

Malaria and the heritability of being infectious

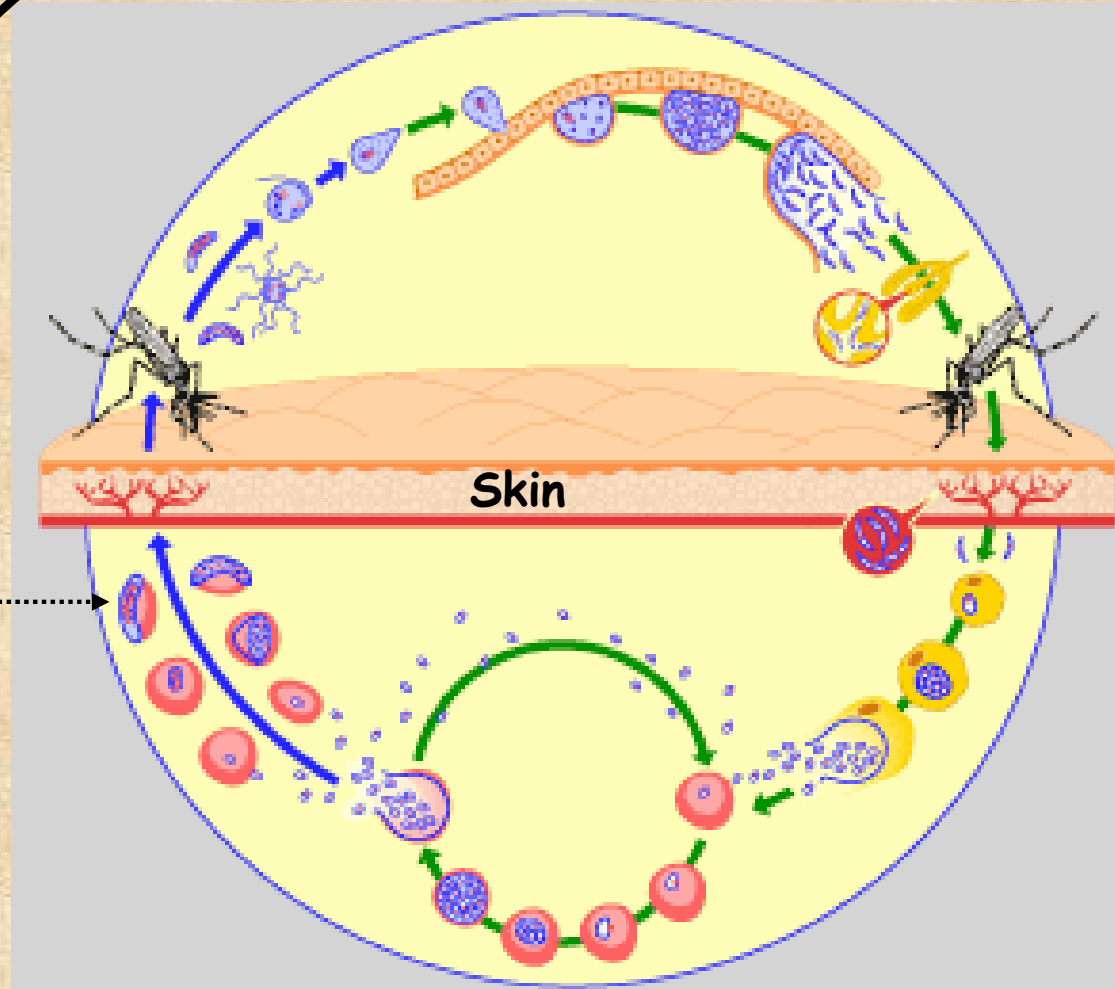
Whose fault is it anyway?

Rick Paul & Anavaj Sakuntabhai
Laboratory of the Genetics of the Human Response to Infection



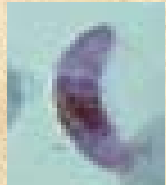
Transmission to

Mosquito



Skin

Man



Male & Female
Gametocytes
(falciforme)
*Plasmodium
falciparum*

Transmission to

Why gametocytes?

Identification of the reservoir of infection

Who & how many?

- Feasibility of targeted intervention
- Re-evaluation of vaccine strategy using Integrated Control Program



Why gametocytes?

Identification of the reservoir of infection

Who & how many?

What risk factors?
(genetic or otherwise)

- Feasibility of targeted intervention
- Re-evaluation of vaccine strategy using Integrated Control Program

- Develop novel approaches based on transmission not disease

Why gametocytes?

Identification of the reservoir of infection

Who & how many?

