

Evaluating the influence of selection for disease resistance on the spread of infections in a simulated aquaculture population when underlying epidemiological traits are correlated

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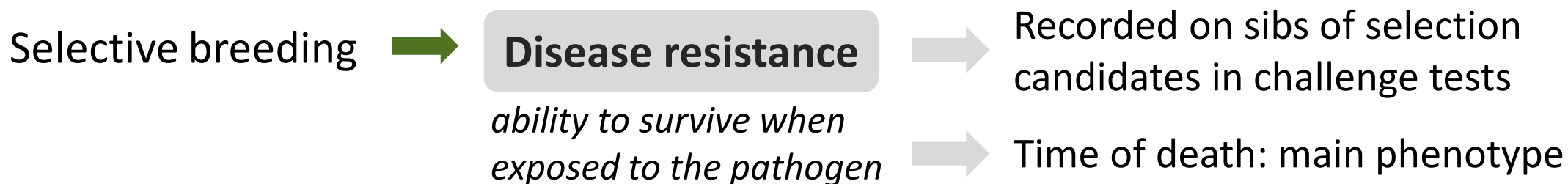


Background

Infectious disease outbreaks

Major threat ➡ economic and environmental sustainability of animal production

Especially in aquaculture production ➡ specific conditions facilitate transmission



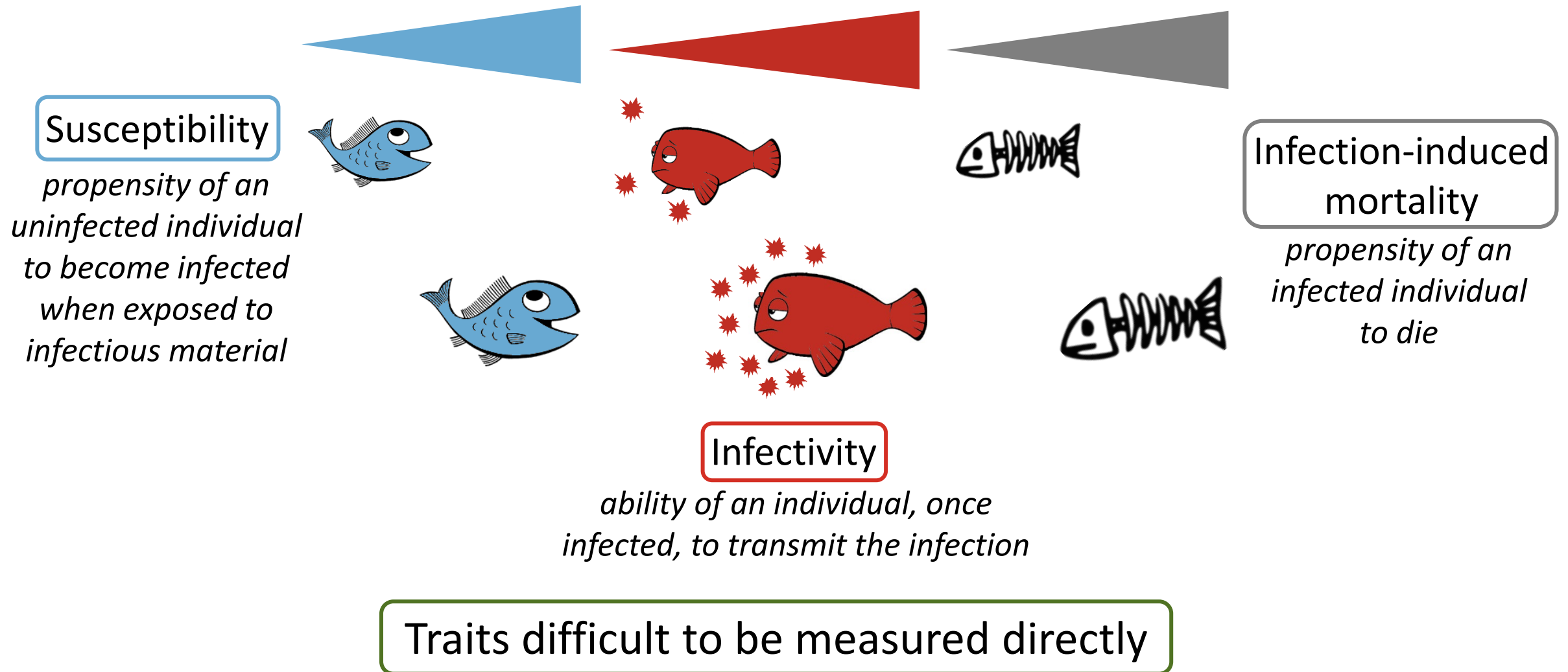
Selection on Disease Resistance ➡ Strengthening an animal's ability to cope with infection

Does this reduce pathogen transmission and thus the incidence and severity of outbreaks?

