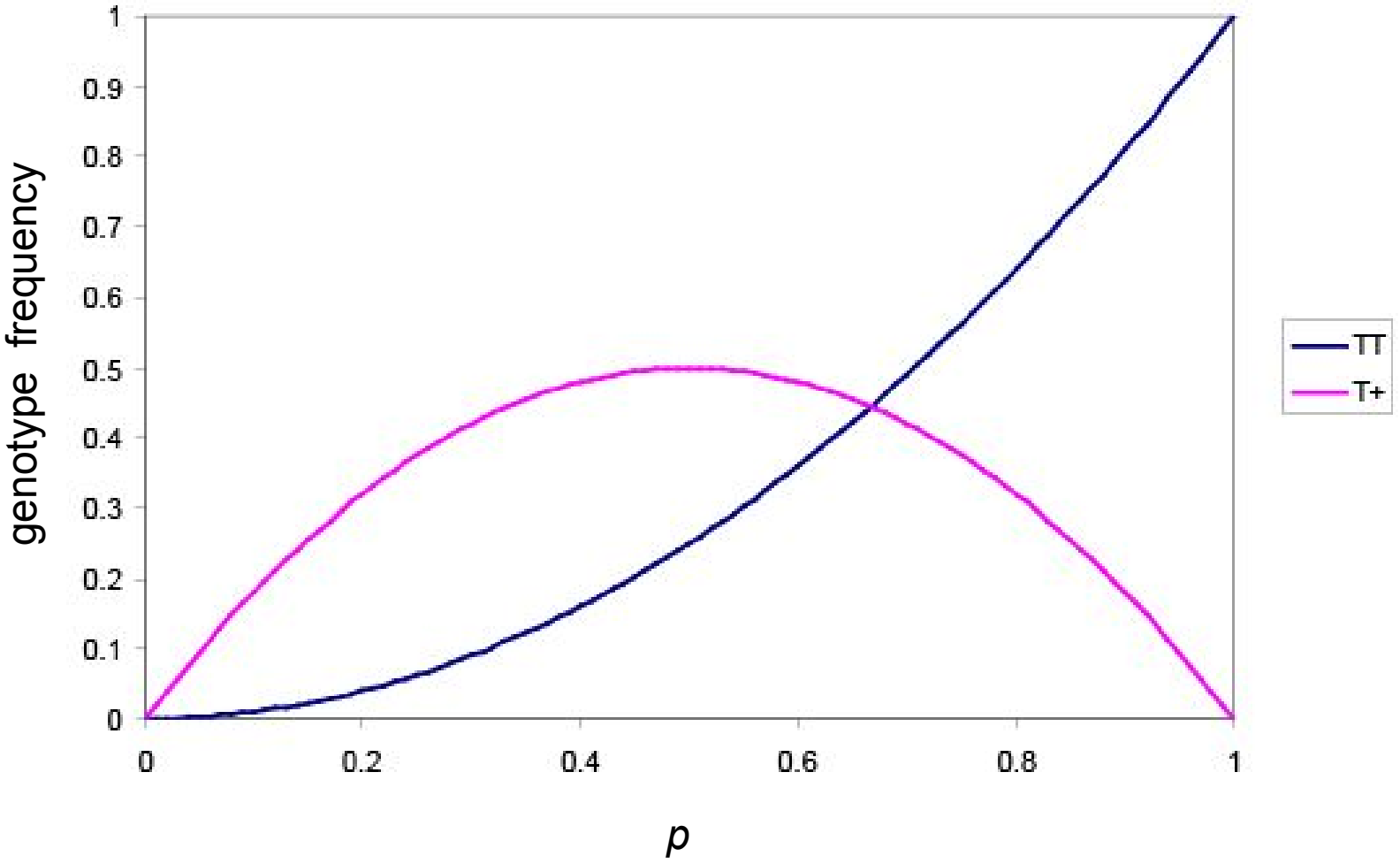
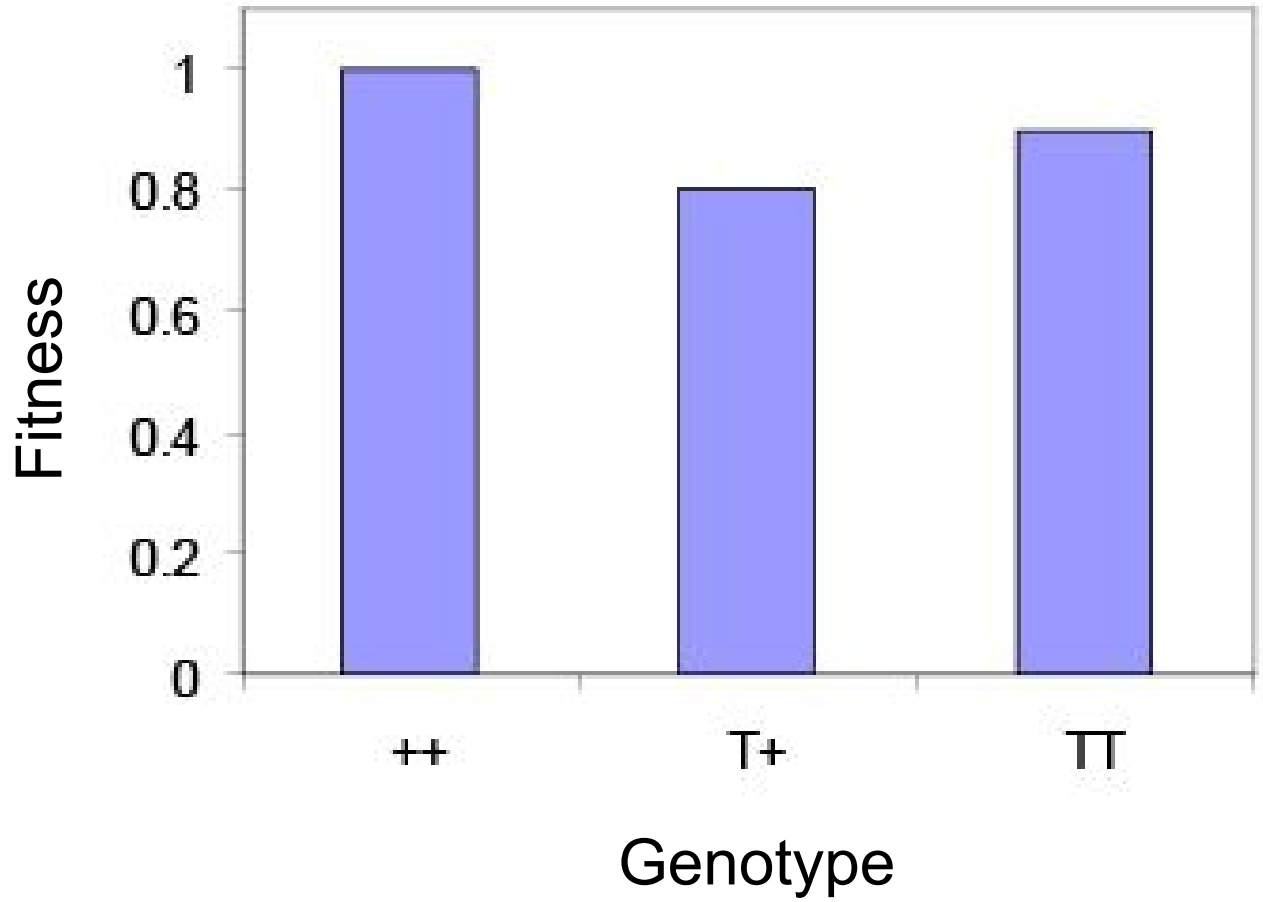
Finally,
empirical
results!

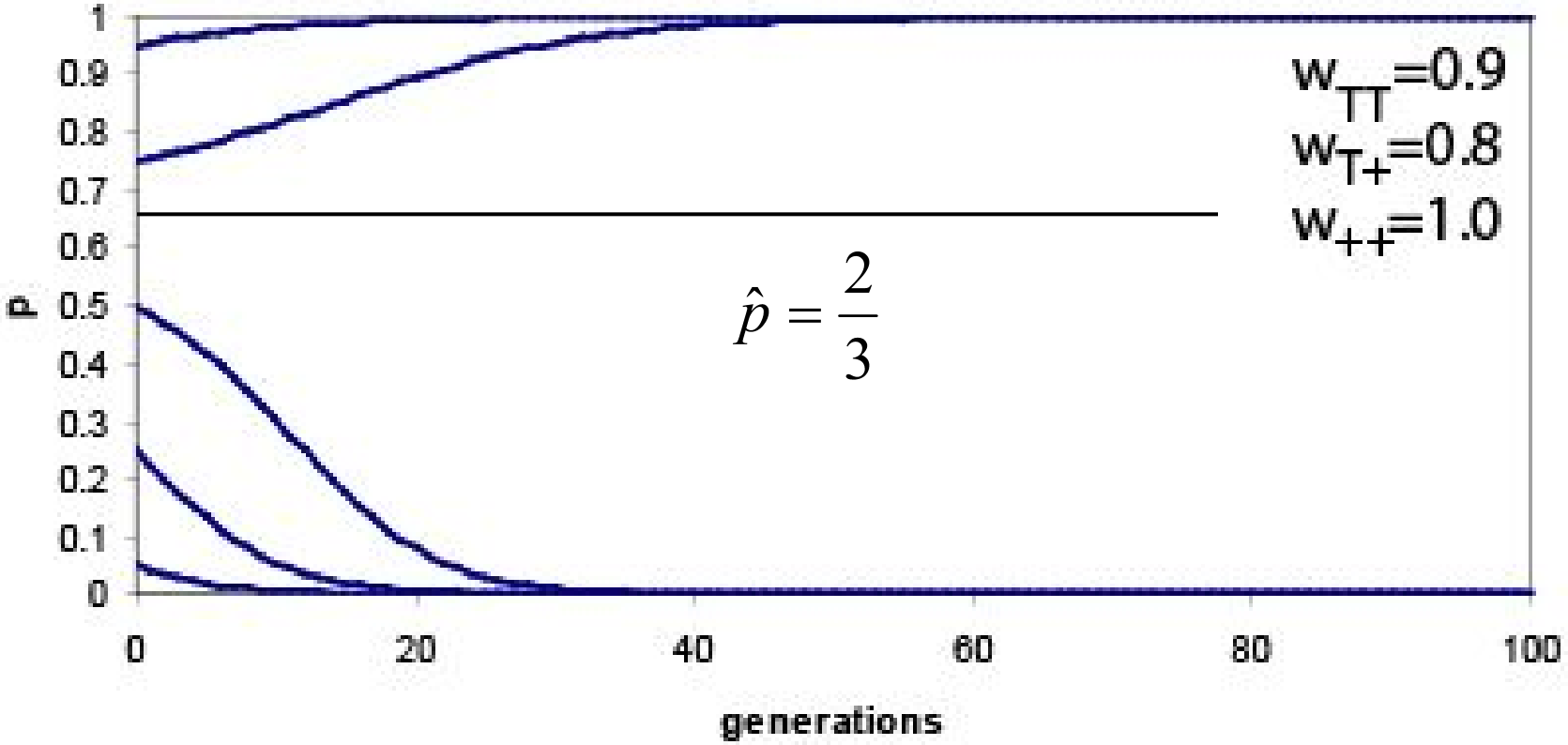
# A rare allele spends more time as a heterozygote than a homozygote