What risk factors?
(genetic or otherwise)

- Feasibility of targeted intervention
- Re-evaluation of vaccine strategy using Integrated Control Program

- Developt novel approaches based on transmission not disease

Understand parasite exploitation of host through its need to transmit

Ross-Macdonald model of malaria (simplified form)

$$R_0 = \frac{ma^2bc}{\mu\gamma}$$

R_0 : the number of secondary cases arising from a single primary case in a naive population.



Ross-Macdonald model of malaria

$$R_0 = \frac{ma^2bc}{\mu\gamma}$$

R_0 : the number of secondary cases arising from a single primary case in a naive population.

The primary case remains infected for a period of $1/\gamma$ days.



Ross-Macdonald model of malaria

$$R_0 = \frac{ma^2bc}{\mu\gamma}$$

R_0 : the number of secondary cases arising from a single primary case in a naive population.

The primary case remains infected for a period of $1/\gamma$ days.

During this time, this 1° case will be bitten (am/γ) times and a proportion c will infect the biting mosquitoes giving (amc/γ) infected mosquitoes.



Ross-Macdonald model of malaria

$$R_0 = \frac{ma^2bc}{\mu\gamma}$$

R_0 : the number of secondary cases arising from a single primary case in a naive population.

The primary case remains infected for a period of $1/\gamma$ days.

During this time, this 1° case will be bitten (am/γ) times and a proportion c will infect the biting mosquitoes

giving (amc/γ) infected mosquitoes.

Each of these mosquitoes lives ($1/\mu$) days and makes a total number (ab/μ) infectious bites in her lifetime.



Ross-Macdonald model of malaria

$$R_0 = \frac{ma^2bc}{\mu\gamma}$$

R_0 : the number of secondary cases arising from a single primary case in a naive population.

The primary case remains infected for a period of $1/\gamma$ days.

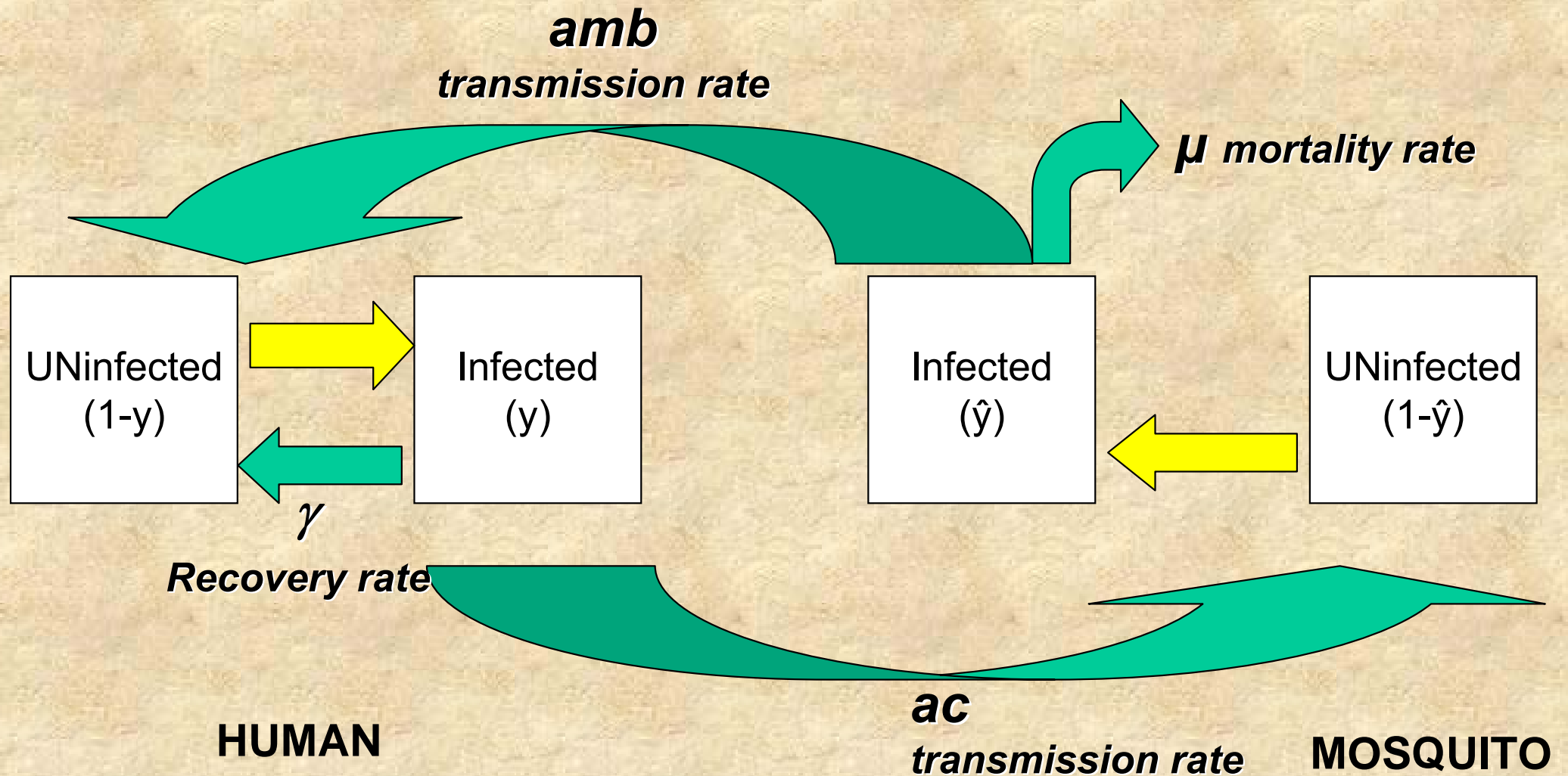
During this time, this 1° case will be bitten (am/γ) times and a proportion c will infect the biting mosquitoes