Basic reproductive ratio (R_0) ➡ number of secondary infections

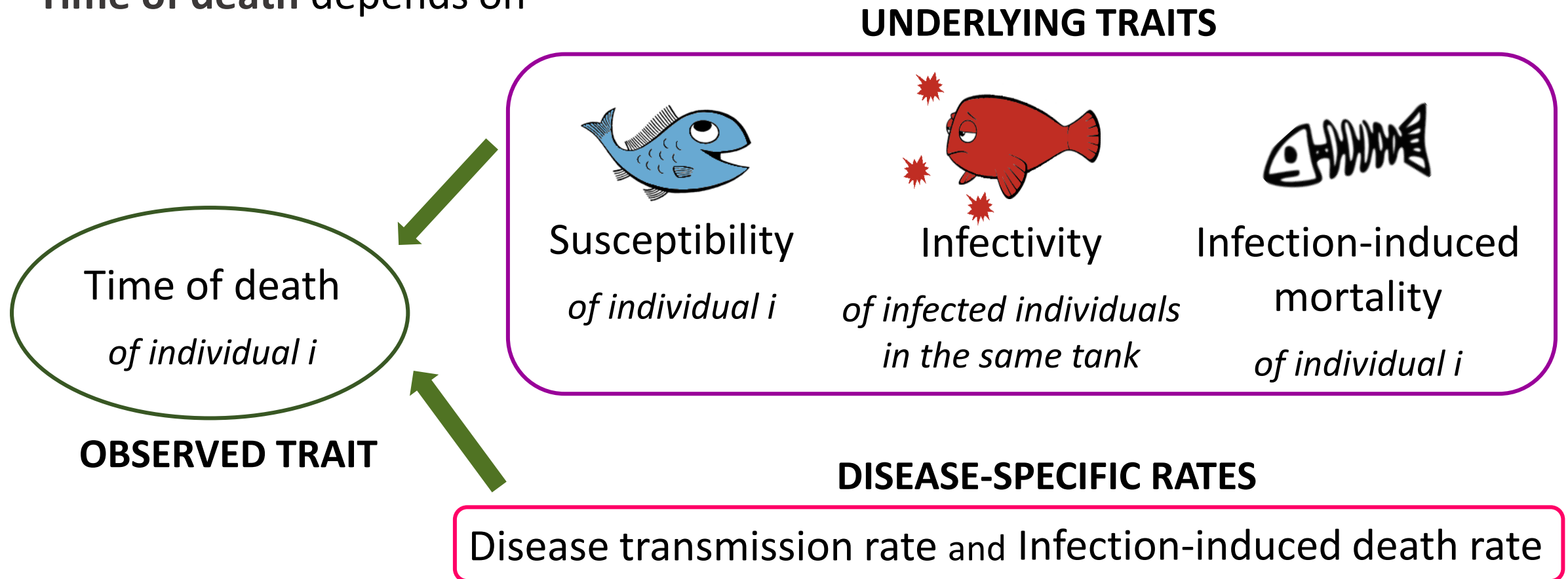
Background

Pathogen transmission is affected by three underlying epidemiological host traits



Background

Time of death depends on



What impact does selection for time of death have on the three underlying traits? And on the dynamic of the infection?

Objective

Predict the impact of **selection for disease resistance** measured as time of death on the three **underlying traits** and the **spread of the disease**



*through computer simulations
mimicking a salmon population*



Material and Methods

- Genome
30 Chromosomes
30 Morgan total genome length



Atlantic salmon

- Breeding program

100 ♂, 200 ♀



→ 200 full-sib families

→ 100 half-sib families

30 fish per FS family → 10 selection candidates

- Each generation
→ 20 sibs → challenge tests → time of death

Number of fish	Selection candidates	Sibs (challenge tests)	Number of full-sib families	Number of half-sib families
6,000	2,000	4,000	200	100

- 10 generations of selection

M&M – Underlying traits

TBV for **Susceptibility** **Infectivity** and **Infection-induced mortality**

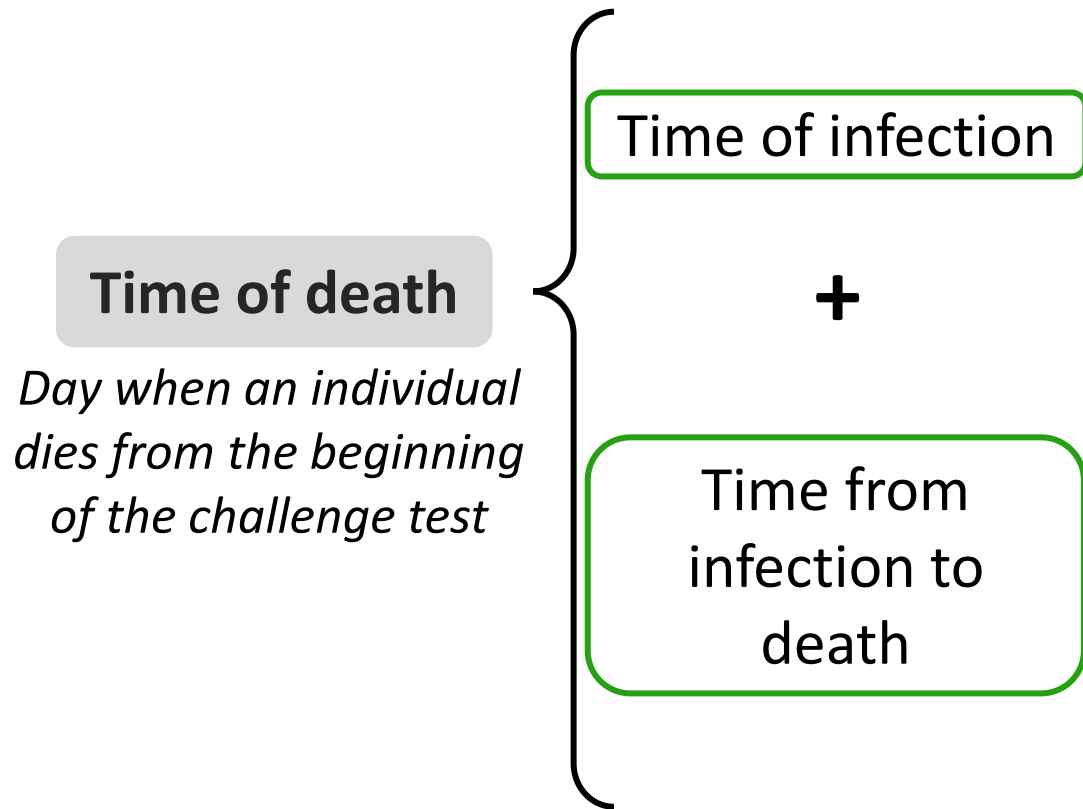
all fish (selection candidates + sibs)

- 1,000 additive loci controlling simultaneously the three traits
- Phenotypic variance for the three traits = 1

	Susceptibility	Infectivity	Infection-induced mortality
Susceptibility	0.5		
Infectivity	0.5		
Infection-induced mortality	$\rho = 0, 0.5 \text{ or } -0.5$		0.5

➡ Heritability for the **observed trait (time of death)** = 0.2

M&M – Observable trait



SIR epidemiological model

Transition rates:

-  
Susceptible → Infected

j : infected fish in the same tank

force of infection $\lambda_i = \beta \text{Susceptibility}_i \sum_j \text{infectivity}_j$
↓
disease transmission rate

