH})}{(P_h+c)}$, $\varepsilon_2 = \frac{(\theta\varpi_{HH})}{(P_h+c)}$, $\varepsilon_3 = \frac{(\theta\varpi_{F\gamma})}{(P_h+c)}$, $\varepsilon_4 = \frac{(\theta\varpi_{H\gamma})}{(P_h+c)}$

and

$$D_0 = \frac{P_vP_h\gamma\alpha_1(\varepsilon_1\varepsilon_3(1+\tau_h)+\varepsilon_2\varepsilon_4(\delta_1+\tau_h))}{(\delta_1+\tau_h)(P_vP_h\gamma\varepsilon_2\varepsilon_4+\tau_h(1+\tau_h)\tau_v^2)}$$

It can be seen from the above equations that the steady state solution is positive for $D_0 > 1$ .The local stability of each equilibrium point is determined by the sign of eigenvalues for each steady state. If all eigenvalues have negative real parts, then that steady state is local stability [9]. The eigenvalues are obtained by solving the following characteristic equation

$$\det(J-\psi I_8)=0$$

where I_8 the identity matrix dimension 8x8 .

For the disease free steady state $S_0 = (\frac{P_h\gamma}{\tau_h},0,0,0,0,0,\frac{P_v}{\tau_v},0)$, the *Jacobian* matrix is given by

$$\begin{bmatrix}
(-(\tau_1)-(\alpha_1\varepsilon_1Ai)-((1-\alpha_1)(\varepsilon_1)Ai))-\psi & 0 & 0 & 0 & 0 & 0 & 0 & -(\alpha_1\varepsilon_1Ds)-((1-\alpha_1)(\varepsilon_1)Ds) \\
(\alpha_1\varepsilon_1Ai) & (-(\tau_2)-(\delta_1))-\psi & 0 & 0 & 0 & 0 & 0 & (\alpha_1\varepsilon_1Ds) \\
((1-\alpha_1)(\varepsilon_2)Ai) & 0 & (-(\tau_3)-(\beta)-(1-\beta))-\psi & 0 & 0 & 0 & 0 & ((1-\alpha_1)(\varepsilon_2)Ds) \\
0 & 0 & \beta & (-(\tau_4)-(\delta_2))-\psi & 0 & 0 & 0 & 0 \\
0 & 0 & (1-\beta) & 0 & (-(\tau_5)-(\tau_d)-(\delta_3))-\psi & 0 & 0 & 0 \\
0 & \delta_1 & 0 & \delta_2 & \delta_3 & -(\tau_6)-\psi & 0 & 0 \\
0 & -(\varepsilon_2Ai) & -(\varepsilon_4Ai) & 0 & 0 & 0 & (-(\varepsilon_2Fi)-(\varepsilon_4Hi)-(\tau_v))-\psi & 0 \\
0 & (\varepsilon_2Ai) & (\varepsilon_4Ai) & 0 & 0 & 0 & (\varepsilon_2Fi)+(\varepsilon_4Hi) & (-\tau_v)-\psi
\end{bmatrix}$$

where

$\psi = -\tau_h$, $\psi = -\tau_h, \psi = -\tau_h-\delta_2, \psi = -\tau_h-\delta_3-\tau_d, \psi = -\tau_v,$

The characteristic equation is defined by $\psi^3 + A_1\psi^2 + A_2\psi + A_3$.

where

$A_1 = 1+\delta_1+2\tau_h+\tau_v,$

$$A_2 = (1+\tau_h)+(\delta_1+\tau_h)-\frac{P_h P_v \gamma(\alpha_1\varepsilon_1\varepsilon_3+\varepsilon_2\varepsilon_4-\alpha_1\varepsilon_2\varepsilon_4)}{\tau_h\tau_v}+(1+\delta_1+2\tau_h)\tau_v,$$

$$A_3 = \frac{1}{\tau_h\tau_v}(-P_h P_v \gamma(\alpha_1\varepsilon_1\varepsilon_3-(-1+\alpha_1)\varepsilon_2\varepsilon_4\delta_1+(\alpha_1\varepsilon_1\varepsilon_3+\varepsilon_2\varepsilon_4-\alpha_1\varepsilon_2\varepsilon_4)\tau_h)+\tau_h(1+\tau_h)(\delta_1+\tau_h)\tau_v^2$$

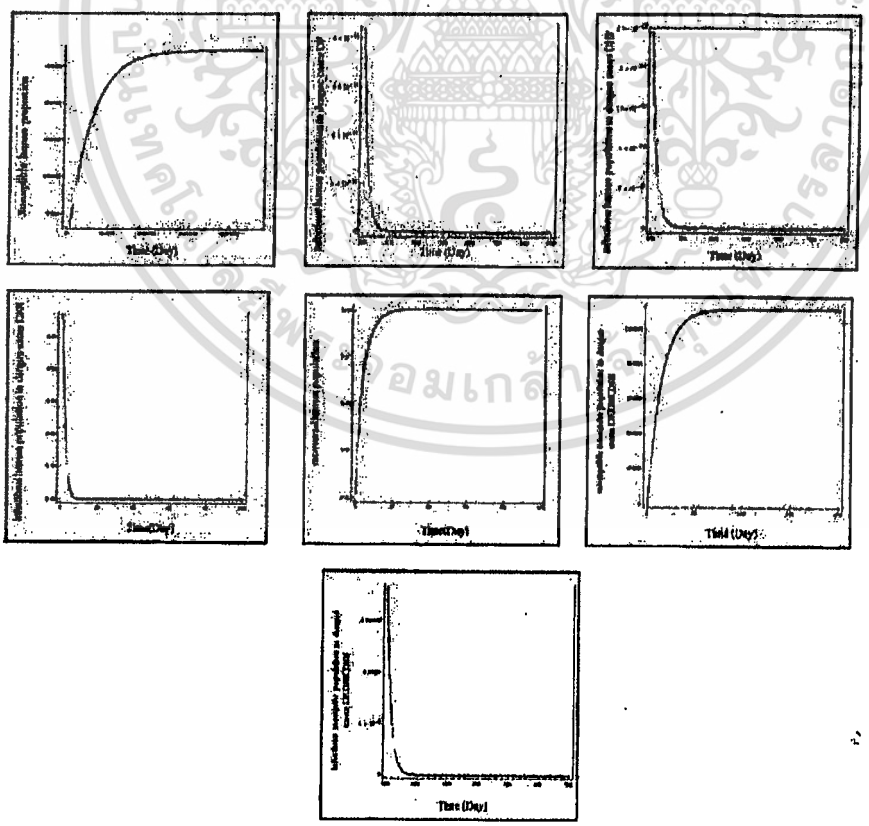
We check the sign of eigenvalues by using Routh Hurwitz criteria can impact eigenvalues with negative real parts. If the characteristic equation satisfy Routh Hurwitz criteria, we can say that the steady state is local stability. Thus, this disease free state will be local stability when $D_0 < 1$.On similarly method, we found that the disease endemic state will be local stability when $D_0 > 1$.

5. Numerical results

The parameters are given as follows: $\tau_h = 1/(365*74.6)$ corresponds to the life expectancy of 74.6 years for human, $\delta_1 = 1/5$ corresponds to the 5 days at which quarantine human change to be recovered human for DF, $\delta_2 = 1/6$ corresponds to the 6 days at which quarantine human change to be recovered human for DHF, $\delta_3 = 1/3$ corresponds to the 3 days at which quarantine human change to be recovered human for DSS. The other parameters are arbitrary chosen

Cases1. $D_0 < 1$;

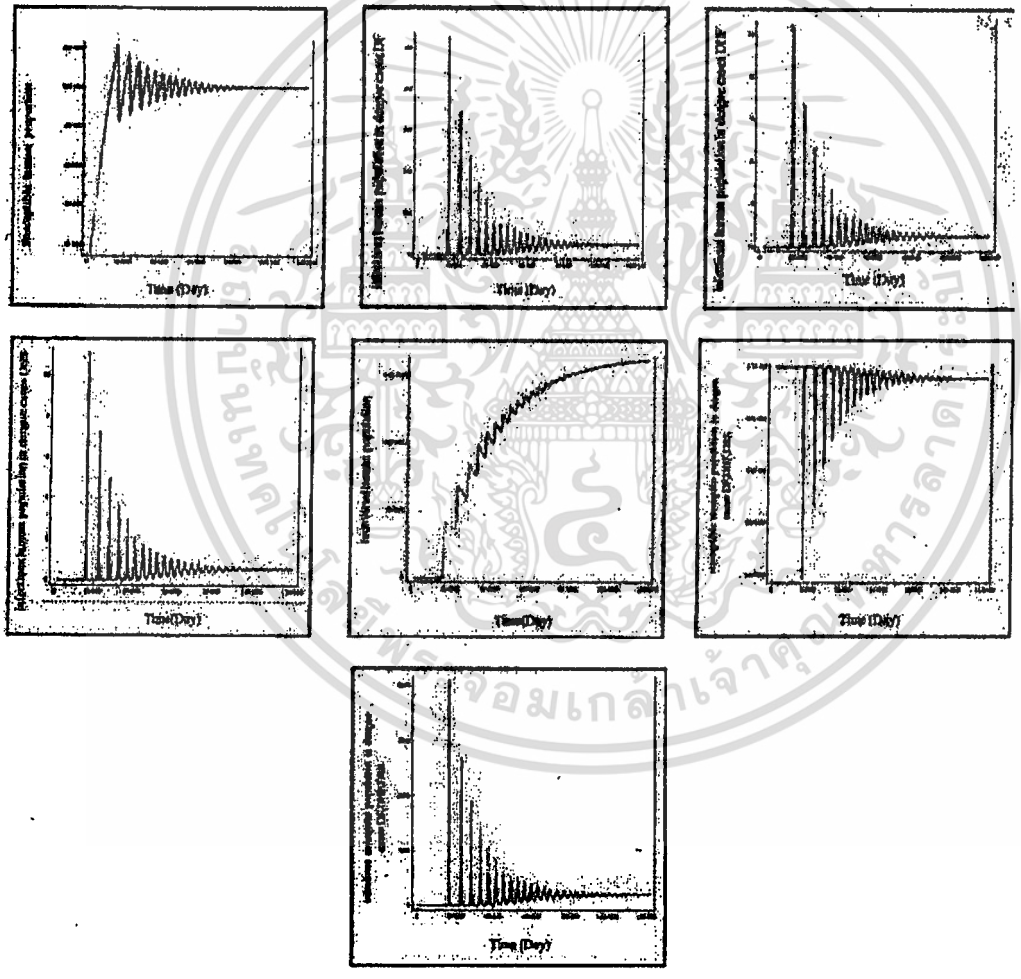
Figure 2 : Times series solutions of susceptible, DF infectious human, DHF infectious human, DSS infectious human, susceptible mosquito population, infectious mosquito population, respectively.



The parameters are
$\tau_h = 1/(365*74.6)$, $\delta_1 = 1/5$, $\delta_2 = 1/6$, $\delta_3 = 1/3$, $P_h = 100{,}000$, $P_v = 8000$, $\omega_{FH} = 1/8$, $\omega_{HH} = 1/10$, $\omega_{FV} = 1/3$, $\omega_{HV} = 1/7$, $\tau_d = 1/2$, $\alpha_1 = 0.7$, $\beta = 0.007$, $D_0 = 0.319108$. The solutions converge to the disease free states (272290, 0, 0, 0, 0, 0, 98000, 0)

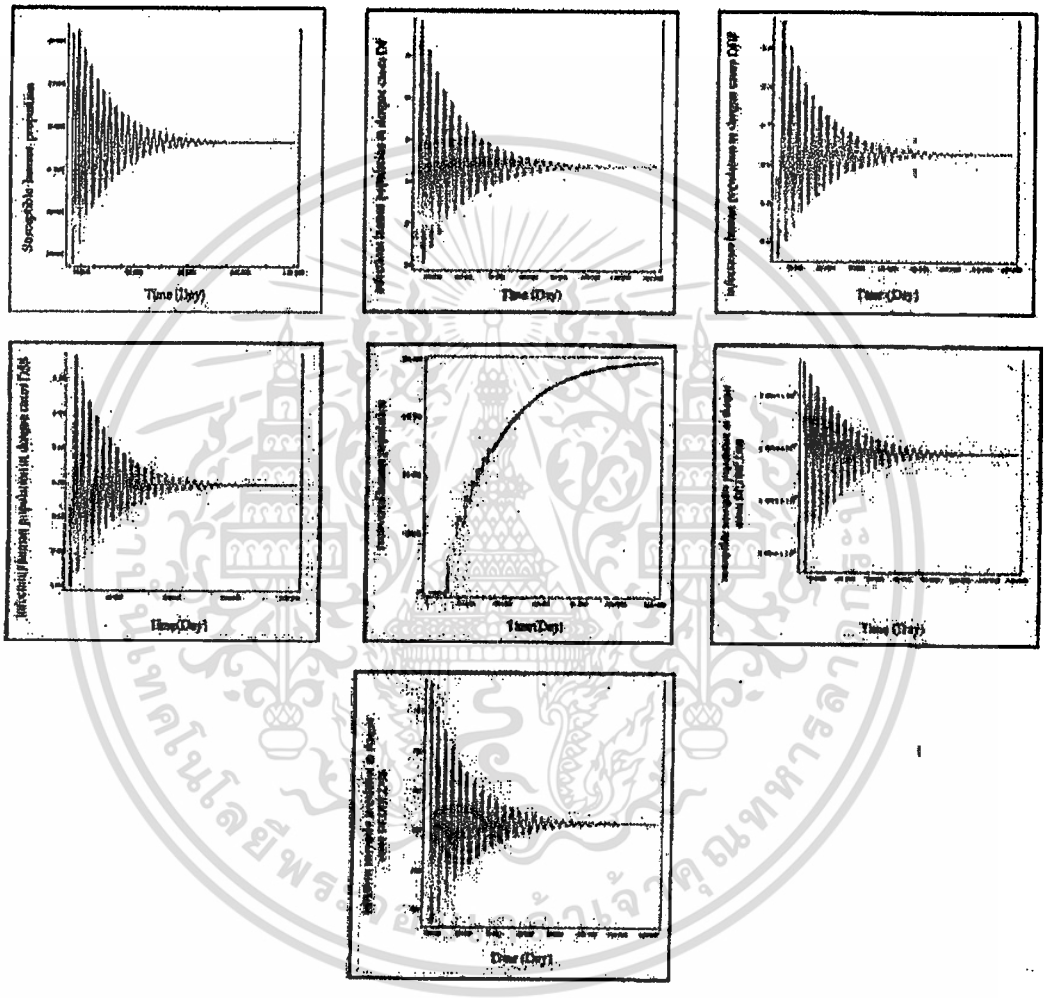
Cases2. $D_0 > 1$;

Figure 3 : Times series solutions of susceptible, DF infectious human, DHF infectious human, DSS infectious human, susceptible mosquito population, infectious mosquito population, respectively.



The parameters are $\tau_h = 1/(365*74.6)$, $\delta_1 = 1/5$, $\delta_2 = 1/6$, $\delta_3 = 1/3$, $P_h = 100{,}000$, $P_v = 48000$, $\omega_{FH} = 1/8$, $\omega_{HH} = 1/10$, $\omega_{FV} = 1/3$, $\omega_{HV} = 1/7$, $\tau_d = 1/2$, $\alpha_1 = 0.9$, $\beta = 0.04$, $D_0 = 2.3622$. The solutions oscillate to the endemic disease states (100182, 26.1172, 0.515961, 0.113488, 0.550336, 164588, 671749, 206.223).

Figure 4 : Times series solutions of susceptible , DF infectious human, DHF infectious human, DSS infectious human, susceptible mosquito population, infectious mosquito population, respectively.



The parameters are $\tau_h = 1/(365*74.6)$, $\delta_1 = 1/5$, $\delta_2 = 1/6$, $\delta_3 = 1/3$, $P_h = 100{,}000$, $P_v = 78000$, $\omega_{FH} = 1/8$, $\omega_{HH} = 1/10$, $\omega_{FV} = 1/3$, $\omega_{HV} = 1/7$, $\tau_d = 1/2$, $\alpha_1 = 0.7$, $\beta = 0.007$, $D_0 = 3.43912$. The solutions oscillate to the endemic disease states (61654.8, 31.9637, 0.631462, 0.138894, 0.673532, 201432, 0.000001091, 410.1).

When value of probability of infection with DF (α_1) and probability of patient with type DHF plasma leakage is not in shock (β), as a results Fig 3 converge to endemic faster than Fig 4.

6. Discussion and conclusion

In this study, we constructed the mathematical model of dengue cases (DF,DHF,DSS) and analyzed the results by using standard dynamical modeling method. The basic reproductive number is defined by D_0 .From Fig 3 ,parameter values are $\alpha_1 = 0.9$, $\beta = 0.04$ and Fig 4, parameter values are $\alpha_1 = 0.7$, $\beta = 0.007$,so that the convergence of the graph are different. The others parameter were, too. Therefore, we know that, when values α_1 (the probability of infection with DF) and β (the probability of patient with type DHF plasma leakage is not in shock), the convergence to endemic state are different. The time series parameter inference shows different dynamic behaviours, depending on the data collection to be described via the modeling approaches. The output of this model should introduce the way for reducing the transmission of this disease.

Acknowledgment

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Transmission model of Dengue disease with the effect of temperature in Thailand

Puntani Pongsumpun *

Department of Mathematics, Faculty of Science,

King Mongkut's institute of Technology Ladkrabang,

Chalongkrung road, Ladkrabang, Bangkok 10520, Thailand

* Corresponding author, e-mail: puntani_p@yahoo.com, kppuntan@kmitl.ac.th

Abstract: Tropical disease which is found in Thailand called as dengue disease. This disease is occurred in Thailand for many years. This disease has three forms: Dengue Fever (DF), Dengue hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS). The *Aedes* mosquitoes are vector for this disease. We formulate the dynamical model of dengue disease using the knowledge of Mathematics and epidemiology. The different temperatures are considered as the factors for the transmission of this disease. After that, we use standard dynamical modeling theorem to analyze our equations. Numerical simulations are found to confirm our analytical results.

Keywords: dengue, standard dynamical modeling theorem, temperature, Thailand.

INTRODUCTION

The tropical disease usually found in Thailand called as dengue disease. Four serotypes of dengue virus are D1, D2, D3 and D4. People has permanent immunity if he/she infected with the same serotypes but only temporary to the other serotypes. Dengue Fever (DF), Dengue hemorrhagic fever (DHF) and Dengue shock syndrome (DSS) are three forms of dengue disease. The transmission cycle of dengue virus by the *Aedesaegypti* starts with a dengue infectious person. Most dengue cases have virus circulating in the blood (viremia) that lasts for about five days but may last up to 12 days [1]. During the period of viremic, an uninfected female *Aedesaegypti* mosquito bites the person and ingests blood that contains dengue virus. Within the vector, the viruses replicate during an extrinsic incubation period of eight to twelve days. After an extrinsic incubation period of vector, its salivary glands become infected and the virus is transmitted when the infectious vector bites and injects the salivary fluid into the wound of the human. The vector can bite a susceptible person and could transmit the virus to him or her, as well as to every other susceptible person. The mosquito bites for the rest of its lifetime. The virus then replicates in the person during an intrinsic incubation period of four to seven days and

produces infection [2,3]. DF was recognized for at least several hundred years since Benjamin Rush from Philadelphia. First time, we called DF as "breakbone fever" in 1780. This disease is occurring as an epidemic in tropical and subtropical regions of Asia and Africa. Transmission has been geographically increasing during the past few decades. Successive introduction and circulation of all four serotypes into Central, South America and the Caribbean have occurred since 1977. DHF epidemic was first reported in the Caribbean in 1981.Evolving transmission patterns are probably the results of a combination of changing human demographics, expanding vector populations, and alterations in viral virulence. Dengue disease can be found wherever the mosquito vector is introduced. One hundred million cases of this disease are reported yearly by WHO, making it one of the most important viral diseases in the world. Cases seen in the US are imported from the Caribbean region, the others arriving from South America, Africa or Asia. Transmission of dengue virus is often seasonal, with rates increasing during hot, humid months. The vector *Aedesaegypti* breeds in peridomestic fresh water as might be stored in natural and artificialcontainers in and around human dwellings (e.g., old tires, flowerpots, water storage containers). From the data of dengue disease in Thailand, we found that the temperature effect to the transmission of this disease. The appropriated temperature for vector is about 28-35^0 c .

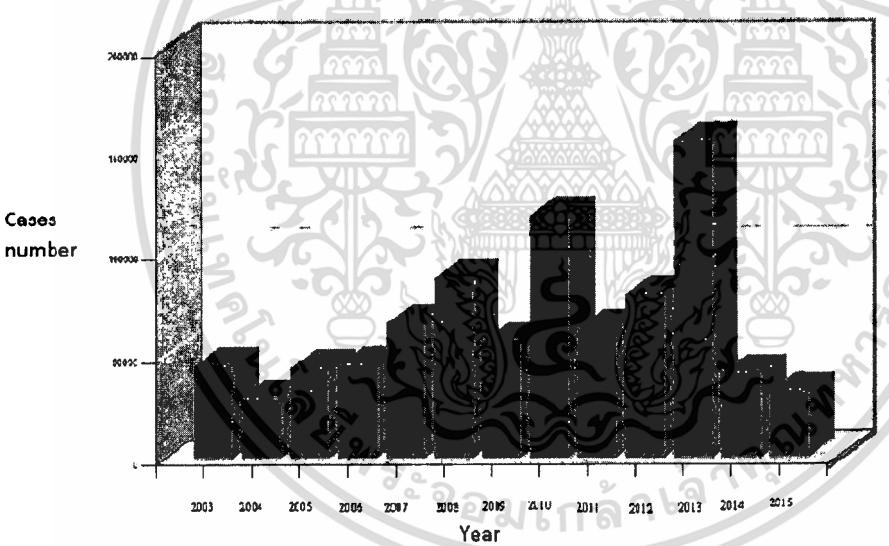


Figure 1. Number of dengue cases in Thailand from 2003 to 2015 [4]

Mathematical model is applied to many diseases. From the data of dengue cases in Thailand in figure 1, we can see that dengue cases are appeared every year. In 1998, Esteva and Vargas [5] proposed their mathematical model for the transmission of dengue virus infection in a constant human population They supposed that the population can be infected only one time. In 2008, we incorporated the influence of incubation to our model [6]. Recently, we formulated the transmission model of dengue disease considering the transmission of two types of *Aedes* mosquito. We apply standard dynamical modeling method to our model to find the method for

reducing the outbreak of this disease [7]. In this paper, we formulate the transmission model of dengue disease with the effect of temperature. The application of dynamical modeling method is used in this study.

MATERIALS AND METHODS

We formulate our model by separating the population into 2 groups such as human and vector populations. Human is separated into 3 groups such as susceptible, infected and recovered groups. Vector is separated into 2 groups such as susceptible and infected groups. We separate the infected human into 2 classes. Class of infected human population when the temperature is28-35^{0}c and class of infected vector population when the temperature is not 28-35^{0}c The variables and parameters of our model is described as follows:

variable/parameter	definition
S	Number of susceptible human
I_{t_a}	Number of infected humanwhen the temperature is 28-35^{0}c
I_{t_b}	Number of infected humanwhen the temperature is not 28-35^{0}c
R	Number of recovered human
S_v	Number of susceptible vector
I_v	Number of infectious vector
b	Birth rate of human
N_T	Total human
μ_h	Death rate of human population
β_{t_a}	Transmission rate of dengue virus from vector to human population when the temperature is 28-35^{0}c
β_{t_b}	Transmission rate of dengue virus from vector to human population when the temperature is not 28-35^{0}c
r	Recovery rate of human population
C_v	Constant recruitment rate of vector population
β_v	Transmission rate of dengue virus from human to vector population

μ_v	Death rate of vector population

Using the knowledge of mathematical model and the transmission behavior of this disease, we can obtain the differential equations as follows:
For human population:

$$\begin{aligned}
\frac{d}{dt}S &= bN_T - (\beta_{I_a} + \beta_{I_b})SI_v - \mu_h S \\
\frac{d}{dt}I_{I_a} &= \beta_{I_a} SI_v - (r + \mu_h)I_{I_a} \\
\frac{d}{dt}I_{I_b} &= \beta_{I_a} SI_v - (r + \mu_h)I_{I_b} \qquad (1) \\
\frac{d}{dt}R &= r(I_{I_a} + I_{I_b}) - \mu_h R
\end{aligned}$$

For vector population:

$$\begin{aligned}
\frac{d}{dt}S_v &= C_v - \beta_v S_v(I_{I_a} + I_{I_b}) - \mu_v S_v \\
\frac{d}{dt}I_v &= \beta_v S_v(I_{I_a} + I_{I_b}) - \mu_v I_v \qquad (2)
\end{aligned}$$

with the conditions: $N_T = S + I_{I_a} + I_{I_b} + R$ and $N_v = S_v + I_v$.

We normalize our equations (1)-(2) by introducing the new variables:

$$s = \frac{S}{N_T}, i_{I_a} = \frac{I_{I_a}}{N_T}, i_{I_b} = \frac{I_{I_b}}{N_T}, r_h = \frac{R}{N_T}, s_v = \frac{S_v}{N_v} \text{ and } i_v = \frac{I_v}{N_v}. \qquad (3).$$

Note that $s, i_{I_a}, i_{I_b}, r_h, s_v$ and i_v are the fractions of susceptible human, infected human when the temperature is 28-35^{0}c , infected human when the temperature is not 28-35^{0}c , recovered human, susceptible vector and infectious vector, respectively.

S	Number of susceptible human
I_{I_a}	Number of infected humanwhen the temperature is 28-35^{0}c
I_{I_b}	Number of infected humanwhen the temperature is not 28-35^{0}c
R	Number of recovered human

The reduced equations become

$$\begin{aligned}
\frac{d}{dt}s &= \mu_h(1-s) - (\beta_{t_a} + \beta_{t_b})(C_v/\mu_v)s\,i_v \\
\frac{d}{dt}i_{t_a} &= \beta_{t_a}(C_v/\mu_v)s\,i_v - (r+\mu_h)i_{t_a} \\
\frac{d}{dt}I_{t_b} &= \beta_{t_b}(C_v/\mu_v)s\,i_v - (r+\mu_h)i_{t_b} \\
\frac{d}{dt}i_v &= \beta_v(1-i_{t_a}-i_{t_b})(i_{t_a}+i_{t_b})N_T - \mu_v i_v
\end{aligned} \tag{4}$$

with the conditions: $1 = s + i_{t_a} + i_{t_b} + r_h$ and $1 = s_v + i_v$.