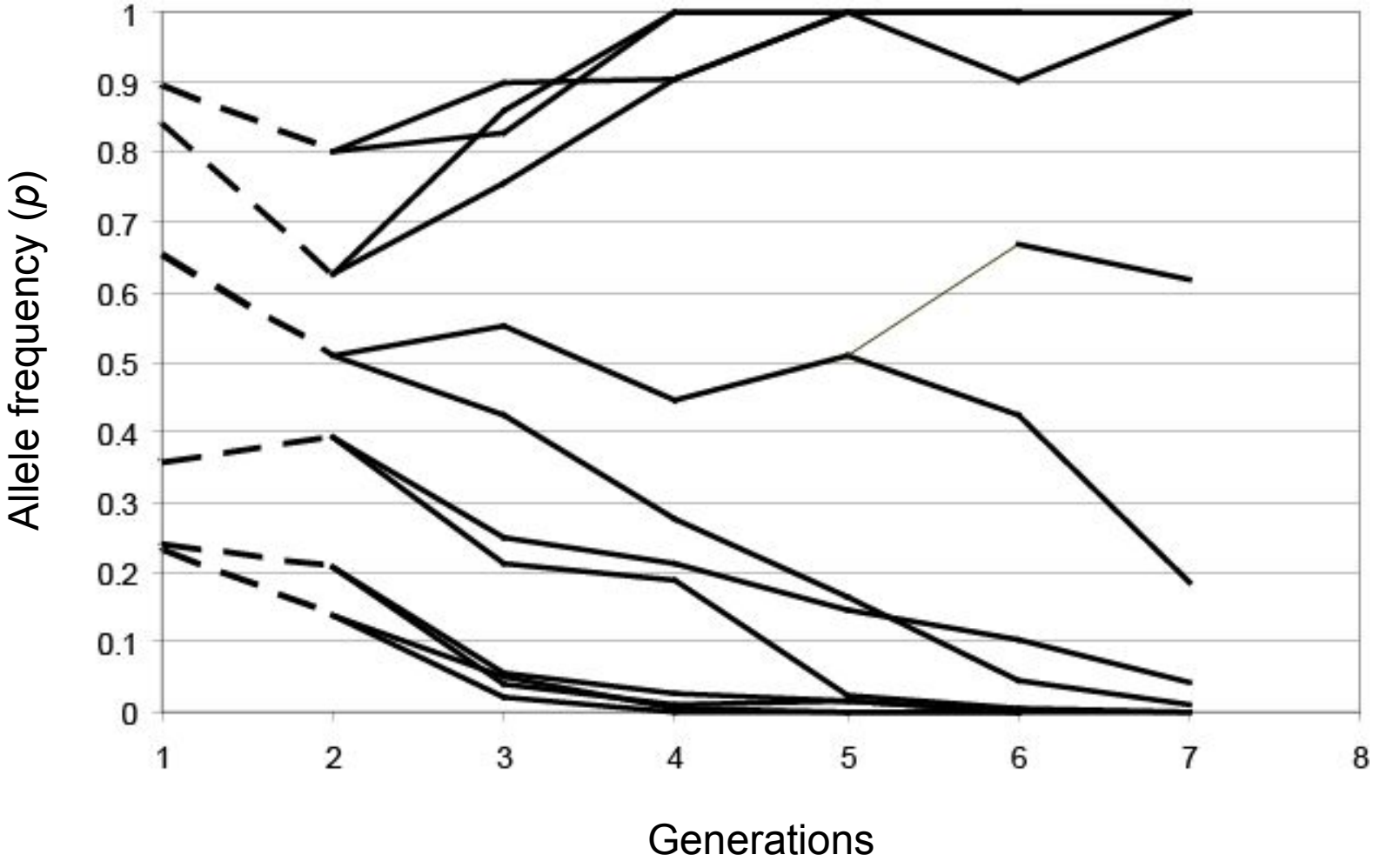
# A heterozygote disadvantage corresponds to a rare allele disadvantage



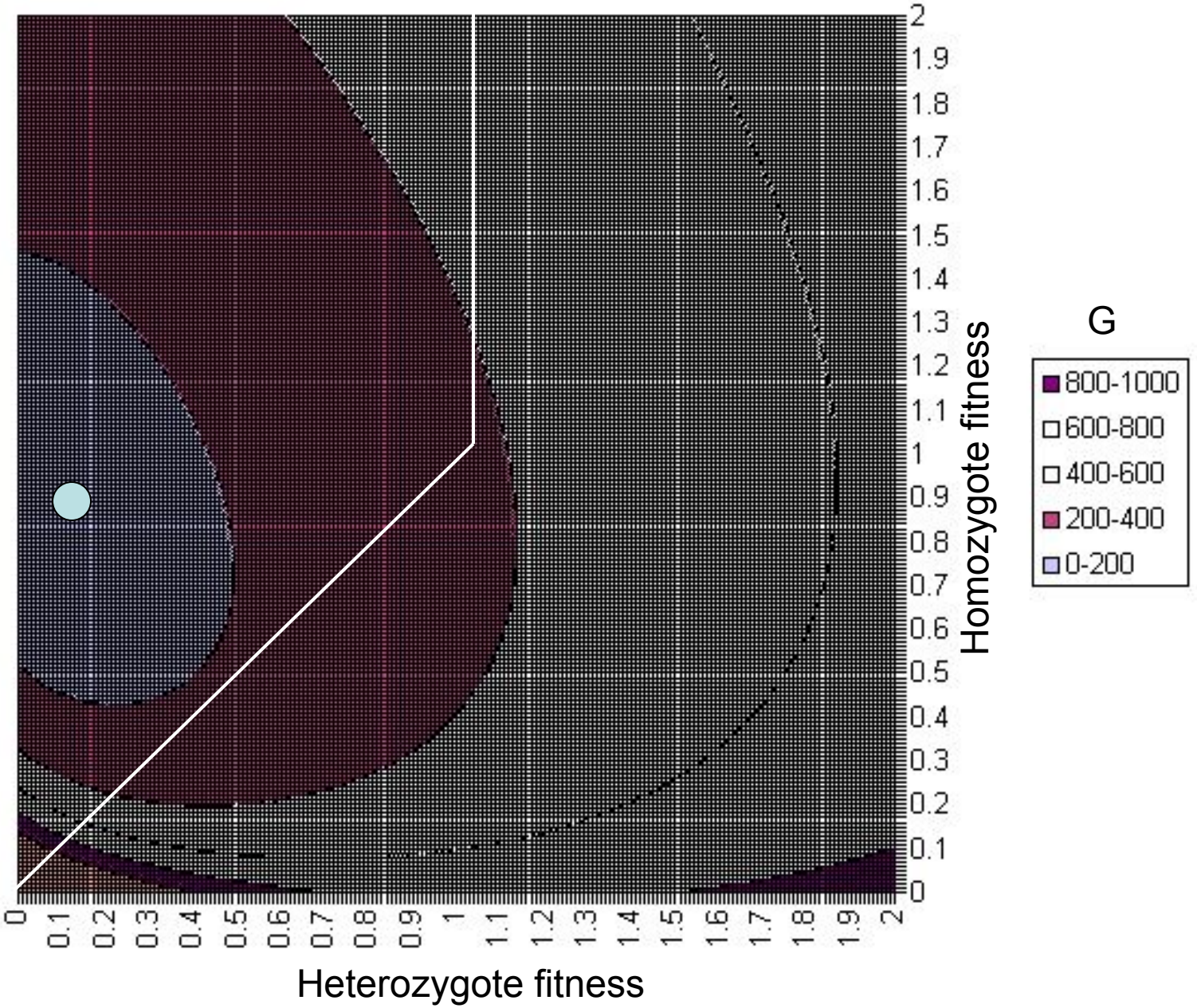
With underdominance, if starting at a high enough frequency, an allele less fit than wildtype can stably fix in a population.