giving (amc/γ) infected mosquitoes.

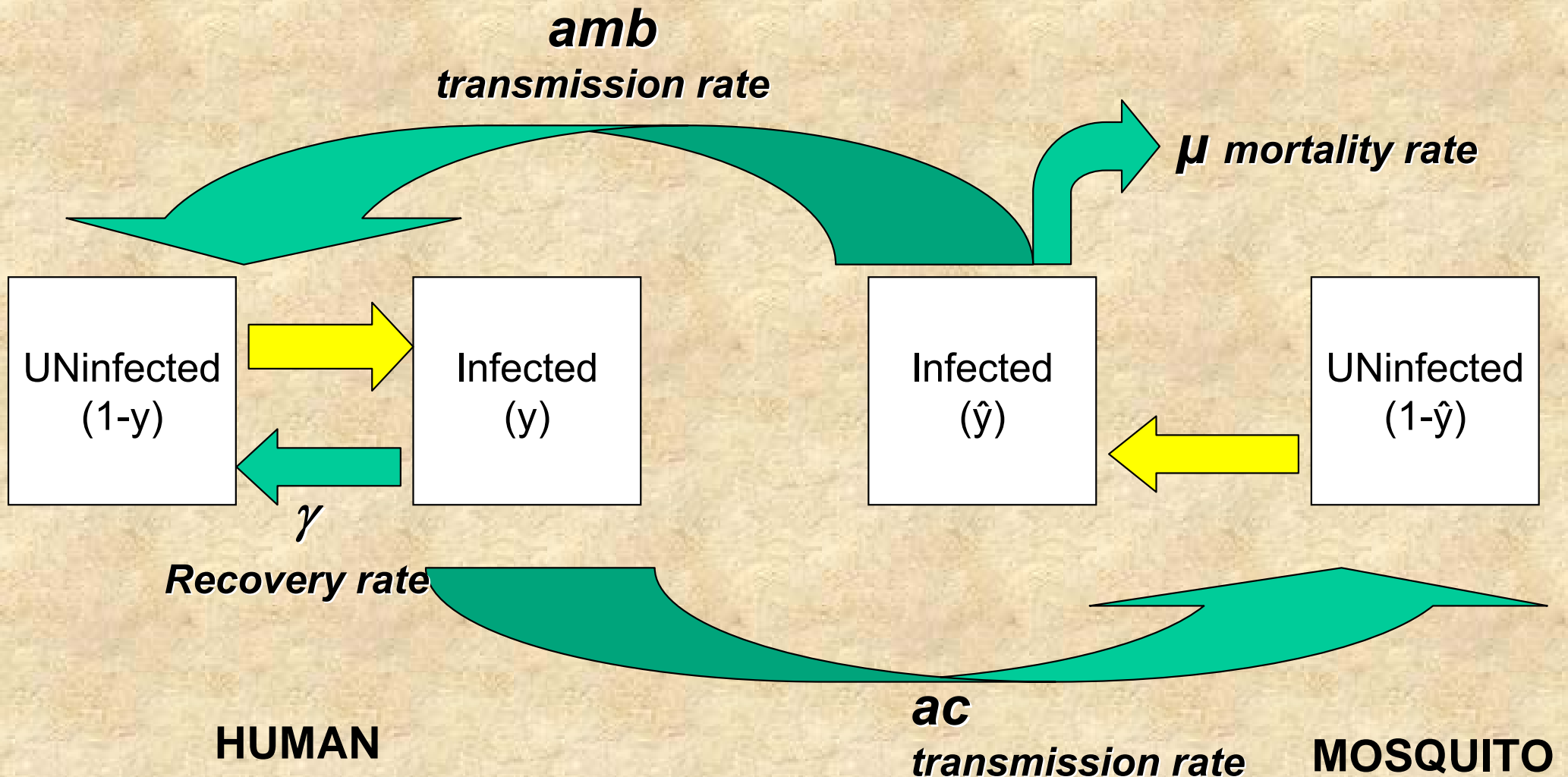
Each of these mosquitoes lives ($1/\mu$) days and makes a total number (ab/μ) infectious bites in her lifetime.