To follow the method of dynamical modeling method, the steady states of our equations are found. They are from setting (4) to zero, thus the steady states are (1,0,0,0) and the positive steady state $(s^*, i^*_{t_a}, i^*_{t_b}, i^*_v)$ is defined by

$$s^* = \frac{\mu_h\mu_v}{(\beta_{t_a}+\beta_{t_b})C_v i^*_v + \mu_h\mu_v}, i^*_{t_a} = \frac{\beta_{t_a}C_v i^*_v s^*}{\mu_v(\mu_h+r)}, i^*_{t_b} = \frac{\beta_{t_b}C_v i^*_v s^*}{\mu_v(\mu_h+r)} \text{ where}$$

i^*_v is found from solving (5).

$$\begin{aligned}
&\mu_h^2\mu_v(((\beta_{t_a}+\beta_{t_b})C_v i^*_v + \mu_h\mu_v)^2 - (\beta_{t_a}+\beta_{t_b})\beta_v C_v\mu_h N_T) + \mu_h((\beta_{t_a}+\beta_{t_b})C_v i^*_v + \mu_h\mu_v) \\
&-(\beta_{t_a}+\beta_{t_b})\beta_v C_v N_T)r + \mu_v((\beta_{t_a}+\beta_{t_b})C_v i^*_v + \mu_h\mu_v)^2 r^2 = 0
\end{aligned} \tag{5}$$

Next, we check the local stability of each steady state by looking the sign of eigenvalues, where the eigenvalues are evaluated by $\det(J-\lambda I)=0$; $\det(J-\lambda I)=0$; I is the identity matrix. If all eigenvalues have negative real parts, then that steady state will be local stability[8-10].
For the first steady state(disease free state) : (1,0,0,0), jacobian matrix is given by

$$J_1 = \begin{pmatrix}
-\mu_h & 0 & 0 & -\dfrac{(\beta_{t_a}+\beta_{t_b})C_v}{\mu_v} \\
0 & -\mu_h - r & 0 & \dfrac{\beta_{t_a}C_v}{\mu_v} \\
0 & 0 & -\mu_h - r & \dfrac{\beta_{t_b}C_v}{\mu_v} \\
0 & \beta_v N_T & \beta_v N_T & -\mu_v
\end{pmatrix}.$$

The eigenvalues are

$$\mu_h,\ \mu_h,\ r, \frac{1}{2\mu_v}(-\mu_h\mu_v - \mu_v^2 - \mu_v r \pm \sqrt{\mu_v(4(\beta_{t_a}+\beta_{t_b})\beta_v C_v N_T + \mu_v(\mu_h+\mu_v+r)^2)}).$$

We can see that all eigenvalues have negative real parts when $A_0 < 1$;

where $A_0 = \dfrac{(\beta_{t_a} + \beta_{t_b})\beta_v C_v N_T}{\mu_v^2(\mu_h + r)}$.

The positive steady state(endemic state): $(s^*, i_{t_a}^*, i_{t_b}^*, i_v^*)$,

Jacobian matrix is defined by

$$J_2 = \begin{bmatrix} -\mu_h - \dfrac{(\beta_{t_a}+\beta_{t_b})C_v i_v^*}{\mu_h} & 0 & 0 & -\dfrac{(\beta_{t_a}+\beta_{t_b})C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)} \\ \dfrac{\beta_{t_a}C_v i_v^*}{\mu_h} & -\mu_h - r & 0 & \dfrac{\beta_{t_a}C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)} \\ \dfrac{\beta_{t_b}C_v i_v^*}{\mu_h} & 0 & -\mu_h - r & \dfrac{\beta_{t_b}C_v}{\mu_v} \\ 0 & -\dfrac{(\beta_{t_a}+\beta_{t_b})\beta_v C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)(r+\mu_h)} N_T i_v^* & \beta_v N_T\left(1 - \dfrac{2(\beta_{t_a}+\beta_{t_b})C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)(r+\mu_h)}\right) & -\mu_v \\ & + \beta_v N_T\left(1 - \dfrac{(\beta_{t_a}-\beta_{t_b})C_v\mu_h}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)(r+\mu_h)}\right) i_v^* & & \end{bmatrix}$$

Using the same method as before, eigenvalues are obtained by solving $\lambda^3 + A\lambda^2 + B\lambda + C = 0$;

where $A = \dfrac{(\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_v(2\mu_h + \mu_v + r)}{\mu_v}$,

$$B = -\frac{1}{L_4\mu_v((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)^2}((-\beta_{t_a}^3 - \beta_{t_b}^3)C_v^3 i_v^{*3} L_3 L_4$$

$$- \beta_{t_b} C_v\mu_v(L_4\mu_h\mu_v(-i_v^* L_1 + \beta_v\mu_h N_T(\mu_h - r))) - L_4\mu_h^2\mu_v^3(\mu_h(\mu_h + 2\mu_v) + (\mu_h + \mu_v)r)$$

$$\beta_{t_a} C_v(3\beta_{t_b}^2 C_v^2 i_v^{*3} L_3 L_4 + L_4\mu_h\mu_v^2(i_v^* L_1 + \beta_v\mu_h N_T) + \beta_{t_a} C_v i_v^*(3\beta_{t_a} C_v i_v^* L_3 L_4$$

$$+ \mu_v(i_v^* L_2 L_4 + \beta_v\mu_h N_T(\mu_h - r))) - 2\beta_{t_b} C_v i_v^*\mu_v(i_v^* L_2 L_4 - \beta_v\mu_h N_T r))),$$

$$C = \frac{\mu_h(((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)^2 - (\beta_{t_a}+\beta_{t_b})\beta_v C_v\mu_h N_T}{(\beta_{t_a}+\beta_{t_b})C_v i_v^* - \mu_h\mu_v} + ((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)r$$

$$+ \frac{2(\beta_{t_a}^2 + \beta_{t_a}\beta_{t_b} + \beta_{t_b}^2)\beta_v C_v^2 i_v^{*2}\mu_h^3 N_T}{((\beta_{t_a}+\beta_{t_b})C_v i_v^* + \mu_h\mu_v)^2(\mu_h + r)},$$

where

$L_1 = 3\mu_h^2 + 5\mu_h\mu_v + 3\mu_h r + 2\mu_v r,$

$L_2 = 3\mu_h^2 + 4\mu_h\mu_v + 3\mu_h r + \mu_v r,$

$L_3 = \mu_h + \mu_v + r,$

$L_4 = \mu_h + r$

From Routh Hurwitz criteria [8,10], the eigenvalues have negative real parts when the following conditions are satisfied:

i) $A > 0$

ii) $C > 0$

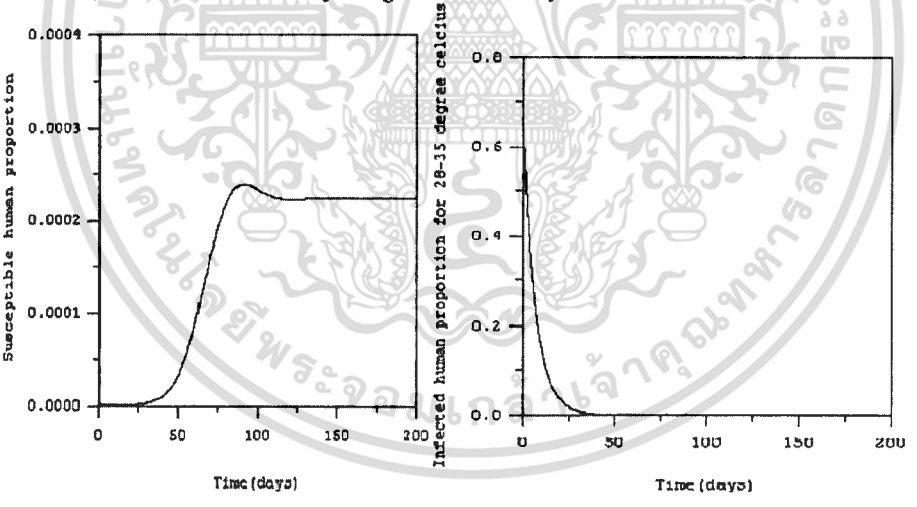
iii) $AB > C$.

From our evaluations, we can say that the above conditions are satisfied when $A_0 > 1$;

where $A_0 = \dfrac{(\beta_{1a} + \beta_{1b})\beta_v C_v N_T}{\mu_v^2(\mu_h + r)}$.

We can conclude that the first steady state is local stability when $A_0 < 1$ and the second steady state is local stability when $A_0 > 1$.

Next, we show our results by using numerical analysis.



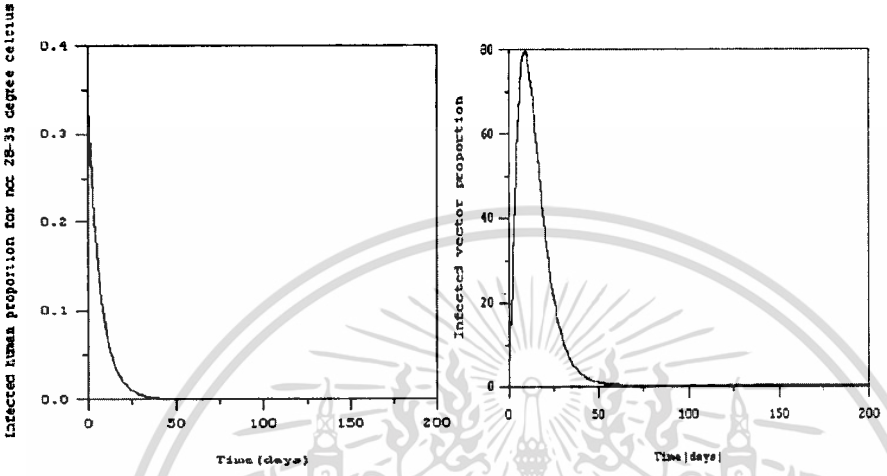


Figure 2. Time series of each population group for $\Lambda_0 = 4.480$. The parameters used in this study are $\mu_h = 0.0000457$, $\mu_v = 0.25$, $\beta_{t_a} = 0.0007$, $\beta_{t_b} = 0.0003$, $\beta_v = 1$, $r = 0.1428$, $N_T = 100$, $C_v = 400$. The solutions converge to the steady state (0.000223266,0.000223893,0.000095,0.127899).

From figure 2, it can be seen that the solutions converge to the endemic steady state for $\Lambda_0 > 1$.

RESULTS AND DISCUSSION

The threshold number is defined by $\Lambda_0 = \frac{(\beta_{t_a} + \beta_{t_b})\beta_v C_v N_T}{\mu_v^2(\mu_h + r)}$. For $\Lambda_0 < 1$, the disease free state is local stability and the endemic state is local stability for $\Lambda_0 > 1$. The basic reproductive number is defined by $\hat{\Lambda}_0 = \sqrt{\Lambda_0}$, it represents the average number of secondary cases produced from primary cases. This values are used for reduced the outbreak of this disease. Next, we compare the behavior of solutions for the different total human population.

การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

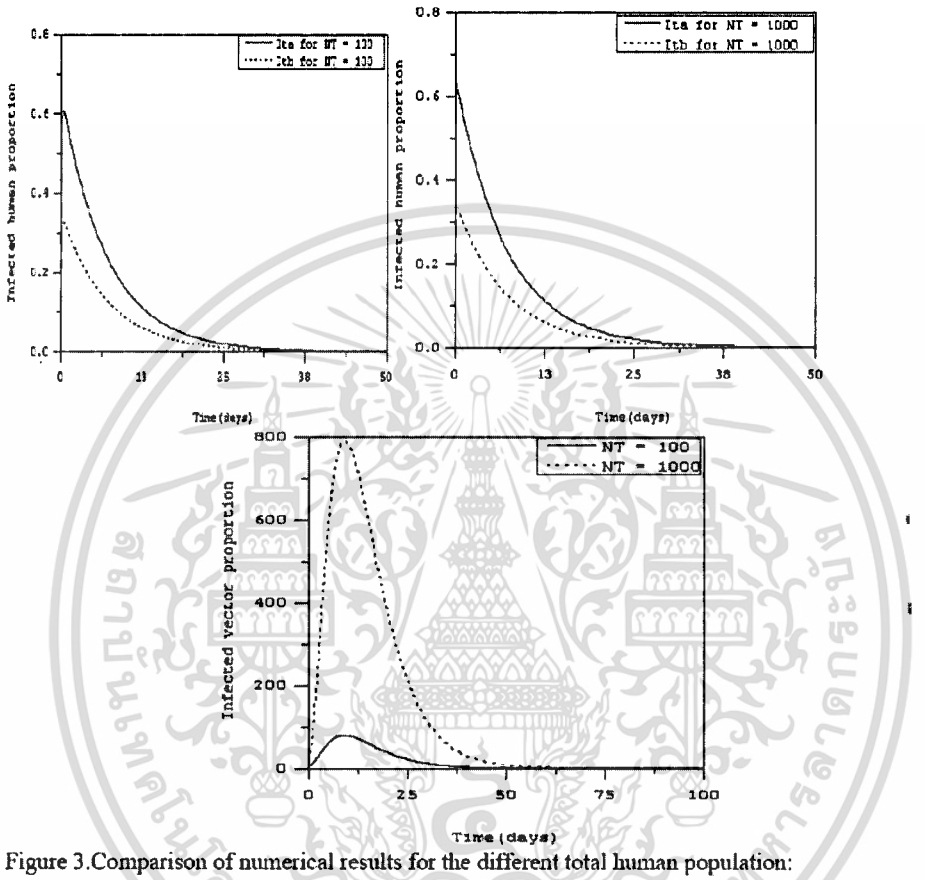


Figure 3.Comparison of numerical results for the different total human population: $N_T = 100$ and $N_T = 1000$.

We can see that the fraction of vector population and the outburst time are depending on the total human population. The fraction of dengue cases are depending on the temperature, as we can see from figure 3. The fraction of dengue cases for $28\text{-}35^0$ c are greater than the other temperatures because the appropriated temperature for the growth of mosquito population.

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DYNAMICAL MODEL OF DENGUE TRANSMISSION IN *AEDES ALBOPICTUS* AND *AEDES AEGYPTI* VECTORS WITH RAINING

Puntani Pongsumpun

King Mongkut's Institute of Technology Ladkrabang, Thailand

Dengue disease is a frequent occurrence in Thailand. This disease is due to biting by *Aedes Albopictus* or *Aedes Aegypti* mosquitoes. This study examines the transmission of the disease between vectors. The volume of rain is considered to be one factor for the transmission of two species of vectors. The dynamical model is formulated by blending mathematics and epidemiology. Our model is analyzed and numerical solutions are offered to the reader.

Keywords: *Aedes Aegypti*, *Aedes Albopictus*, Dengue disease, Dynamical model, Raining.

Introduction

The tropical disease usually found in Thailand, called as dengue disease. DEN-1, DEN-2, DEN-3 and DEN-4 are four serotypes of dengue virus. This disease has appeared as a worldwide problem since the 1950s[1]. More than one-third of the world's population living in areas at risk for dengue infection. Dengue virus is a leading cause of illness and death in the tropics and subtropics. In each year, there are 400 million people are infected. Dengue is caused by any one of four serotypes. The virus is transmitted to human by bitting of *Aedes Albopictus* or *Aedes Aegypti* mosquitoes. After people be infected with dengue virus, people can be appeared as DF(Dengue Fever), DHF(Dengue Hemorrhagic Fever) and DSS(Dengue Shock Syndrome). It depends on the severity of the disease [2]. After world warII, the dengue epidemiology changed. A primary infection intoduces a classic primary-type immunologic response characterized by the initially appearance of dengue antibodies of the immunoglobulin M (IgM) class [3,4]. Dengue viruses are transmitted between people by biting of infected female *Aedes* mosquitoes. *Aedes albopictus and Aedes aegypti* are the most important epidemic vectors[5]. *Aedes albopictus* belongs to the same subgenus (*Stegomyia*) as *Aedes aegypti*. This species can be found in Asia from tropical to temperate countries. This species has extended its range to North and South America, the Caribbean, Africa, Southern Europe and some Pacific islands. It is a forest species that has become adapted to rural, suburban and urban human environments. It oviposits and develops in tree holes, bamboo stumps and leaf axils in forest habitats. In some areas of Asia and in the Seychelles, *Aedes albopictus* has been occasionally incriminated as the vector of dengue epidemic [6]. *Aedes aegypti* can be found in tropical and subtropical areas of South-East Asia, and is common in most urban areas. It can be found around the globe, usually between latitudes 35^0 N and 35^0 S. It is one of the most efficient mosquito vectors for arboviruses, because it is highly antropophilic and thrives in close proximity to humans and often lives indoors [7]. The studies of disease transmission occurred for long time ago. In 2000, Esteva and Vargas [8] constructed non-linear system of differential equations that models the

dynamics of vertical and mechanical transmission in the vector population, and studied the effects that these types of transmission have on the dynamics of the disease. Recently [9], we studied the SIR transmission model of dengue disease with two species of mosquitoes and age structure of human population. We studied the transmission model of dengue disease in the flooding area [10]. From the data of dengue disease in Thailand[11], It indicates that there is the higher rate of dengue patients in rainy season. From the behaviors of *Aedes* vectors, the humidity and temperature effect to the growth of eggs' mosquitoes. In this paper, we formulate the transmission model of dengue disease by considering the vertical transmission in *Aedes albopictus and Aedes aegypti* vectors with the volume of raining.

Mathematical Model

Our model is formulated by considering the two species of vectors, *Aedes albopictus* and *Aedes aegypti*. Each species is separated in to 3 classes, Eggs(O), Exposed(E) and Infectious(I) classes. The volume of raining effects to the number of eggs' mosquitoes. The dynamical equations are explained as follows:

For *Aedes albopictus* vector,

$$O_A'(t) = va_1A - a_2O_A(t) - \mu_A O_A(t), \tag{1}$$

$$E_A'(t) = a_2O_A(t) - \frac{1}{EP_A}E_A(t) - \mu_A E_A(t), \tag{2}$$

$$I_A'(t) = \frac{1}{EP_A}E_A(t) - \mu_A I_A(t). \tag{3}$$

with $N_A(t) = O_A(t) + E_A(t) + I_A(t)$.

For *Aedes aegypti* vector,

$$O_B'(t) = vb_1B - b_2O_B(t) - \mu_B O_B(t), \tag{4}$$

$$E_B'(t) = b_2O_B(t) - \frac{1}{EP_B}E_B(t) - \mu_B E_B(t), \tag{5}$$

$$I_A'(t) = \frac{1}{EP_B}E_B(t) - \mu_B I_B(t). \tag{6}$$

with $N_B(t) = O_B(t) + E_B(t) + I_B(t)$.

We define varaiables and parameters as follows:

$O_A(t)$ is the number of eggs' *Aedes albopictus* vector.

$O_B(t)$ is the number of eggs' *Aedes aegypti* vector.

$E_A(t)$ is the number of exposed *Aedes albopictus* vector.

$E_B(t)$ is the number of exposed *Aedes aegypti* vector.

$I_A(t)$ is the number of infectious *Aedes albopictus* vector.

$I_B(t)$ is the number of infectious *Aedes aegypti* vector.

v is the probability of producing eggs' mosquitoes at the time of raining.

a_1 is the rate of producing eggs per 1 *Aedes albopictus* vector.

b_1 is the rate of producing eggs per 1 *Aedes aegypti* vector.

a_2 is the survival rate of eggs of *Aedes albopictus* vector.

b_2 is the survival rate of eggs of *Aedes aegypti* vector

A is the constant recruitment rate of *Aedes albopictus* vector.

B is the constant recruitment rate of *Aedes aegypti* vector.

EP_A is the incubation period of *Aedes albopictus* vector.

EP_B is the incubation period of *Aedes aegypti* vector.

μ_A is the death rate of *Aedes albopictus* vector.

μ_B is the death rate of *Aedes aegypti* vector.

N_A is the total number of *Aedes albopictus* vector.

N_B is the total number of *Aedes aegypti* vector.

To reduce our equations, we introduce the new variables: $\tilde{O}_A(t), \tilde{O}_B(t), \tilde{E}_A(t), \tilde{E}_B(t), \tilde{I}_A(t)$ and $\tilde{I}_B(t)$ as the proportion of each population group that is $\tilde{O}_A(t) = O_A(t)/N_A, \tilde{O}_B(t) = O_B(t)/N_B, \tilde{E}_A(t) = E_A(t)/N_A, \tilde{E}_B(t) = E_B(t)/N_B, \tilde{I}_A(t) = I_A(t)/N_A$ and $\tilde{I}_B(t) = I_B(t)/N_A$. Then we obtain 4 reduced equations:

$$\tilde{O}_A'(t) = -(a_2 + \mu_A)O_A(t) + \frac{Aa_1 v}{N_A}, \tag{7}$$

$$\tilde{I}_A'(t) = (1/EP_A)(1 - O_A(t) - I_A(t)) - I_A(t)\mu_A, \tag{8}$$

$$\tilde{O}_B'(t) = -(b_2 + \mu_b)O_B(t) + \frac{Bb_1 v}{N_B}, \tag{9}$$

$$\tilde{I}_B'(t) = (1/EP_B)(1 - O_B(t) - I_B(t)) - I_B(t)\mu_B, \tag{10}$$

where $\tilde{O}_A(t) + \tilde{E}_A(t) + \tilde{I}_A(t) = 1$ and $\tilde{O}_B(t) + \tilde{E}_B(t) + \tilde{I}_B(t) = 1$.

The standard dynamical modeling method is used in this study[12]. First, we find equilibrium states by setting eqs.(7) – (10) to zero, then we get an equilibrium state $(\tilde{O}_A', \tilde{E}_A', \tilde{O}_B', \tilde{E}_B')$ where

$$\tilde{O}_A' = \frac{Aa_1 v}{(a_2 + \mu_A)N_A},$$

$$\tilde{I}_A' = \frac{Aa_1 a_2 v}{(a_2 + \mu_A)(\mu_A + EP_A\mu_A^2)N_A},$$

$$\tilde{O}_B' = \frac{Bb_1 v}{(b_2 + \mu_B)N_B},$$

$$\tilde{I}_B' = \frac{Bb_1 b_2 v}{(b_2 + \mu_B)(\mu_B + EP_B\mu_b^2)N_B}.$$

To determine the local stability of this equilibrium state, we evaluate the eigenvalues (λ) from $\det(J - \lambda I) = 0$; where J is the Jacobian matrix and I is the identity matrix.

J is defined by

$$J = \begin{pmatrix} \frac{\partial F_1}{\partial \tilde{O}_A} & \frac{\partial F_1}{\partial \tilde{I}_A} & \frac{\partial F_1}{\partial \tilde{O}_B} & \frac{\partial F_1}{\partial \tilde{I}_B} \\ \frac{\partial F_2}{\partial \tilde{O}_A} & \frac{\partial F_2}{\partial \tilde{I}_A} & \frac{\partial F_2}{\partial \tilde{O}_B} & \frac{\partial F_2}{\partial \tilde{I}_B} \\ \frac{\partial F_3}{\partial \tilde{O}_A} & \frac{\partial F_3}{\partial \tilde{I}_A} & \frac{\partial F_3}{\partial \tilde{O}_B} & \frac{\partial F_3}{\partial \tilde{I}_B} \\ \frac{\partial F_4}{\partial \tilde{O}_A} & \frac{\partial F_4}{\partial \tilde{I}_A} & \frac{\partial F_4}{\partial \tilde{O}_B} & \frac{\partial F_4}{\partial \tilde{I}_B} \end{pmatrix} \quad \text{when}$$

$$F_1(t) = -(a_2 + \mu_A)O_A(t) + \frac{Aa_1 v}{N_A}, \tag{7}$$

$$F_2(t) = (1/EP_A)(1 - O_A(t) - I_A(t)) - I_A(t)\mu_A, \tag{8}$$

$$F_3(t) = -(b_2 + \mu_b)O_B(t) + \frac{Bb_1 v}{N_B}, \tag{9}$$

$$F_4(t) = (1/EP_B)(1 - O_B(t) - I_B(t)) - I_B(t)\mu_B. \tag{10}$$

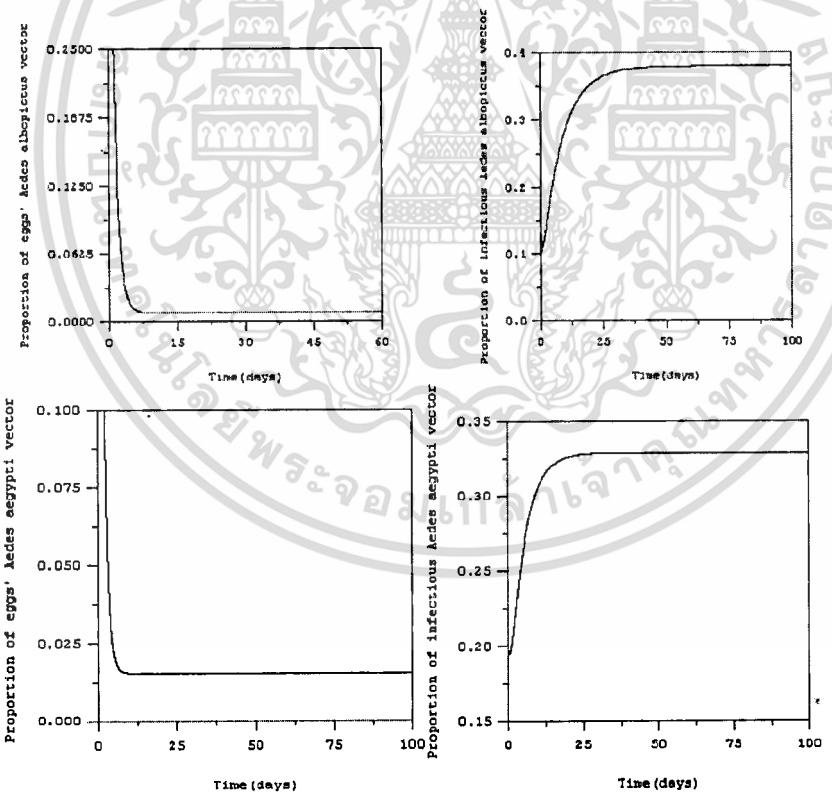
After calculation, the characteristic equation of our equilibrium state is

$$(\lambda^2 + (a_2 + 1/EP_A + 2\mu_A)\lambda + a_2/EP_A + a_2\mu_A + \mu_A/EP_A + \mu_A^2)$$
$$(\lambda^2 + (b_2 + 1/EP_B + 2\mu_B)\lambda + a_2/EP_B + a_2\mu_B + \mu_B/EP_B + \mu_B^2) = 0. \tag{11}$$

The eigenvalues are $\lambda_1 = -a_2 - \mu_A$, $\lambda_2 = -(1/EP_A)(1 + EP_A\mu_A)$, $\lambda_3 = -b_2 - \mu_b$ and $\lambda_2 = -(1/EP_B)(1 + EP_B\mu_B)$.