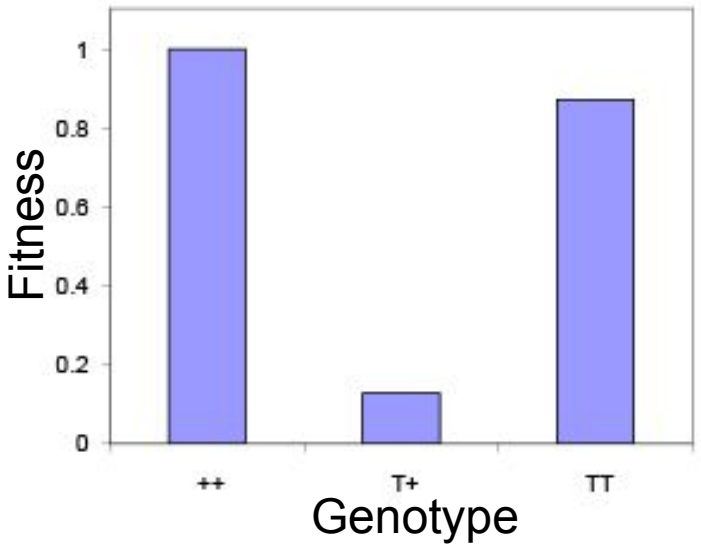
# Allele frequency changes over replicated populations

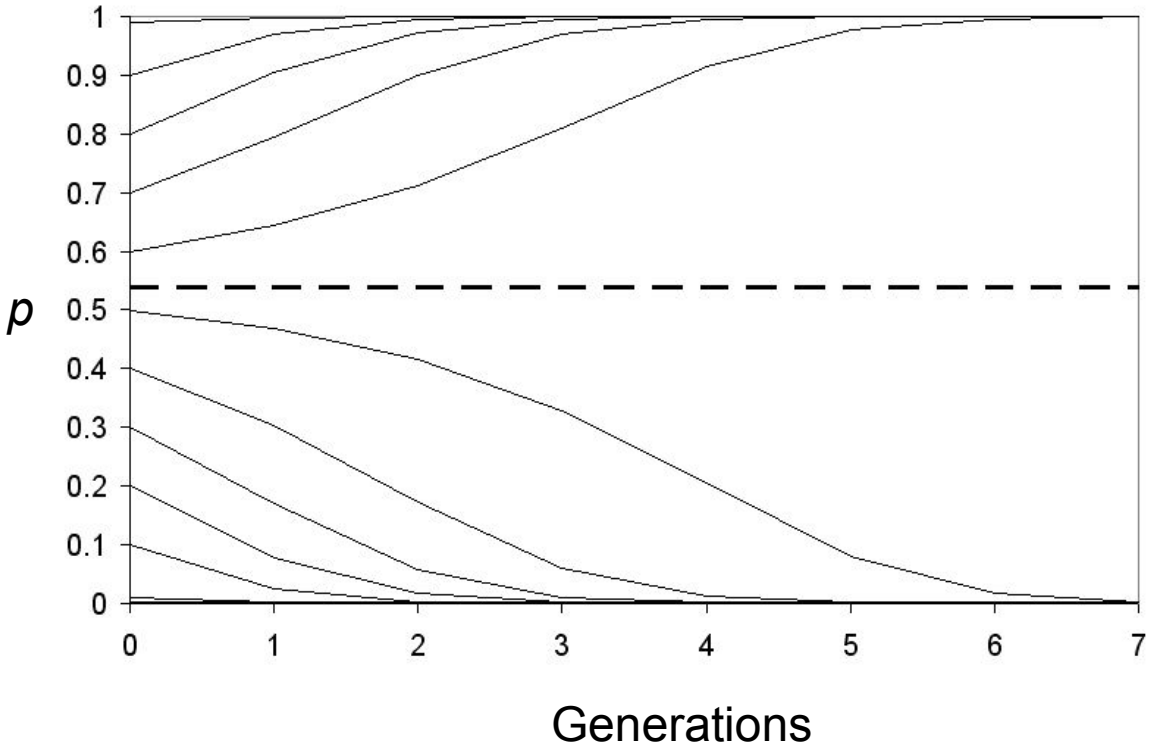


# The model is fit to the data to estimate relative genotype fitnesses

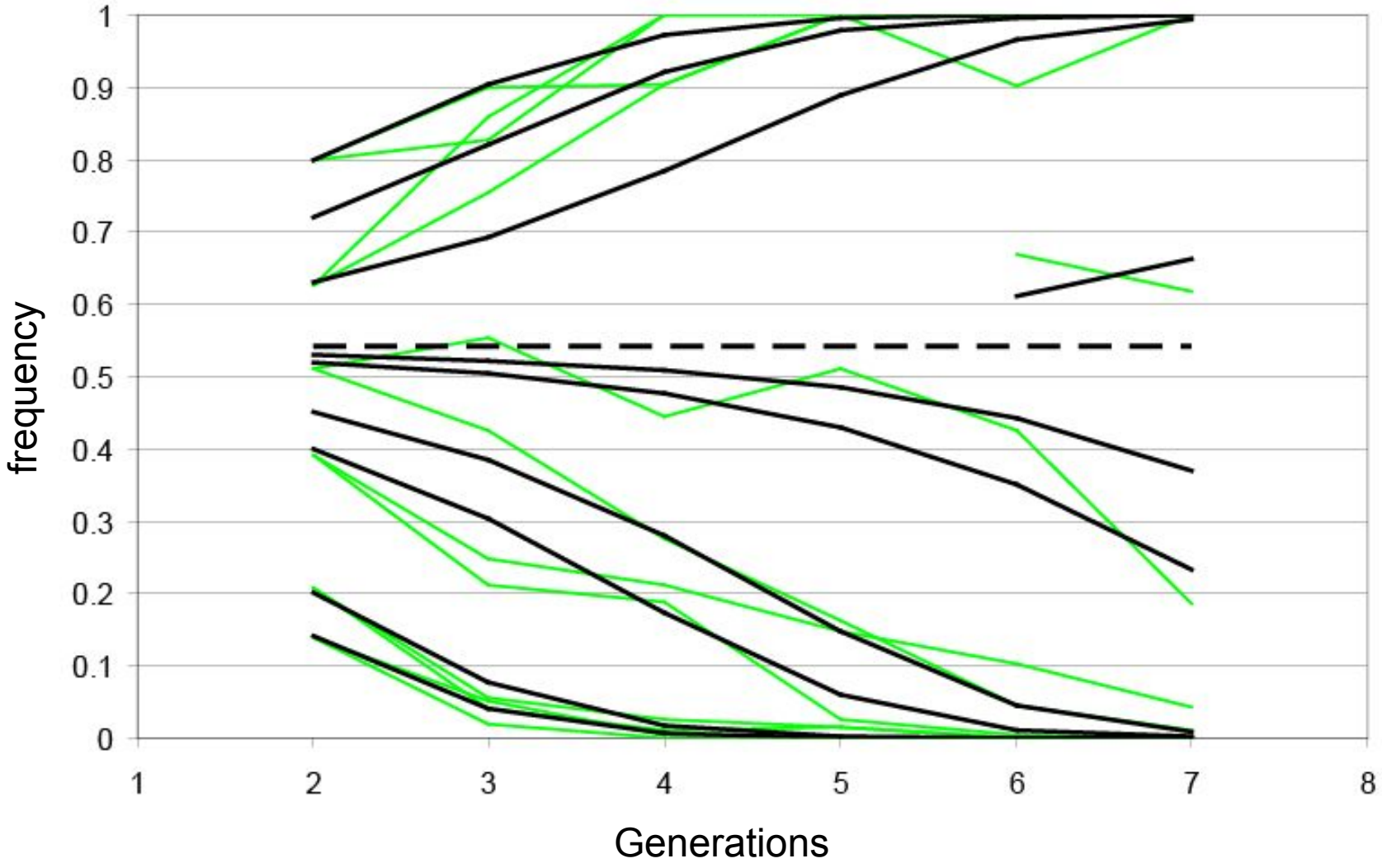


The maximum-likelihood estimate predicts the following fitness configuration and changes in allele frequency.



# Theory and Data



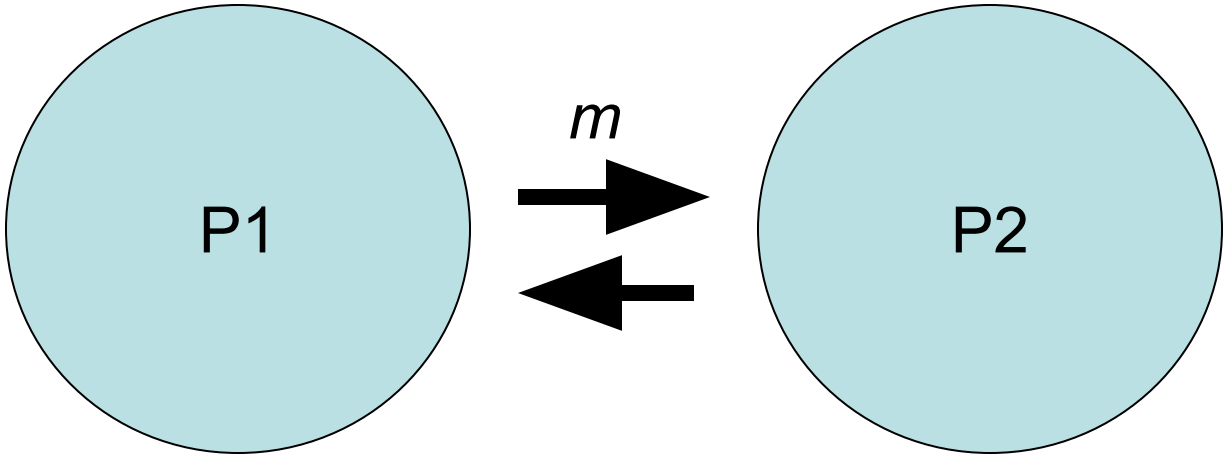
# Stability of an underdominant polymorphism in the presence of migration