The number of secondary cases is thus $(ab/\mu)(amc/\gamma)$

Transmission and infection is dynamic



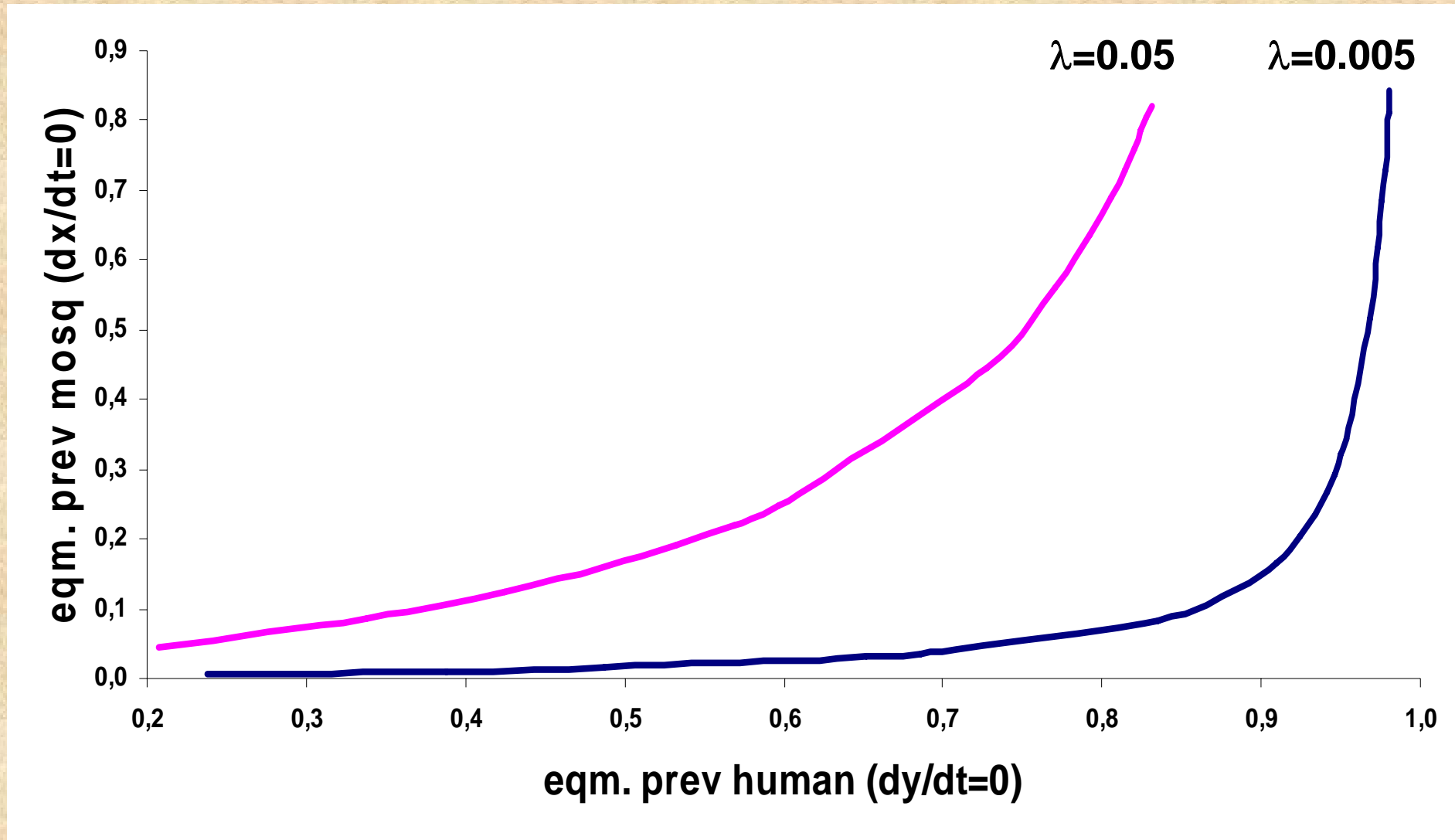
Transmission and infection is dynamic



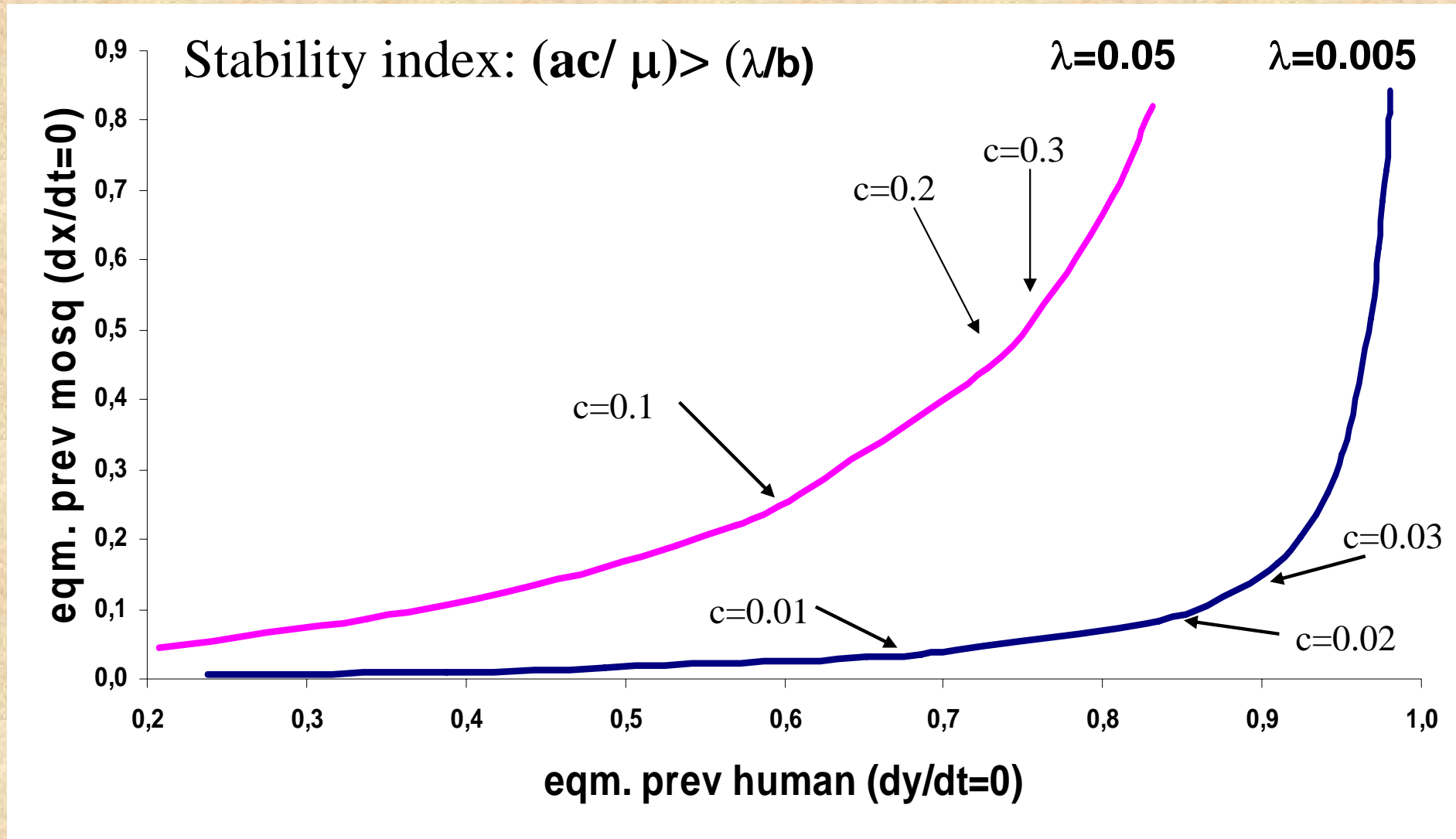
$$\frac{dy}{dt} = (abm) \hat{y}(1-y) - \gamma y$$

$$\frac{d\hat{y}}{dt} = acy(1-\hat{y}) - \mu \hat{y}$$

The effect of « c » on the prevalence of infection

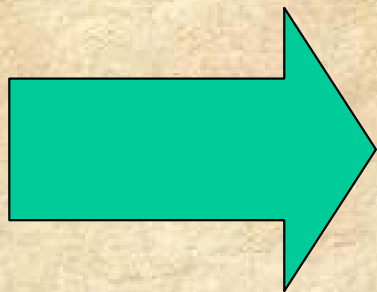


The effect of « c » on the prevalence of infection



Risk factors for gametocyte carriage

1. Anaemia
2. Hyperparasitaemia
3. Reaction to antimalarial drug treatment



All in symptomatic infections

Gametocytes in asymptomatic infections

1. No acquired immunity to gametocytes
(only to gametes – transmission-blocking vaccines)
2. No real decrease with age and exposure
3. Seasonal variations



Genetic predisposition to carry gametocytes?