From local stability theorem[12], the equilibrium state is local stability when the eigenvalues give the negative signs, It can be seen that all eigenvaluaes are negative. Therefore, we can conclude that the equilibrium state is local stability.

Next, we show the results by using numerical results. The parameters used in this study follow the real situations.



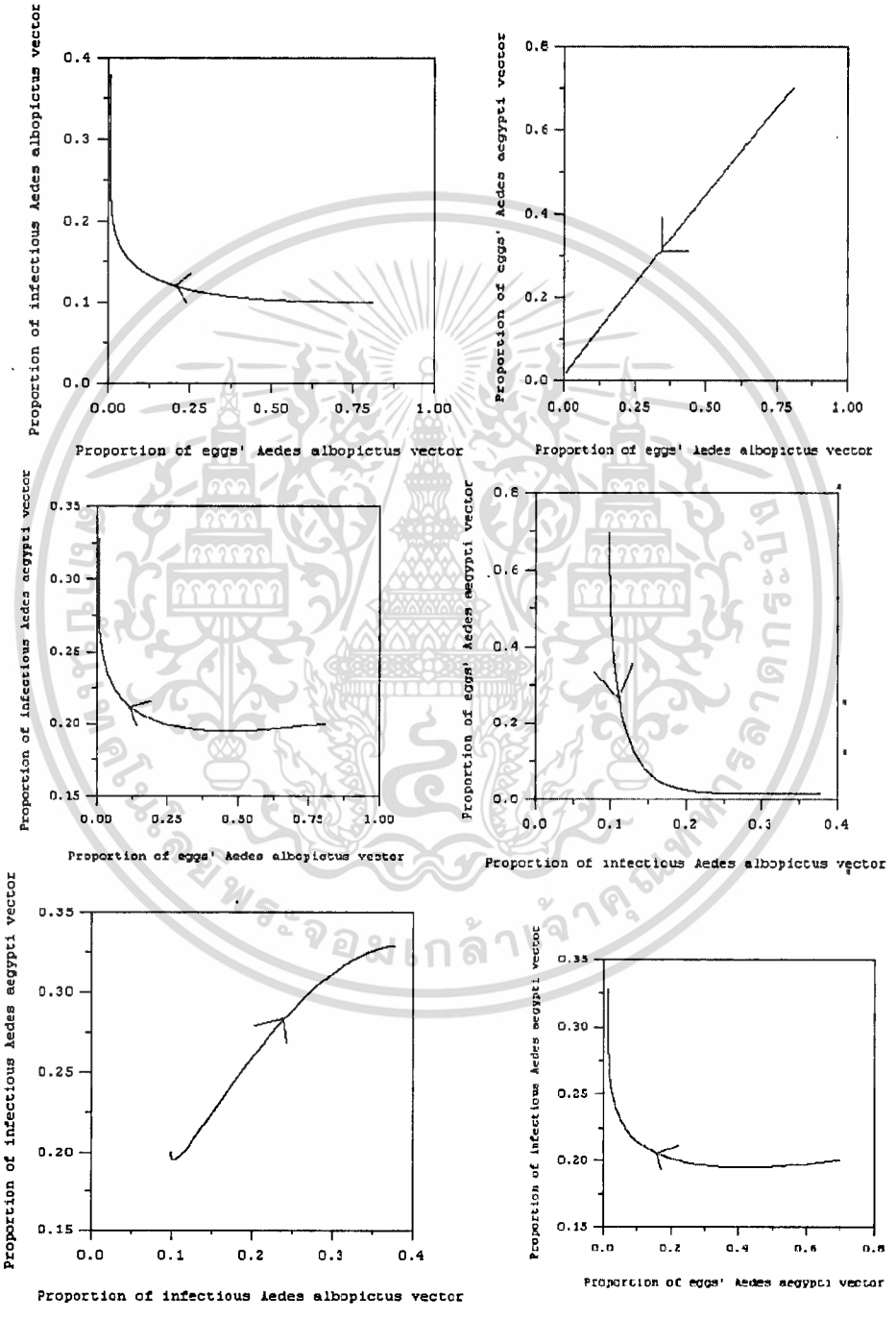


Figure 1. Numerical solutions of our equations(7)-(10). The parameters used in this study are v =0.1, $a_1 = 0.8$, A=7,000. $a_2 = 0.9$, $\mu_A = 1/13$, $EP_A = 21$, $b_1 = 0.6$, B = 10,000, $b_2 = 0.8$, $\mu_B = 1/7$, $EP_B = 14$.

We will see that the solutions converge to the equilibrium state (0.00787402,0.379342, 0.0151515,0.328283) corresponding to the analytical results.

Results and Discussion

Mathematical model is formulated corresponding to the characteristics of dengue disease.The effect of raining is considered in this study. Mathematics is applied to many diseases [13,14]. We simulate our solutions when there are the different probabilities of producing eggs' mosquitoes at the time of raining.

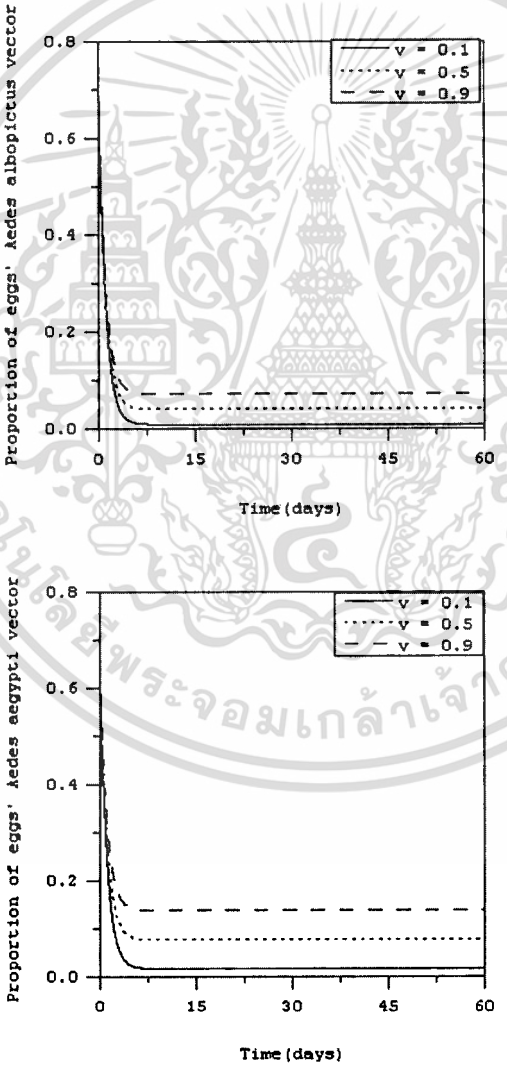


Figure 2. Time series solutions of proportion of eggs' *Aedes albopictus* and *Aedes aegypti* vectors for the different probability of producing eggs' mosquitoes at the time of raining

From fig.2, we can see that the volume of raining effects to the eggs of two species of vectors(*Aedes albopictus* and *Aedes aegypti*). When there is the higher volume of raining, the higher proportion of vectors. This corresponding to the real situation in Thailand [11].

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Household Distribution of Dengue Epidemic of the Flooding Area

P.Pongsumpun

***Abstract*—Dengue disease is transmitted to human by biting of infected *Aedes* mosquitoes. From dengue data in Bangkok, Thailand, we found that there is the high rate of dengue cases when there is the flood in Bangkok. The movement of human and the flying of mosquitoes are always happen. Thus, the above three factors effect to the transmission of dengue disease. In this paper, we formulate the dynamical network model and the behaviors of solutions to our model are shown for the different set of parameters. The simulation outputs are shown to introduce the way for reduce the dengue outbreak.**

Index Terms*—*Aedes mosquito, flood, dengue, movement dynamical equations.

I. Introduction

DENGUE disease is considered to be the most tropical disease in Thailand. Four serotypes of this disease are denoted as DEN-1, DEN-2, DEN-3 and DEN-4.Dengue disease is classified into three types: Dengue Fever(DF). DengueHemorrhagic Fever(DHF) and Dengue Shock Syndrome(DSS).Dengue virus is transmitted from person to person by biting of infected female *Aedes* mosquitoes. *Aedes albopictus* and *Aedes polynesiensis*, members of *Aedesscutellaris complex* have also been incriminated as secondary vectors [1].The appropriated temperature of dengue transmission is above 20^0 C, and it never transmit virus at 16 ^{0}C. The changed season is effected to dengue transmission. Dengue transmission is always decreasingwith the approach of cold temperatures. The person can produce life-long immunity of dengue virus to that infected serotype when he/she is infected with dengue virus for the first time but only partial protection to the other three serotypes. Transmission of dengue virus from an infected human to a mosquito is determined by the magnitude and duration of viremia in the human host. Person with high viremia provides a higher infectious dose of virus to feeding mosquito. This normally leads to a greater percentage of feeding mosquitoes becoming infected. Some mosquito vectors may however become infectious when there is only a very low level of virus in the blood [1.2]. The dengue virus epidemic in Australia ceased as the temperature dropped to 14-15 ^{0}C at the beginning of winter. Temperature may also effect the maturation of mosquitoes, higher temperature producing smaller females which are forced to take more blood meals to obtain the protein needed for egg production[3]. The temperature and humidity are influence to the extrinsic incubation period of the mosquitoes and is an important variable in causing epidemic transmission [4]. The extrinsic incubation period of the mosquito in the low temperature is greater than that in the high temperature [5]. If the climate is too cold, the development of virus is slow then the mosquitoes can not survive long enough to become infectious [6]. The mosquitoes never recover from the infection since their infective period ends with their death [2].Because 2011 is the year which has many flooding areas in Bangkok, then we compare 2 years between 2010 and 2011 to see the distribution of dengue cases. We compare the data of dengue cases in Bangkok, Thailand for each area between year 2010 and 2011. We can see that the flooding effect to the transmission of dengue virus as shown in fig.1 [7].

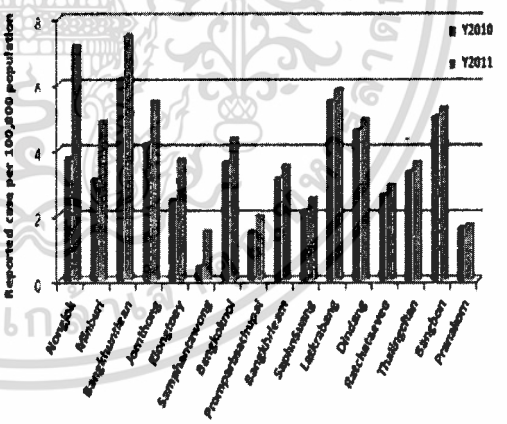

Fig.1.The reported cases of dengue disease in each area of Bangkok, Thailand between year 2010 and 2011.

Esteva and Vargas [8] formulated the mathematical model of dengue disease in 1998. They considered the transmission of dengue disease between human and mosquito. The total human and vector population have constant sizes. In 2008, the dynamical model of dengue disease is considered with the incubation of dengue virus [9]. In this paper, we consider the dynamical equations of dengue disease considering the traveling of human and mosquitoes with the effect of flooding.

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P. Pongsumpun is with Department of Mathematics, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Chalongkrung road, Ladkrabang, Bangkok, THAILAND,10520(corresponding author to provide phone: (662)-329-8000; e-mail:kppuntan@kmitl.ac.th).

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II. DYNAMICAL MODEL

Dengue virus is transmitted between human and mosquitoes. We assume that people can move between houses. The mosquitoes can fly to any houses. In the beginning, there is only one dengue case and he/she can stay in any house. The people can travel to any house but at the ending day, he/she will come back to the house same as the beginning day. The flood effects to the transmission of dengue virus, thus the rate of flooding is considered in our model. The discrete dynamical equations can be described as the following equations:

$$\Delta Sh_{t,k} = -\varphi f_h\left(\frac{r}{r_{\max}}\right) Iv_{t,k} Sh_{t,k} + w\left(\frac{r}{r_{\max}}\right) Rh_{t,k}$$

$$\Delta Ih_{t,k} = \varphi f_h\left(\frac{r}{r_{\max}}\right) Iv_{t,k} Sh_{t,k} - aIh_{t,k}$$

$$\Delta Rh_{t,k} = aIh_{t,k} - w\left(\frac{r}{r_{\max}}\right) Rh_{t,k}$$

$$\Delta Sv_{t,k} = -\varphi f_v\left(\frac{r}{r_{\max}}\right) Ih_{t,k} Sv_{t,k} - \mu_v Sv_{t,k}$$

$$\Delta Iv_{t,k} = \varphi f_v\left(\frac{r}{r_{\max}}\right) Ih_{t,k} Sv_{t,k} - \mu_v Iv_{t,k}$$

The parameters are defined as in the following table:

TABLE I
THE DEFINITIONS OF VARIABLES/PARAMETERS IN OUR DYNAMICAL EQUATIONS.

Variable/Parameter	Definition
$Sh_{t,k}$	Number of susceptible persons of k^{th}house at time t.
$Ih_{t,k}$	Number of infectious persons of k^{th} house at time t.
$Rh_{t,k}$	Number of recovered persons of k^{th} house at time t.
φ	Percentage of flooding.
$Sv_{t,k}$	Number of susceptible vector of k^{th} house at time t.
$Iv_{t,k}$	Number of infectious vector of k^{th} house at time t.
$Rv_{t,k}$	Number of recovered vector of k^{th} house at time t.
f_h	Infectious rate of dengue virus from vector to human.
r	The distant of flying 's mosquito.
$r_{\max}$	The maximum distant of flying 's mosquito
w	The rate at which the recovered persons can become to be susceptible persons.
a	The recovery rate of human.
f_v	Infectious rate of dengue virus from human to vector.
μ_v	The death rate of vector.

Our dynamical equations are calculated by simulating the different set of parameters. The solutions are shown in the next section.

A. Analysis of our equations

We simulate the different sets of parameters. The considered parameters are Percentage of flooding (φ),Infectious rate of dengue virus from vector to human (f_h).The distant of flying 's mosquito(r) and Infectious rate of dengue virus from human to vector(f_v). The different sets of parameters are shown in the following table. The results are the total number of dengue cases from all houses.

TABLE II
THE DIFFERENT SET OF PARAMETERS IN THIS SIMULATIONS.

Parameter	Values			
φ	80%	60%	40%	20%
f_h	0.9	0.6	0.3	0.1
r	400	300	200	100
f_v	1.0	0.75	0.5	0.25

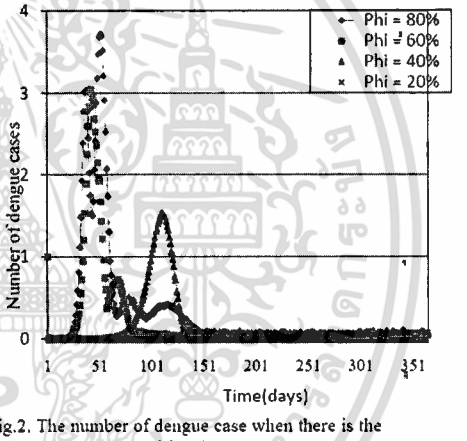

Fig.2. The number of dengue case when there is the different percentage of flooding.

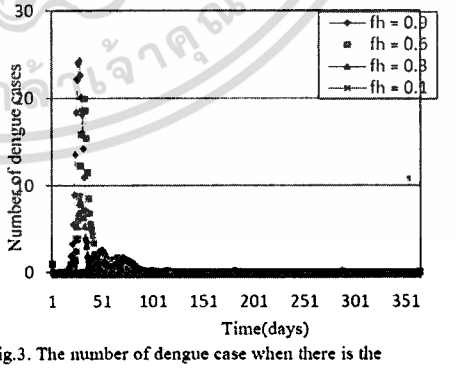

Fig.3. The number of dengue case when there is the different infectious rate of dengue virus from vector to human.

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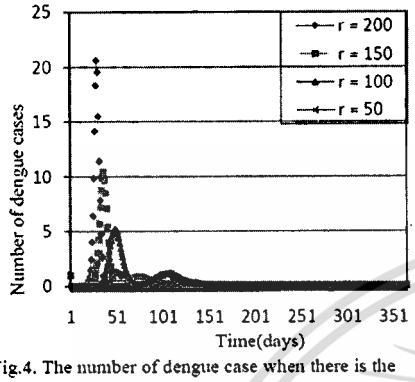

Fig.4. The number of dengue case when there is the different distant of flying's mosquito.

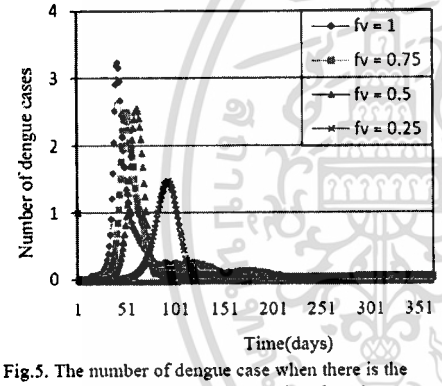

Fig.5. The number of dengue case when there is the different infectious rate of dengue virus from human to vector.

Moreover, we consider when there are the different total human and the number of houses. The results are shown in fig.6 and fig.7.

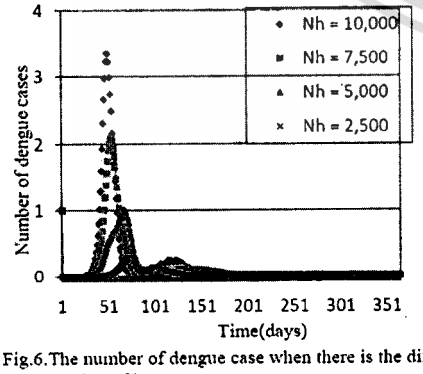

Fig.6.The number of dengue case when there is the different total number of human.

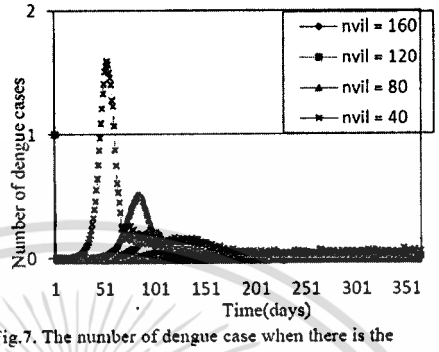

Fig.7. The number of dengue case when there is the different number of houses.

III. Discussion and Conclusion

In this study, we simulate the different set of parameters to see the factors effect to the transmission of this disease. From our simulations, we found that when percentage of flooding (φ), Infectious rate of dengue virus from vector to human(f_h) are increasing. The distant of flying 's mosquito(r) and the total human population is increasing. the infectious dengue case is increasing and the outburst time of dengue epidemic is longer. But when the number of house is increasing, the number of dengue case is decreasing and the outburst of dengue epidemic is shorter.The preliminary results of this study should suggest the factors influence to dengue transmission.

Acknowledgment

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การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรคไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์

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ENVIRONMENTAL IMPACT ON THE SPREAD OF DENGUE VIRUS WHEN TWO MOSQUITO SPECIES CIRCULATE

Rattiya Sungchasit[1,2], Puntani Pongsumpun[1] and I Ming Tang[3]

[1]Department of Mathematics
Faculty of Science
King Mongkut's Institute of Technology Ladkrabang
Chalongkrung Road
Ladkrabang, Bangkok 10520
Thailand
e-mail: kppuntan@kmitl.ac.th

[2]Mathematics Program
Faculty of Science Technology
Phuket Rajabhat University
Phuket 83000, Thailand

[3]Department of Materials Science
Faculty of Science
Kasetsart University
50 Ngam Wong Wan Road
LatYao Chatuchak
Bangkok 10900, Thailand

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2 Rattiya Sungchasit, Puntani Pongsumpun and I Ming Tang

Abstract

We study the environmental impact on the dengue fever epidemic when two species of mosquitoes namely the *Aedes aegypti* and *Aedes albopictus* circulate. The infected populations of the humans and of mosquito species are each divided into two groups, the being infected but not infectious and the other infected and infectious (I). A SEIR model and SEI model are developed for the human and the two mosquito populations, respectively. The dynamical behaviors of the three populations are obtained by simulating the behaviors by numerically solving the differential equations which describe the models. Changes in the trajectories when the values of the environment dependent parameters are changed reveal the influence of the environment on the spread of the dengue virus. Often the values of the parameters in the two SEI models will depend on how a particular mosquito specie interacts with the environment and so the values of the parameters will be different in the two SEI models. This makes possible that the basic production numbers of the two species ($S_{aegypti}$ and $S_{albopictus}$) will be different giving different S_i's which give the following combinations ($S_{aegyptii} > 1$, $S_{albopictus} > 1$), ($S_{aegyptii} > 1$, $S_{albopictus} < 1$), ($S_{aegyptii} < 1$, $S_{albopictus} > 1$) and ($S_{aegyptii} < 1$, $S_{albopictus} < 1$). When the different conditions are satisfied, nature will have both species present, only one specie present or no species present.

1. Introduction

Dengue fever (DF) is one of the arthropod-borne diseases that is endemic in more than 100 tropical and subtropical countries mostly in Africa, Central America and Southeast Asia [1]. It can also infect countries in southern Europe, in particular, Italy and Spain. The World Health Organization (WHO) has labeled DF as being the most important vector borne disease since there are more than 2.5 billion people at risk to this disease [2]. The disease is caused by any one of the four serotypes of the dengue virus, labeled DEN1, DEN2, DEN3 and DEN4. Infection by one serotype does not lead to immunity to infections by another type of the virus [3].

The virus is spread to a human by the bite of two species of the *Aedes* mosquitoes, the *A. aegypti* and the *A. albopictus* mosquitoes. The discovery that DF can be spread by the latter species has caused concern among the public health officials around the world since the *A. albopictus* mosquito can survive at colder temperatures [4], making it possible for DF to appear in the northern Europe and the United States (USA). Understanding the spread of this disease is of special importance to Thailand since epidemics involving three or more different serotypes of the dengue virus have occurred in the country. In most countries, the epidemic is due to only one of the serotypes [5]. Furthermore, both the *A. aegypti* and *A. albopictus* mosquitoes exist in Thailand [6]. The *A. aegypti* mosquitoes are found in the urban areas since the females lay their eggs in manmade containers such as discarded tires, cans or broken bottles. The *A. albopictus* mosquitoes are found in the rural areas since the females lay their eggs in natural crevices between the individual banana or bamboo trees which grow in clusters in the clearing in the jungle. The *A. albopictus* mosquito has however adapted itself so that it can also survive in the urban environment.

The females of both species lay their eggs above the water line of the breeding pool [7]. Therefore the eggs will only hatch when the eggs are inundated by water. In Thailand and other countries in South East Asia, this happens only after a heavy rainfall. In dry area such as in southwest United States, the water can come from the human watering of the crops [8]. Without the inundating water, the eggs will not hatch and there will be no more adult mosquitoes until the next rainy season. If there are no mosquitoes in the environment, there would no further infection humans. There should therefore be a correlation between the number of dengue infection and the start of the rain fall. In Figure 1 which is a plot of the number of cases of dengue fever in each month, the mean temperature and the cumulative rainfall in southern Thailand in 2010 [9], we do indeed see that the highest incidence of dengue infections occurs during the rainy season.

The temperature also affects the development of the dengue virus. The virus develops inside the mosquitoes in hot weather. But as the temperature

decreases, the incubation period increases. At 16°C, the incubation period can be longer than the life time of the mosquitoes. Thus the mosquito will die before it becomes infectious. After the last rainfall of the season, the eggs laid do not shrivel up and die since the eggs of both species at this time are desiccate resistant and survive for a long period during the dry season (between 3 to 8 months for the *A. aegypti* eggs [10-11] and 340 days for the *A. albopictus* eggs [12]). This long desiccation resistance time for the *A. aegypti* eggs made it possible for the *A. aegypti* mosquitoes to be reintroduced into Cuba when used tires carrying the eggs were imported into Cuba from SE Asia [13]. Harrigton et al., have forecasted the effects of temperature and rain fall on the incidence of dengue fever [14, 15].

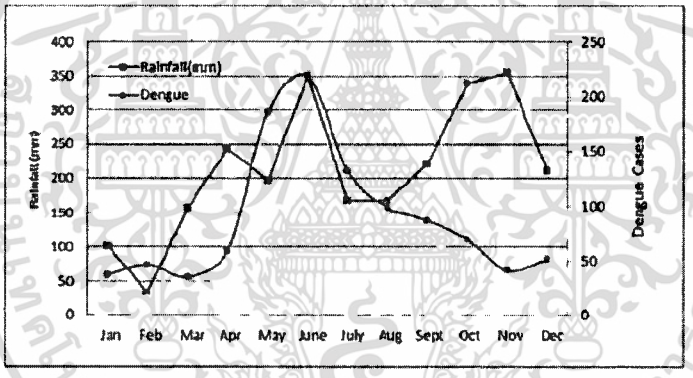

Figure 1. Reported cases of Dengue cases, mean temperature and rainfall southern Thailand in 2010.