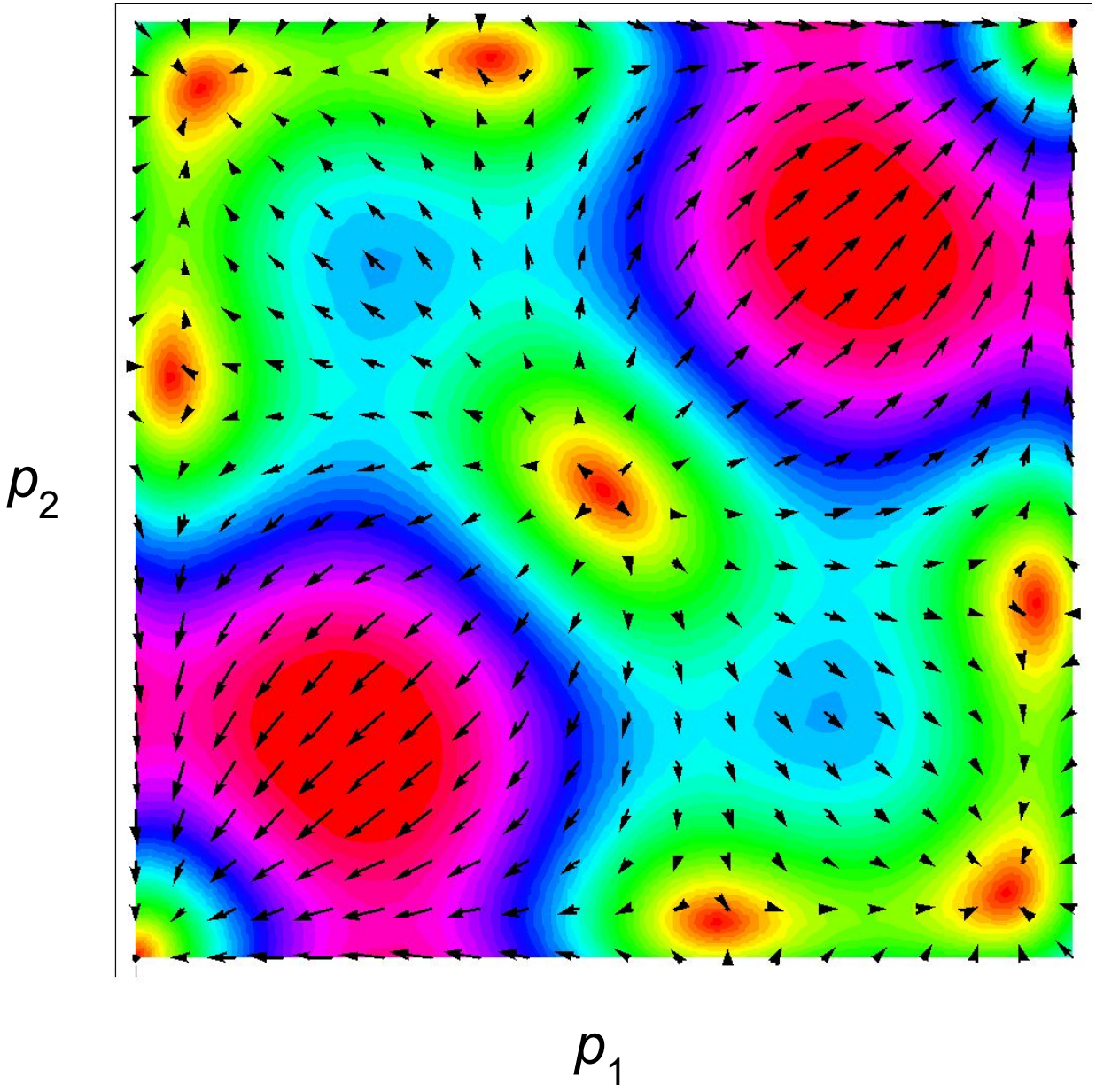
Philipp M. Altrock[a*], Arne Traulsen[a†], R. Guy Reeves[b‡], and Floyd A. Reed[b⋆]

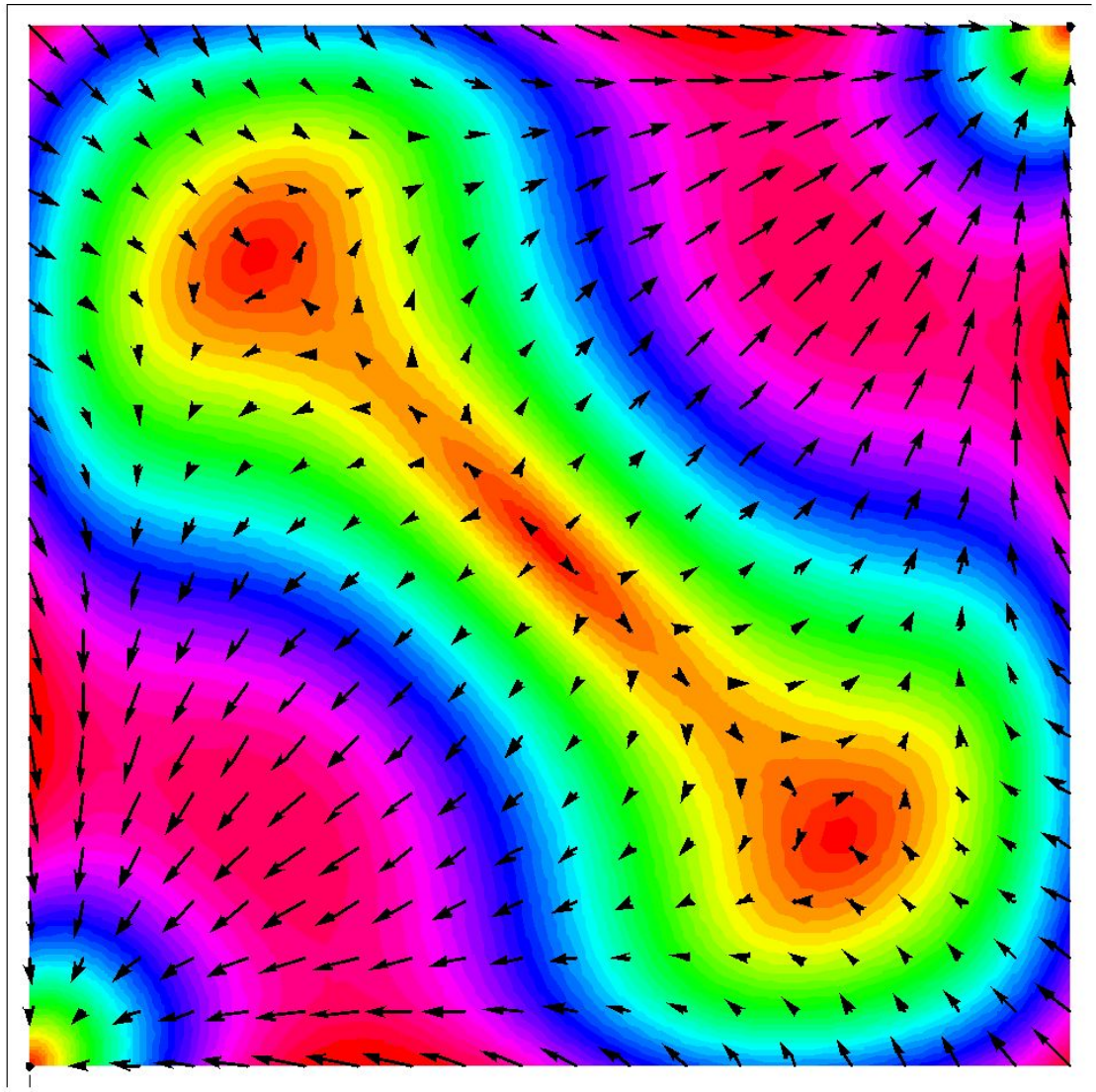
In revision at JTB

http://static.squidoo.com/resize/squidoo_images/-1/draft_lens2155261module13296141photo_1231023406fruit_fly_reading_newpaper.

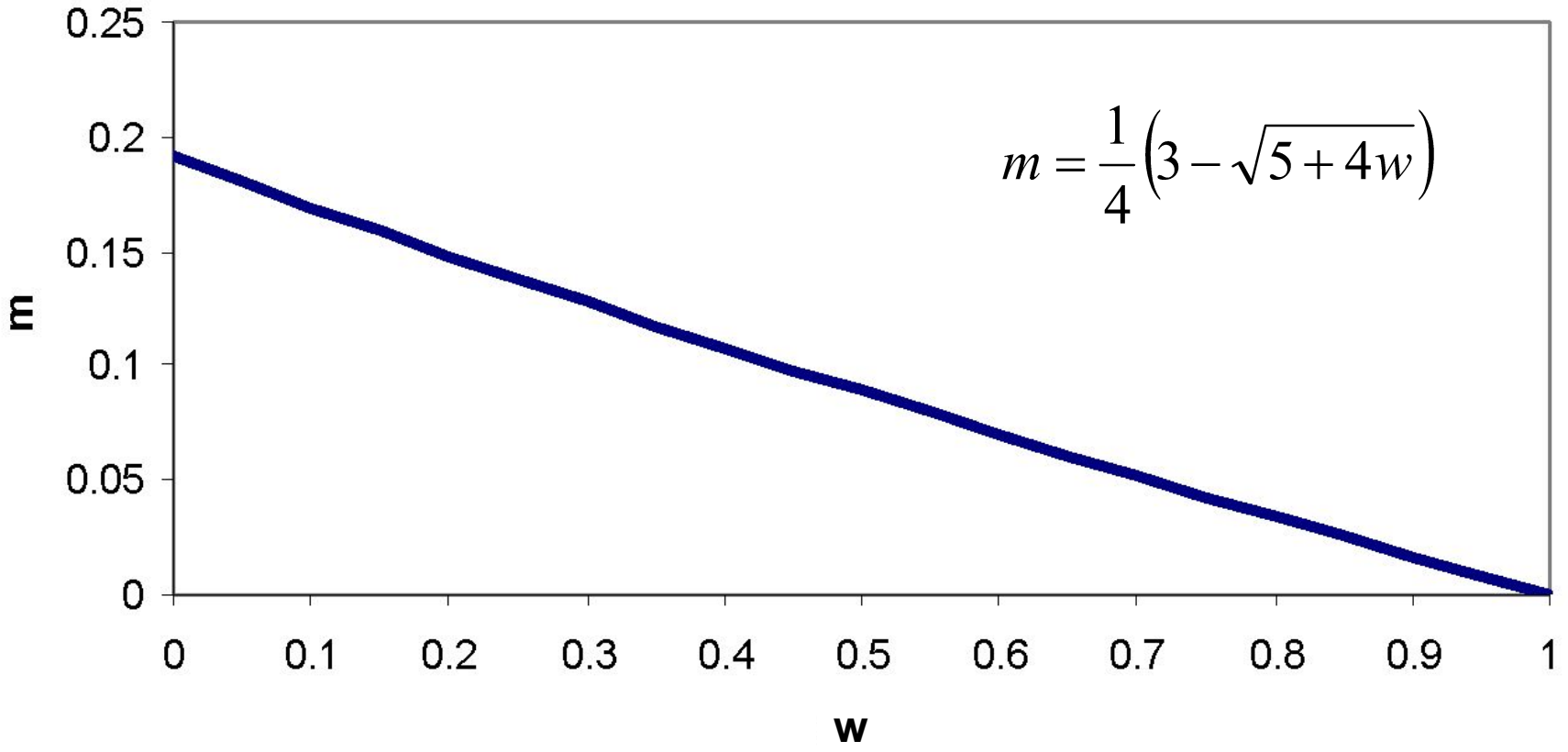
The simplest model to investigate the spatial properties of underdominance is one of a single locus in two populations exchanging migrants each generation.