-  
Infected → Dead

$w_i = \gamma \text{mortality}_i$
↓
infection-induced death rate

Phenotypes were generated only for the sibs sent to the disease challenge

M&M – Challenge test

ISA virus disease

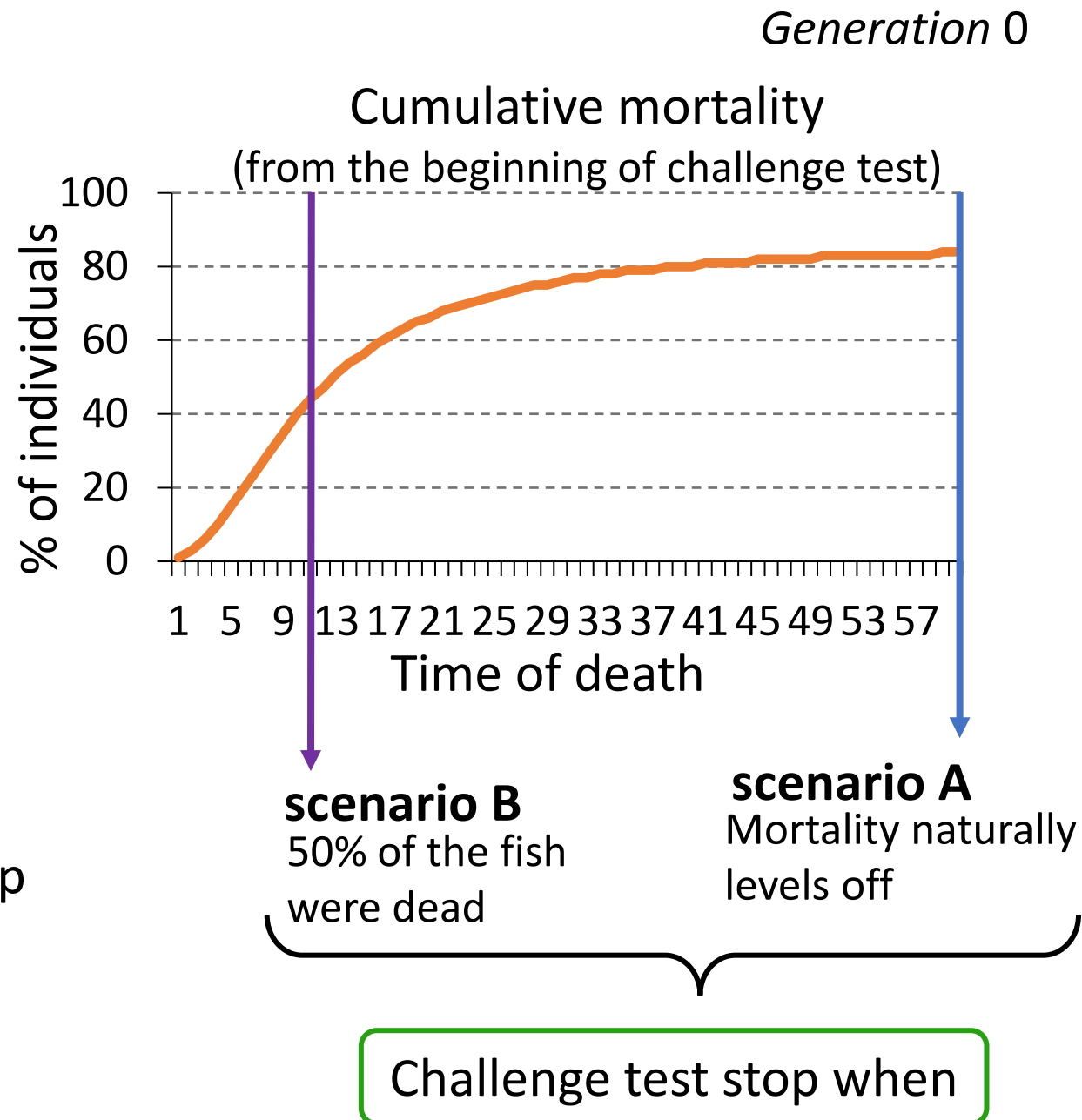


Severe outbreak:

- Disease transmission rate = 0.8
- Infection induced death rate = 0.4
- Heritability of time of death = 0.2

Challenge test

- 20 groups/tanks
 - 200 fish (one of each family) per group
 - 5 fish per group as initially infected



M&M – Evaluation, selection and mating

- **Evaluation Model**

$$\begin{array}{c} \text{additive genetic effects} \\ \uparrow \\ \text{Phenotypes} \leftarrow \mathbf{y} = \underset{\substack{\downarrow \\ \text{mean}}}{\mu} + \mathbf{Zu} + \mathbf{e} \rightarrow \text{residual effects} \\ \text{Time of death} \end{array}$$