Other climatic effects that affect the survival of the different species have been reported by Juliano et al. [16]. They reported that the proportion of bleeding sites occupied by the *A. albopictus* eggs at the start of the rainy season was significantly lower than the proportions well into the rainy season. This difference in the number of breeding sites occupied by the *A. aegypti* eggs did not appear to be affected by whether one was at the beginning or middle (or end) of the rainy season. This could be the reason for the seasonal shift in the relative abundance of the *A. aegypti* and the *A. albopictus* mosquitoes observed by Mogi et al. [6] in Chiang Mai, northern Thailand. The *A. aegypti* mosquitoes being the most abundant at the

beginning of the rainy season and the *A. albopictus* mosquitoes being the more abundant towards the end of the rainy season. Esteva and Vargas [17] were the first to develop a model for dengue disease transmission and which incorporated the dynamics of the *Aedes aegypti* mosquito into a standard SIR (S-susceptible, I-infected, R-recovered) model for the human population and SI model for vector. Pongsumpun and Kongnuy [18] utilized the Lyapunov function to determine the effect of maternal antibodies on the dengue disease in newly born infants. In order to take into account the fact that the dengue viruses need to incubate inside the human and mosquitoes before they can be transmitted to a different host, the infected class needs to be divided into an infected but not infectious class and an infectious class, the I class in the original model should be replaced by an E (exposed) and an I (Infectious) class. Thus the SIR model becomes a SEIR model while the SI model for the mosquitoes becomes a SEI model. If there are more than one serotype of the dengue virus around, the recovered class can become a new susceptible class which can be infected by the second serotype. For dengue virus, the infection by one serotype confers immunity to human to that serotype but not to the other serotypes. Sriprom, Barbazan and Tang [19] have developed a SEIRS model to study the destabilization effect of the host immune status on the sequential transmission dynamics of the DF infection.

For this study of dengue infection when there are two species of mosquitoes present, we use the SIERS model to describe the dynamics of the DF virus in the humans and two SEI models to describe the dynamics in the two species of mosquitoes. In this research, we use the data of dengue disease in southern Thailand, 2010 to create the model. Analysis of the model shows that there is a reproductive ratio S_0 that conceptualizes the rate of spread of a dengue disease and determines a threshold: when $S_0 < 1$, a typical infection give rise, on average, to less than one secondary infection, and the disease will die out. When $S_0 > 1$, the disease will become endemic.

2. Formulation of Model for Dengue Disease

Sungchasit et al. [20, 21] used a SIR model for describing the dengue

transmission by *Aedes aegypti* and *Aedes albopictus*. Since we are interested in the effects of environment factors on the spread of DF in Thailand, we have used the SEIRS (host (human) population (the recovered can be susceptible to infection by another serotypes of the DENV) model to describe the transmission of the DF in Thailand. We have taken the mean temperature, and cumulative rainfall to be the values for those southern Thailand. In the flow chart appearing in Figure 2, $N_{a(b)}$ is the total human population which will be bitten by an *A. aegypti* mosquito (denoted by the subscript (a)) or by an *A. albopictus* mosquito (now dented by the subscript (b)). The two human populations are each divided into five compartments, $S_i(t)$, $E_i(t)$, $I_i(t)$, $R_i(t)$ and $S_i'(t)$ are the numbers of humans who are susceptible to the dengue virus carried by a specie '*i*' mosquito (*i* is a if the specie is *A. aegypti* and is "*b*" if the specie is *A. albopictus* the *i*-th specie of mosquitoes, infected but not infectious, infectious, recovered and susceptible to infection by the second serotype virus, respectively. Denoting the total numbers of *A. aegypti* mosquitoes and *A. albopictus* mosquitoes as N_{va} or N_{vb}. If a second serotype virus is present, then the recovered humans would be susceptible to infection by the second serotype virus. The last group however is immune to further infections by the same serotype of virus. The populations of each species of the mosquitoes are separated into three subclasses, S_{vi} (susceptible '*i*' specie mosquito), E_{vi} (infected but not infectious '*i*' specie mosquito) and I_{vi} (infectious '*i*' specie mosquito). The flow charts for the different classes are shown in Figure 2.

The dynamical equations for the different population are obtained by inspection and are

$$\frac{dS_a(t)}{dt} = aN_h - \left(T_{va}\Psi_a\gamma_{vah}\frac{I_{va}(t)}{N_h + b} + \delta_h\right)S_a(t) + \theta_a R_a(t) \qquad (1)$$

$$\frac{dE_a(t)}{dt} = \left(T_{va}\Psi_a\gamma_{vah}\frac{I_{va}(t)}{N_h + b}\right)S_a(t) - (\delta_h + \alpha_a)E_a(t) \qquad (2)$$

$$\frac{dI_a(t)}{dt} = \alpha_a E_a(t) - (\delta_h + \beta_a) I_a(t) \tag{3}$$

$$\frac{dR_a(t)}{dt} = \beta_a I_a(t) - (\delta_h + \theta_a) R_a(t) \tag{4}$$

$$\frac{dS_b(t)}{dt} = (1-a)N_h - \left(T_{vb}\psi_b\gamma_{vbh}\frac{I_{vb}(t)}{N_h + b} + \delta_h\right) S_b(t) + \theta_b R_b(t) \tag{5}$$

$$\frac{dE_b(t)}{dt} = \left(T_{vb}\psi_b\gamma_{vbh}\frac{I_{vb}(t)}{N_h + b}\right) S_b(t) - (\delta_h + \alpha_b) E_b(t) \tag{6}$$

$$\frac{dI_b(t)}{dt} = \alpha_b E_b(t) - (\delta_h + \beta_b) I_b(t) \tag{7}$$

$$\frac{dR_b(t)}{dt} = \beta_b I_b(t) - (\delta_h + \theta_b) R_b(t) \tag{8}$$

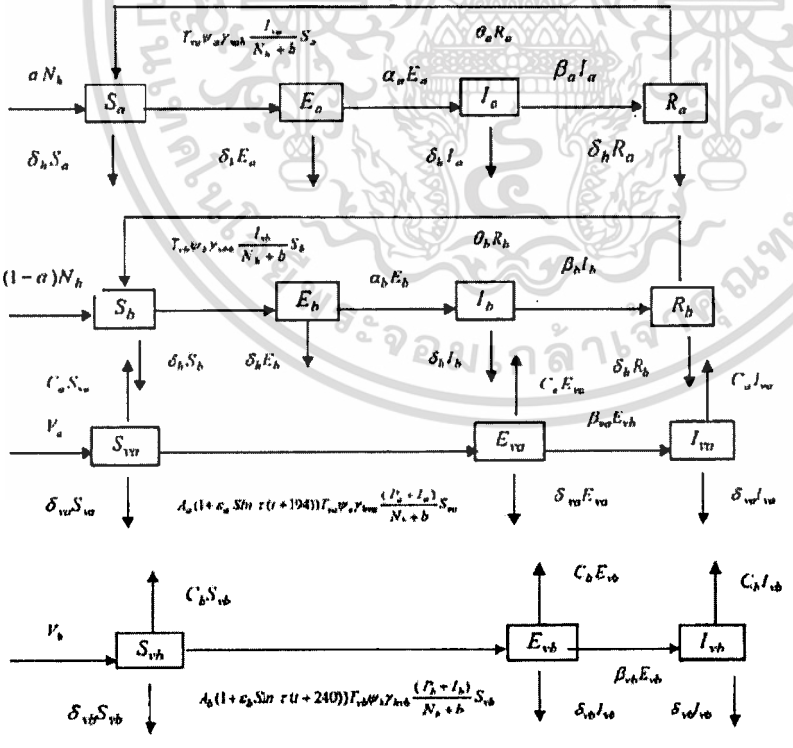

Figure 2. Flow Chart of the Model.

The dynamical systems are described by following equations.

$$\frac{dS_{va}(t)}{dt} = V_a$$

$$-\left(A_a(1+\varepsilon_a Sin\tau(t+194))T_{va}\psi_a\gamma_{hva}\frac{(P_a+I_a(t))}{N_h+b}+C_a+\delta_{va}\right)S_{va}(t) \quad (9)$$

$$\frac{dE_{va}(t)}{dt} = \left(A_a(1+\varepsilon_a Sin\tau(t+194))T_{va}\psi_a\gamma_{hva}\frac{(P_a+I_a(t))}{N_h+b}\right)S_{va}(t)$$

$$-(C_a+\delta_{va}-\beta_{va})E_{va}(t) \quad (10)$$

$$\frac{dI_{va}(t)}{dt} = \beta_{va}E_{va}(t)-(C_a+\delta_{va})I_{va}(t) \quad (11)$$

$$\frac{dS_{vb}(t)}{dt} = V_b$$

$$-\left(A_b(1+\varepsilon_b Sin\tau(t+240))T_{vb}\psi_b\gamma_{hvb}\frac{(P_b+I_b(t))}{N_h+b}+C_b+\delta_{vb}\right)S_{vb}(t) \quad (12)$$

$$\frac{dE_{vb}(t)}{dt} = \left(A_b(1+\varepsilon_b Sin\tau(t+240))T_{vb}\psi_b\gamma_{hvb}\frac{(P_b+I_b(t))}{N_h+b}\right)S_{vb}(t)$$

$$-(C_b+\delta_{vb}-\beta_{vb})E_{vb}(t) \quad (13)$$

$$\frac{dI_{vb}(t)}{dt} = \beta_{vb}E_{vb}(t)-(C_b+\delta_{vb})I_{vb}(t) \quad (14)$$

with

$$N_h = S_a(t)+E_a(t)+I_a(t)+R_a(t)+S_b(t)+E_b(t)+I_b(t)+R_b(t), \quad (15)$$

$$N_{va} = S_{va}(t)+E_{va}(t)+I_{va}(t),\ N_{va} = S_{vb}(t)+E_{vb}(t)+I_{vb}(t). \quad (16)$$

The parameters of our dynamical system are defined in the Table 1. Taking the time derivative of N_h and N_{va} (and N_{vb}) and substituting the time derivates of the subpopulations equations (1) to (14), we find that

$$\frac{dN_h}{dt} = 0,\ \frac{dN_{va}}{dt} = 0 \text{ and } \frac{dN_{va}}{dt} = 0$$

meaning that N_h, N_{va} and N_{vb} are independent of time, i.e., they are constants. Dividing equations (1)-(14) by these constants and introducing the new variables.

$$\widetilde{S}_a(t) = \frac{S_a(t)}{N_h},\ \widetilde{E}_a(t) = \frac{E_a(t)}{N_h},\ \widetilde{I}_a(t) = \frac{I_a(t)}{N_h},\ \widetilde{R}_a(t) = \frac{R_a(t)}{N_h},$$

$$\widetilde{S}_b(t) = \frac{S_b(t)}{N_h},\ \widetilde{E}_b(t) = \frac{E_b(t)}{N_h},\ \widetilde{I}_b(t) = \frac{I_b(t)}{N_h},$$

$$\widetilde{R}_b(t) = \frac{R_b(t)}{N_h},\ \widetilde{S}_{va}(t) = \frac{S_{va}(t)}{V_a/(\delta_{va} + C_a)},\ \widetilde{E}_{va}(t) = \frac{E_{va}(t)}{V_a/(\delta_{va} + C_a)},$$

$$\widetilde{I}_{va}(t) = \frac{I_{va}(t)}{V_a/(\delta_{va} + C_a)},\ \widetilde{S}_{vb}(t) = \frac{S_{vb}(t)}{V_b/(\delta_{vb} + C_b)},$$

$$\widetilde{E}_{vb}(t) = \frac{E_{vb}(t)}{V_b/(\delta_{vb} + C_b)},\ \widetilde{I}_{vb}(t) = \frac{I_{vb}(t)}{V_b/(\delta_{vb} + C_b)}.$$

Table 1. Definition of variables and parameters in the model

Parameters	Definition
δ_h	The death rate of host population
T_{va}	The development rate of adult female *Aedes aegypti* mosquitoes [7, 23]
T_{vb}	The development rate of adult female *Aedes albopictus* mosquitoes [23]
ψ_a	The biting rate of *Aedes aegypti* population
ψ_b	The biting rate of *Aedes albopictus* population
γ_{vah}	The transmission probability (from *Aedes aegypti* to human population)
γ_{vbh}	The transmission probability (from *Aedes albopictus* to human population)

γ_{hva}	The transmission probability (from human population to *Aedes aegypti*)
γ_{hvb}	The transmission probability (from human population to *Aedes albopictus*)
α_a	The viral development rate of *Aedes aegypti* in human
α_b	The viral development rate of *Aedes albopictus* in human
β_{va}	The viral development rate of *Aedes aegypti* bodies
β_{vb}	The viral development rate of *Aedes albopictus* bodies
β_a	The recovery rate of human population who be infected with *Aedes aegypti*
β_b	The recovery rate of human population who be infected with *Aedes albopictus*
δ_{va}	The death rate of *Aedes aegypti*
δ_{vb}	The death rate of *Aedes albopictus*
C_a and C_b	The control effort rates in *Aedes aegypti* and *Aedes albopictus*
ε_a and ε_b	The measure of influence on the transmission
V_a	The constant recruitment rate of *Aedes aegypti*
V_b	The constant recruitment rate of *Aedes albopictus*

we obtain the new set of equations

$$\frac{d\tilde{S}_a(t)}{dt} = a - \left(T_{va}\psi_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b} + \delta_h \right)\tilde{S}_a(t) + \theta_a\tilde{R}_a(t) \quad (17)$$

$$\frac{d\tilde{E}_a(t)}{dt} = \left(T_{va}\psi_a\gamma_{vah}\frac{\tilde{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b} \right)\tilde{S}_a(t) - (\delta_h+\alpha_a)\tilde{E}_a(t) \quad (18)$$

$$\frac{d\tilde{I}_a(t)}{dt} = \alpha_a \tilde{E}_a(t) - (\delta_h + \beta_a)\tilde{I}_a(t) \tag{19}$$

$$\frac{d\tilde{S}_b(t)}{dt} = (1-a) - \left(T_{vb}\psi_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b} + \delta_h \right)\tilde{S}_b(t)$$

$$+ \theta_b \tilde{R}_b(t) \tag{20}$$

$$\frac{d\tilde{E}_b(t)}{dt} = \left(T_{vb}\psi_b\gamma_{vbh}\frac{\tilde{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b} \right)\tilde{S}_b(t) - (\delta_h + \alpha_b)\tilde{E}_b(t) \tag{21}$$

$$\frac{d\tilde{I}_b(t)}{dt} = \alpha_b \tilde{E}_b(t) - (\delta_h + \beta_b)\tilde{I}_b(t) \tag{22}$$

$$\frac{d\tilde{E}_{va}(t)}{dt} = \left(A_a(1+\varepsilon_a Sin\,\tau(t+194))T_{va}\psi_a\gamma_{hva}\frac{(P_a + \tilde{I}_a(t) * N_h)}{N_h+b} \right)$$

$$\times (1 - \tilde{E}_{va}(t) - \tilde{I}_{va}(t)) - (C_a + \delta_{va} - \beta_{va})\tilde{E}_{va}(t) \tag{23}$$

$$\frac{d\tilde{I}_{va}(t)}{dt} = \beta_{va}\tilde{E}_{va}(t) - (C_a + \delta_{va})\tilde{I}_{va}(t) \tag{24}$$

$$\frac{d\tilde{E}_{vb}(t)}{dt} = \left(A_b(1+\varepsilon_b Sin\,\tau(t+240))T_{vb}\psi_b\gamma_{hvb}\frac{(P_a + \tilde{I}_b(t) * N_h)}{N_h+b} \right)$$

$$\times (1 - \tilde{E}_{vb}(t) - \tilde{I}_{vb}(t)) - (C_b + \delta_{vb} - \beta_{vb})\tilde{E}_{vb}(t) \tag{25}$$

$$\frac{d\tilde{I}_{vb}(t)}{dt} = \beta_{vb}\tilde{E}_{vb}(t) - (C_b + \delta_{vb})\tilde{I}_{vb}(t) \tag{26}$$

with $\tilde{S}_a + \tilde{E}_a + \tilde{I}_a + \tilde{R}_a = 1$, $\tilde{S}_{va} + \tilde{E}_{va} + \tilde{I}_{va} = 1$, $\tilde{S}_{vb} + \tilde{E}_{vb} + \tilde{I}_{vb} = 1$. The peak number of mosquito population in a given year are determined by $(A_a(1+\varepsilon_a Sin\,\tau(t+194)))$ and $(A_b(1+\varepsilon_b Sin\,\tau(t+240)))$ [19].

In this paper, we took the period of *A. aegypti* reproduction to be 194 and of the *A. albopictus*, to be 240.

3. Equilibrium Points for SEIRS Model

The equilibrium points are obtained by setting the RHS of equations (17)-(26) to zero. We only consider solutions in the domains

$$\Omega_a = \{(\tilde{S}_a, \tilde{E}_a, \tilde{I}_a, \tilde{E}_{va}, \tilde{I}_{va}) : \tilde{S}_a, \tilde{E}_a, \tilde{I}_a, \tilde{E}_{va}, \tilde{I}_{va} \geq 0,$$
$$\tilde{S}_a + \tilde{E}_a + \tilde{I}_a, \tilde{E}_{va} + \tilde{I}_{va} \leq 1\}$$
$$\Omega_b = \{(\tilde{S}_b, \tilde{E}_b, \tilde{I}_b, \tilde{E}_{vb}, \tilde{I}_{vb}) : \tilde{S}_b, \tilde{E}_b, \tilde{I}_b, \tilde{E}_{vb}, \tilde{I}_{vb} \geq 0,$$
$$\tilde{S}_b + \tilde{E}_b + \tilde{I}_b, \tilde{E}_{vb} + \tilde{I}_{vb} \leq 1\}$$

since the flow generated by vector field of equation (17)-(26) in these regions will be positive invariant and the trajectories must not pass into the exterior region of Ω_a and Ω_b otherwise some of the populations would become negative which is impossible. The equilibrium points in our model are

(i) Disease free equilibrium point: $S_{0a} = (1, 0, 0, 0, 0)$ if the infecting mosquito is *A. aegypti* and $S_{0b} = (1, 0, 0, 0, 0)$ if the infecting mosquito is *A. albopictus*.

(ii) Endemic disease equilibrium point: $S^*_{0a} = (S''_a, E''_a, I''_a, E''_{va}, I''_{va})$ when the infecting mosquito is *Aedes aegypti* and $S^*_{0b} = (S''_b, E''_b, I''_b, E''_{vb}, I''_{vb})$ if the infecting mosquito is *A. albopictus*.

The equilibrium populations are

$$S''_a = \frac{-a - \theta_a + I''_a\theta_a + \dfrac{A_a(I''_aN_h + P_a)\omega_5(a + \theta_a - I''_a\theta_a)}{\omega_3 + A_a(I''_aN_h + P_a)\omega_4}}{\delta_h + \theta_a + \dfrac{(I''_aN_h + P_a)\omega_6}{\omega_7 + A_a(I''_aN_h + P_a)\omega_8}} \tag{27}$$

$$E''_a = \frac{A_a(I''_aN_h + P_a)\beta_{va}(a + \theta_a - I''_a\theta_a)\omega_1\omega_2}{\omega_3 + A_a(I''_aN_h + P_a)\omega_4} \tag{28}$$

$$I''_a = \frac{1}{(2A_bN_b(\alpha_a\beta_{va}\theta_a\omega_1\omega_2 + (\beta_a + \delta_h)\omega_4))}$$

$$\times (aA_aN_h\alpha_a\beta_{va}\omega_1\omega_2 + A_aN_h\alpha_a\theta_a\beta_{va}\omega_1\omega_2$$

$$- A_aP_a\alpha_a\beta_{va}\theta_a\omega_1\omega_2 - \beta_a\omega_3 + \delta_b\omega_3A_aP_a\beta_a\omega_4 + A_aP_a\delta_h\omega_4$$

$$+ \sqrt{\begin{array}{l}4(A_a^2N_hP_a\alpha_a\beta_{va}(a+\theta_a)\omega_1\omega_2(\alpha_a\beta_{va}\theta_a\omega_1\omega_2 + (\beta_a+\delta_h)\omega_4 \\ + (-A_a\alpha_a\beta_{va}(aN_h + (N_h - P_a)\theta_a)\omega_1\omega_2 + (\beta_a+\delta_h)\omega_3 \\ + A_aP_a(\beta_a+\delta_h)\omega_4)^2))\end{array}} \quad (29)$$

$$E''_{va} = \frac{A_a(I''_aN_h + P_a)\omega_2(-\omega_7 + A_a(I''_aN_h + P_a)(\beta_{va}\omega_2 - \omega_8))}{(\omega_9 + A_a(I''_aN_h + P_a)\omega_2)(\omega_7 + A_a(I''_aN_h + P_a)\omega_8)} \quad (30)$$

$$I''_{va} = \frac{A_a(I''_aN_h + P_a)\beta_{va}\omega_2}{\omega_7 + A_a(I''_aN_h + P_a)\omega_8} \quad (31)$$

$$S''_b = \frac{-1 + a - \theta_b + I''_b\theta_b + \dfrac{A_b(I''_bN_h + P_b)\beta_{vb}\theta_b(-1 + a + (-1 + I''_b)\theta_b)\mu_1\mu_2}{\mu_3 + A_b(I''_bN_h + P_b)\mu_4}}{\delta_h + \theta_b + \dfrac{A_b(I''_bN_h + P_b)\mu_{10}}{\mu_6 + A_b(I''_bN_h + P_b)\mu_7}} \quad (32)$$

$$E''_b = \frac{A_b(I''_bN_h + P_b)\beta_{vb}(-1 + a + (-1 + I''_b)\theta_b)\mu_1\mu_2}{\mu_3 + A_b(I''_bN_h + P_b)\mu_4} \quad (33)$$

$$I''_b = \frac{1}{(2A_bN_h(\alpha_b\beta_{vb}\theta_b\mu_1\mu_2 + (\beta_b+\delta_h)\mu_4))}$$

$$\times (A_b\alpha_bN_h\alpha_a\beta_{vb}(P_b\theta_b + N_h(1 - a + \theta_b)) + \mu_1\mu_2$$

$$+ (\beta_b+\delta_h)\mu_3 + A_bP_b(\beta_b+\delta_h)\mu_4$$

$$+ \sqrt{\begin{array}{l}((\beta_b+\delta_h)^2\mu_3^2 + 2A_b(\beta_b+\delta_h)\mu_3(\alpha_b\beta_{vb}(N_h - aN_h\theta_b - P_b\theta_b)\mu_1\mu_2 \\ + \sqrt{+P_b(\beta_b+\delta_h)\mu_4}) + (A_b\alpha_b\beta_{vb}((-1+a)N_h \\ - (N_h + P_b)\theta_b)\mu_1\mu_2 + A_bP_b(\beta_b+\delta_h)\mu_4)^2))\end{array}} \quad (34)$$

$$I''_{vb} = \frac{A_b(I''_bN_h + P_b)\beta_{vb}\mu_2}{\mu_6 + A_b(I''_bN_h + P_b)\mu_7} \quad (35)$$

$$E''_{vb} = \frac{A_b(I''_b N_h + P_b)\mu_2(-\mu_6 + A_b(I''_b N_h + P_b)\mu_9)}{\mu_8 + A_b(I''_b N_h + P_b)\mu_2(\mu_6 + A_b(I''_b N_h + P_b)\mu_7)}, \quad (36)$$

where

$$\omega_1 = \frac{\gamma_{vah} T_{va} V_a \psi_a}{(N_h + b)(\delta_{va} + C_a)}, \ \omega_2 = \frac{\gamma_{hva} T_{va} \psi_a (1 + \varepsilon_a Sin\, \tau(t + 194))}{N_h + b},$$

$$\omega_3 = (\alpha_a + \delta_h)(\delta_{va} + C_a)(C_a + \beta_{va} + \delta_{va})(\delta_h + \theta_a).$$

$$\omega_4 = ((\alpha_a + \delta_h)(C_a - \beta_{va} + \delta_{va})(\delta_h + \theta_a) + \beta_{va}(\alpha_a + \delta_h + \theta_a)\omega_1)\omega_2,$$

$$\omega_5 = \beta_{va}\theta_a\omega_1\omega_2, \ \omega_6 = A_a\beta_{va}\omega_1\omega_2,$$

$$\omega_7 = (\delta_{va} + C_a)(C_a + \beta_{va} + \delta_{va}), \ \omega_8 = (C_a - \beta_{va} + \delta_{va})\omega_2,$$

$$\omega_9 = C_a + \beta_{va} + \delta_{va}$$

$$\mu_1 = \frac{\gamma_{vbh} T_{vb} V_b \psi_b}{(N_h + b)(\delta_{vb} + C_b)}, \ \mu_2 = \frac{\gamma_{vbh} T_{vb} \psi_b (1 + \varepsilon_b Sin\, \tau(t + 240))}{N_h + b},$$

$$\mu_3 = (\alpha_b + \delta_h)(\delta_{vb} + C_b)(C_b + \beta_{vb} + \delta_{vb})(\delta_h + \theta_b),$$

$$\mu_4 = ((\alpha_b + \delta_h)(C_b - \beta_{vb} + \delta_{vb})(\delta_h + \theta_b) + \beta_{vb}(\alpha_b + \delta_h - \theta_h)\mu_1)\mu_2,$$

$$\mu_6 = (\delta_{vb} + C_b)(C_b + \beta_{vb} + \delta_{vb}).$$

$$\mu_7 = (C_b - \beta_{vb} + \delta_{vb})\mu_2, \ \mu_8 = C_b + \beta_{vb} + \delta_{vb},$$

$$\mu_9 = \beta_{vb}\mu_2 - \mu_7, \ \mu_{10} = \beta_{vb}\mu_1\mu_2.$$

4. Local Stability of SEIRS Model

The local stability of an equilibrium point is determined from the Jacobian matrix of the system of equations (17)-(26) evaluated at the equilibrium points. If all the eigenvalues have negative real parts, then the equilibrium point will be locally asymptotically stable. The standard dynamical modeling method [20] is used in this study. From (17)-(26), the