$p_2$
$p_1$
$m$=0.05
$w$=0.5
Direction of change
Rate of change
high
low


$p_2$
$p_1$
$m$=0.1
$w$=0.5
Direction of change
Rate of change
high
low

The maximum migration rate that allows local underdominant stability.



**Prediction of maximum migration rate with asymmetric fitness.**

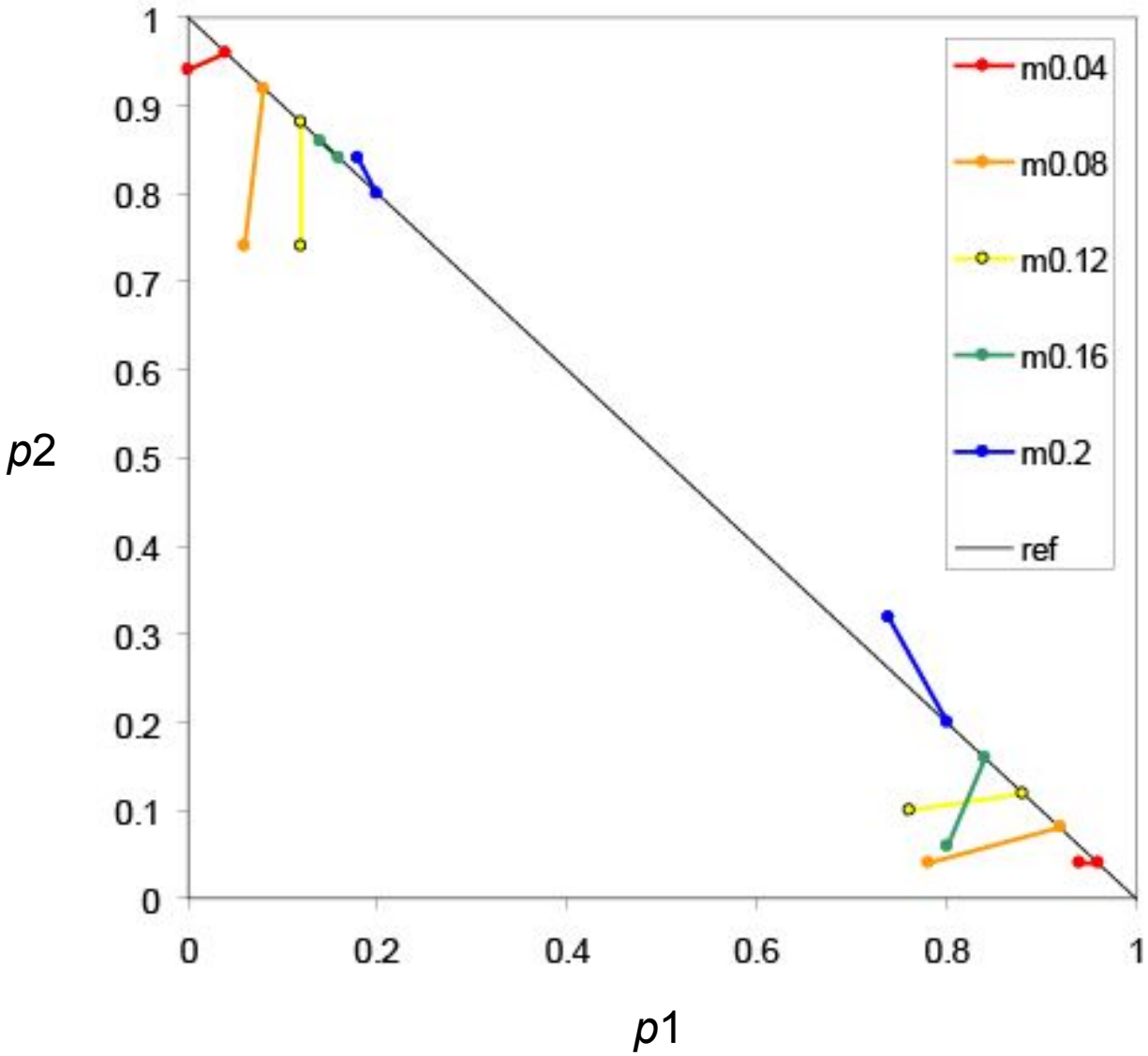
$$\mu_2(\omega) = \frac{1}{4}\left(3 - \sqrt{5 + 4\,\omega}\right)$$

$$\mu_{\mathrm{w}}(\omega, \nu) = \mu_3(\omega, \nu)(1 - \nu) + \frac{\mu_2(\omega)(\nu - \omega)^2}{(1 - \omega)^2}.$$

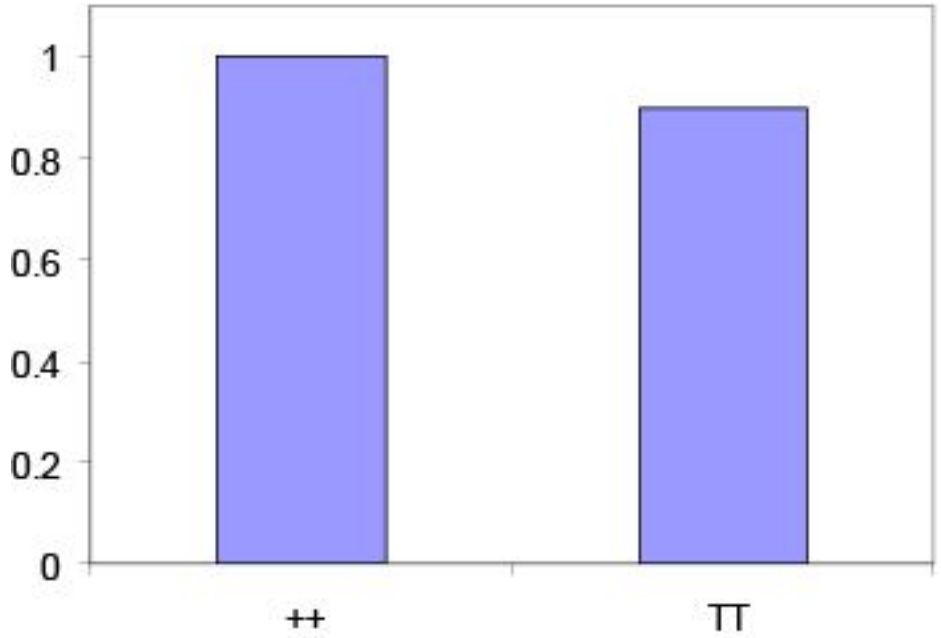
$$\mu_3(\omega, \nu) = \frac{\nu(2 - 2\omega + \nu) - \omega^2 - 2\sqrt{\nu(1 + \nu - 2\omega)(\nu - \omega^2)}}{(\nu - \omega)^2}.$$

**or about 14% migration**

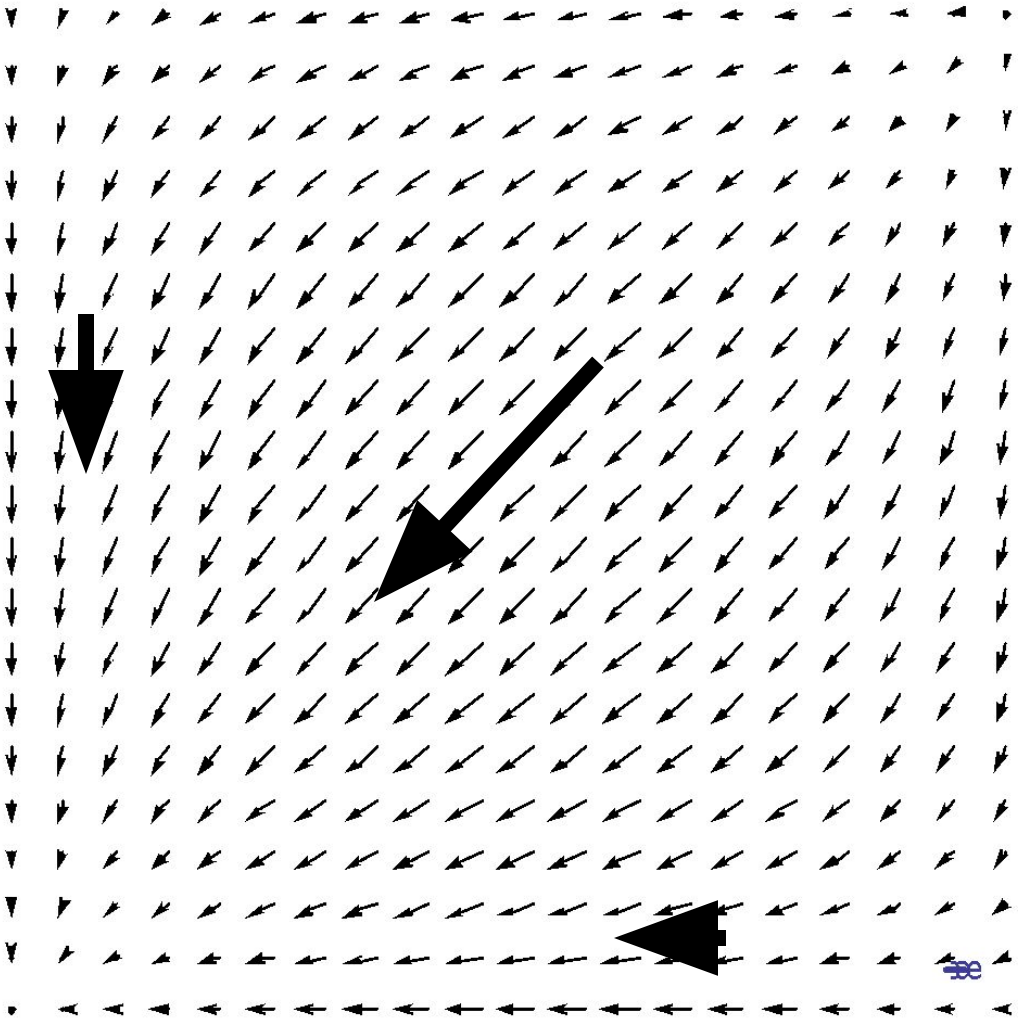
First generation, 2-popualtion results!



