Vector born and macro-parasite diseases

D. Guranie
I. Vector mediated transmission

**Viral:** RVF, Dengue, Yellow fever, ...

**Protozoa:** Malaria, leishmaniasis, ...

**Macro-parasites** (worms): Schistosomiasis, Filariasis, ...
Malaria Life Cycle

Mosquito Stages:
1. Oocyst
2. Ruptured oocyst
3. Release of sporozoites
4. Mosquito takes a blood meal (injects sporozoites)
5. Macrogamocyte
6. Microgamete entering macrogamete
7. Exflagellated microgamocyte
8. Macrogamete

Sporogonic Cycle:
9. Ookinetes
10. Oocysts

Human Liver Stages:
11. Liver cell
12. Infected liver cell

Exo-erythrocytic Cycle:
13. Ruptured schizont
14. Schizont

Human Blood Stages:
15. Immature trophozoite (ring stage)
16. Mature trophozoite

Erythrocytic Cycle:
17. Ruptured schizont
18. Schizont

Gametocytes:
19. Gametocytes

CDC Logo

http://www.dpd.cdc.gov/dpxd
Coupled “host-vector” systems

Host:

Vector:

SEIR

SEIR

SIR

SIR
Classical Ross model of malaria (1912)

**Human:**
- $x = 1 - z$
- $z$

**Mosquito:**
- $w$
- $u = 1 - w$

**Forces of infection:**
- $\lambda = bm\omega w$
- $\Lambda = a\omega z$

**BRN:**
- $R_0 = \frac{abm\omega^2}{r\mu}$

**Endemic Equilibria:**
- $z^* = \frac{(1 - 1/R_0)}{1 + r/bm\omega}$
- $w^* = \frac{(1 - 1/R_0)}{1 + \mu/a\omega}$

**Prevalence DE**
- $\dot{z} = \lambda (1 - z) - rz$
- $\dot{w} = \Lambda (1 - v) - \mu w$

**Parameters**

<table>
<thead>
<tr>
<th>$r$</th>
<th>H. recovery</th>
<th>$\mu$</th>
<th>Mosquito mortality</th>
</tr>
</thead>
<tbody>
<tr>
<td>$b$</td>
<td>Probability of H –infection /bite</td>
<td>$a$</td>
<td>Probability of M – infection /bite</td>
</tr>
<tr>
<td>$m$</td>
<td>Mosquito no/host</td>
<td>$\omega$</td>
<td>Mosquito biting rate</td>
</tr>
</tbody>
</table>

**Mosquito control:** $m, \omega$ ?
Extended “Ross” model with latency (Diezt,...)

<table>
<thead>
<tr>
<th></th>
<th>H</th>
<th>M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Latency</td>
<td>L=?</td>
<td>T=10-14d</td>
</tr>
<tr>
<td>Recovery/Mortality</td>
<td>r=?</td>
<td>μ = 4week</td>
</tr>
</tbody>
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\[
\begin{align*}
\dot{y} &= \lambda x - e^{-rL} (\lambda x) |_{L} - ry; \quad x = 1 - y - z \\
\dot{z} &= e^{-rL} (\lambda x) |_{L} - rz \\
\dot{v} &= \Lambda u - e^{-\mu T} (\Lambda u) |_{T} - \mu v; \quad u = 1 - v - w \\
\dot{w} &= e^{-\mu T} (\Lambda u) |_{T} - \mu w
\end{align*}
\]

\[R_{0} = \frac{abm\omega^{2}}{r \mu} e^{-(\mu T + rL)}\]
Basic parameters

Model Parameters:

$m = \frac{\text{mosq. #}}{\text{host}}$

$\omega = \frac{\text{biting rate}}{\text{mosq}}$

$\mu = \text{mosq. mortality}$

$\tau = \text{mosq. latency}$

$b = \frac{\text{prob. M-infection}}{\text{infected bite}}$

$a = \frac{\text{prob. H-infection}}{\text{infected bite}}$

$$\Rightarrow \lambda_0 = \frac{abm\omega^2 e^{-\mu\tau}}{\mu} \text{ - vectorial capacity}$$

$$R_0 = \frac{\lambda_0}{r + \delta} = \frac{abm\omega^2 e^{-\mu\tau}}{\mu(r + \delta)}$$

$R_0 > 1 \Rightarrow \text{stable (endemic) equilibrium (} y > 0 \text{)}$

$R_0 < 1 \Rightarrow \text{stable equilibrium } y = 0 \text{ (eradication)}$
Examples of dynamic simulations with Mathematica: infection outbreak

1. Standard outbreak

2. Reduced biting by 60% (ITN)

3. Comparison 1 and 2:
   H- and M (dashed) infection prevalences
Macro-parasites: schistosome life cycle

This diagram is provided by Center for Disease Control and Prevention (CDC).
“Mean burden” (host) + prevalence (“vector”)

For macro-parasites *infection intensity* (burden) is more important than *prevalence*!

Macdonald (1965)

\[
\frac{dw}{dt} = (\alpha \eta N) y - \gamma w = A y - \gamma w
\]

\[
\frac{dy}{dt} = (\beta \eta H) w(1 - y) - \mu y = B w(1 - y) - \mu y
\]

w=mean worm burden of H population; y=prevalence of shedding snail
A,B – transmission coefficients: “snail->human” and “human -> snail”

Premises:
• Steady snail population and environment
• Homogeneous human population, and transmission patterns (contact /contamination rates, worm establishment ets)

BRN: \[ R_0 = \frac{AB}{\gamma \mu} \] => equilibria, analysis and control