Jacobian matrices are:

$$A_{aa} = \begin{pmatrix} -\left(T_{va}\forall_a\gamma_{va h}\frac{\bar{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}+\delta_h\right) & 0 & 0 & 0 & -\left(T_{va}\forall_a\gamma_{va h}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b}\right)\bar{S}_a(t) \\ \left(T_{va}\forall_a\gamma_{va h}\frac{\bar{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}\right) & -(\delta_h+\alpha_a) & 0 & 0 & \left(T_{va}\forall_a\gamma_{va h}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b}\right)\bar{S}_a(t) \\ 0 & \alpha_a & -(\delta_h+\beta_a) & 0 & 0 \\ 0 & 0 & \left(A_a(1+\varepsilon_a Sin\pi(t+194))T_{va}\forall_a\gamma_{hva}\frac{(P_a+N_h)}{N_h+b}\right) & -(C_a+\delta_{va}-\beta_{va}) & 0 \\ 0 & 0 & (1-\bar{E}_{va}(t)-\bar{I}_{va}(t)) & \beta_{va} & -(C_a+\delta_{va}) \end{pmatrix}$$

$$= 0 \qquad (37a)$$

$$A_{bb} = \begin{pmatrix} -\left(T_{vb}\forall_b\gamma_{vb h}\frac{\bar{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}+\delta_h\right) & 0 & 0 & 0 & -\left(T_{vb}\forall_b\gamma_{vb h}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b}\right)\bar{S}_b(t) \\ \left(T_{vb}\forall_b\gamma_{vb h}\frac{\bar{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}\right) & -(\delta_h+\alpha_b) & 0 & 0 & \left(T_{vb}\forall_b\gamma_{vb h}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b}\right)\bar{S}_b(t) \\ 0 & \alpha_b & -(\delta_h+\beta_b) & 0 & 0 \\ 0 & 0 & \left(A_b(1+\varepsilon_b Sin\pi(t+240))T_{vb}\forall_b\gamma_{hvb}\frac{(P_b+N_h)}{N_h+b}\right) & -(C_b+\delta_{vb}-\beta_{vb}) & 0 \\ 0 & 0 & (1-\bar{E}_{vb}(t)-\bar{I}_{vb}(t)) & \beta_{vb} & -(C_b+\delta_{vb}) \end{pmatrix}$$

$$= 0 \qquad (37b)$$

The characteristic equation is determined from

$$|A_{aa}-\lambda I|$$

$$\begin{pmatrix} -\left(T_{va}\forall_a\gamma_{va h}\frac{\bar{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}+\delta_h\right)-\lambda & 0 & 0 & 0 & -\left(T_{va}\forall_a\gamma_{va h}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b}\right)\bar{S}_a(t) \\ \left(T_{va}\forall_a\gamma_{va h}\frac{\bar{I}_{va}(t)(V_a/(\delta_{va}+C_a))}{N_h+b}\right) & -(\delta_h+\alpha_a)-\lambda & 0 & 0 & \left(T_{va}\forall_a\gamma_{va h}\frac{(V_a/(\delta_{va}+C_a))}{N_h+b}\right)\bar{S}_a(t) \\ 0 & \alpha_a & -(\delta_h+\beta_a)-\lambda & 0 & 0 \\ 0 & 0 & \left(A_a(1+\varepsilon_a Sin\pi(t+194))T_{va}\forall_a\gamma_{hva}\frac{(P_a+N_h)}{N_h+b}\right) & -(C_a+\delta_{va}-\beta_{va})-\lambda & 0 \\ 0 & 0 & (1-\bar{E}_{va}(t)-\bar{I}_{va}(t)) & \beta_{va} & -(C_a+\delta_{va})-\lambda \end{pmatrix}$$

$$= 0 \qquad (38a)$$

when A_{aa} is Jacobian matrix for endemic equilibrium point of *Aedes aegypti*, λ is the eigenvalue, I is the identity matrix and

$$|A_{bb}-\lambda I|$$

$$\begin{pmatrix} -\left(T_{vb}\forall_b\gamma_{vb h}\frac{\bar{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}+\delta_h\right)-\lambda & 0 & 0 & 0 & -\left(T_{vb}\forall_b\gamma_{vb h}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b}\right)\bar{S}_b(t) \\ \left(T_{vb}\forall_b\gamma_{vb h}\frac{\bar{I}_{vb}(t)(V_b/(\delta_{vb}+C_b))}{N_h+b}\right) & -(\delta_h+\alpha_b)-\lambda & 0 & 0 & \left(T_{vb}\forall_b\gamma_{vb h}\frac{(V_b/(\delta_{vb}+C_b))}{N_h+b}\right)\bar{S}_b(t) \\ 0 & \alpha_b & -(\delta_h+\beta_b)-\lambda & 0 & 0 \\ 0 & 0 & \left(A_b(1+\varepsilon_b Sin\pi(t+240))T_{vb}\forall_b\gamma_{hvb}\frac{(P_b+N_h)}{N_h+b}\right) & -(C_b+\delta_{vb}-\beta_{vb})-\lambda & 0 \\ 0 & 0 & (1-\bar{E}_{vb}(t)-\bar{I}_{vb}(t)) & \beta_{vb} & -(C_b+\delta_{vb})-\lambda \end{pmatrix}$$

$$= 0 \qquad (38b)$$

when A_{bb} is the Jacobian matrix for endemic equilibrium point of *A. albopictus* case, λ is the eigenvalue, I is the identity matrix.

The eigenvalues of $|A_{aa} - \lambda I|$ in *A. aegypti* and $|A_{bb} - \lambda I|$ in *A. albopictus* are obtained by solving $\det(A_{aa} - \lambda I_5) = 0$ and $\det(A_{bb} - \lambda I_5) = 0$, where A_{aa} and A_{bb} are Jacobian matrix for the two species, equations (37a) and (37b) respectively. We are interested in the stabilities of the endemic equilibrium points.

Lemma. *If $S_0 > 1$, the endemic equilibrium S^*_{0a} and S^*_{0b} of equations* (17)-(26) *is locally asymptotically stable in Ω_a and Ω_b, with the basic reproduction number S_0 is given by* [22]

$$S_0 = Max\{S_{0a}, S_{0b}\},$$

where

$$S_{0a} = (aA_aN_h\alpha_a\beta_{va}\omega_1\omega_2 + A_aN_h\alpha_a\beta_{va}\theta_a\omega_1\omega_2 + \delta_h\omega_3 + \sqrt{4(A_a^2N_hP_a\alpha_a\beta_{va}(a+\theta_a)\omega_1\omega_2(\alpha_a\beta_{va}\theta_a\omega_1\omega_2 + (\beta_a+\delta_h)\omega_4 + (-A_a\alpha_a\beta_{va}(aN_h + (N_h - P_a)\theta_a)\omega_1\omega_2 + (\beta_a+\delta_h)\omega_3 + A_aP_a(\beta_a+\delta_h)\omega_4)^2)))$$
$$/(\beta_a\omega_3 + A_bP_a(\alpha_a\theta_a\beta_{va}\omega_1\omega_2 + (\beta_a+\delta_h)\omega_4)), \quad (39)$$

$$S_{0b} = (A_bN_h\alpha_b\beta_{vb}\mu_1\mu_2 + A_bN_h\alpha_b\beta_{vb}\theta_b\mu_1\mu_2 + \beta_b\mu_3 + \delta_h\mu_3 + A_bP_b\beta_b\mu_4 + A_bP_b\delta_h\mu_4 + \sqrt{((\beta_b+\delta_h)^2\mu_3^2 + 2A_b(\beta_b+\delta_h)\mu_3(\alpha_b\beta_{vb}(N_h - aN_h + N_h\theta_b - P_b\theta_b)\mu_1\mu_2 + P_b(\beta_b+\delta_h)\mu_4) + (A_b\alpha_b\beta_{vb}((-1+a)N_h - (N_h+P_b)\theta_b)\mu_1\mu_2 + A_bP_b(\beta_b+\delta_h)\mu_4)^2)))$$
$$/a(A_bN_h\alpha_b\beta_{vb}\mu_1\mu_2 + A_b\alpha_bP_b\beta_{vb}\theta_b\mu_1\mu_2) \quad (40)$$

with

$$\Omega_a = \{(\tilde{S}_a, \tilde{E}_a, \tilde{I}_a, \tilde{E}_{va}, \tilde{I}_{va}) : \tilde{S}_a, \tilde{E}_a, \tilde{I}_a, \tilde{E}_{va}, \tilde{I}_{va} \geq 0,$$
$$\tilde{S}_a + \tilde{E}_a + \tilde{I}_a, \tilde{E}_{va} + \tilde{I}_{va} \leq 1\}.$$

Proof. After evaluating the eigenvalue equation, equation (38a), i.e., we need to solve $\det(A_a - \lambda I_5) = 0$. Doing this, we obtain

$$(\alpha_a + \delta_h + \lambda)(\beta_a + \delta_h + \lambda)(\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3) = 0, \tag{41}$$

where

$$A_1 = 2C_a + \beta_{va} + \delta_h + 2\delta_{va} + \frac{A_a(I_a''N_h + P_a)\beta_{va}\omega_1\omega_2}{\omega_7 + A_a(I_a''N_h + P_a)\omega_8},$$

$$\begin{aligned}
A_2 = {} & C_a^2 + \delta_{va}(2\delta_h + \delta_{va}) \\
& + C_a\left(\beta_{va} + 2\delta_h + 2\delta_{va} + \frac{2A_a(I_a''N_h + P_a)\beta_{va}\omega_1\omega_2}{\omega_7 + A_a(I_a''N_h + P_a)\omega_8}\right) \\
& + \beta_{va}\left(\delta_h + \frac{\delta_{va}(\omega_7 + A_a(I_a''N_h + P_a)(2\omega_1\omega_2 + \omega_8))}{\omega_7 + A_a(I_a''N_h + P_a)\omega_8}\right) \\
& + (A_aN_h\alpha_a(a + \theta_a - I_a''\theta_a)\omega_1\omega_2(\omega_3 + A_a(I_a''N_h + P_a)(\omega_4 - \omega_5)) \\
& (\omega_7 + A_a(I_a''N_h + P_a)\omega_8)(2A_a(I_a''N_h + P_a)\omega_2 + \omega_9)) \\
& /((\omega_3 + A_a(I_a''N_h + P_a)\omega_4)((\delta_h + \theta_a)\omega_7 + (I_a''N_h + P_a) \\
& (\omega_6 + A_a(\delta_h + \theta_a)\omega_8))(A_a(I_a''N_h + P_a)\omega_2 + \omega_9))) \\
& + (A_a(I_a''N_h + P_a)\beta_{va}^2\omega_1\omega_2(A_a(I_a''N_h + P_a)\omega_2\omega_3(I_a''N_h\omega_6 \\
& + P_a\omega_6 + (\delta_h + \theta_a)\omega_7 - 2A_a^4N_h(I_a''N_h + P_a)^3\alpha_a(a + \theta_a - I_a''\theta_a)\omega_2^2 \\
& (\omega_4 - \omega_5)\omega_8 + \omega_3(I_a''N_h\omega_6 + P_a^2\omega_4\omega_6 + (\delta_h + \theta_a)\omega_7)\omega_9 \\
& + A_a(I_a''^2N_h^2\omega_4\omega_6 + P_a^2\omega_4\omega_6 - N_h\alpha_a(a + \theta_a)\omega_2\omega_3\omega_7 \\
& + P_a(\delta_h + \theta_a)(\omega_4\omega_7 + \omega_3\omega_8) + I_a''N_h(2P_a\omega_4\omega_6 + \alpha_a\theta_a\omega_2\omega_3\omega_7 \\
& + (\delta_h + \theta_a)(\omega_4\omega_7 + \omega_3\omega_8)))\omega_9 + A_a^2(I_a''N_h + P_a) \\
& (I_a''^2N_h^2\omega_2\omega_4\omega_6 + P_a^2\omega_2\omega_4\omega_6 + P_a(\delta_h + \theta_a)(\omega_2\omega_4\omega_7
\end{aligned}$$

$$+ \omega_2\omega_3\omega_8 - \omega_4\omega_8\omega_9) - N_h\alpha_a(a + \theta_a)\omega_2(2\omega_2\omega_3\omega_7 + (\omega_4\omega_7$$
$$- \omega_5\omega_7 + \omega_3\omega_8)\omega_9) + I_a''N(2P_a\omega_2\omega_4\omega_6 + \alpha_a\theta_a\omega_2(2\omega_2\omega_3\omega_7$$
$$+ \omega_4\omega_7\omega_9 - \omega_5\omega_7\omega_9 + \omega_3\omega_8\omega_9) + (\delta_h + \theta_a)(\omega_2\omega_4\omega_7$$
$$+ \omega_2\omega_3\omega_8 + \omega_4\omega_8\omega_9))) + A_a^2(I_a''N_h + P_a)^2\omega_2(P_a(\delta_h + \theta_a)\omega_4\omega_8$$
$$+ aN_h\alpha_a(-2\omega_2(\omega_4\omega_7 - \omega_5\omega_7 + \omega_3\omega_8) + (-\omega_4 + \omega_5)\omega_8\omega_9)$$
$$+ N_h(I_a''(\delta_h + \theta_a)\omega_4\omega_8 + (-1 + I_a'')\alpha_a\theta_a(2\omega_2(\omega_4\omega_7 - \omega_5\omega_7 + \omega_3\omega_8)$$
$$+ (-\omega_4 + \omega_5)\omega_8\omega_9)))))/((\omega_3 + A_a(I_a''N_h + P_a)\omega_4(\omega_7$$
$$+ (I_a''N_h + P_a)\omega_8)((\delta_h + \theta_a)\omega_7 + (I_a''N_h + P_a)(\omega_6$$
$$+ (I_a''N_h + P_a)\omega_8))(A_a(I_a''N_h + P_a)\omega_2 + \omega_9))$$

The first two eigenvalues are $\lambda_1 = -\alpha_a - \delta_h$ and $\lambda_2 = -\beta_a - \delta_h$. They are always negative. The other eigenvalues λ_3, λ_4 and λ_5 which are the solutions to the cubic equation

$$\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3 = 0. \tag{42}$$

According the Routh-Hurwitz theory, the three solutions to the characteristic equations in the form of the cubic equations above will all be negative if the coefficients A_1, A_2 and A_3 satisfy the relations

$$A_1 > 0,\ A_3 > 0,\ A_1A_2 > 0. \tag{43}$$

We have plotted the values of A_1, A_2 and A_3 for a set of fixed values appropriate to the *A. aegypti* mosquitoes and a range of viral development rates in this specie of mosquitoes β_{va}. It should be remembered that this rate depends on the temperature of the environment. The fixed values of the other parameters are

$$\theta = \frac{2\pi}{365},\ \delta_h = 1/(365 * 74.6)\text{day}^{-1},\ a = 0.077,\ N_h = 200,000,$$

$\beta_a = 1/14$, $\alpha_a = 1/6$, $\beta_{va} = 0.11$, $\psi_a = 1/11$, $\gamma_{vah} = 0.0048$,

$\gamma_{hva} = 0.0086$, $T_{va} = 0.2$, $A_a = 3000$, $P_a = 0.07$, $C_a = 0.008$,

$\theta_a = 1/6$, $b = 6{,}000$, $V_a = 90{,}000$ and $\delta_{va} = 1/3$.

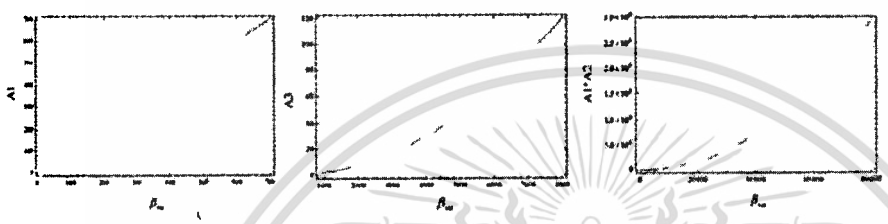

Figure 3. The parameters spaces for the endemic equilibrium point which satisfies the Routh-Hurwitz criteria with the value of parameters in S_a'', E_a'', I_a'', E_{va}'' and I_{va}'' for the parameter values listed in the text.

These values will lead to $S_0 > 1$. Looking at the three graphs in Figure 3, we see that the conditions stated in equation (40) are satisfied and so the equilibrium state S_{0a}^* is locally asymptotically stable.

To see whether S_{0b}^* is locally asymptotically stable, we evaluate equation (38b) to get

$$(\alpha_b + \delta_h + \lambda)(\beta_b + \delta_h + \lambda)(\lambda^3 + B_1\lambda^2 + B_2\lambda + B_3) = 0, \qquad (44)$$

where

$$B_1 = 2C_b + \beta_{vb} + \delta_h + 2\delta_{vb} + \frac{A_b(I_b''N_h + P_b)\beta_{vb}\mu_1\mu_2}{\mu_6 + A_b(I_b''N_h + P_b)\mu_7},$$

$$B_2 = C_b^2 + \delta_{vb}(2\delta_h + \delta_{vb})$$

$$+ C_b\left(\beta_{vb} + 2\delta_h + 2\delta_{vb} + \frac{2A_b(I_b''N_h + P_b)\beta_{vb}\mu_1\mu_2}{\mu_6 + A_b(I_b''N_h + P_b)\mu_7}\right)$$

$$+ (A_b^3N_h(I_b''N_h + P_b)^2\alpha_b\beta_{vb}^3\theta_b(-1 + (-1 + I_b'')\theta_b\mu_1^2\mu_2^3)/((\mu_3$$

$$+ A_b(I_b''N_h + P_b)\mu_4)((2\delta_h + \theta_b)\mu_6 + A_b(I_b''N_h + P_b)$$

$$
\begin{aligned}
&(\mu_{10} + (\delta_h + \theta_b)\mu_7))) \\
&+ \beta_{vb}\Bigg(\delta_h + \frac{\delta_{vb}(\mu_6 + A_b(I_b'' N_h + P_b)(2\mu_1\mu_2 + \mu_7))}{\mu_6 + A_b(I_b'' N_h + P_b)\mu_7} \\
&- (A_b N_h \alpha_b(-1 + (-1 + I_b'')\theta_b)\mu_1\mu_2(\mu_6\mu_8 \\
&+ A_b(I_b'' N_h + P_b)(2\mu_2\mu_6 + \mu_7\mu_8) \\
&+ A_b^2(I_b'' N_h + P_b)^2\mu_2(\mu_7 - \mu_9)))/(((\delta_h + \theta_b)\mu_6 \\
&+ A_b(I_b'' N_h + P_b)(\mu_{10} + (\delta_h + \theta_b)\mu_7))(A_b(I_b'' N_h + P_b)\mu_2 + \mu_8))) \\
&+ (A_b(I_b'' N_h + P_b)\beta_{vb}^2\mu_1\mu_2(A_b(I_b'' N_h + P_b)(\delta_h + \theta_b)\mu_2\mu_3\mu_6 \\
&+ (\delta_h + \theta_b)\mu_3\mu_6\mu_8 + A_b(N_h\alpha_b(-1 + a - \theta_b)\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6) \\
&+ P_b(\mu_{10}\mu_3 + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7)) + I_b'' N_h(\mu_{10}\mu_3 \\
&+ \alpha_b\theta_b\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6) + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7)))\mu_8 \\
&+ A_b^2(I_b'' N_h + P_b)(P_b\mu_2(\mu_{10}\mu_3 + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7)) \\
&+ P_b\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7)\mu_8 + N_h\alpha_b \\
&(-1 + a - \theta_b)\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6) \\
&+ (\mu_4\mu_6 + (\mu_3 - 2\theta_b\mu_1\mu_6)\mu_7)\mu_8 + I_b'' N_h(\mu_{10}(\mu_2\mu_3 + \mu_4\mu_8) \\
&+ (\delta_h + \theta_b)(\mu_2\mu_4\mu_6 + \mu_2\mu_3\mu_7 + \mu_4\mu_7\mu_8) \\
&+ \alpha_b\theta_b\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6) + (\mu_4\mu_6 + \mu_3\mu_7 - 2\theta_b\mu_1\mu_6\mu_7)\mu_8))) \\
&+ A_b^4 N_h(I_b'' N_h + P_b)^3\alpha_b(-1 + a + (-1 + I_b'')\theta_b)\mu_2^2\mu_7(\mu_4 \\
&+ \theta_b\mu_1(-\mu_7 + \mu_9)) + A_b^3(I_b'' N_h + P_b)^2\mu_2(P_b\mu_4(\mu_{10} \\
&+ (\delta_h + \theta_b)\mu_7) + N_h\alpha_b(-1 + a - \theta_b)(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8 \\
&+ \mu_2(\mu_3\mu_7 + \mu_6(\mu_4\mu_2 + \theta_b\mu_1(-3\mu_7 + \mu_9))))
\end{aligned}
$$

$$+ I_b'' N_h(\mu_{10}\mu_4 + (\delta_h + \theta_b)\mu_4\mu_7 + \alpha_b\theta_b(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8$$

$$+ \mu_2(\mu_3\mu_7 + \mu_6(\mu_4\mu_2 + \theta_b\mu_1(-3\mu_7 + \mu_9)))))))/((\mu_3$$

$$+ A_b(I_b'' N_h + P_b)\mu_4)(\mu_6 + A_b(I_b'' N_h + P_b)\mu_7)((\delta_h + \theta_b)\mu_6$$

$$+ A_b(I_b'' N_h + P_b)(\mu_{10} + (\delta_h + \theta_b)\mu_7))A_b(I_b'' N_h + P_b)\mu_2 + \mu_8))$$

$$B_3 = \delta_h\delta_{vb}^2 + (C_b^2(\delta_h\mu_6 + A_b(I_b'' N_h + P_b)\beta_{vb}\mu_1\mu_2 + \delta_h\mu_7)))/(\mu_6$$

$$+ A_b(I_b'' N_h + P_b)\mu_7) + (C_b(\beta_{vb} + 2\delta_{vb})\delta_h\mu_6$$

$$+ A_b(I_b'' N_h + P_b)(\beta_{vb}\mu_1\mu_2 + \delta_h\mu_7)))/(\mu_6 + A_b(I_b'' N_h + P_b)\mu_7)$$

$$+ (A_b^3 N_h(I_b'' N_h + P_b)^2\alpha_b\beta_{vb}^3\delta_h\theta_b(-1 + a(-1 + I_b'')\theta_b\mu_1^2\mu_2^3)/((\mu_3$$

$$+ A_b(I_b'' N_h + P_b)\mu_4)((\delta_h + \theta_b)\mu_6 + A_b(I_b'' N_h + P_b)$$

$$(\mu_{10} + (\delta_h + \theta_b)\mu_7))) + \beta_{vb}\left(\frac{A_b(I_b'' N_h + P_b)\delta_{vb}^2\mu_1\mu_2}{\mu_6 + A_b(I_b'' N_h + P_b)\mu_7}\right.$$

$$+ (\delta_h(A_b(I_b'' N_h + P_b)\delta_{vb}(\delta_h + \theta_b)\mu_2\mu_6 + \delta_{vb}(\delta_h + \theta_b)\mu_6\mu_8$$

$$+ A_b(N_h\alpha_b(1 - a + \theta_b)\mu_1\mu_2\mu_6 + P_b\delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7)$$

$$+ I_b'' N_h(-\alpha_b\theta_b\mu_1\mu_2\mu_6 + \delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7)))$$

$$+ \mu_8 + A_b^2(I_b'' N_h + P_b)\mu_2(P_b\delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7)$$

$$- N_h\alpha_b(-1 + a - \theta_b)\mu_1(2\mu_2\mu_6 + \mu_7\mu_8)$$

$$+ I_b'' N_h(\delta_{vb}(\mu_{10} + (\delta_h + \theta_b)\mu_7) - \alpha_b\theta_b\mu_1(2\mu_2\mu_6 + \mu_7\mu_8)))$$

$$- A_b^3 N_h(I_b'' N_h + P_b)^2\alpha_b(-1 + a(-1 + I_b'')\theta_b\mu_1\mu_2^2(\mu_7 - \mu_9)))$$

$$/(((\delta_h + \theta_b)\mu_6) + A_b(I_b'' N_h + P_b)((\mu_{10} + (\delta_h + \theta_b)\mu_7))$$

$$(A_b(I_b'' N_h + P_b)\mu_2 + \mu_8))) + (A_b(I_b'' N_h + P_b)\beta_{vb}^2\mu_1\mu_2$$

$$(A_b(I_b'' N_h + P_b)\delta_{vb}(\delta_h + \theta_b)\mu_2\mu_3\mu_6 + \delta_{vb}(\delta_h + \theta_b)\mu_3\mu_6\mu_8$$

$$+ A_b(N_h\alpha_b\delta_h(-1 + a - \theta_b)\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6)$$

$$+ P_b\delta_{vb}(\mu_{10}\mu_3 + (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7))$$

$$+ I_b''N_h(\alpha_b\delta_h\theta_b\mu_2\mu_6(\mu_3 - \theta_b\mu_1\mu_6) + \delta_{vb}(\mu_{10}\mu_3$$

$$+ (\delta_h + \theta_b)(\mu_4\mu_6 + \mu_3\mu_7))))\mu_8 + A_b^2(I_b''N_h + P_b)$$

$$(N_h\alpha_b\delta_h(-1 + a - \theta_b)\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6)$$

$$+ (\mu_4\mu_6 + \mu_3\mu_7 - 2\theta_b\mu_1\mu_6\mu_7)\mu_8) + P_b\delta_{vb}(\mu_{10}(\mu_2\mu_3 + \mu_4\mu_8)$$

$$+ (\delta_h + \theta_b)(\mu_2\mu_4\mu_6 + \mu_2\mu_3\mu_7 + \mu_4\mu_7\mu_8))$$

$$+ \delta_{vb}\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7)\mu_8 + \alpha_b\delta_h\theta_b\mu_2(\mu_2\mu_6(\mu_3 - 2\theta_b\mu_1\mu_6)$$

$$+ (\mu_4\mu_6 + \mu_3\mu_7 - 2\theta_b\mu_1\mu_6\mu_7)\mu_8)))$$

$$+ A_b^4N_h(I_b''N_h + P_b)^3\alpha_b\delta_h(-1 + a + (-1 + I_b'')\theta_b)\mu_2^2\mu_7(\mu_4$$

$$+ \theta_b\mu_1(-\mu_7 + \mu_9)) + A_b^3(I_b''N_h + P_b)^2\mu_2(P_b\delta_{vb}\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7)$$

$$+ N_h\alpha_b\delta_h(-1 + a - \theta_b)(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8 + \mu_2(\mu_3\mu_7$$

$$+ \mu_6(\mu_4 + \theta_b\mu_1(-3\mu_7 + \mu_9)))) + I_b''N_h(\delta_{vb}\mu_4(\mu_{10} + (\delta_h + \theta_b)\mu_7)$$

$$+ \alpha_b\delta_h\theta_b(\mu_7(\mu_4 - \theta_b\mu_1\mu_7)\mu_8 + \mu_2(\mu_3\mu_7 + \mu_6(\mu_4$$

$$+ \theta_b\mu_1(-3\mu_7 + \mu_9)))))))/((\mu_3 + A_b(I_b''N_h + P_b)\mu_4)$$

$$(\mu_6 + A_b(I_b''N_h + P_b)\mu_7)((\delta_h + \theta_b)\mu_6 + A_b(I_b''N_h + P_b)$$

$$(\mu_{10} + (\delta_h + \theta_b)\mu_7))A_b(I_b''N_h + P_b)\mu_2 + \mu_8)).$$

Again we see that the first two eigenvalues $\lambda_1 = -\alpha_b - \delta_h$ and $\lambda_2 = -\beta_b - \delta_h$ are negative. The other three eigenvalues are the solutions of the characteristic equation $(\lambda^3 + B_1\lambda^2 + B_2\lambda + B_3) = 0$, where the B's are given above. Just like before, the three eigenvalues will be negative if (i) $B_1 > 0$, (ii) $B_3 > 0$, (iii) $B_1B_2 > 0$. As before, we have evaluate the values of the

B's numerically using the following parameter values

$$\theta = \frac{2\pi}{365},\ \delta_h = 1/(365 * 74.6)\text{day}^{-1},\ a = 0.077,\ N_h = 200{,}000,$$

$$\beta_b = 1/19,\ \alpha_b = 1/13,\ \beta_{vb} = 0.8,\ \psi_b = 1/19,\ \gamma_{vbh} = 0.083,$$

$$\gamma_{hvb} = 0.068,\ T_{vb} = 0.6,\ A_b = 35000,\ P_b = 0.97,$$

$$C_b = 0.7,\ \theta_b = 1/9,\ b = 10{,}000,\ V_b = 960{,}000 \text{ and } \delta_{va} = 1/9.$$

These values are appropriate for the *A. albopictus* mosquitoes. Looking at Figure 4, we see that for the values of the parameters used, the B's satisfy the Routh-Hurwitz criteria and so will be locally asymptotically stable. The expressions for S_b'', E_b'', I_b'', E_{vb}'' and I_{vb}'' are defined by equations (32)-(36).