So far, first generation, only homozygotes have been present.
This is directional selection with no spatial stability.



# Directional Selection

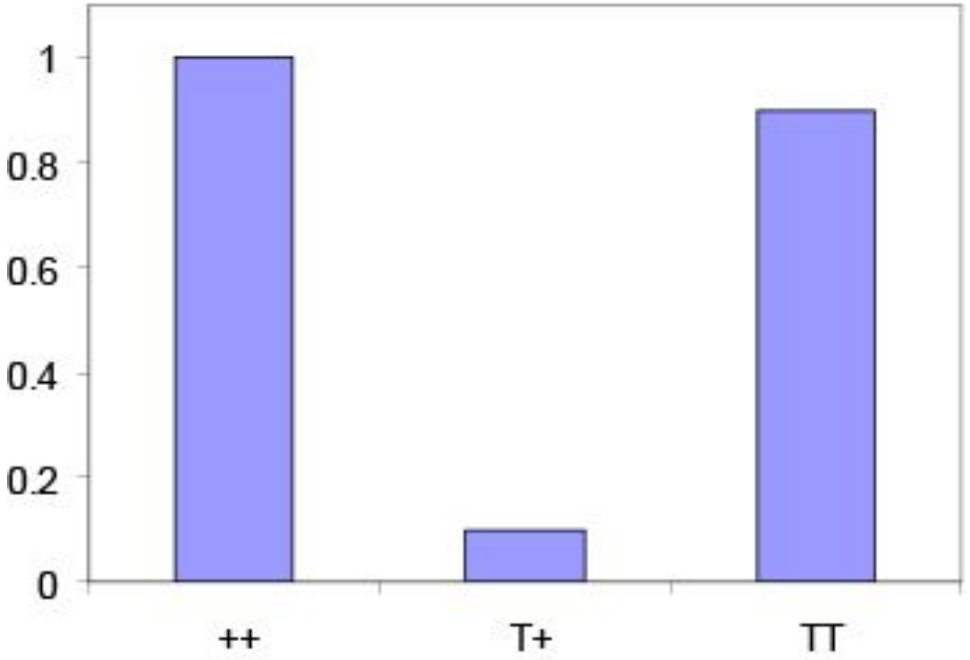


*m*=0.1

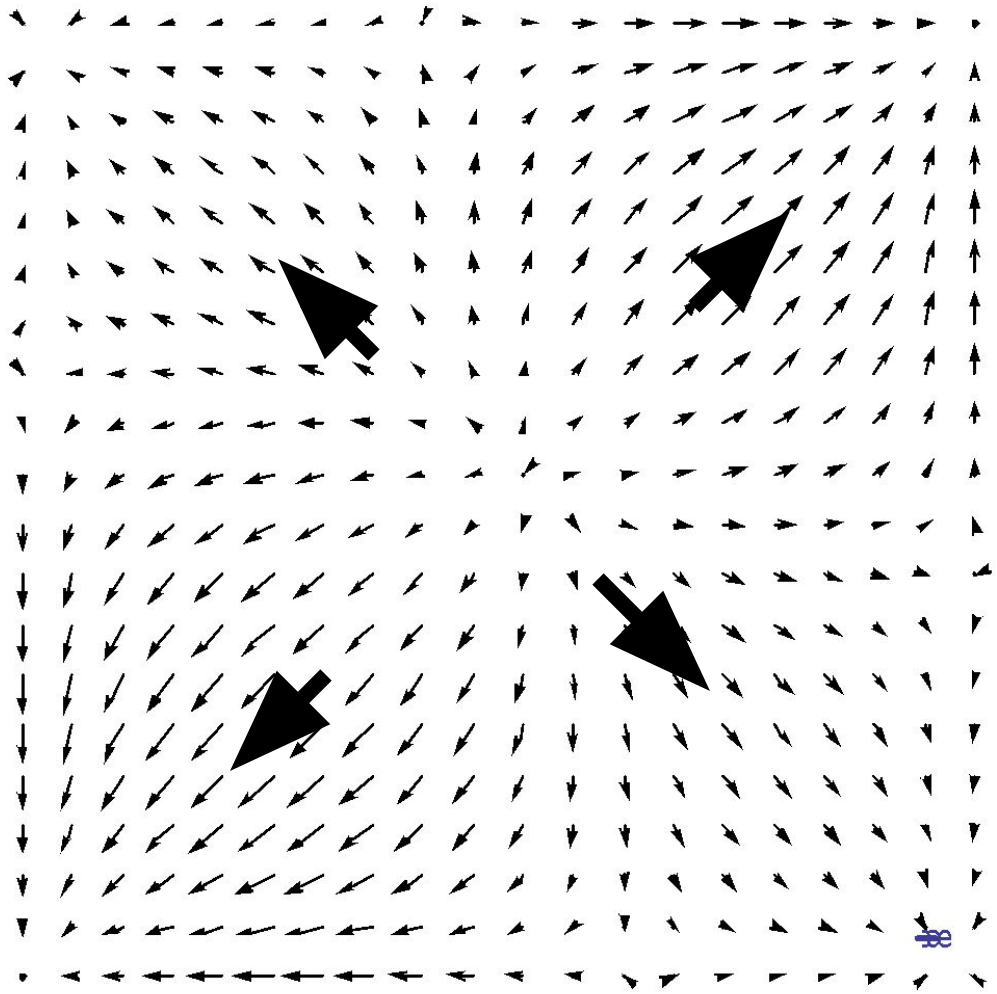
*p*2

*p*1

In the next generation (next week!) heterozygotes should appear and give a stabilizing effect.