Evaluation method for **time of death**: **GBLUP**

$$\mathbf{V}(\mathbf{u}) = \mathbf{G}\sigma_u^2$$

G: genomic relationship matrix

45,000 SNPs

1,500 SNPs/Morgan

- **Selection**

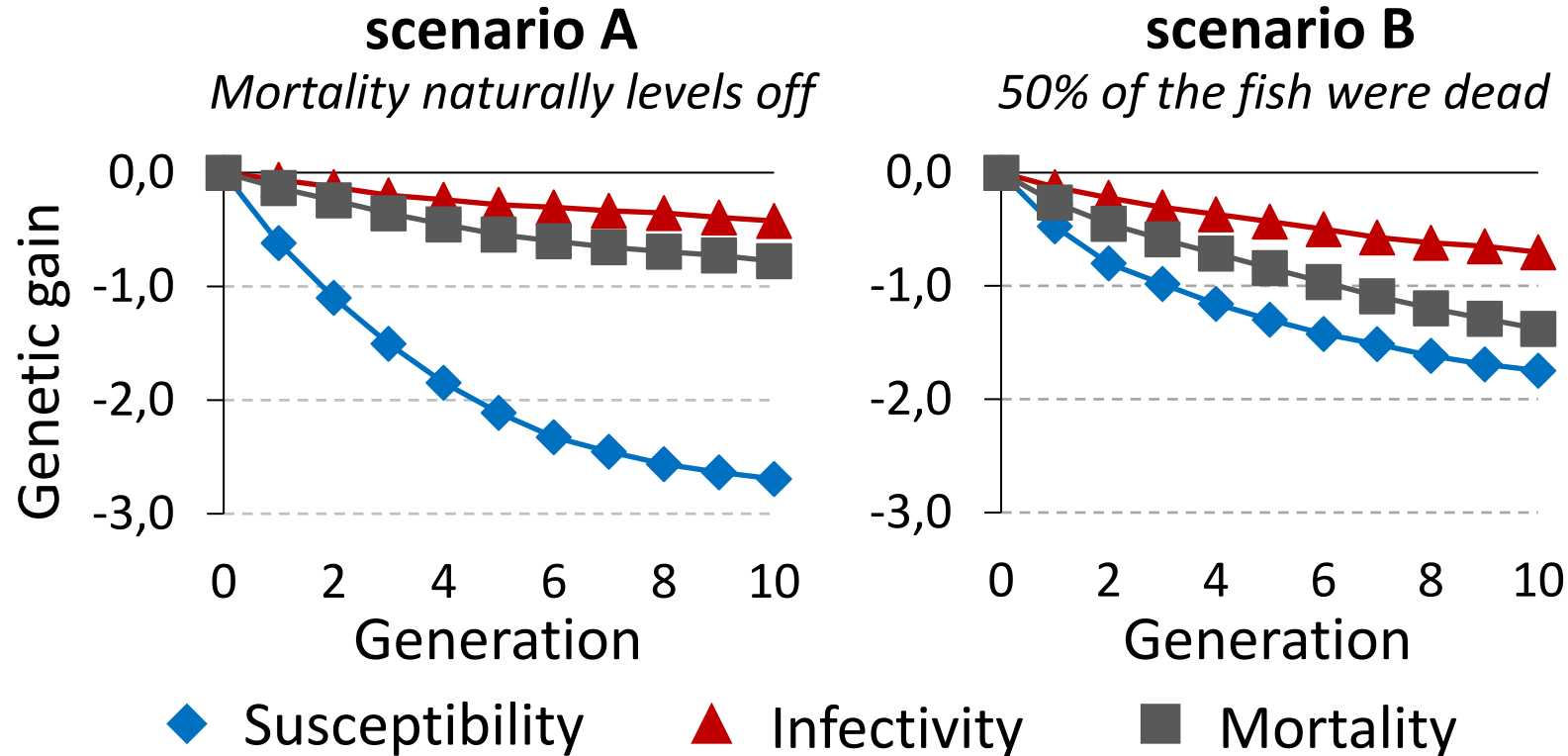
100 ♂ & 200 ♀ with the highest GEBVs 10 generations

- **Mating**

Random mating (1 ♂ x 2 ♀) ➡ 30 fish

Results - Uncorrelated

Cumulative genetic gain across generations



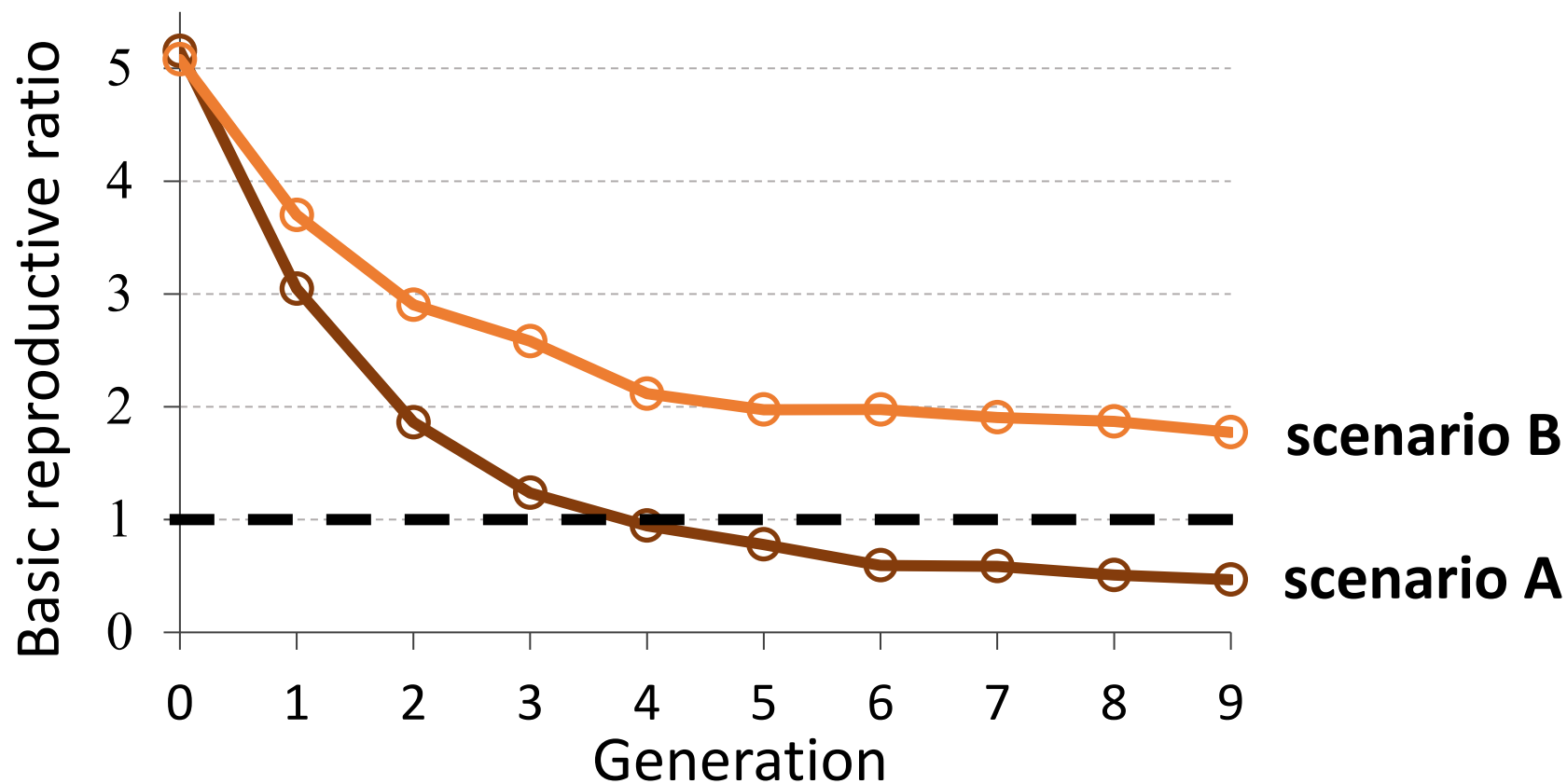
Selection for disease resistance ➡ reduction in the three underlying traits

