

# Definition and utilization of heritable variation in reproduction ratio $R_0$

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# Background

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- **Genetic variation between animals**

resistance

infectivity

tolerance etc...

- **Utilize existing heritable variation *via* Selective breeding**

- **Ultimately...**

Reduce size of an epidemic/level of Endemic Equilibrium



# Back ground

- **Reproduction ratio  $R_0$  - Important parameter**

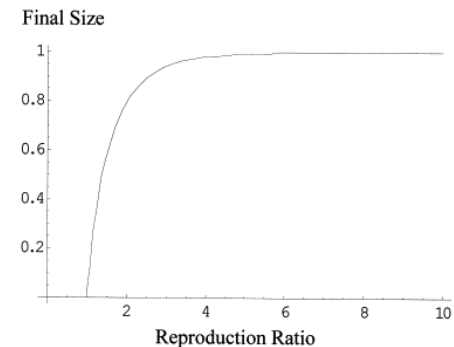
Average # new cases/ infectious life time

Size of epidemic and level of endemic equilibrium

- **Threshold value**

< 1 Disease will die out

> 1 possible major disease outbreak



Reduce epidemic :- reduce  $R_0$



# Genetics Vs. Epidemiology

- **Breeding to reduce  $R_0$**

Breeding values

Heritable variation

- **However...**

Quantitative Epidemiology

Quantitative Genetics



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# Objective

**To define breeding value and heritable variation in  $R_0$**

**What selection schemes allow us to utilize this heritable  
variation ?**



# Epidemiological model

- SIR- compartmental model



# of new cases per unit of time

- Transmission of an infection depends on

- susceptibility( $\gamma_i$ ) of the recipient  $i$
- infectivity( $\varphi_j$ ) of infectious individual  $j$

## Genetically Heterogeneous population

$$\beta_{ij} = \gamma_i \varphi_j$$



# Genetic model

- Genetically heterogeneous - Diploid population

Two loci

Susceptibility( $\gamma$ )

Infectivity( $\varphi$ )

Two allele

**g**/G

**f**/F

- Hardy Weinberg Equilibrium (HWE)
- No Linkage Disequilibrium (LD)
- Additive effect without dominance



# Can we define breeding values and heritable variation in $R_0$ ?





# Total breeding value $R_0$

- Population  $R_0$  : Next Generation Matrix

$$R_0 = \frac{\bar{\gamma} \bar{\varphi}}{\alpha}$$

Breeding value in  $R_0$  ([Bijma 2011](#))

$$A_{R_0,i} = \frac{\gamma_i \varphi_i}{\alpha}$$

And Population  $R_0 = \overline{A_{R_0}}$ ,

- **Heritable variance: variance in Breeding value**



# Heritable variance in $R_0$

$$\text{var}(A_{R_0}) = \left\{ \left[ 4p_g^2 g^2 + 2p_g(1-p_g)(g+G)^2 + 4(1-p_g)^2 G^2 \right] \right. \\ \left. \left[ 4p_f^2 f^2 + 2p_f(1-p_f)(f+F)^2 + 4(1-p_f)^2 F^2 \right] - \bar{\varphi}^2 \bar{\gamma}^2 \right\} \frac{c}{\alpha}$$

$$\Delta R_0 = i\rho \sqrt{\text{var}(A_{R_0})}$$

where  $i$  is selection intensity,  $\rho$  is correlation coefficient and  $\sqrt{\text{var}(A_{R_0})}$  is variance in BV in  $R_0$