# Underdominance, pushing toward the corners

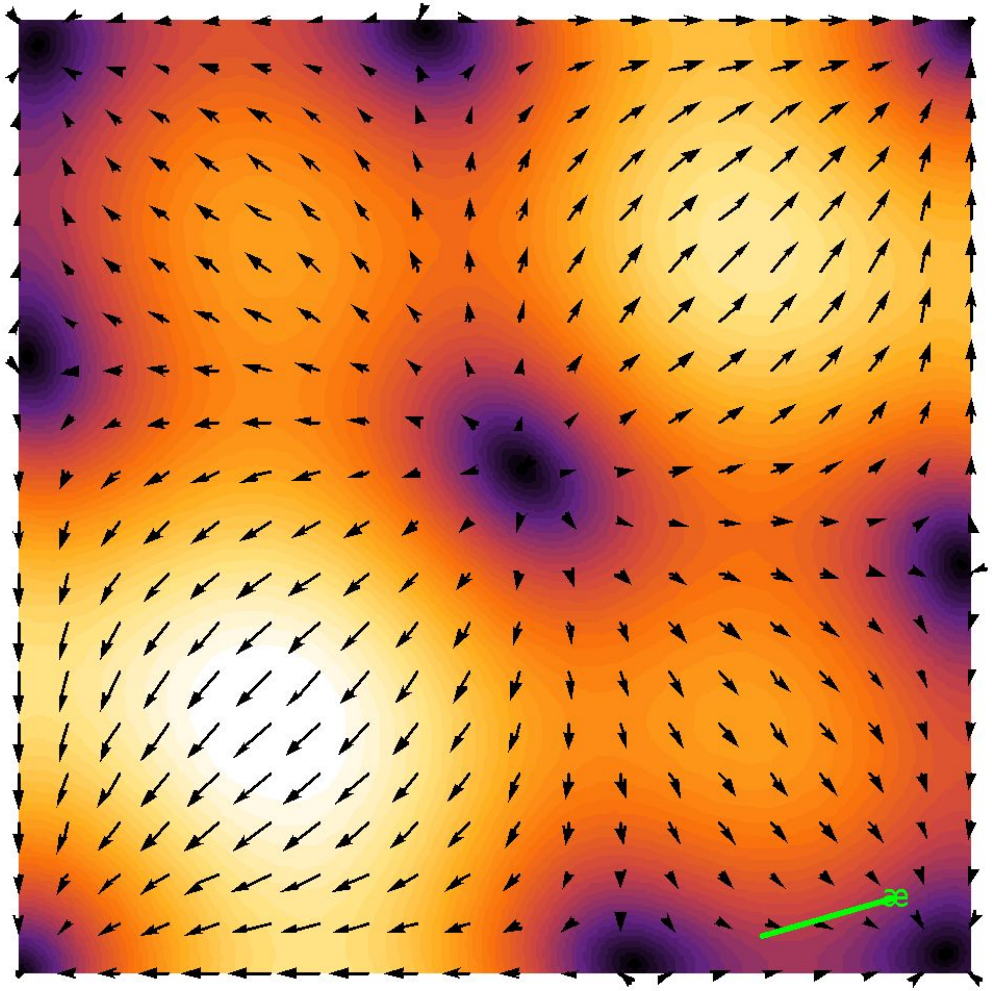


*m*=0.08

*p*2

*p*1

# Potential period of stability

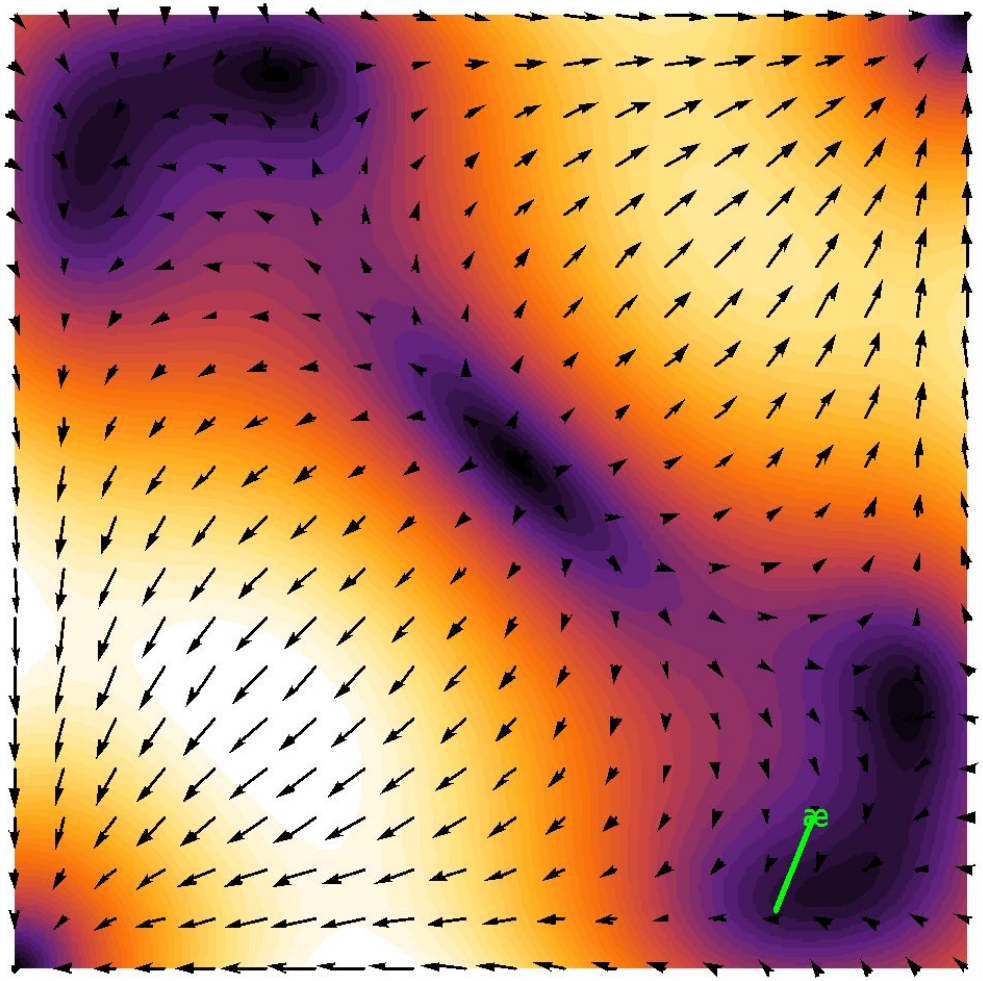


*m*=0.08

*p*2

*p*1

# No stability



*p*2

*p*1

*m*=0.16

## Conclusion

**We have created an underdominant system!**

**In a large population, it (should) allow local stable transformations with migrations rates as high as 14%!**

**Next:**

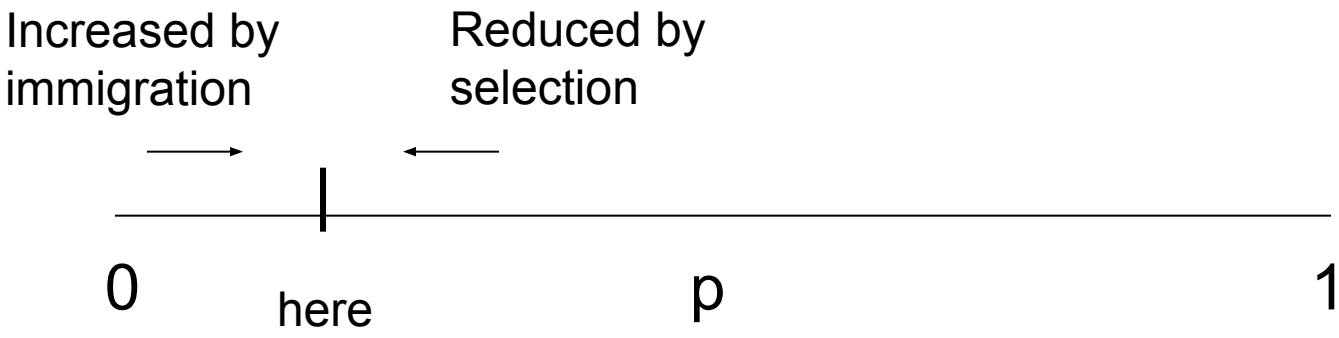
- **Follow more generations**
- **Estimate effective population size in our experiments**
- **Simulate the effects of genetic drift on stability.**
- **Develop a more complete model of the effects of mating prior to migration (and mating discrimination)**

## Acknowledgements

Philipp Altrock – Theory (and fly counting!)
Chip Aquadro (Cornell U) – Global Fly Lines
Kevin Cook (Indiana U) – Drosophila Genetics
Chaitanya Gokhale – Theory
Kent Golic (U of Utah) – FLP-FRT translocations
Fred Gould (NC State U) – Gene Drive Systems
Francis Jiggins (U of Edinburgh) – Sigma Virus
Kata Langer – Internship
The Max Planck Society – Support
Anita Möller – Technician
Hagen Müller – Internship
The Monday Theory/Chalk Talk Group (MPI Plön)
**Guy Reeves – Engineering and everything else!**
Diethard Tautz – Support
Arne Traulsen – Theory
Kata Weiß – Internship

Extra slides for questions

In contrast to the single-population prediction, underdominance can maintain a stable polymorphism among multiple populations connected by migration.



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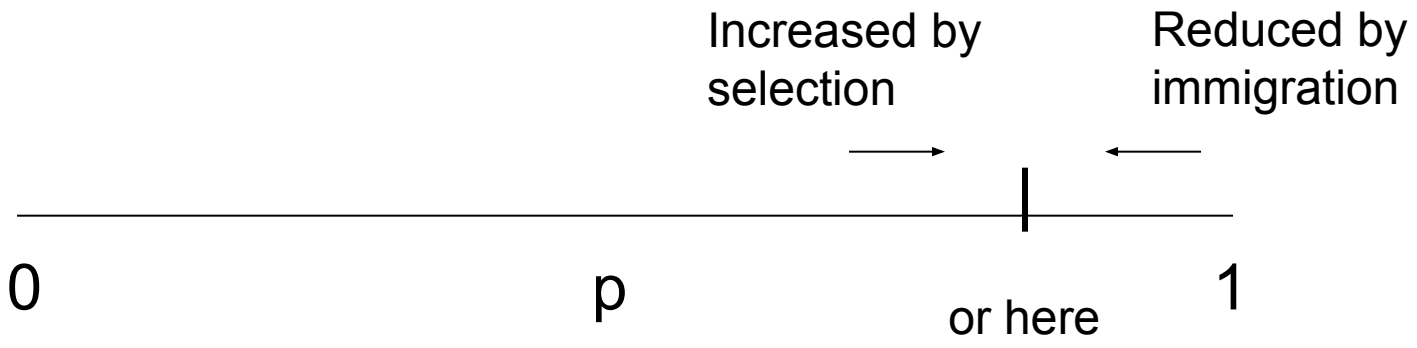
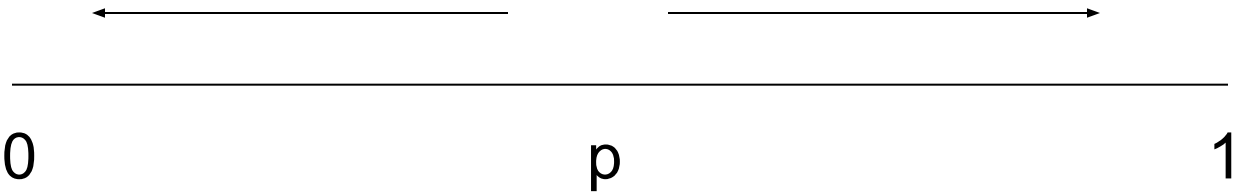
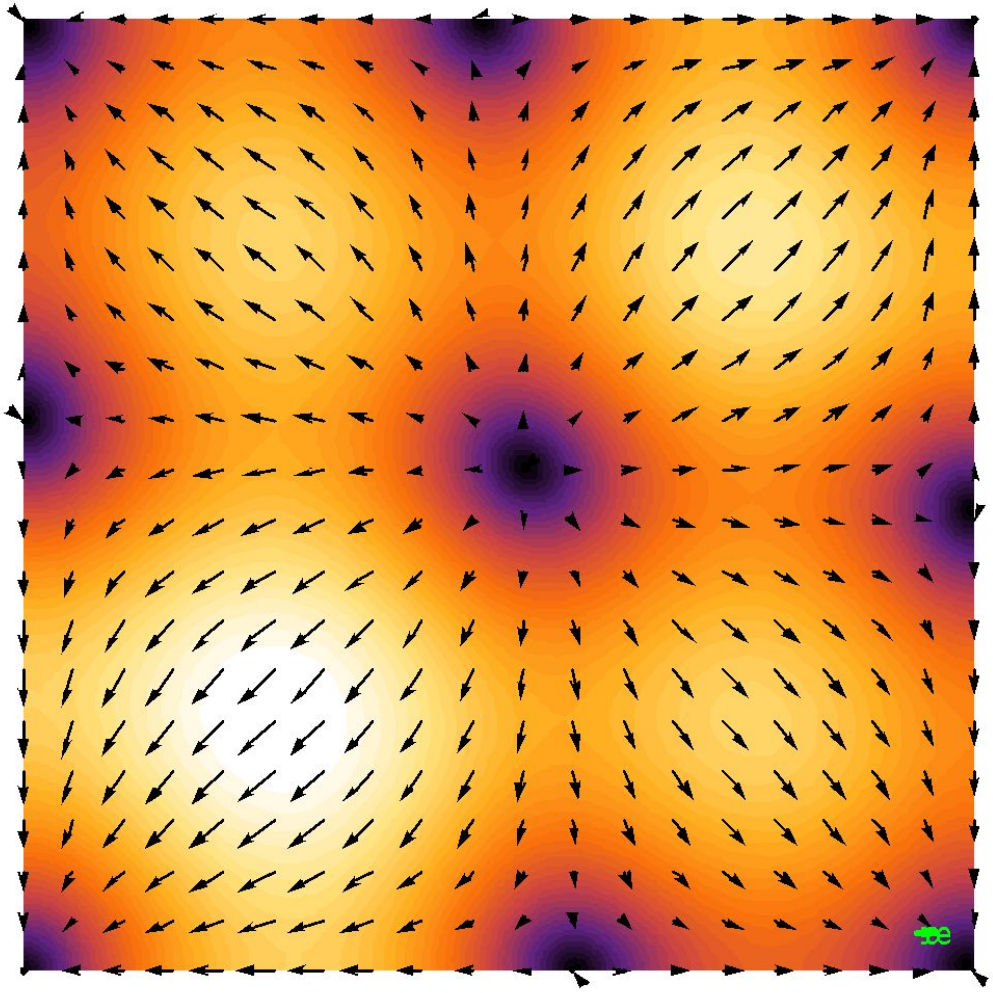


In contrast to the single-population prediction, underdominance can maintain a stable polymorphism among multiple populations connected by migration.