scenario A ➡ genetic gain was mainly for susceptibility

scenario B ➡ genetic gain for the three traits became more similar

Results - Uncorrelated

Basic reproductive ratio (R_0) across generations



In all scenarios selection for time of death decreased R_0

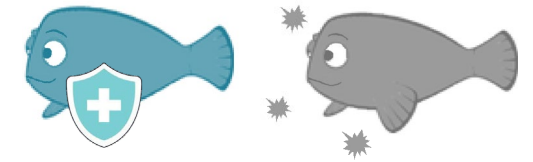
Scenario A led to $R_0 < 1$

Results – Positively correlated

$$R_0 \sim 4 \quad t = 0$$

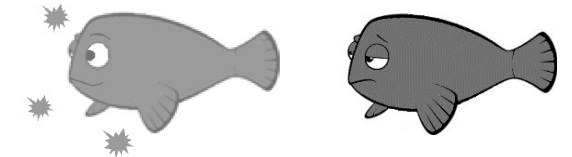
- Susceptibility and infectivity

Favorable: *fish with low susceptibility are less infective*



- Infectivity and Infection-induced mortality

Unfavorable: *fish with low infectivity died later*



Time to death $R_0 < 1 \quad t = 4$ ➡ *Disease eradicated*

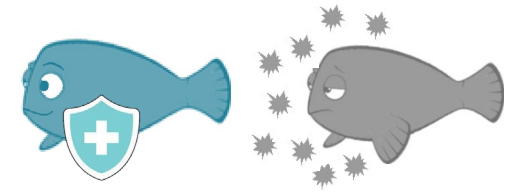
Dead/alive status $R_0 \sim 1 \quad t = 10$ ➡ *Outbreaks decreased*

Results – Negatively correlated

$$R_0 \sim 4 \quad t = 0$$

- Susceptibility and infectivity

Unfavorable: *fish with low susceptibility are more infective*



- Infectivity and Infection-induced mortality

Favorable: *fish with low infectivity died sooner*

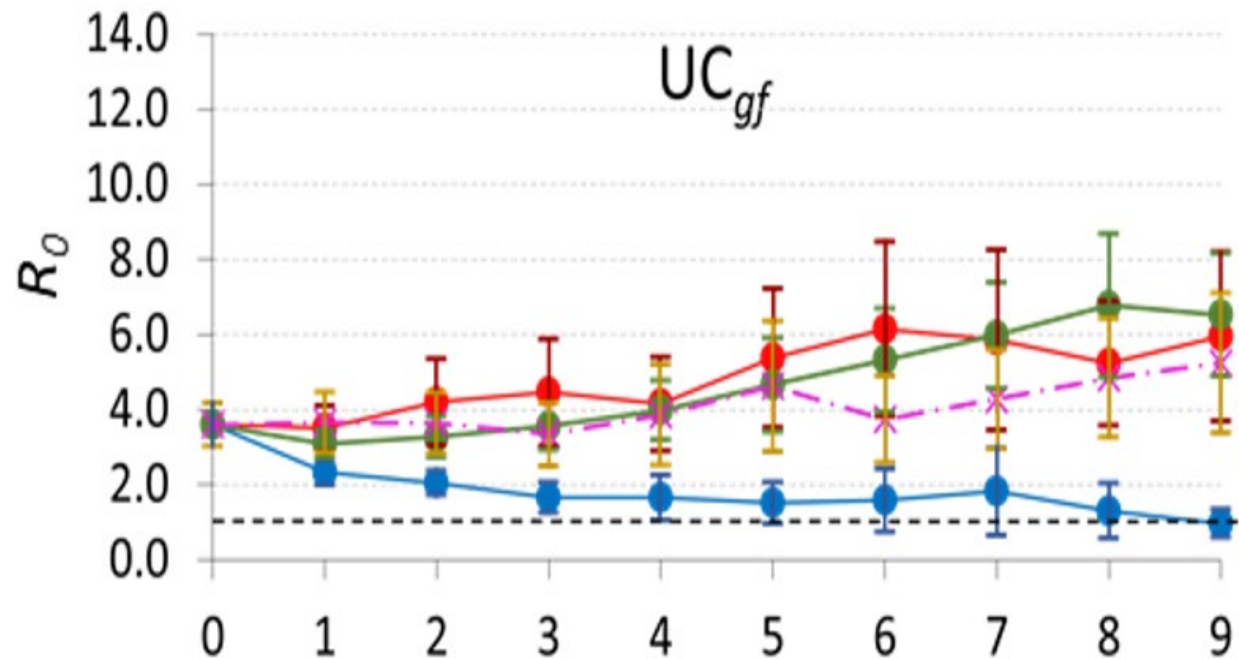


Time to death (A) $R_0 \sim 1$ $t = 10$ ➡ *Outbreaks decreased*

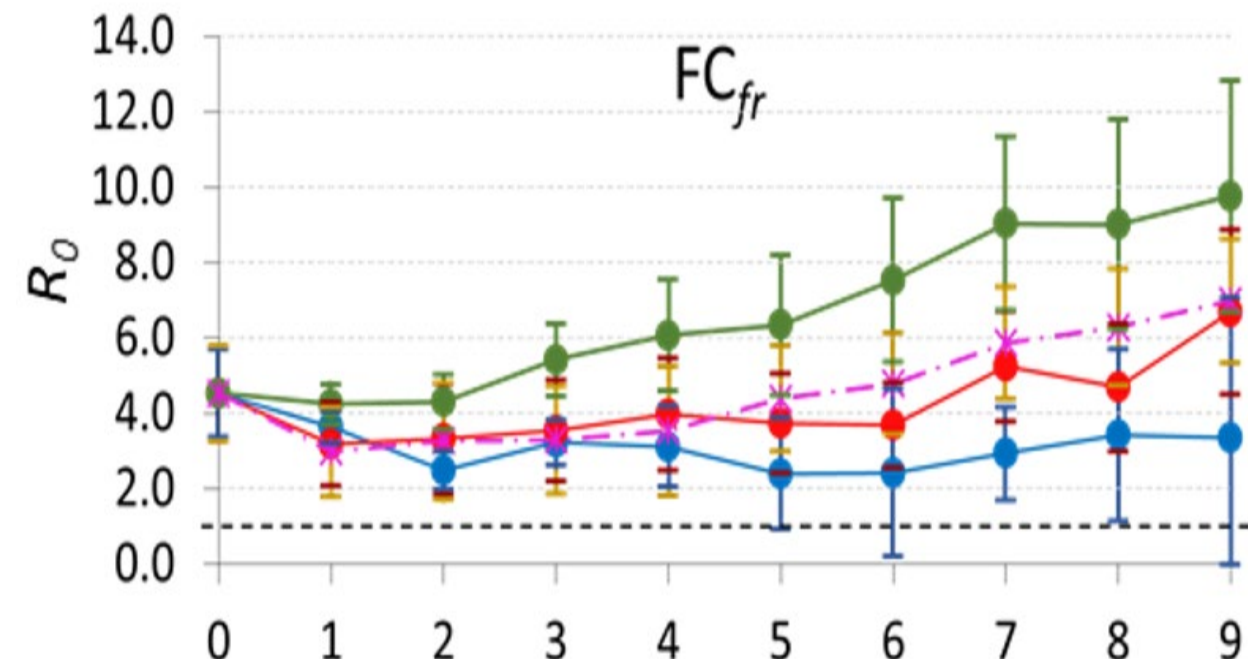
Dead/alive status **$R_0 \sim 7$** **$t = 10$** ➡ ***Outbreaks increased***