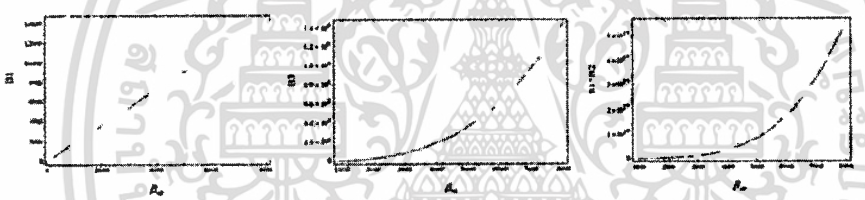

Figure 4. The parameters spaces for the endemic equilibrium point which satisfies the Routh-Hurwitz criteria with the value of parameters listed in the text.

5. Numerical Simulation

After showing that the equilibrium populations during a dengue epidemic in which two species of mosquitoes, *A. aegypti* and *A. albopictus* are co circulating is locally asymptotically stable, we now simulated the trajectories of the epidemic by numerically solving equations (17) to (26) [23-24]. The values of parameters used the numerical simulations are $\delta_h = 1/(365 * 74.6)$ per day, corresponding to a life expectancy of 74.6 years; $\alpha_a = 1/6$ and $\alpha_b = 1/17$, corresponds to the exposed rate of human population; $\beta_a = 1/6$ and $\beta_b = 1/19$, corresponding to the recovery rate of human population due to biting of *A. aegypti* and *A. albopictus*, respectively. The transmission

probability of *A. aegypti* (ψ_a) and *A. albopictus* (ψ_b) are arbitrary chosen. We assume that no alternative host. The other parameters were arbitrarily chosen. The numerical solutions of (16)-(26) are shown in following figures.

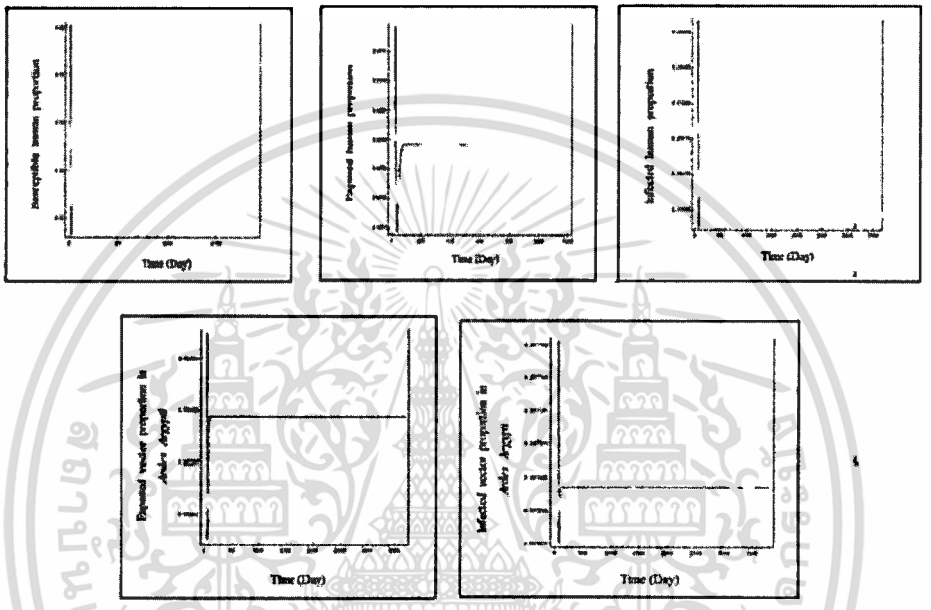

Figure 5. Numerical solutions of (16)-(26), which shows the times series behavior of populations (when $S_0 > 1$) of S_a'', E_a'', I_a'', E_{va}'' and I_{va}''.

For the case of *Aedes Aegypti* when seasonal change in the total number of this species does not influence the behavior (achieved by setting $\varepsilon_a = 0$) of the populations. To obtain the trajectories, the following numerical values

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365 * 74.6)\text{day}^{-1}$, $a = 0.00077$, $N_h = 200{,}000$,

$\beta_a = 1/14$, $\alpha_a = 1/9$, $\beta_{va} = 0.11$, $\psi_a = 1/16$, $\gamma_{vah} = 0.00018$,

$\gamma_{hva} = 0.66$, $T_{va} = 0.05$, $A_a = 4000$, $P_a = 0.09$, $C_a = 0.008$, $\theta_a = 1/6$,

$b = 3{,}000$, $V_a = 9{,}000{,}000$, $\varepsilon_a = 0$ and $\delta_{va} = 1/3$, $S_{0a}^{*} = 31.0712$.

These values lead to the following equilibrium state (0.5323, 0.1079, 0.2516, 0.5820, 0.2872).

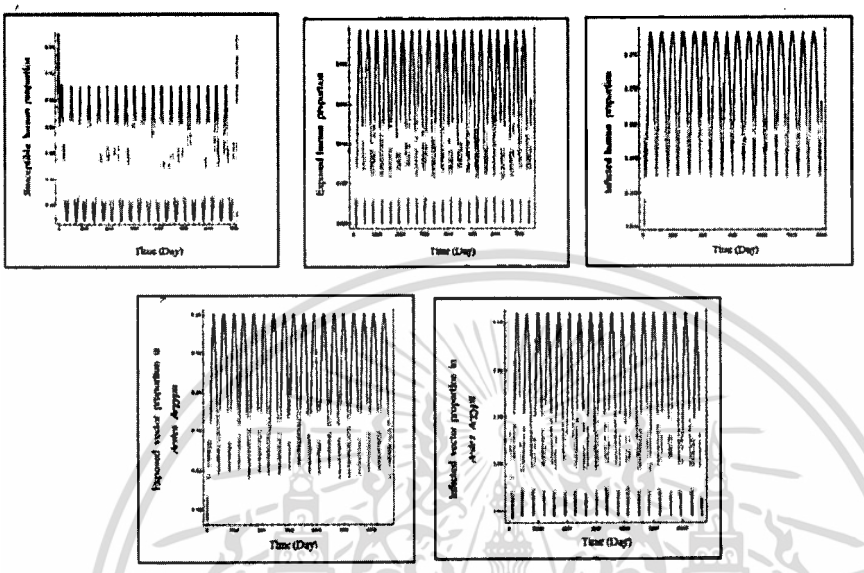

Figure 6. Numerical solutions demonstrate the solution trajectories of S_a'', E_a'', I_a'', E_{va}'' and I_{va}''. The values of the parameters are given in the text of the paper.

For the case where the influence when the influence of the seasonal variation is taken into account (case $\varepsilon_a \neq 0$). The numerical values of the parameters have been changed to

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365 * 74.6)\text{day}^{-1}$, $a = 0.000007777$, $N_h = 200{,}000$,

$\beta_a = 1/14$, $\alpha_a = 1/6$, $\beta_{va} = 0.11$, $\psi_a = 1/18$, $\gamma_{vah} = 0.00018$,

$\gamma_{hva} = 0.0026$, $T_{va} = 0.4$, $A_a = 7000$, $P_a = 0.7$, $C_a = 0.08$,

$\theta_a = 1/6$, $b = 6{,}000$, $V_a = 90{,}000{,}000$, $\varepsilon_a = 0.5$ and $\delta_{va} = 1/3$.

Plotting the series development of two of the populations on the same figures. we see limit cycle behaviors. The values of the parameters are the same as those used to get Figure 6. can occur.

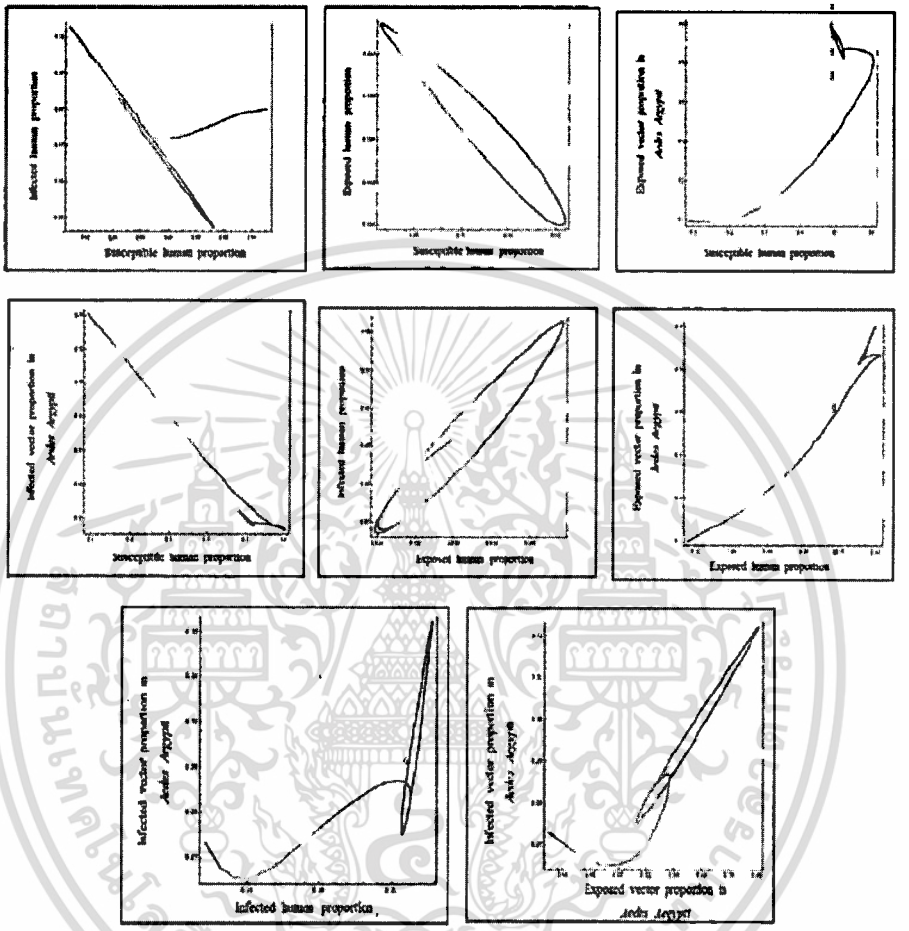

Figure 7. Numerical solutions demonstrate the solution trajectories, projected onto the $(S_a'', I_a''), (S_a'', E_a''), (S_a'', E_{va}''), (S_a'', I_{va}''), (E_a'', I_a''), (E_a'', E_{va}''), (I_a'', I_{va}'')$ and (E_{va}'', I_{va}'') space.

Case where the infecting mosquitoes are *A. Albopictus* when the seasonal changes of the mosquitoes population is negected (achieved by setting $\varepsilon_b = 0$). The numerical values of the parameters used in solving equations are now changed to

$$\theta = \frac{2\pi}{365},\ \delta_h = 1/(365 * 74.6)\text{day}^{-1},\ a = 0.00077,\ N_h = 200{,}000,$$

$\beta_b = 1/19$, $\alpha_b = 1/18$, $\beta_{vb} = 0.8$, $\psi_b = 1/12$, $\gamma_{vbh} = 0.093$,

$\gamma_{hvb} = 0.48$, $T_{vb} = 0.8$, $A_b = 45000$, $P_b = 0.00697$, $C_b = 0.00007$,

$\theta_b = 1/9$, $b = 100$, $V_b = 660{,}000$, $\varepsilon_b = 0$ and $\delta_{vb} = 1/3$.

These values lead to equilibrium state population of $S^*_{0b} = 1.8572$. The time evolutions of the different population are plotted in Figure 8. This figure corresponds to Figure 5 for the time evolutions of the different populations when the infecting mosquito is the *A. aegypti* mosquito. The endemic equilbrium point (0.6305, 0.9272, 0.9781, 0.2000, 0.7998).

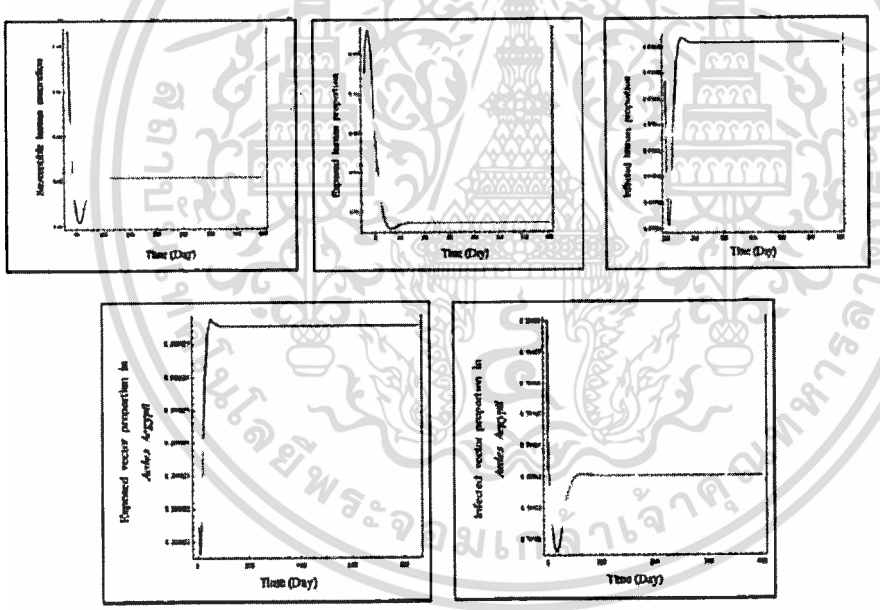

Figure 8. Numerical solutions of (16)-(26), show the time evolutions of S''_b, E''_b, I''_b, E''_{vb} and I''_{vb} when the mosquitoes responsible for the epidemic is *A. albopictus*. The values of the parameters are given in the text.

Case when the influence of the seasonal variation of the number of *A. albopictus* is taken into account (achived by setting $\varepsilon_b \neq 0$). The values of the parameters are now set to

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365 * 74.6)\text{day}^{-1}$, $a = 0.000007777$, $N_h = 200{,}000$,

$\beta_b = 1/19$, $\alpha_b = 1/12$, $\beta_{vb} = 0.8$, $\psi_b = 1/7$, $\gamma_{vbh} = 0.073$,

$\gamma_{hvb} = 0.068$, $T_{vb} = 0.04$, $A_b = 25000$. $P_b = 0.03$, $C_b = 0.08$,

$\theta_b = 1/9$, $b = 20{,}000$. $V_b = 3{,}000{,}000$, $\varepsilon_b = 0.6$ and $\delta_{vb} = 1/5$.

The time series behaviors of the different populations are show on Figure 9. The values of the parameters used to obtain the curves shown in Figure 9 are

$\theta = \frac{2\pi}{365}$, $\delta_h = 1/(365 * 74.6)\text{day}^{-1}$, $a = 0.000007777$, $N_h = 200{,}000$,

$\beta_b = 1/19$, $\alpha_b = 1/12$, $\beta_{vb} = 0.8$, $\psi_b = 1/7$, $\gamma_{vbh} = 0.073$,

$\gamma_{hvb} = 0.068$, $T_{vb} = 0.04$, $A_b = 25000$, $P_b = 0.03$, $C_b = 0.08$,

$\theta_b = 1/9$, $b = 20{,}000$, $V_b = 3{,}000{,}000$, $\varepsilon_b = 0.6$ and $\delta_{vb} = 1/5$.

Pairing up the solutions shown in Figure (9) and plotting them on a two plot i.e., (S_b'', E_b''), (S_b'', E_{vb}''), (S_b'', I_b''), (S_b'', I_{vb}''), (I_b'', E_b''), (I_b'', E_{vb}''), (I_b'', I_{vb}''), $(E_b''. E_{vb}'')$ and (E_b'', I_{vb}'') we see the limit cycle behaviors appearing on Figure 10. Similar limit cycle behaviors to those seen in Figures (7) and (10) will be seen when ε_a is between 0.25 and 0.7 and when ε_b is between 0.3 and 0.65. There appears to be a loss of stability when other values are changed especially changes in the biting rates of the two species, ψ_a (biting rate of *A. aegypti* mosquitoes) and ψ_b (biting rate of *A. albopictus* mosquitoes).

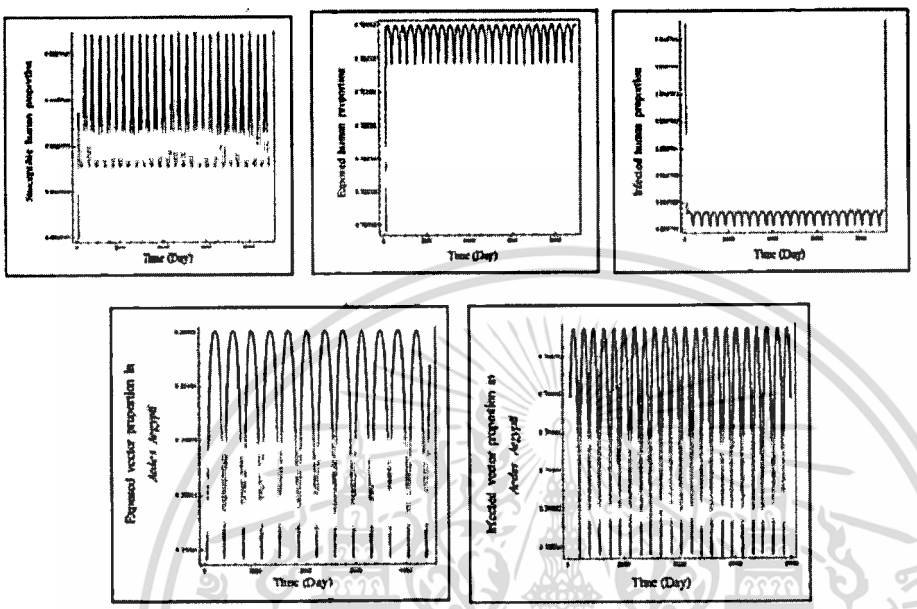

Figure 9. Numerical solutions shows the time series behaviors of the different populations S_b'', E_b'', I_b'', E_{vb}'' and I_{vb}''. The values of the parameters are given in the test.

6. Discussion and Conclusion

We are interested in the transmission of a single serotype of dengue virus when two species of mosquitoes, *A. aegypti* and *A. albopictus* are co circulating among a human population. The threshold number or basic reproduction of this model is defined as S_0, where is the maximum of S_{0a} and S_{0b} are defined by equations (39a) and (39b). The square root of this number represents the average number of secondary case that can be produce a when one initial infection is produced by a bite of one (either specie) mosquito. If $S_0 < 1$, the number of infections will go to 0 as time progresses. If however $S_0 > 1$, the number of infection will increase as time progress and the dengue virus infection will become endemic. The transmission of dengue virus depends on the values of $A_a(1 + \varepsilon_a Sin\,\tau(t + 194))$ and $A_b(1 + \varepsilon_b Sin\,\tau\ \ (t + 240))$ is the virus is being transmitted by the *A. aegypti*

and *A. albopictus* mosquitoes, respectively. The behaviors of our solution depend on the value of ε_a and ε_b.

We have seen that the equilibrium points $S^*_{0a} = (S''_a, E''_a, I''_a, E''_{va}, I''_{va})$ and $S^*_{0b} = (S''_b, E''_b, I''_b, E''_{vb}, I''_{vb})$ when $\varepsilon_a = 0$ and $\varepsilon_b = 0$ are locally asymptotically stable when $S_0 > 1$. Figure 5 and Figure 8 show the behaviors of human and two species of vectors $(S''_a, E''_a, I''_a, E''_{va}, I''_{va})$ and $(S''_b, E''_b, I''_b, E''_{vb}, I''_{vb})$ as time passes.

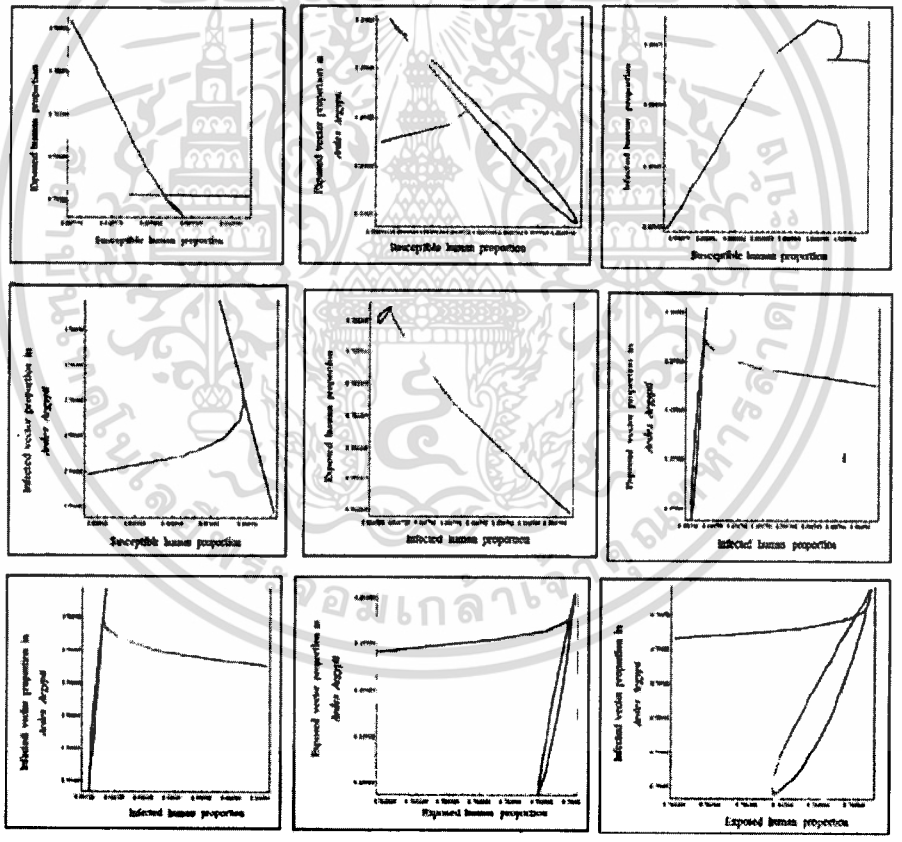

Figure 10. Limit Cycle Behavior of the populations in the model of dengue fever when the DENV is pbing transmitted by *A. Albopictus* mosquitoes in different 2D space. The trajectories in the 2D space (S''_b, E''_b), (S''_b, E''_{vb}), (S''_b, I''_b), (S''_b, I''_{vb}), (I''_b, E''_b), (I''_b, E''_{vb}), (I''_b, I''_{vb}), (E''_b, E''_{vb}) and (E''_b, I''_{vb}) exhibit limit cycle behaviors.

Each of the populations quickly reaches their equilibrium value and remains at the equilibrium values (Lemma 1). When $\varepsilon_a \neq 0$ and $\varepsilon_b \neq 0$, the endemic equilibrium point $S^*_{0a} = (S''_a, E''_a, I''_a, E''_{va}, I''_{va})$ and $S^*_{0b} = (S''_b, E''_b, I''_b, E''_{vb}, I''_{vb})$ are again locally stability when the other parameter values lead $S_0 > 1$. The two dimensional plots however indicate another type of behavior (see Figures 6-7 and Figures 9-10). Instead of quickly coming to their equilibrium values, trajectories exhibit limit cycle behaviors (Figures (7) and (10)). Varying the values of ε_a between 0.25 and 0.70 and ε_b between 0.3 and 0.65 for the cases of *A. aegypti* and *A. albopictus* vectors, respectively, we get behaviors similar to those of Figures (5) and (8) and those of Figures (6), (7), (9) and (10) when ε_a and ε_b are greater or less than some critical values (ε^*_a and ε^*_b) which we call the bifurcation values. When its value $\varepsilon_a = 0$ and $\varepsilon_b = 0$ or less than ε^*_a and ε^*_b, the time behaviors do not exhibit any oscillation, but if the values ε_a and ε_b are greater than ε^*_a and ε^*_b oscillations are seen. The bifurcation diagrams of equations (17)-(26) are shown in the above figures.

In conclusion, we showed that the endemic equilibrium point is local stable, when the threshold number is greater than one. The local stability of all equilibrium states are determined by the threshold numbers S_0. This study shows that by modifying how one reacts to the environment so as to change the values of the parameters, it would be possible to control the spread of dengue fever when two species of mosquitoes, the *A. aegypti* and *A. albopictus* are co-circulating.