Perry (1914) Madras

Dombo people vs. Pojoras

- Dombo are recent immigrants
- Dombo suffer more clinically
- Dombo have increased spleen rates

<16yr old	Prev Rate (%)	%infections with gametocytes
Dombos	51	5
Pojoras	78	41

Genetic effect: estimation of heritability

Variance components

$$H_0: \quad V_p = V_e$$

$$H_1: \quad V_p = V_e + V_g$$

$$\text{statistic} \quad \chi^2, df 1 = 2 \ln(L_1/L_0)$$

V_p = variation of phenotype

V_e = variation due to environment

V_g = variation due to genetics (additive)

$$\text{Heritability} = V_g/V_p$$



Family-based longitudinal cohort studies



Dielmo & Ndiop, Senegal



Suanpung, Thailand



Study Populations

Population	N	Nuclear families
Dielmo, Senegal	589	190
Ndiop, Senegal	644	208
Suanpung, Thailand	3484	603



Collection of phenotypes

Intensive survey period

Blood smear regardless of symptoms

Dielmo: twice weekly from June-September (1990)

Ndiop: once-twice weekly for 1 year (1992)

Suanpung, Thailand: once a month for 2 years (1994-1996)

Follow up period

Record clinical malaria attacks

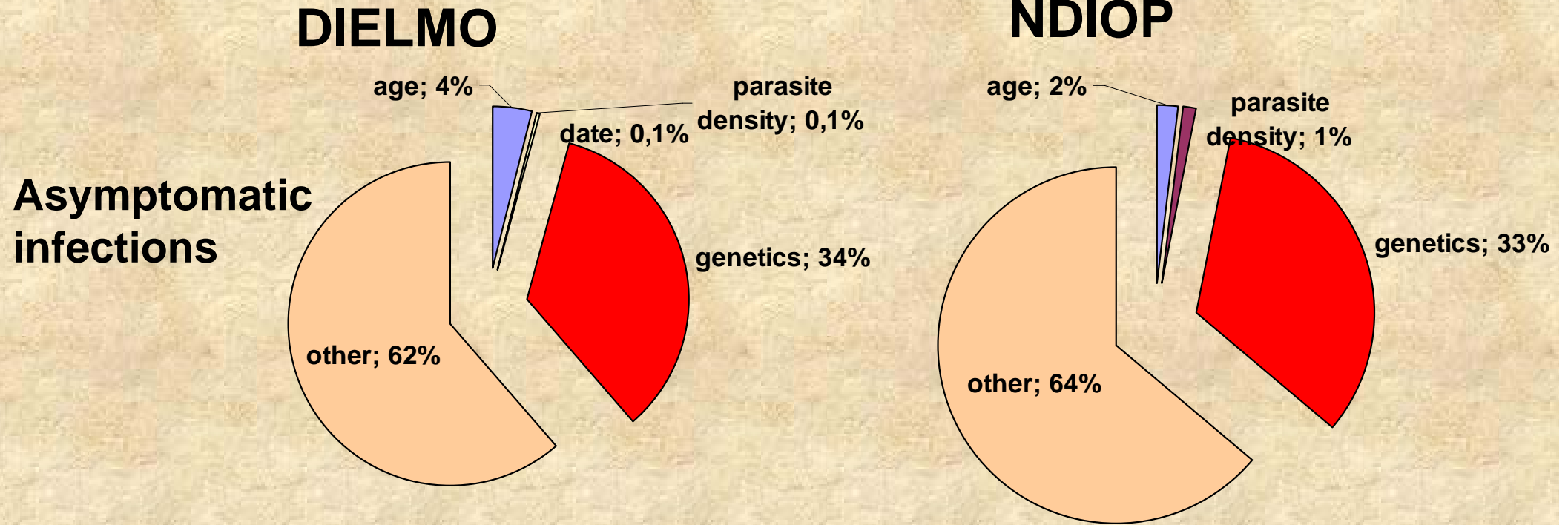
Dielmo: 1990-1999

Ndiop: 1992-2000

Suanpung, Thailand: 1998-2005



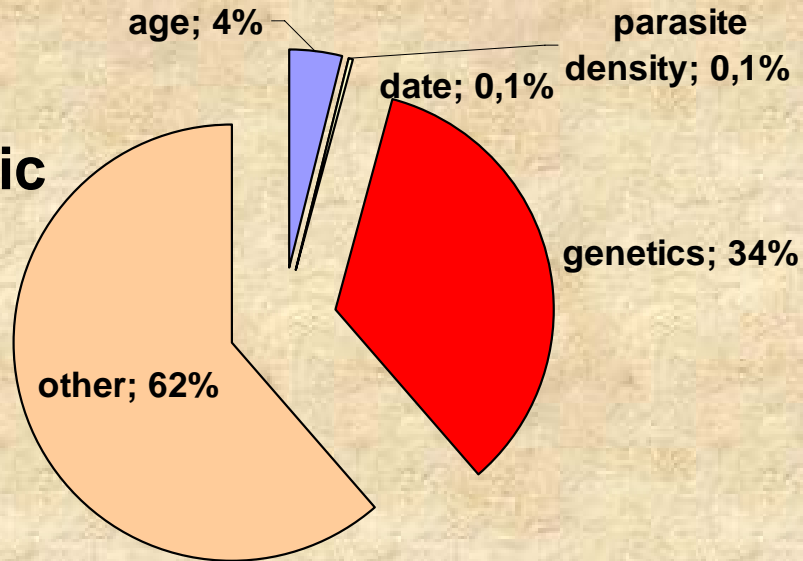
% variability in the proportion of infections that have gametocytes explained by « environmental » and genetic (heritability) factors (1)



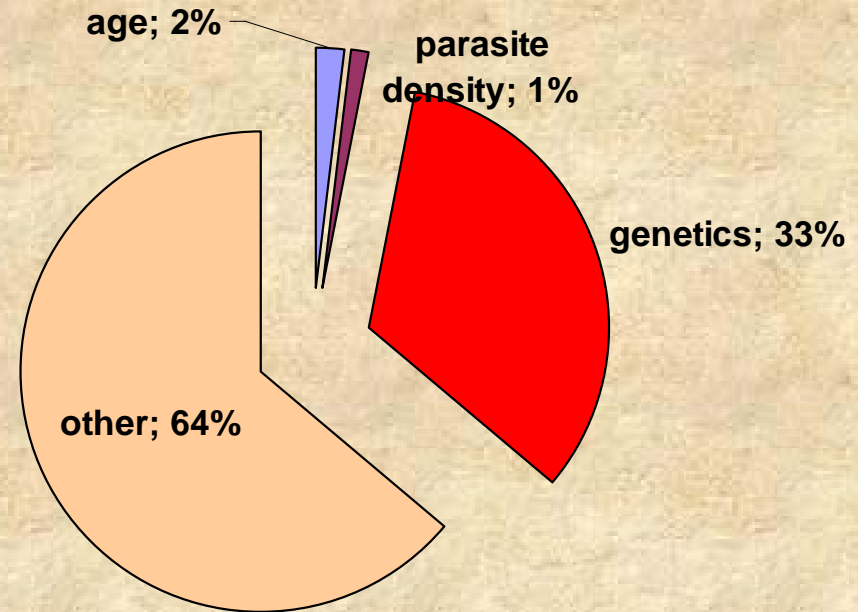
% variability in the proportion of infections that have gametocytes explained by « environmental » and genetic (heritability) factors (2)