Results

Susceptibility-Infectivity



Infectivity-Mortality



- Selection for time of death, test lasting 60 days
- Selection for time of death, test lasting 15 days
- Selection for time of death, test lasting 7 days
- Selection dead/alive status

Summary

- The three underlying **traits** are genetically **uncorrelated**
 - **Selection for time of death**
 - ➔ Reduction in the genetic mean for the three underlying traits
 - ➔ Not only increase survival, but also contributes to reduce the disease transmission in a severe outbreak
- For **correlated** underlying **traits**
 - ➔ Depending on the particular correlations
 - ➔ Significant reduction in R_0 in many combinations
- The **greatest decrease in R_0** (reaching values < 1) when the challenge **test continued until mortality naturally levels off**

Conclusions

Genomic selection against mortality measured as time to death can simultaneously reduce mortality and disease transmission

Acknowledgements



75th EAAP Annual Meeting
1/5 September 2024 - Florence, Italy

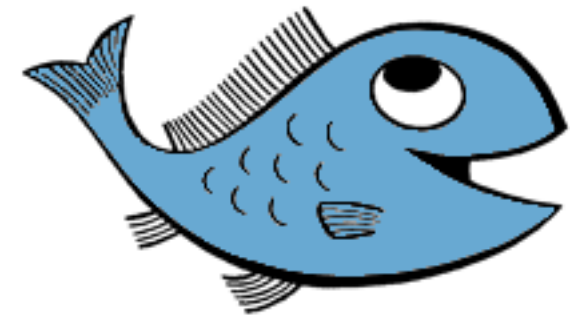


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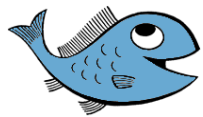
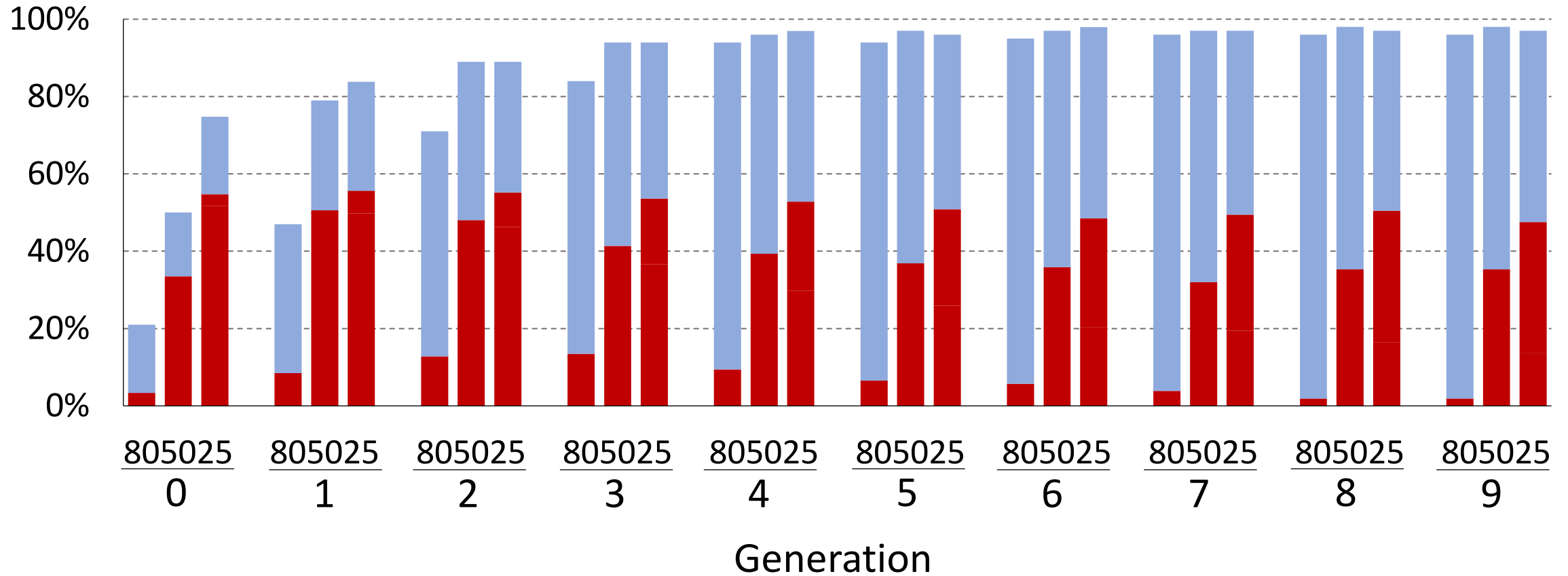
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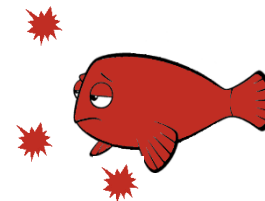