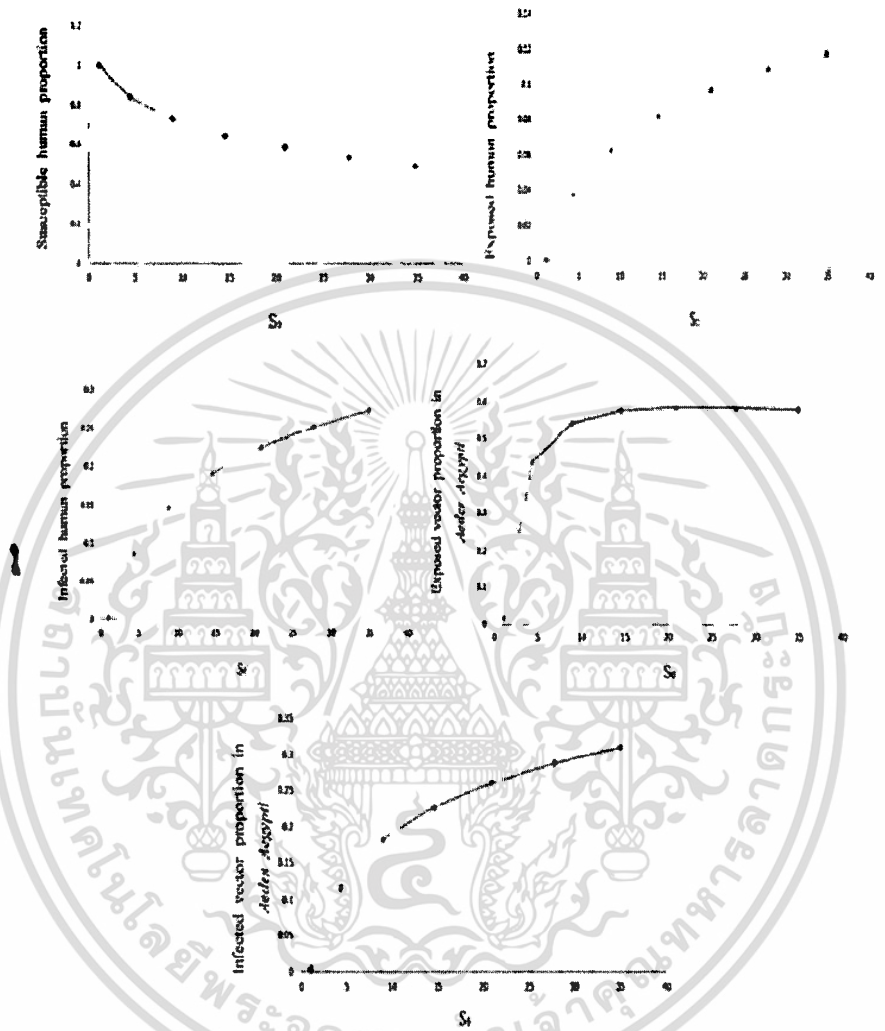

Figure 11. Bifurcation diagrams of the solutions to (16)-(26), plotted onto (S_0, S_a''), (S_0, E_a''), respectively for the different values of S_0 denote the stable solutions.

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LYAPUNOV FUNCTION FOR A DENGUE MODEL WHERE TWO SPECIES OF MOSQUITOES ARE PRESENT: GLOBAL STABILITY

P. Pongsumpun[1,*], R. Sungchasit[1] and I. M. Tang[2]

[1]Department of Mathematics
Faculty of Science
King Mongkut's Institute of Technology Ladkrabang
Chalongkrung Road. Ladkrabang
Bangkok 10520, Thailand
e-mail: kppuntan@kmitl.ac.th

[2]Department of Materials Science
Faculty of Science
Kasetsart University
50 Ngam Wong Wan Road
Lat Yao Chatuchak
Bangkok 10900, Thailand
e-mail: fsciimt@ku.ac.th

Abstract

In this study, we are interested in the newly observed endemic due to the ZIKA virus. In the absence of a full knowledge of the dynamics of the infection due to this virus, we consider a model of the closely

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*Corresponding author

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related dengue virus when there are two species of mosquitoes, A. aegypti and A. albopictus mosquitoes which are both capable of transmitting the two viruses. We use a SIR (susceptible-infected-recovered) model to describe the infection of the human populations. We obtain the basic reproduction ratio (R_0) and show that if R_0 is less than 1, the disease free equilibrium state is global asymptotically stable. If R_0 is greater than 1, we use the Lyapunov function approach to find the conditions for the unique dengue endemic equilibrium state to be globally stable. We then point out the insights into the global stability of the ZIKA epidemic that can be gained by looking at the global stability of a model for the dengue infection in the presence of two species of mosquitoes that can transmit the disease.

Introduction

The big scare in the world public health community right now (January 2016) is the ZIKA virus 1 [WHO (2016)]. This virus was discovered in the Zika forest in Uganda, Africa. In the 2007 outbreak in the Federated States of Micronesia, 5000 ZIKA infections were reported in a population of 67002 (Petersen (2016)] Since the virus at the time was thought to cause only a mild febrile fever 3 (Simpson [3]), not much attention was paid to the virus. However, in the recent outbreak in Brazil, some of the babies born to pregnant female patients developed microcephaly (a disease which causes the heads of newly born babies to be undersize and the brain to be malformed4 (Miakar et al. [4]). The possible connection between the ZIKA virus and microcephaly was the reason for WHO1 (World Health Organization) on Feb. 1, 2016 to declare the possible ZIKA pandemic to be a global health emergency5. On April 13, 2016, CDC (Center for Disease Control (USA)) announced that the ZIKA virus met the conditions for causality of microcephaly by the ZIKA virus 6 (Rasmussen [6]). This new complication arising from this disease led the President 7 of the USA ask the US Congress for 1.8 billion dollar to combat this disease and scientists to a promise that a vaccine against this disease could be made in eighteen months.

The virus belongs to the family Flavivindae genius Flavivirus. Another member of this family and genius is the dengue virus. The vectors of both of

these viruses are mosquitoes of the Aedes family, the A. aegypti mosquitoes 8, 9 in urban areas [Koenraadt (1988); Chadee [9]] and the A. albopictus mosquitoes 10, 11 in rural areas (Hawley [10]; Mori (1972)]. The (normal) symptoms caused by these two viruses are similar, i.e., mild fever, skin rashes, muscle and joint pains and headaches. In this paper we propose to gain some insights in the spread of the ZIKA virus in Brazil when the presence of both the A. aegypti and A. albopictus mosquitoes are taken into account 12 (Serpa et al. [12]). The reason for taking into account the presence of two species is due to difference in the effects of the different environments in the different parts of Florida, USA on the two species caused the pattern of the infections to be different in the different parts of Florida 13, 14 [Costanzo et al. [13]: Julaino (2002)].

Since a full understanding of the ZIKA epidemic (how it is spread) is not known. we propose to look at the global stability of the solutions of a transmission model of the related disease, dengue fever 15, 16 (Keeling and Rohani [15]: Diekmann and Heesterbeek [16]) in which there are two species of mosquitoes transmitting the virus. The present authors have already established the conditions for local asymptotic stability of a dengue model in which two species of mosquitoes are present (Sungchasit et al. [17]). In that paper, the authors showed that when there were seasonal variations in the rates at which of the dengue infections are transmitted from the two species to the human, limit cycle was seen n the trajectories of the two mosquitoes populations and that the endemic equilibrium state was locally asymptotically stable when the basic reproduction number is greater than one. We use the same parameter values used in that paper which lead to the fraction of *A* aegypti mosquitoes oscillating between 0.261 and 0.04587 and the fraction of *A*. albopictus oscillating between 0.01024 6 and 00002. In this paper, we wish to establish the global stability of this model using the Lyapunov approach. The aim is to gain insights into the stability of an illness caused by the related ZIKA virus whose nature or means of transmission are not completely known.

Li and Muldowney [18] have studied the global stability of the solutions of the SEIR 91 (susceptible-exposed-infected-recovered) model commonly

used in epidemiological modeling. They showed that the endemic equilibrium which is locally asymptotically stable when the contact number (defined in their paper) $\sigma \leq 1$ and becomes globally asymptotically stable when $\sigma > 1$. Beretta and Capasso [19] found the conditions needed for the endemic equilibrium of a SIR model with constant population size to be globally stable. At the present stage of knowledge of the ZIKA epidemic, it is not known if there is an exposed stage in the humans so we will use a simpler model to describe the dynamics of this disease in humans, the SIR model. We will be looking at a similar model except that there will be two species of mosquitoes present. In this paper, we use a generalized Lyapunov function to analysize the global dynamic of the eigth-dimensional model of dengue disease of the human population and different Aedes mosquitoes (Aedes aegypti and Aedes albopictus). where an infected human can be one who was infected by a bite of an A. Aegypti mosquitoes or by an A. albopictus mosquitoes. We will prove the global stability of the equilibrium states using Lyapunov functions 20 [La Salle (1991)]. Discussion and conclusion are given in the last section.

Model Formulation and Stability Analysis

We use the susceptible-infected-recovered (SIR) for human and susceptible-infected (SI) for both species of the Aedes mosquitoes. In fact, there has been no report of which species of the mosquitoes is involved in the transmission of the ZIKA virus. We consider the presence of the two (the A. aegypti and A. albopictus mosquitoes) since both are present in Brazil. One of the reasons for mentioning only the first specie is that the alarm is centered in the urban areas of Brazil. The initial outbreak was in the city Recife in northeastern Brazil. Evidence has been accumulating that A. albopictus has adapted itself so that it can thrive in urban environments 21 (Benedict et al. [21]). The great fear is that it will spread to Rio de Janeiro, the site of the 2016 Olympics where many people from the rest of the world will come. Cancelling the Olympics is out of the question. There are studies which show that both species of the mosquitoes are present in parts of Brazi

113 and if we are to look at the transmission of the diseases in Brazil, we should take into account the presence of both species.

The dengue virus (Gubler [22]) is spread by the bite of adult female Aedes mosquitoes only, since the female needs the blood to complete the ovigenesis cycle. Only in the viraemic period which ranges from 2 to 12 days with an average of 4-5 days, is an infected person capable of transmitting the virus. During this period, a dengue-infected person is capable of transmitting the dengue virus to the two species (A. aegypti and A. albopictus) of vectors when they are bitten by the mosquitoes (Guga-Sapir [23]). During the blood meal, the females ingest the dengue virus from an infectious human where the virus goes into the gut of the mosquitoes. The dengue virus then undergoes an extrinsic incubation period (of approximately 8-12 days in the Aedes mosquitoes) before the mosquitoes become infectious and can transmit the virus to the humans. The presence of the incubation period causes a time which we ignore since it has not been established that this occurs with the ZIKA virus. If the temperature is low enough, the incubation period can be longer then the life time of the mosquitoes, in which case no transmission of the virus will occur.

1. Parameters of Model

Let N_T, N_{va} and N_{va} represent the total number of human. In this paper, the total number of population is to be constant for each category. The human population of sizes NT consists of susceptible humans (S), infected humans due to a bite of an *A.* aegypti (I_a) mosquito or of an *A.* albopictus (I_b) mosquito and recovered human (*R*), i.e, $N_T = S + I_a + I_b + R$. For vector population of sizes N_{va}, is total number of an adult A. aegypti mosquito which consist of the susceptible (S_{va}) and infectious mosquitoes (I_{va}), i.e., $N_{va} = S_{va} + I_{va}$. N_{vb} is the total number of *A.* albopictus mosquitoes, i.e., $N_{vb} = S_{vb} + I_{vb}$ and S_{vb} is susceptible mosquito, I_{vb} is infectious mosquito. Note that μ_h and μ_d are the average constant natural death rate of human population and death rate of human population due to

the disease, μ_{va} and μ_{va} are the average constant death rate in A. aegypti and A. albopictus mosquitoes, respectively. As we have mentioned earlier, the seasonal variation is simulated by introducing sinusoidal dependence into the rates of transmission of the virus to the humans and not into the death rates as is done by most researchers. The reason for this was given earlier.

The other parameters are defined as follows: κ is the birth rate of human population, N_h is the total human population at time t. ω_a and ω_b are the biting rates of Aedes aegypti population and Aedes albopictus population, λ_a and λ_b are the measure of influence on the transmission process from human population to Aedes aegypti and Aedes albopictus. α_{ha} and α_{hb} are the recovery rate of human population who be infected by an A. aegypti and A. albopictus mosquitoes. It is well known that a person infected with one serotype of the Dengue virus cannot be re infected by the same serotype but can be infected by a different serotype which may result in death causing illness. For vector population, it is assumed a constant recruitment rate Q_a and Q_b of A. aegypti and A. albopictus, λ_{va} and λ_{vb} are the measure of influence on the transmission process from A. aegypti and A. albopictus, respectively to human population, β_{va} and β_{vb} are the transmission probability of dengue disease from vector populations (A. aegypti and A. albopictus) to human population, as well as the number of infectious and susceptible of each species. In reality, the rate at which the adult mosquitoes are recruited depends on how many eggs are laid, on whether the eggs hatch and how many of the larvae survive the metamorphosis process to become adults. For our simple model, we ignore all of this and insert the sinusoidal dependence into the rates of transmission since these depend on the number of bites the mosquitoes must make to obtain the necessary amount of blood needed for the ovigenesis cycle. Our model equations are shown in the next section.

2. Equations of Model

In this paper, we study the transmission of dengue disease in a human population where there are two species of mosquitoes, A. aegypti and A.

albopictus mosquitoes. We assume that there is only one type of dengue virus present, even though there are four serotypes; DEN1, DEN2, DEN3 and DEN 4. Infection by one type confers life-long immunity to further infection by that type. There is no immunity to infection by the others. However, infection by a different serotype opens up the possibility an allergic reaction to the antibodies of the first type, resulting in a more severe form of the disease, dengue hemorrhagic fever. Figure 1 shows the monthly incidence of dengue fever in Thailand in the period 2003 to 201124 [MOPH (2011)]. The figure does not show a systematic yearly increase of the disease. The incidences can be larger or smaller year to year. They all show a sinusoidal behavior. We have therefore included sinusoidal dependence in the rates of transmission of the virus to the humans from an infectious mosquito of either species and of the transmission of the virus to either specie of mosquito from an infected human. The rates of transmissions between a human and mosquito usually contains factor giving the number of contacts between the two. If there is no contact, the rates of transmission would be zero. Other studies (Fisman [25]; Greenfell [26]) have introduced a sinusoidal dependence in the death rates, reasoning that when the weather gets cold enough, the mosquitoes will die. Our choice of where to introduce the sinusoidal dependence is based on the fact that the Ades mosquitoes breeding habits are different from the other mosquito genius. The females of the Ades mosquitoes lay their eggs above the water line of the breeding pond. The eggs will hatch only after they are inundated with water from a new rain fall. If there is no new rain fall, there will be more mosquitoes unless humans replenish the water by artificially spraying the area.

The flow chart for the transmission of the dengue virus when there are two species of mosquitoes present is shown in Figure 2.

3. The mathematical representation of the flow chart.

The mathematical representation of the model is given by the following system of ordinary differential equations.

$$\frac{dS}{dt} = \kappa N_h - \omega_a(1+\lambda_a \sin \eta t) I_{va} S - \mu_d S - \mu_h S - \omega_b(1+\lambda_b \sin \eta t) I_{vb} S \quad (1)$$

$$\frac{dI_a}{dt} = \omega_a(1 + \lambda_a \sin \eta t) I_{va} S - \mu_d I_d - \mu_h I_a - \alpha_{ha} I_b \quad (2)$$

$$\frac{dI_b}{dt} = \omega_b(1 + \lambda_b \sin \eta t) I_{va} S - \mu_d I_b - \mu_h I_b - \alpha_{hb} I_b \quad (3)$$

$$\frac{dR}{dt} = -\mu_d R - \mu_h R + \alpha_{ha} I_a + \alpha_{hb} I_b \quad (4)$$

$$\frac{dS_{va}}{dt} = Q_a - \beta_{va}(1 + \lambda_{va} \sin \eta t) S_{va} I_a - \mu_{va} S_{va} \quad (5)$$

$$\frac{dI_{va}}{dt} = \beta_{va}(1 + \lambda_{va} \sin \eta t) S_{va} I_a - \mu_{va} I_{va} \quad (6)$$

$$\frac{dS_{va}}{dt} = Q_b - \beta_{vb}(1 + \lambda_{vb} \sin \eta t) S_{vb} I_b - \mu_{vb} S_{vb} \quad (7)$$

$$\frac{dI_{va}}{dt} = \beta_{vb}(1 + \lambda_{va} \sin \eta t) S_{va} I_b - \mu_{vb} I_{vb}. \quad (8)$$

All parameters in our model are non- negative. We will now show that the solutions to the equations given by (1)-(8), in the non-negative octant R_+^8 are positive invariant (where R_+^8 denotes the non-negative region). With respect to system (1)-(8), we have the following results.

Proposition 1. *Let* $(S(t), I_a(t), I_b(t), R(t), S_{va}(t) I_{va}(t), S_{vb}(t), I_{vb}(t))$ *be the solution of* (1)-(8) *with the initial condition* $(S(0), I_a(0), I_b(0), R(0), S_{va}(0) I_{va}(0), S_{vb}(0), I_{vb}(0))$ *and the compact set*

$$\Omega_a = \left\{(S, I_a, I_b, R, S_{va}, I_{va}, S_{vb}, I_{vb}) \in R_+^8, W_1 \le N_T = \frac{\kappa N_h}{\mu_d + \mu_h},\right.$$

$$\left. W_2 \le N_{va} = \frac{Q_a}{\mu_{va}}, W_3 \le N_{vb} = \frac{Q_b}{\mu_{vb}}\right\}.$$

Then, under the flow described by (1)-(8), Ω_a *is a positively invariant set that attracts all solutions in* R_+^8.

Proof. We choose the Lyapunov function

$$W(t) = (W_1(t), W_2(t), W_3(t))$$

$$= (S + I_a + I_b + R, S_{va} + I_{va} + S_{vb} + I_{vb})$$

to be positive definite on R_+^∞ and we have

$$\frac{dW}{dt} = \left(\frac{dW_1}{dt}, \frac{dW_2}{dt}, \frac{dW_3}{dt}\right)$$

$$= \left(\frac{dS}{dt} + \frac{dI_a}{dt} + \frac{dI_b}{dt} + \frac{dR}{dt}, \frac{dS_{va}}{dt} + \frac{dI_{va}}{dt}, \frac{dS_{vb}}{dt} + \frac{dI_{vb}}{dt}\right)$$

$$= (\kappa N_h - (\mu_d + \mu_h)(S + I_a + I_b + R), Q_a - \mu_{va}(S_{va} + I_{va}), Q_b - \mu_{vb}(S_{vb} + I_{vb}))$$

$$= (\kappa N_h - (\mu_d + \mu_h)N_T, Q_a - \mu_{va}N_{va}, Q_b - \mu_{vb}N_{vb}).$$

We used the fact that $N_T = \frac{\kappa N_h}{\mu_d + \mu_h}$, $N_{va} = \frac{Q_a}{\mu_{va}}$ and $N_{vb} = \frac{Q_b}{\mu_{vb}}$.

With this in mind, it is not difficult to show that

$$\frac{dW_1}{dt} = \kappa N_h - (\mu_d + \mu_h)W_1 \le 0, \text{ for } W_1 \ge \frac{\kappa N_h}{\mu_d + \mu_h} \tag{9}$$

$$\frac{dW_2}{dt} = Q_a - \mu_{va}W_2 \le 0, \text{ for } W_2 \ge \frac{Q_a}{\mu_{va}} \tag{10}$$

$$\frac{dW_3}{dt} = Q_a - \mu_{vb}W_3 \le 0, \text{ for } W_3 \le \frac{Q_b}{\mu_{vb}}. \tag{11}$$

From the above equations (9)-(11) one has that $\frac{dW}{dt} \le 0$ which implies that Ω_a is a positively invariant set. In other words, by solving (9)-(11), we obtain

$$0 \le (W_1(t), W_2(t), W_3(t)) \le ((\kappa N_h/(\mu_d + \mu_h)) + W_1(0)e^{-(\mu_d + \mu_h)t},$$

$$(Q_a/\mu_{va}) + W_2(0)e^{-\mu_{va}t}, (Q_b/\mu_{vb}) + W(0)e^{-\mu_{vb}t}),$$

where $W_1(0)$, $W_2(0)$ and $W_3(0)$ are respectively, the initial conditions of $W_1(t)$, $W_2(t)$ and $W_3(t)$. Thus, as $t \to \infty$, $0 \le (W_1(t), W_2(t), W_3(t)) \le (\kappa N_h/\mu_d + \mu_h, Q_a/\mu_{va}, Q_b/\mu_{vb}) = (N_T, N_{va}, N_{vb})$ and one can conclude that Ω_a is an attractive set.

4. Equilibrium points

From equations (1)-(8), we set the right hand side of all equations to zero. We obtain two equilibrium points:

(I) If $R_0 \le 1$. the only equilibrium is the disease free equilibrium point

$$J_1(S, I_a, I_b, R, S_{va}, I_{va}, S_{va}, I_{vb})$$

$$= J_1 = \left(\frac{\kappa N_h}{\mu_d + \mu_h}, 0, 0, 0, \frac{Q_a}{\mu_{va}}, I_{va}, \frac{Q_b}{\mu_{vb}}, 0\right) \in \Omega_a.$$

(II) If $R_0 > 1$, there is the endemic equilibrium point

$$J_2(S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^*) \in \Omega_a,$$

where $S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^* > 0$ satisfy

$$S^* = \frac{(\mu_{va}(I_a^*\gamma_{AA} + \mu_{va})\mu_{vb}(N_h\gamma_{BB}\kappa + (\alpha_{bh} + \mu_d + \mu_h)\mu_{vb}))}{(\gamma_{BB}\mu_{va}^2(\gamma_{HB}Q_b + (\mu_d + \mu_h)\mu_{vb}) + I_a^*\gamma_{AA}\gamma_{BB}(\gamma_{HB}Q_b\mu_{va} + \gamma_{HA}Q_a\mu_{vb} + (\mu_d + \mu_h)\mu_{va}\mu_{vb}))} \quad (12)$$

$$I_b^* = (N_h\gamma_{BB}\gamma_{HB}Q_b\kappa\mu_{va}(I_a^*\gamma_{AA} + \mu_{va}) - (\alpha_{hb} + \mu_d + \mu_h)((\mu_d + \mu_h)\mu_{va}^2$$

$$+ I_a^*\gamma_{AA}(\gamma_{HA}Q_a + \mu_d + \mu_h)\mu_{va}))\mu_{vb}^2)/(\gamma_{BB}(\alpha_{hb} + \mu_d + \mu_h)(\mu_{va}^2\gamma_{HB}Q_b$$

$$+ (\mu_d + \mu_h)\mu_{vb} + I_a^*\gamma_{AA}(\gamma_{BH}Q_b\mu_{va} + \gamma_{HA}Q_b\mu_{vb} + (\mu_d + \mu_h)\mu_{va}\mu_{vb}))) \quad (13)$$

$$R^* = \{(\alpha_{ha}(-\gamma_{BB}\gamma_{BH}Q_b(\alpha_{ha} + \mu_d + \mu_h)\mu_{va} - \gamma_{BB}(N_h\gamma_{AA}\gamma_{HA}Q_a\kappa$$

$$+ (\mu_d + \mu_h)(\alpha_{ha} + \mu_d + \mu_h)\mu_{va}^2)\mu_{vb} + \gamma_{AA}\gamma_{HA}Q_a(\alpha_{hb} + \mu_d + \mu_h)\mu_{vb}^2))/$$

$$(\gamma_{AA}(\alpha_{ha} + \mu_d + \mu_h)(\gamma_{HB}Q_b\mu_{va} + \gamma_{HA}Q_a\mu_{vb} + (\mu_d + \mu_h)\mu_{va}\mu_{vb})$$

$$+(\alpha_{hb}(N_h\gamma_{BB}\gamma_{HB}Q_b\kappa\mu_{va}(I_a^*\gamma_{AA}+\mu_{va})$$

$$-(\alpha_{hb}+\mu_d+\mu_h)((\mu_d+\mu_h)\mu_{va}^2+I_a^*\gamma_{AA}(\gamma_{HA}Q_a+(\mu_d+\mu_h)\mu_{va}))\mu_{vb}^2)/$$

$$((\alpha_{hb}+\mu_d+\mu_h)(\mu_{va}^2(\gamma_{HB}Q_b+(\mu_d+\mu_h)+I_a^*\gamma_{AA}(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}$$

$$+(\mu_d+\mu_h)\mu_{va}\mu_{vb}))\}/\{\gamma_{BB}(\mu_d+\mu_h)\} \quad (14)$$

$$S_{va}^* = \frac{Q_a}{I_a^*\gamma_{AA}+\mu_{va}} \quad (15)$$

$$I_{va}^* = \frac{I_a^*\gamma_{AA}Q_a}{I_a^*\gamma_{AA}\mu_{va}+\mu_{va}^2} \quad (16)$$

$$S_{vb}^* = ((\alpha_{hb}+\mu_d+\mu_h)(\mu_{va}^2(\gamma_{HB}Q_b+(\mu_d+\mu_h)\mu_{vb})$$

$$+I_a^*\gamma_{AA}(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}(\mu_d+\mu_h)\mu_{va}\mu_{vb})))/(\gamma_{HB}\mu_{va}(I_a^*\gamma_{AA}$$

$$+\mu_{va})(N_h\gamma_{BB}\kappa+(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb})) \quad (17)$$

$$I_{vb}^* = (N_h\gamma_{BB}\gamma_{HB}Q_b\kappa\mu_{va}(I_a^*\gamma_{AA}+\mu_{va})-(\alpha_{hb}+\mu_d+\mu_h)$$

$$((\mu_d+\mu_h)\mu_{ab}^2+I_a^*\gamma_{AA}(\gamma_{HA}Q_a+(\mu_d+\mu_h)\mu_{va}))\mu_{vb}^2)/(\gamma_{HB}\mu_{va}(I_a^*\gamma_{AA}$$

$$+\mu_{va})\mu_{vb}(N_h\gamma_{BB}\kappa+(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb})) \quad (18)$$

$$I_a^*(\gamma_{HB}\gamma_{HB}Q_b(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^2-\gamma_{BB}(-N_h\gamma_{AA}\gamma_{HA}Q_a\kappa+(\mu_d+\mu_h)$$

$$(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^2)\mu_{vb}+\gamma_{AA}\gamma_{HA}Q_a(\alpha_{hb}+\mu_d+\mu_h)\mu_{vb}^2)/$$

$$(\gamma_{AA}\gamma_{BB}(\alpha_{ha}+\mu_d+\mu_h)(\gamma_{HB}Q_b\mu_{va}+\gamma_{HA}Q_a\mu_{vb}+(\mu_d+\mu_h)\mu_{va})\mu_{vb})) \quad (19).$$

and

$$\gamma_{HA}=\omega_a(1+\lambda_a(\sin\eta t)),\ \gamma_{HB}=\omega_b(1+\lambda_b(\sin\eta t))$$

$$\gamma_{AA}=\beta_{va}(1+\lambda_{va}(\sin\eta t)),\ \gamma_{BB}=\beta_{vb}(1+\lambda_{vb}(\sin\eta t)).$$

The basic reproduction number for system (1)-(8), is given by

$$R_0 = \frac{\gamma_{AA}\gamma_{HA}Q_a\mu_{va}(N_h\gamma_{BB}\kappa + (\alpha_{hb}+\mu_d+\mu_h)\mu_{bv})}{\gamma_{BB}(\alpha_{ha}+\mu_d+\mu_h)\mu_{va}^2(\gamma_{HB}Q_b+(\mu_d+\mu_h)\mu_{vb})}.$$

5. Global stability of the disease free equilibrium

We study the global behavior of the disease free equilibrium state for the system defined by equations (1)-(8). We define new time dependent components of the death rate of the mosquitoes infected with the virus as

$$\begin{cases}(\mu_{va})(t) = \omega_a(1+\lambda_a sin\eta t)S^*, \\ (\mu_{vb})(t) = \omega_b(1+\lambda_b sin\eta t)S^*, \\ (\mu_d+\mu_h)(t) = \beta_{va}(1+\lambda_{va}sin\eta t)S_{va}^*\beta_b(1+\lambda_{vb}sin\eta t)S_{vb}^*. \end{cases} \quad (20)$$

Then Equations (1), (5) and (7) reduce to

$$\frac{dS}{dt} = \kappa N_h - \mu_h'(t)S, \text{ where}$$

$$\mu_h'(t) = \mu_h + \mu_a + \omega_{va}(1+\lambda_a \sin\eta t)I_{va} + \omega_{vb}(1+\lambda_b \sin\eta t)I_{vb} \quad (1')$$

$$\frac{dS_{va}}{dt} = Q_a - \mu_{va}'(t)S_{va}, \text{ where } \mu_{va}'(t) = \mu_{va} + \beta_{va}(1+\lambda_{va}\sin\eta t)I_a. \quad (5')$$

and

$$\frac{dS_{va}}{dt} = Q_b - \mu_{vb}'(t)S_{va}, \text{ where } \mu_{va}'(t) = \mu_{va} + \beta_{va}(1+\lambda_{va}\sin\eta t)I_a. \quad (7')$$

with the rest of the equations remaining the same.