DIELMO

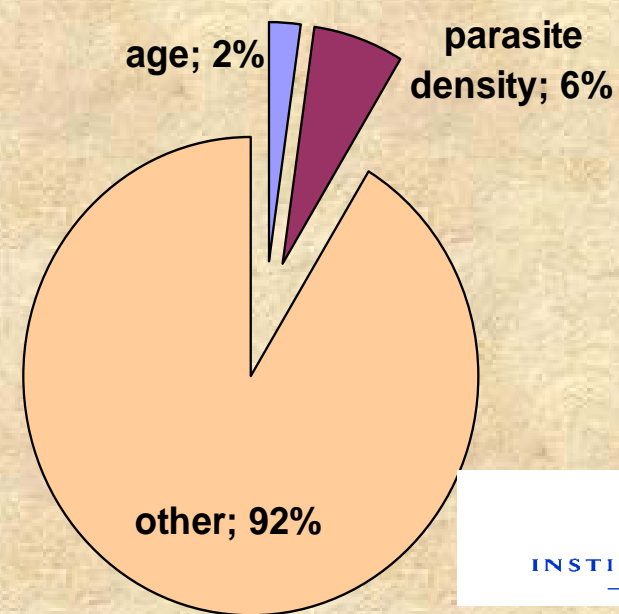
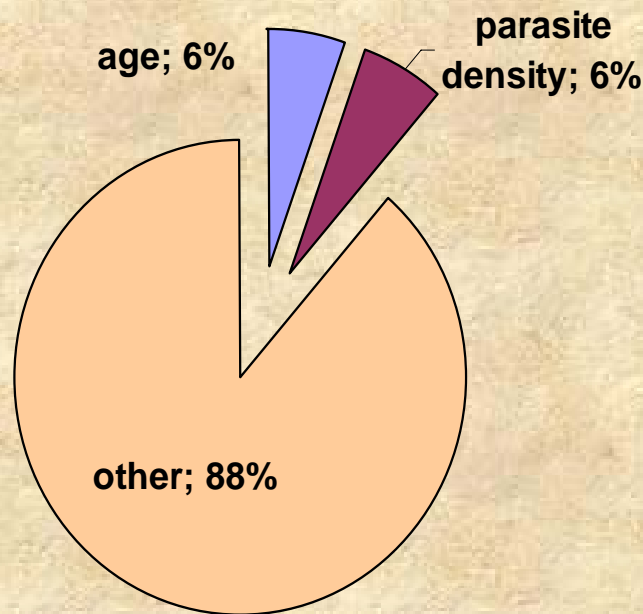
Asymptomatic infections



NDIOP



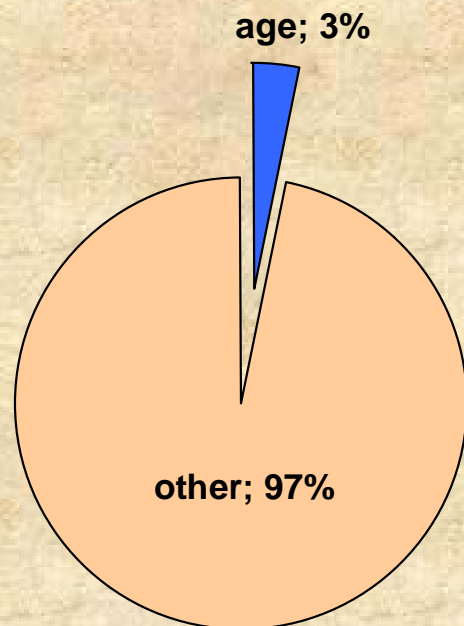
Symptomatic infections



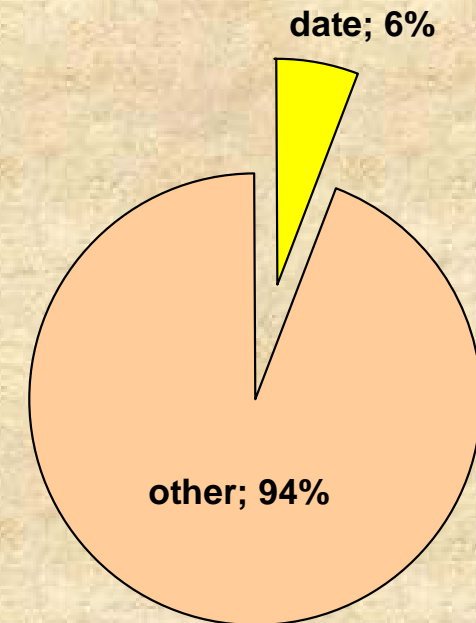
% variability in the proportion of infections that have gametocytes explained by « environmental » and genetic (heritability) factors (3)

Thailand: (virtually) all infections lead to symptomatic episodes

P. falciparum



P. vivax



Correlation of asymptomatic gametocyte prevalence & other parasite phenotypes

Strong positive correlation with asymptomatic asexual parasite density
 $r^2=0.51$ $p<0.0001$ Ndiop and $r^2=0.3$ $p<0.0001$ Dielmo

But heritability greater for gametocyte phenotypes (prevalence or density)
than for asexual parasite density (heritability 30-40% vs. ~20%)

& asexual parasite density explain only 0.1% variation in gametocyte prev.

Conclusions

- Very high heritability for gametocyte carriage
 - biology behind correlation with other phenotypes
 - genome scan & candidate gene selection
- Absence in symptomatic
 - short duration of infection?....
 - differing biological (human) stimuli



Acknowledgement

Our collaborators:

- P. Singhasivanon,
Faculty of Tropical Medicine, Mahidol
University, Thailand

- A. Tall,
Institut Pasteur de Dakar, Senegal

& the participants of the study
cohorts in Thailand and Senegal