Extra

Percentage of survivors per generation



Survivor not infected

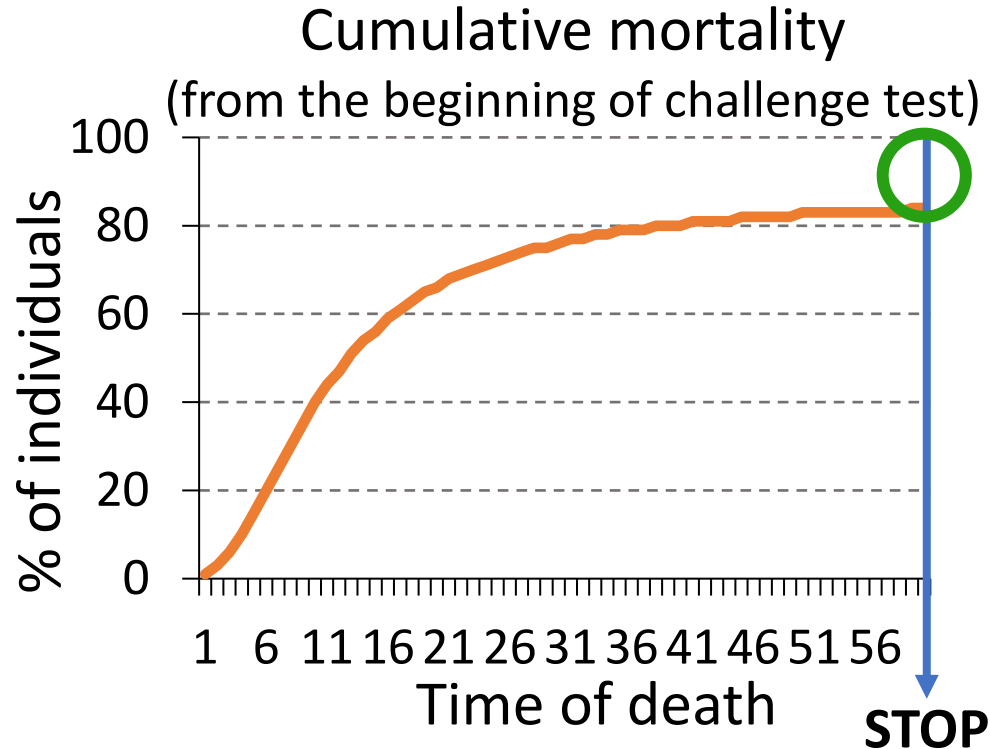


Survivors infected

Results

scenario A

Highest genetic gain was for susceptibility



90% →

Survivors not infected

30% →

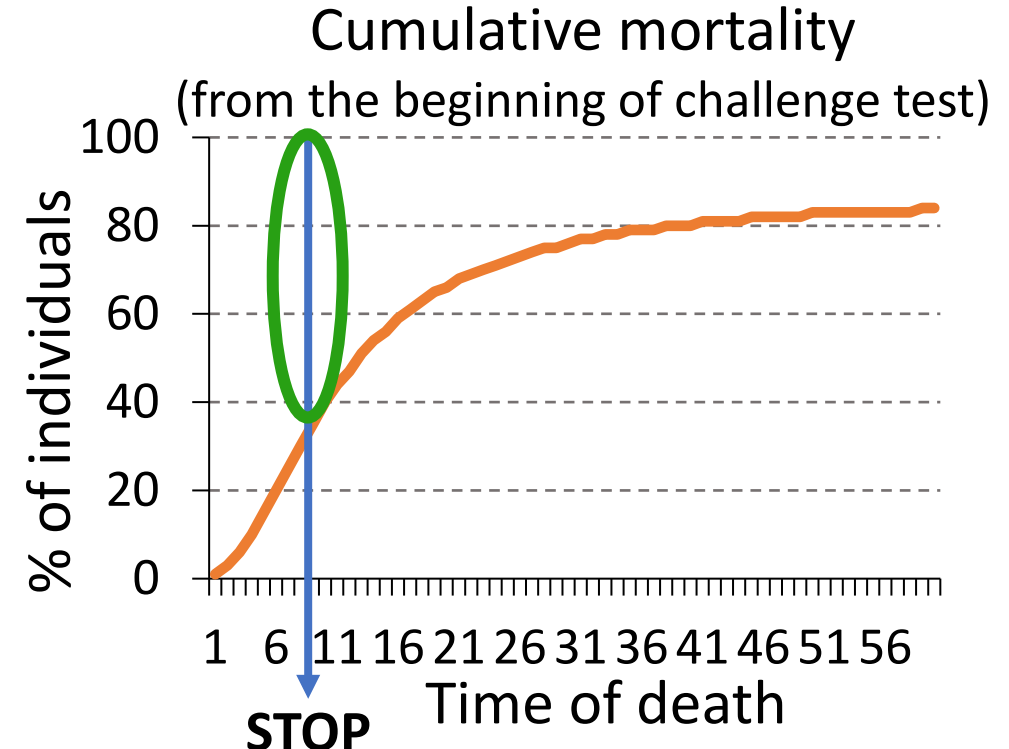
Survivors not infected



Low susceptibility

scenario C

Similar genetic gain for the three traits