Theorem 1. *When* $R_0 \le 1$, *the disease free equilibrium* J_1 *is globally asymptotically stable on* Ω_a.

Proof. Working now with the new set of equations to construct the Lyapunov function on Ω_a., we get

$$\psi(t) = (S - S^* \ln S) + I_a + I_b + R + (S_{va} - S_{va}^* \ln S_{va}) + I_{va} + (S_{va} - S_{va}^* \ln S_{va}) + I_{vb}.$$

The derivative with respect to time yields

$$\frac{d\psi(t)}{dt} = \frac{dS}{dt}\left(1-\frac{S^*}{S}\right) + \frac{dI_a}{dt} + \frac{dI_b}{dt} + \frac{dR}{dt} + \frac{dS_{va}}{dt}\left(1-\frac{S^*_{va}}{S_{va}}\right)$$

$$+ \frac{dI_{va}}{dt} + \frac{dS_{vb}}{dt}\left(1-\frac{dS^*_{vb}}{S_{vb}}\right) + \frac{dI_{vb}}{dt}$$

$$(\kappa N_h - \omega_a(1+\lambda_a \sin\eta t) I_{va} S - \mu_d S - \mu_d S - \mu_h S - \omega_b(1+\lambda_b \sin\eta t) I_{vb} S)\left(1-\frac{S^*}{S}\right)$$

$$+ (\omega_a(1+\lambda_a \sin\eta t) I_{va} S - \mu_d I_a - \mu_h I_a - \alpha_{ha} I_a)$$

$$+ (\omega_b(1+\lambda_b \sin\eta t) I_{vb} S - \mu_d I_b - \mu_h I_b - \alpha_{hb} I_a)$$

$$+ (-\mu_d R - \mu_h R - \alpha_{ha} I_a - \alpha_{hb} I_b)$$

$$+ (Q_a - \beta_{va}(1+\lambda_{va} \sin\eta t) S_{va} I_a - \mu_{va} S_{va})\left(1-\frac{S^*_{vb}}{S_{vb}}\right)$$

$$+ (\beta_{va}(1+\lambda_{va} \sin\eta t) S_{va} I_a - \mu_{va} I_{va})$$

$$+ (Q_b - \beta_{vb}(1+\lambda_{vb} \sin\eta t) S_{vb} I_b - \mu_{vb} S_{vb})\left(1-\frac{S^*_{vb}}{S_{vb}}\right)$$

$$+ (\beta_{vb}(1+\lambda_{vb} \sin\eta t) S_{vb} I_b - \mu_{vb} I_{vb}).$$

Rearranging the terms in the above expression, we get

$$\frac{d\psi(t)}{dt} = \kappa N_h\left(1-\frac{S^*}{S}\right) + Q_a\left(1-\frac{S^*_{vb}}{S_{vb}}\right) + Q_b\left(1-\frac{S^*_{vb}}{S_{vb}}\right)$$

$$+ I_{va}(\omega_a(1+\lambda_a \sin\eta t) S^* - \mu_{va}) + I_{vb}(\omega_b(1+\lambda_b \sin\eta t) S^* - \mu_{vb})$$

$$+ I_a(\beta_{va}(1+\lambda_{va} \sin\eta t) S^*_{va} - (\mu_d + \mu_h)) + I_b(\beta_{vb}(1+\lambda_{vb} \sin\eta t) S^*_{va} - (\mu_d + \mu_h))$$

$$\mu_h S^*\left(1-\frac{S}{S^*}\right)+\mu_d S^*\left(1-\frac{S}{S^*}\right)+\mu_{va}S^*_{va}\left(1-\frac{S_{va}}{S^*_{va}}\right)$$

$$+\mu_{vb}S^*_{vb}\left(1-\frac{S_{vb}}{S^*_{vb}}\right)-\mu_d R-\mu_h R. \qquad (21)$$

Using the new equilibrium states obtained from Equations (1'), (5") and (7')

$S^*=\frac{kN_h}{\mu_d+\mu_h}$, $S^*_{va}=\frac{Q_a}{\mu_{va}}$ and $S^*_{va}=\frac{Q_a}{\mu_{va}}$, expression (21) becomes

$$\frac{d\psi(t)}{dt}=\kappa N_h\left(1-\frac{S^*}{S}\right)+Q_a\left(1-\frac{S^*_{vb}}{S_{vb}}\right)+Q_b\left(1-\frac{S^*_{vb}}{S_{vb}}\right)$$

$$+\mu_h S^*\left(1-\frac{S}{S^*}\right)+\mu_d S^*\left(1-\frac{S}{S^*}\right)+\mu_{va}(t)S^*_{va}\left(1-\frac{S_{va}}{S^*_{va}}\right)$$

$$+\mu_{vb}(t)S^*_{vb}\left(1-\frac{S_{vb}}{S^*_{vb}}\right)-\mu_d R-\mu_h R. \qquad (22)$$

$$\frac{d\psi(t)}{dt}=\kappa N_h\left(2-\frac{S^*}{S}-\frac{S}{S^*}\right)+Q_a\left(2-\frac{S^*_{vb}}{S_{vb}}-\frac{S_{va}}{S^*_{vb}}\right)$$

$$+Q_b\left(2-\frac{S^*_{vb}}{S_{vb}}-\frac{S_{vb}}{S^*_{vb}}\right)-\mu_d R-\mu_h R$$

$$\frac{d\psi(t)}{dt}=-\kappa N_h\frac{(S^*-S)}{S^*S}-Q_a\frac{(S^*_{va}-S_{va})^2}{S^*_{va}S_{va}}$$

$$-Q_b\frac{(S^*_{va}-S_{va})^2}{S^*_{va}S_{va}}-\mu_d R-\mu_h R. \qquad (23)$$

We can see that all terms in (23) are always non-positive. Using the LaSalle's extension to Lyapunov's theorem, we have $\frac{d\psi(t)}{dt}\le 0$ and so the function $\frac{d\psi(t)}{dt}$ is seen to be negative definite. The limit set of each solution

is contained in the largest invariant set for which $S = S^*, S_{va} = S^*_{va}, S_{vb} = S^*_{vb}$ and $R^n = 0$ which is the singleton $\{J_1\}$. Then, the LaSalle's invariant principle implies that the disease free equilibrium J_1 is globally asymptotically stable on Ω_a.

Next, we consider the global property of the endemic equilibrium of (1)-(8).

Theorem 2. *If* $R_0 > 1$, *the endemic equilibrium state*

$$J_2(S^*, I^*_a, I^*_b, R^*, S^*_{va}, I^*_{va}, S^*_{vb}, I^*_{vb}) \in \Omega_a$$

exists and is globally asymptotically stable on Ω_a. *To see this, we now redefine the time dependent components of death rates, Equation* (20), *as*

$$\begin{cases} \mu_{va}(t) = (\omega_a(1 + \lambda_a \sin \eta t)N_h) \\ \mu_{vb}(t) = (\omega_b(1 + \lambda_a \sin \eta t)N_h) \\ (\mu_d + \mu_h + \alpha_{ha})(t) = Q\beta_{va}(1 + \lambda_{va} \sin \eta t)S^*_{vb} \\ (\mu_d + \mu_h + \alpha_{hb})(t) = Q\beta_{va}(1 + \lambda_{vb} \sin \eta t)S^*_{vb} \end{cases} \tag{24}$$

Proof. The Lyapunov function is in the form

$$\rho(t) = (S - S^* \ln S) + I_a + I_b + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)(S_{va} - S^*_{va} \ln S_{va})$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right) + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)(S_{vb} - S^*_{vb} \ln S_{vb})$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right) I_{vb} \tag{25}$$

with

$$A_1(t) = \omega_a(1 + \lambda_a \sin \eta t)$$

$$A_2(t) = \omega_b(1 + \lambda_b \sin \eta t).$$

Its derivative along the trajectories of (1)-(8),

$$\frac{d\rho(t)}{dt} = \frac{dS}{dt}\left(1 - \frac{S^*}{S}\right) + \frac{dI_a}{dt} + \frac{dI_b}{dt} + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)$$

$$\frac{dS_{va}}{dt}\left(1 - \frac{S^*_{va}}{S_{va}}\right) + \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right) + \frac{dI_{va}}{dt}$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)\frac{dS_{vb}}{dt}\left(1 - \frac{dS^*_{vb}}{S_{vb}}\right)$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)\frac{dI_{vb}}{dt} \qquad (26)$$

$$= (\kappa N_h - \omega_a(1 + \lambda_a \sin \eta t) I_{va} S - \mu_d S - \mu_h S - \omega_b(1 + \lambda_b \sin \eta t) I_{vb} S)\left(1 - \frac{S^*}{S}\right)$$

$$+ (\omega_a(1 + \lambda_a \sin \eta t) I_{va} S - \mu_d I_a - \mu_h I_a - \alpha_{ha} I_a)$$

$$+ (\omega_b(1 + \lambda_b \sin \eta t) I_{vb} S - \mu_d I_b - \mu_h I_b - \alpha_{hb} I_a)$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)(Q_a - \beta_{va}(1 + \lambda_{va} \sin \eta t) S_{va} I_a - \mu_{va} S_{va})\left(1 - \frac{S^*_{vb}}{S_{vb}}\right)$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)(\beta_{va}(1 + \lambda_{va} \sin \eta t) S_{va} I_a - \mu_{va} I_{va})$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)(Q_b - \beta_{vb}(1 + \lambda_{vb} \sin \eta t) S_{vb} I_b - \mu_{vb} S_{vb})\left(1 - \frac{S^*_{vb}}{S_{vb}}\right)$$

$$+ \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1 S^*_{va} + A_2 S^*_{vb}}\right)(\beta_{vb}(1 + \lambda_{vb} \sin \eta t) S_{vb} I_b - \mu_{vb} I_{vb}). \qquad (27)$$

Since we assume that total number of populations are constants, so we have $\kappa N_h = N_T(\mu_d + \mu_h)$, $Q_a = N_{va}\mu_{va} = \mu_{va}(S_{va} + I_{va})$ and

$Q_b = N_{vb}\mu_{vb} = \mu_{vb}(S_{vb} + I_{vb})$. Then above equation become

$$\frac{d\rho(t)}{dt} = (\mu_d + \mu_h)N_T\left(1 - \frac{S^*}{S}\right) + Q\mu_{va}N_{va}\left(1 - \frac{S^*_{va}}{S_{va}}\right) + Q\mu_{vb}N_{vb}\left(1 - \frac{S^*_{va}}{S_{va}}\right)$$

$$+ I_{va}(\omega_a(1 + \lambda_a \sin\eta)N_h) - Q\mu_{va}\left(\frac{S_{va}}{S^*_{va}}\right)$$

$$+ I_{vb}(\omega_b(1 + \lambda_b \sin\eta)N_h) - Q\mu_{vb}\left(\frac{S_{va}}{S^*_{va}}\right)$$

$$+ I_a(Q\beta_{va}(1 + \lambda_{va}\sin\eta t)S^*_{va} - (\mu_d + \mu_h + \alpha_{ha}))$$

$$+ I_b(Q\beta_{vb}(1 + \lambda_{vb}\sin\eta t)S^*_{vb} - (\mu_d + \mu_h + \alpha_{ha})) \qquad (28)$$

when $Q = \left(\frac{\mu_d + \mu_h + \alpha_{ha} + \alpha_{hb}}{A_1S^*_{va} + A_2S^*_{vb}}\right)$.

Substituting conditions (24) into (28). we have

$$\frac{d\rho(t)}{dt} = (\mu_d + \mu_h)N_T\left(1 - \frac{S^*}{S}\right) + Q\mu_{va}N_{va}\left(1 - \frac{S^*_{va}}{S_{va}}\right) + Q_1\left(1 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right)$$

$$- QS_{vb}\mu_{va}\left(1 - \frac{S^*_{va}}{S_{va}}\right) + Q_2\left(1 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right)$$

$$+ I_{vb}((\omega_b(1 + \lambda_b \sin\eta t)N_h) - \mu_{va})$$

$$+ I_{vb}((\omega_b(1 + \lambda_b \sin\eta t)N_h) - \mu_{vb})$$

$$+ I_aQ\beta_{va}(1 + \lambda_{va}\sin\eta t)S^*_{va} - (\mu_d + \mu_h + \alpha_{ha})I_a$$

$$+ I_aQ\beta_{va}(1 + \lambda_{va}\sin\eta t)S^*_{va} - (\mu_d + \mu_h + \alpha_{ha})I_b. \qquad (29)$$

In Ω_a, we $Q_1 = I_{va}Q\mu_{va}$ and $Q_2 = I_{vb}Q\mu_{vb}$. The above equation (29) becomes.

$$\frac{d\rho(t)}{dt} = (\mu_d + \mu_h)N_T\left(1 - \frac{S^*}{S}\right) + Q\mu_{va}(t)S_{va}\left(1 - \frac{S^*_{va}}{S_{va}}\right) + Q_1\left(1 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right)$$

$$- QS_{vb}\mu_{va}(t)\left(1 - \frac{S^*_{va}}{S_{va}}\right) + Q_2\left(1 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right)$$

$$+ I_{vb}((\omega_a(1 + \lambda_a \sin \eta t)N_h) - \mu_{va}(t))$$

$$+ I_{vb}((\omega_b(1 + \lambda_b \sin \eta t)N_h) - \mu_{vb}(t))$$

$$+ I_aQ\beta_{va}(1 + \lambda_{va} \sin \eta t)S^*_{va} - (\mu_d + \mu_h + \alpha_{ha})(t)I_a$$

$$+ I_aQ\beta_{va}(1 + \lambda_{va} \sin \eta t)S^*_{va} - (\mu_d + \mu_h + \alpha_{ha})(t)I_b \qquad (30)$$

$$\frac{d\rho(t)}{dt} = -(\mu_d + \mu_h)N_T\frac{(S - S^*)}{SS^*} - Q_a\mu_{va}(t)S_{va}\frac{(S_{va} - S^*_{va})^2}{S_{va}S^*_{va}}$$

$$- Q_1\frac{(S_{va} - S^*_{va})^2}{S_{va}S^*_{va}} - QS_{vb}\mu_{vb}\frac{(S_{va} - S^*_{va})^2}{S_{va}S^*_{va}} - Q_2\frac{(S_{va} - S^*_{va})^2}{S_{va}S^*_{va}} \qquad (31)$$

$$\frac{d\rho(t)}{dt} = (\mu_d + \mu_h)N_T\left(2 - \frac{S^*}{S} - \frac{S^*}{S}\right) + Q\mu_{va}(t)S_{va}\left(2 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right)$$

$$+ Q_1\left(2 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right)$$

$$- QS_{vb}\mu_{va}(t)\left(2 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right) + Q_2\left(2 - \frac{S^*_{va}}{S_{va}} - \frac{S_{va}}{S^*_{va}}\right). \qquad (32)$$

We use the LaSalle's invariant principle to show that $\frac{d\rho(t)}{dt} \le 0$ for all $(S^*, I^*_a, I^*_b, R^*, S^*_{va}, I^*_{va}, S^*_{vb}, I^*_{vb}) \in \Omega_a$, and the strict equality $\frac{d\rho(t)}{dt} = 0$ holds only for $S = S^*$, $I_a = I^*_a$, $I_b = I^*_b$, $R = R^*$, $S_{va} = S^*_{va}$, $I_{va} = I^*_{va}$, $S_{vb} = S^*_{vb}$ and $I_{vb} = I^*_{va}$. Then, the equilibrium state J_2 is the only

invariant set of solutions of the equations (1)-(8) contained entirely in

$$\{(S^*, I_a^*, I_b^*, R^*, S_{va}^*, I_{va}^*, S_{vb}^*, I_{vb}^*)S = S^*, I_a = I_a^*, I_b = I_b^*,$$

$$R = R^*, S_{va} = S_{va}^*, I_{va} = I_{va}^*, S_{vb} = S_{vb}^* \text{ and } I_{vb} = I_{va}^*\}$$

and hence the asymptotic stability theorem, the positive endemic equilibrium state J_2 is global asymptotic stability in Ω_a.

Discussion and Conclusion

Let

$$R_0 = \frac{\gamma_{AA}\gamma_{HA}Q_a\mu_{va}(N_h\gamma_{BB}\kappa + (\alpha_{bb} + \mu_d + \mu_h)\mu_{vb})}{\gamma_{BB}(\alpha_{ha} + \mu_d + \mu_h)\mu_{va}^2(\gamma_{HB}Q_b + (\mu_d + \mu_h)\mu_{vb})}$$

be the threshold parameters. Then, we define $R_0 = \sqrt{R_0}$ as the basic reproductive number of disease. Also, it represents the average number of secondary cases produced from susceptible population. We consider human and vector (A. aegypti and Aedes albopictus) populations. It depends on the transmission rate of dengue virus.

In this paper, we have studied a mathematical model of dengue disease in which the virus is being transmitted by two different species of the Aedes mosquitoes by looking at the global stability of our model. The global stability of transmission of dengue disease in human and vector (Aedes aegypti and A. albopictus) was determined been by using Lyapunov functions. If $R_0 \leq 1$, then to the disease-free equilibrium state is globally asymptotically stable. In the feasible region and the disease dies out of population. If $R_0 > 1$, then there is the unique endemic equilibrium state which is globally asymptotically stable in the interior of feasible region and the disease is present. If the disease is present in the population, then it will persist. Nothing in the model depends directly on the dengue virus directly except for the use of a sinusoidal variation of the transmission rates which were inferred by the behavior seen in Figure 1. Since the ZIKA epidemic has

only been around for less than a year. there has not been enough time to observe what the seasonal dependence is. When that information becomes available, the present work can be modified so that it can be applied to possible ZIKA pandemic which might arise in the near future.

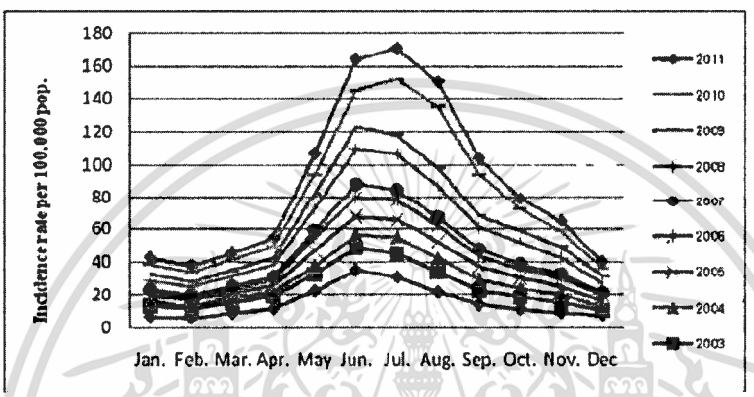

Figure 1. Reported cases of Dengue disease per 100,000 population in Thailand during 2003 and 2011 (month-by-month) [Division of Epidemiology, 2003-2011].

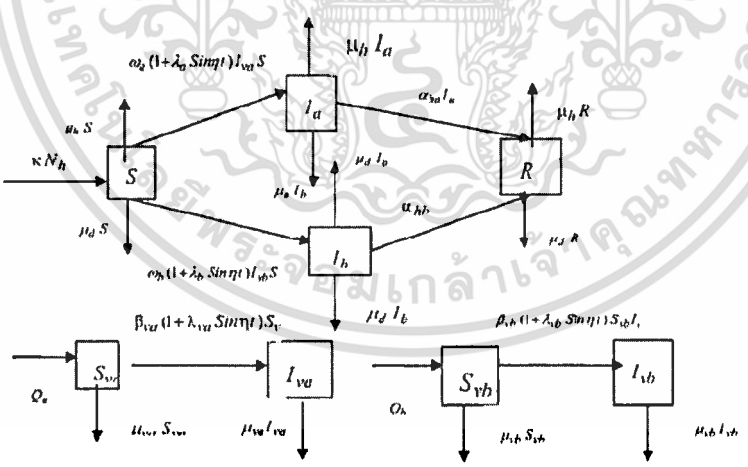

Figure 2. SIR model

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ภาคผนวก ค

ข้อมูลประวัติผู้วิจัย

การศึกษาผลกระทบของภัยพิบัติธรรมชาติอันได้แก่น้ำท่วมในการแพร่ระบาดของโรคที่มียุงเป็นพาหะเช่นโรค
ไข้เลือดออกและโรคมาลาเรียในประเทศไทยโดยใช้แบบจำลองทางคณิตศาสตร์ 302

ข้อมูลประวัติผู้วิจัย

ประวัติส่วนตัว

ชื่อ-สกุล รองศาสตราจารย์ ดร.พันธนี พงศ์สัมพันธ์

ประวัติการศึกษา

ชื่อย่อปริญญา	สาขา	สถาบันที่จบ	ปีที่จบ
ปร.ด.	คณิตศาสตร์ (หลักสูตรนานาชาติ)	มหาวิทยาลัยมหิดล	๒๕๔๗
วท.บ. (เกียรตินิยมอันดับ 2)	คณิตศาสตร์	มหาวิทยาลัยมหิดล	๒๕๔๑

สาขาวิจัยที่มีความชำนาญพิเศษ Mathematical model, Differential equations, Computer simulation และ Numerical Analysis

ทุนการศึกษาและทุนวิจัยที่เคยได้รับ

1. The Royal Golden Jubilee Ph.D. program (RGJ), Thailand Research Fund (TRF), Thailand, 2001-2004.
2. โครงการวิจัย "Spatial approach and mathematical modeling of emerging infectious disease Transmission" แหล่งผู้ให้ทุนคือ สำนักงานคณะกรรมการการอุดมศึกษาและประเทศฝรั่งเศส ปี 2548-2551
3. โครงการวิจัย "Transmission model for Plasmodium Vivax Malaria" แหล่งผู้ให้ทุนคือ สำนักงานกองทุนสนับสนุนการวิจัย ปี 2550-2551
4. โครงการวิจัย "Mathematical model for the transmission by age structure and serotypes of Dengue disease" ทุนสนับสนุนงานวิจัยจากเงินรายได้ประจำปีงบประมาณ 2552 คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง
5. โครงการวิจัย "Franco-Thai Network for Mathematical and Epidemiological Modeling of Infectious Diseases in Thailand" แหล่งผู้ให้ทุนคือ สำนักงานคณะกรรมการการอุดมศึกษา

และประเทศฝรั่งเศส ปี 2552-2553

6. โครงการวิจัย "Transmission model for Chikungunya Fever in Thailand" ทุนสนับสนุนงานวิจัยจากเงินรายได้ประจำปีงบประมาณ 2553 คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

7. โครงการวิจัย"Transmission model for Influenza Pandemic Due to a New-strain of theH1N1 Influenza A Virus" กองทุนวิจัยลาดกระบัง สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง ปี 2554-2556

8. โครงการวิจัย "Mathematical model of Malaria transmission by age group of patients and season in Thailand "ทุนสนับสนุนงานวิจัยจากเงินรายได้ประจำปีงบประมาณ 2555 คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

9. โครงการวิจัย "Using the techniques of formulating the mathematical model, stochastic process and geographic information system for studying the transmission of Malaria" Research Grant from National Research Council of Thailand, 2011-2013.

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11. โครงการวิจัย "Studying the relation of human, rat and season for the spreading of Leptospirosis in Thailand by using Mathematical model"ทุนสนับสนุนงานวิจัยจากเงินรายได้ประจำปีงบประมาณ 2556 คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

12. โครงการวิจัย "Simulation model for distribution of Herpes zoster in Thailand" ทุนสนับสนุนงานวิจัยจากเงินรายได้ประจำปีงบประมาณ 2557 คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

13. โครงการวิจัย "Studying on the risk of cervical cancer by a mathematical model" ทุนสนับสนุนงานวิจัยจากเงินรายได้ประจำปีงบประมาณ 2558 คณะวิทยาศาสตร์ สถาบันเทคโนโลยีพระจอมเกล้าเจ้าคุณทหารลาดกระบัง

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การเสนอผลงานในงานประชุมวิชาการระดับชาติ/นานาชาติ

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