$i$  and  $\rho$  – scale free parameters

$\text{var}(A_{R_0})$  – potential of the population to selection



**What selection schemes allow us to utilize this  
heritable variation ?**



# Simulation

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- **Diploid population**

100 groups/100 size

degree of relatedness  $r : 0 - 1$

Epidemic started by one random individual

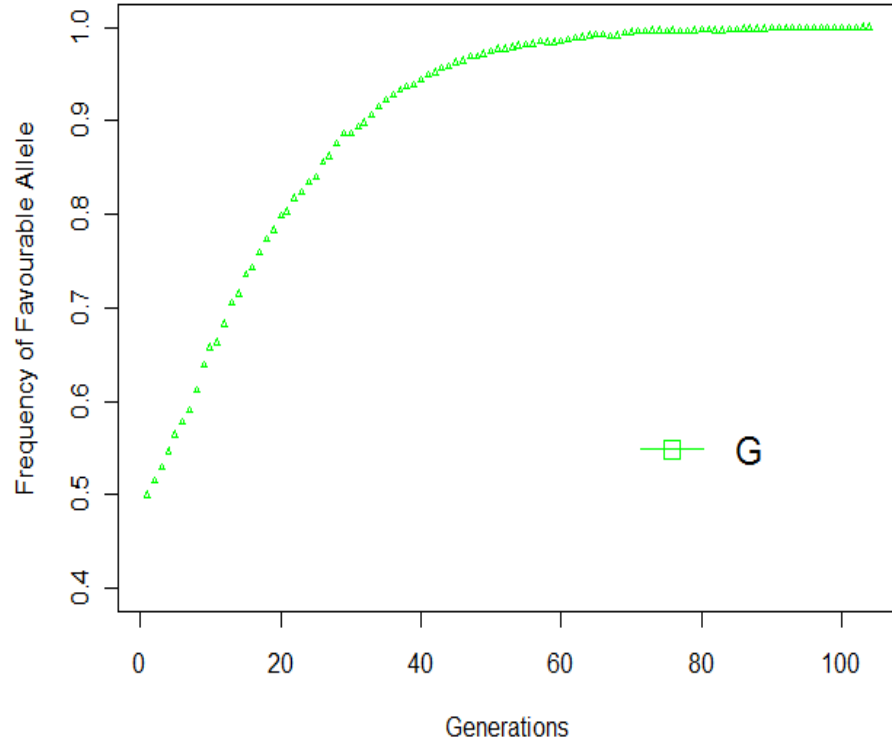
Phenotypic selection – escaped ones

Discrete generations

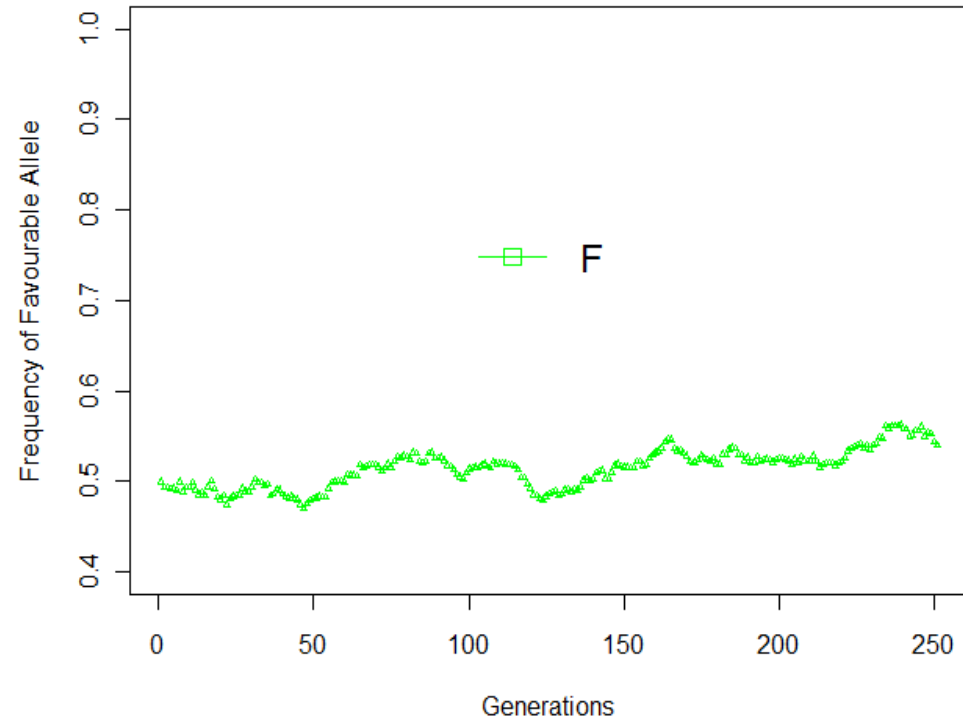