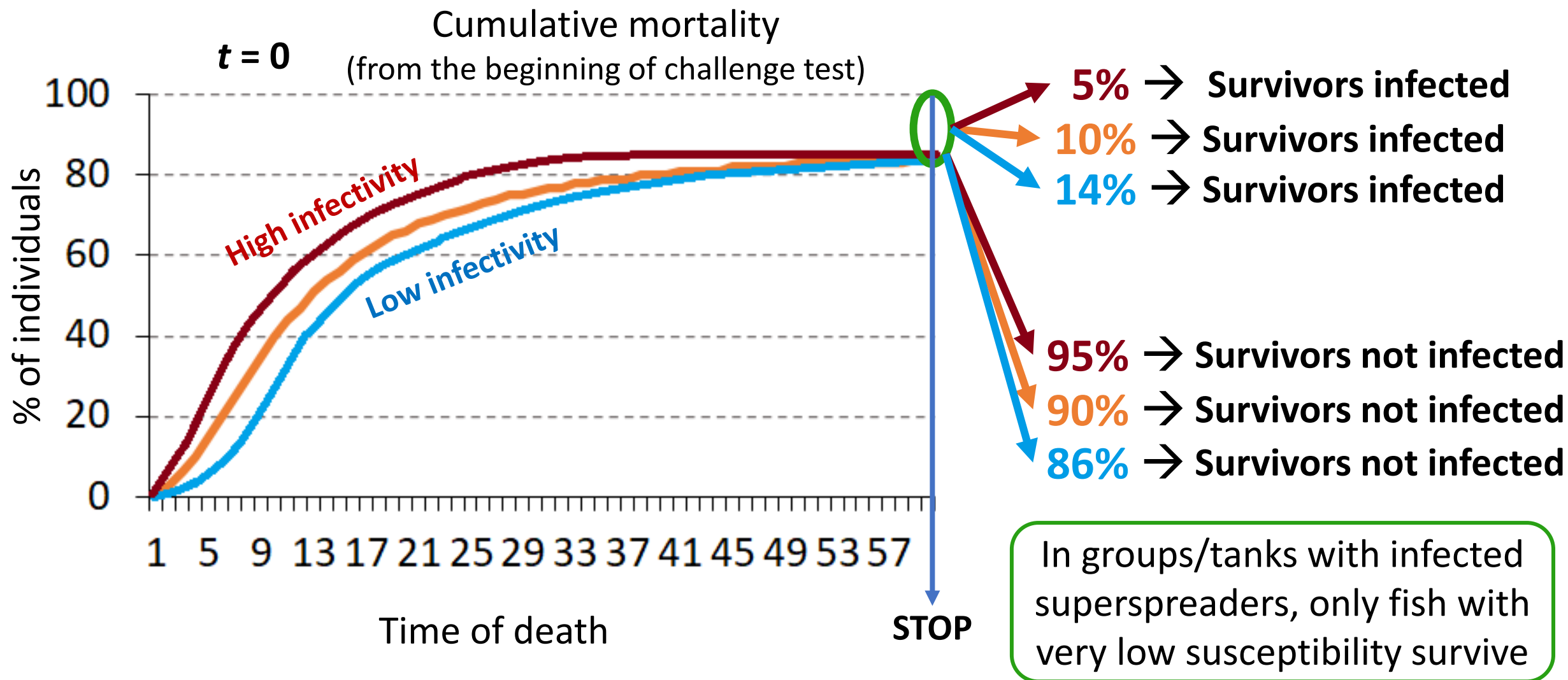


Generation 0

Extra

scenario A

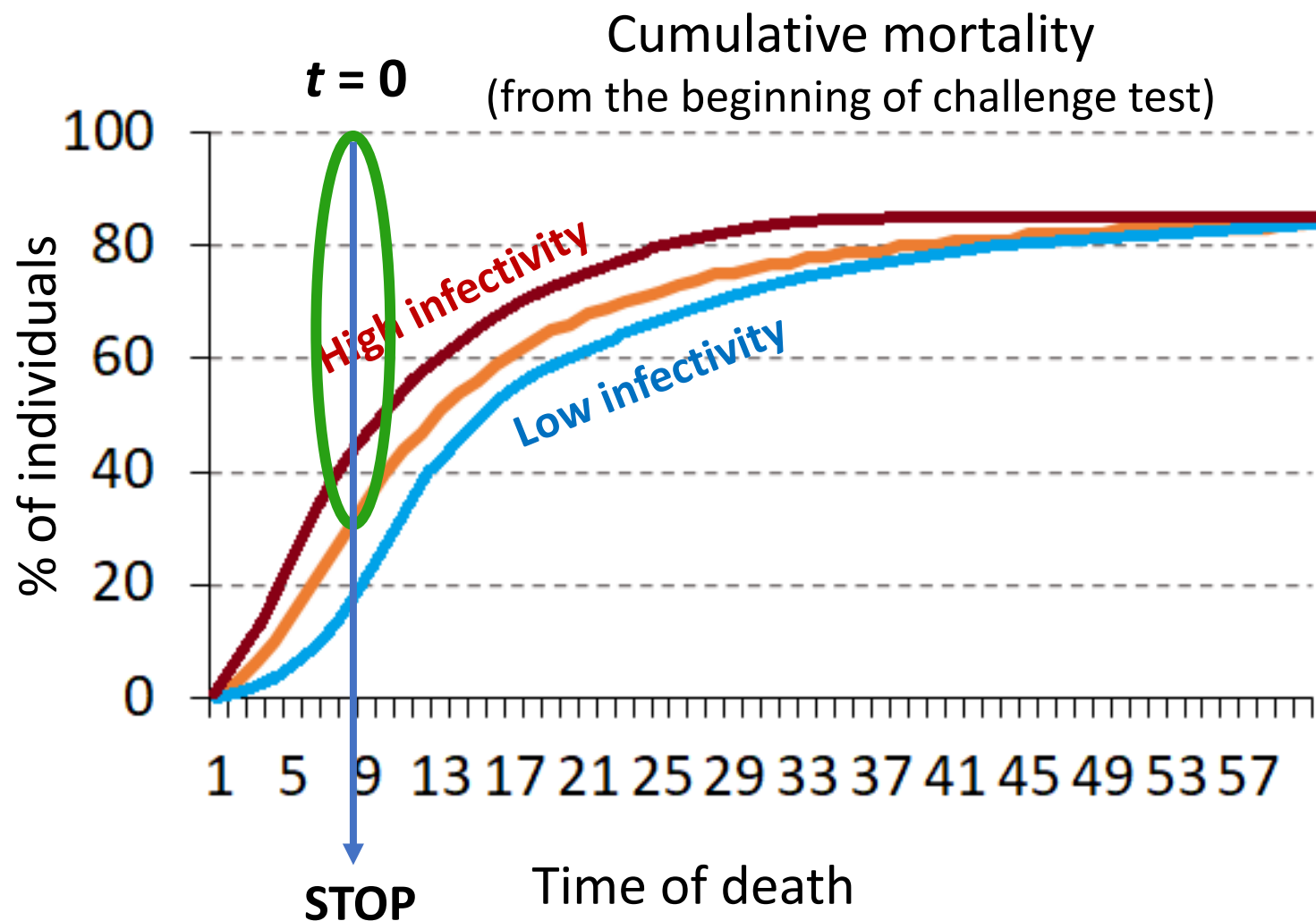
High infectivity → faster transmission → fish infected sooner



Extra

scenario C

High infectivity → faster transmission → fish infected sooner



60% → Survivors

75% → Survivors

80% → Survivors

Groups/tanks without
infected superspreaders
have more survivors