# Results: without relatedness

## Susceptibility

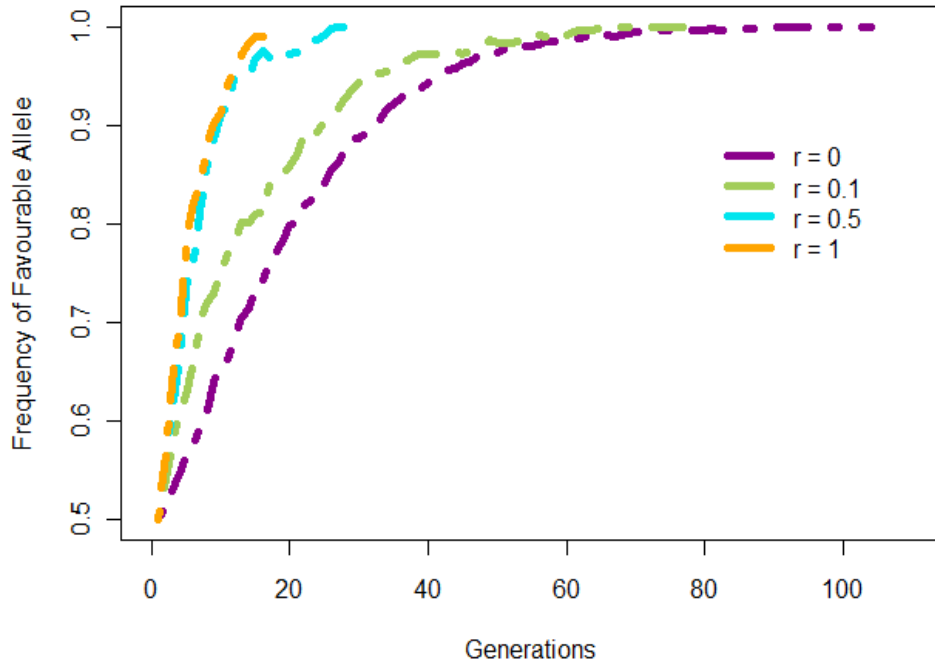


## Infectivity

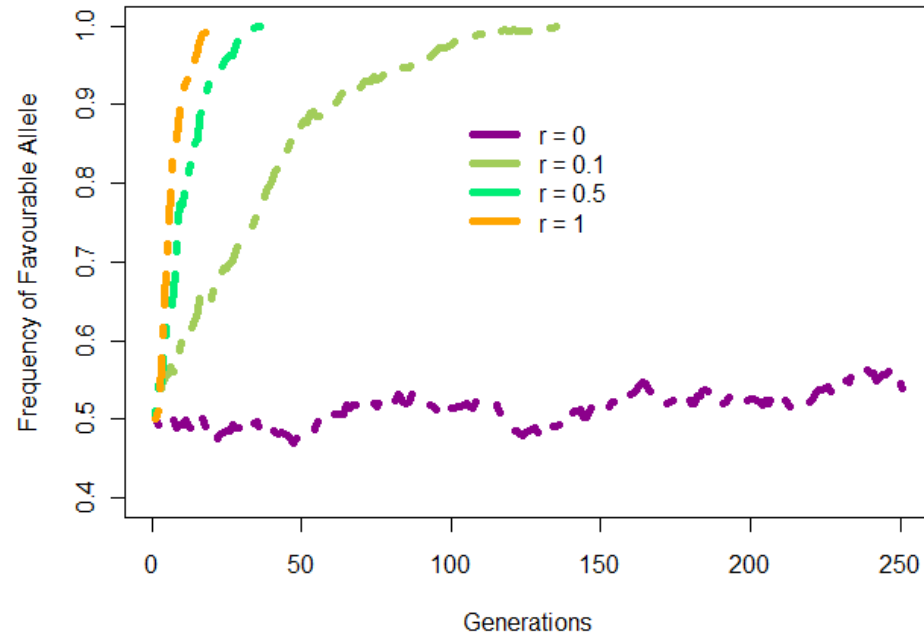


# With relatedness

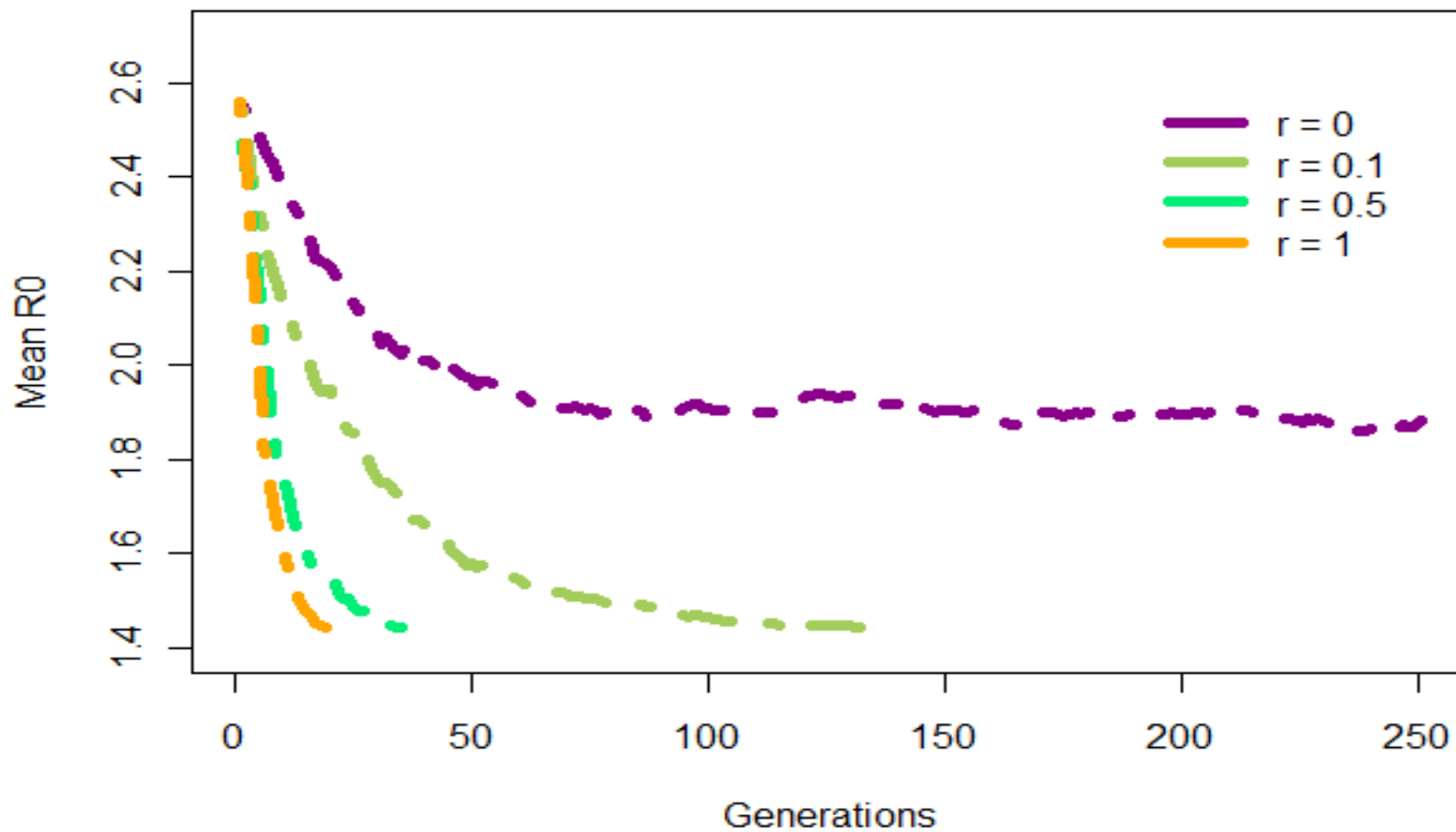
## Susceptibility



## Infectivity



# Population $R_0$



# Conclusion

- **Conceptually**

define Breeding Value and heritable variation in  $R_0$

Next :- extend to polygenic loci

- **Amount of selection response depends on**

Relatedness among interacting individuals

increase in correlation( $\rho$ ) b/n  $A_{R_0}$  and disease phenotype (0/1)

$$\rho_{unrelated} = 0.033$$

$$\rho_{related} = 0.094$$

$$\Delta R_0 = i\rho \sqrt{\text{var}(A_{R_0})}$$





# Remarkably !

- **Susceptibility**

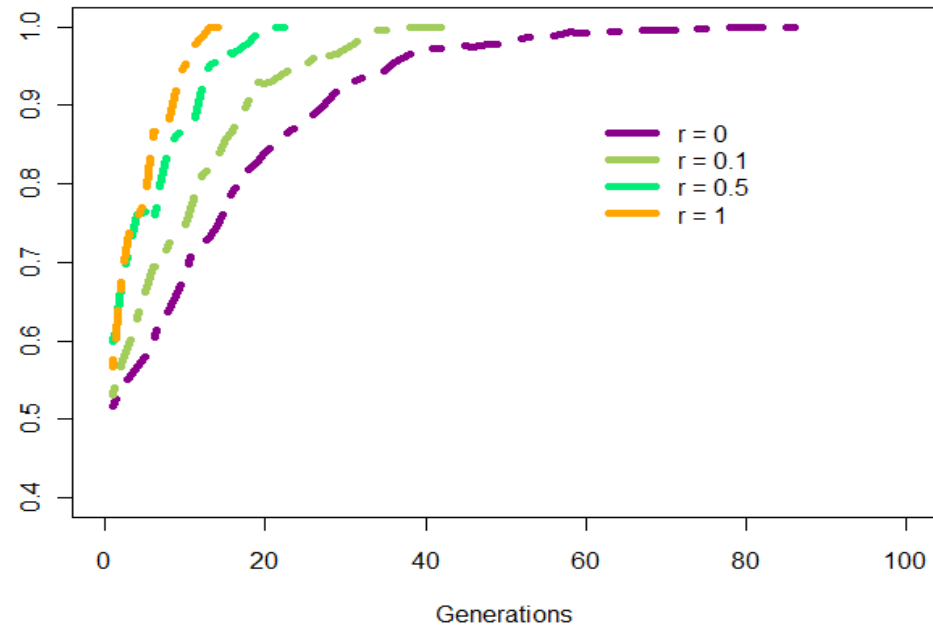
Direct genetic effect

Indirect genetic effect

- **Consequently**

underestimation of heritable variance

underestimated heritability



**Thank you for your  
attention !**

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