However, if the migration rate is too high, the system behaves like a single population and polymorphism is lost.

# Potential period of stability

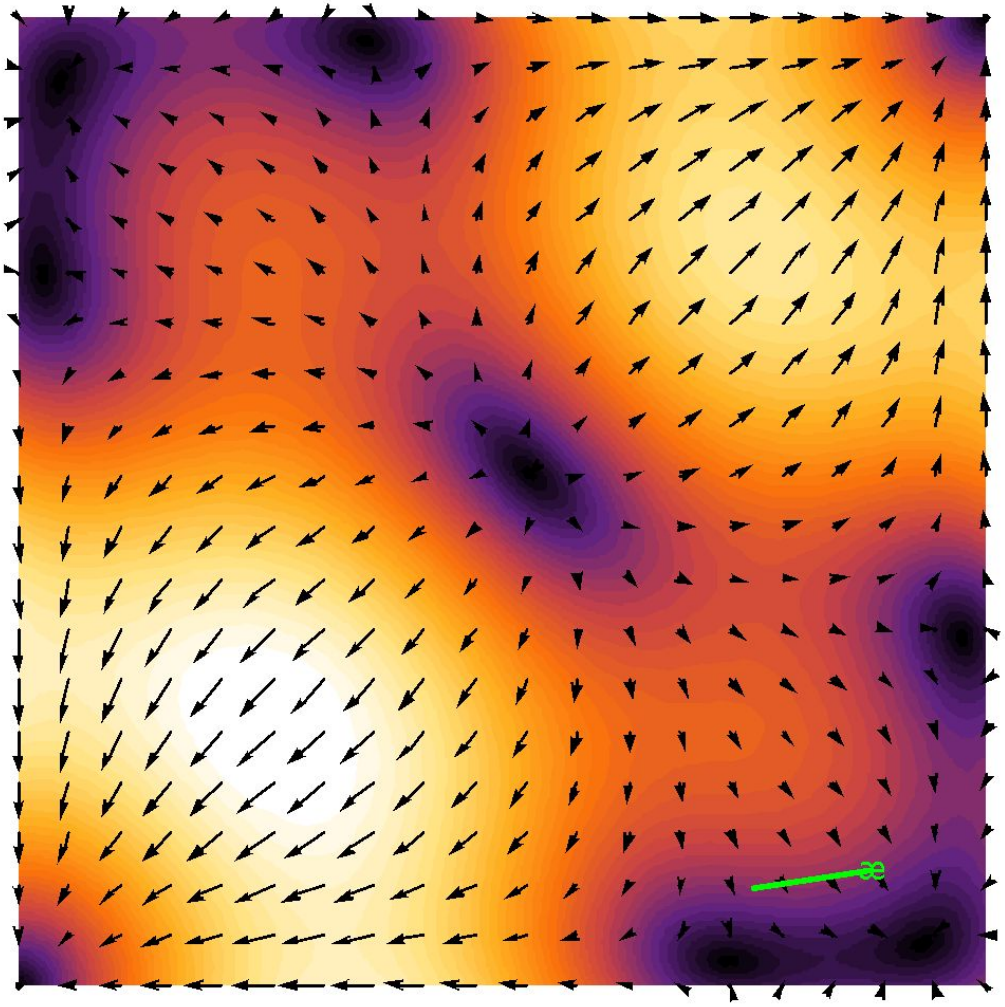


*p*2

*p*1

*m*=0.04

# Potential period of stability

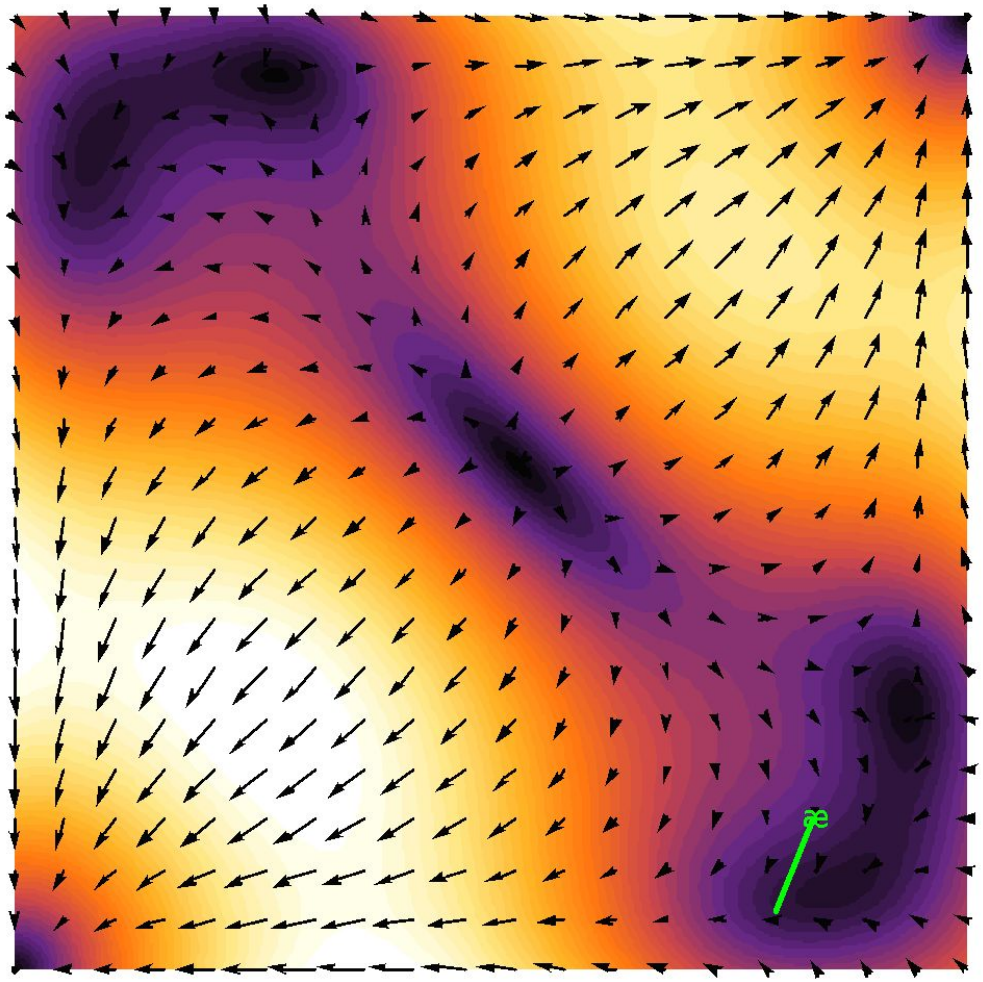


*p*2

*p*1

*m*=0.12

# No stability

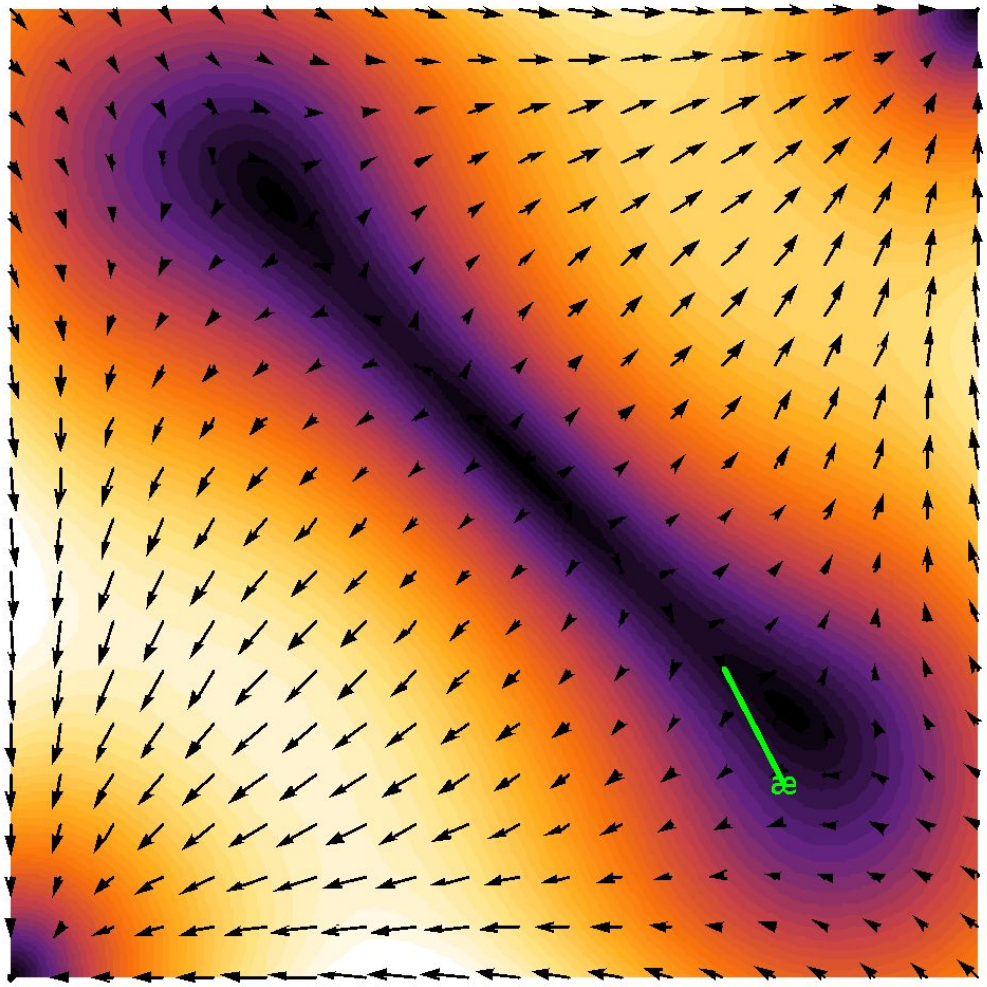


*m*=0.16

*p*2

*p*1

# No stability

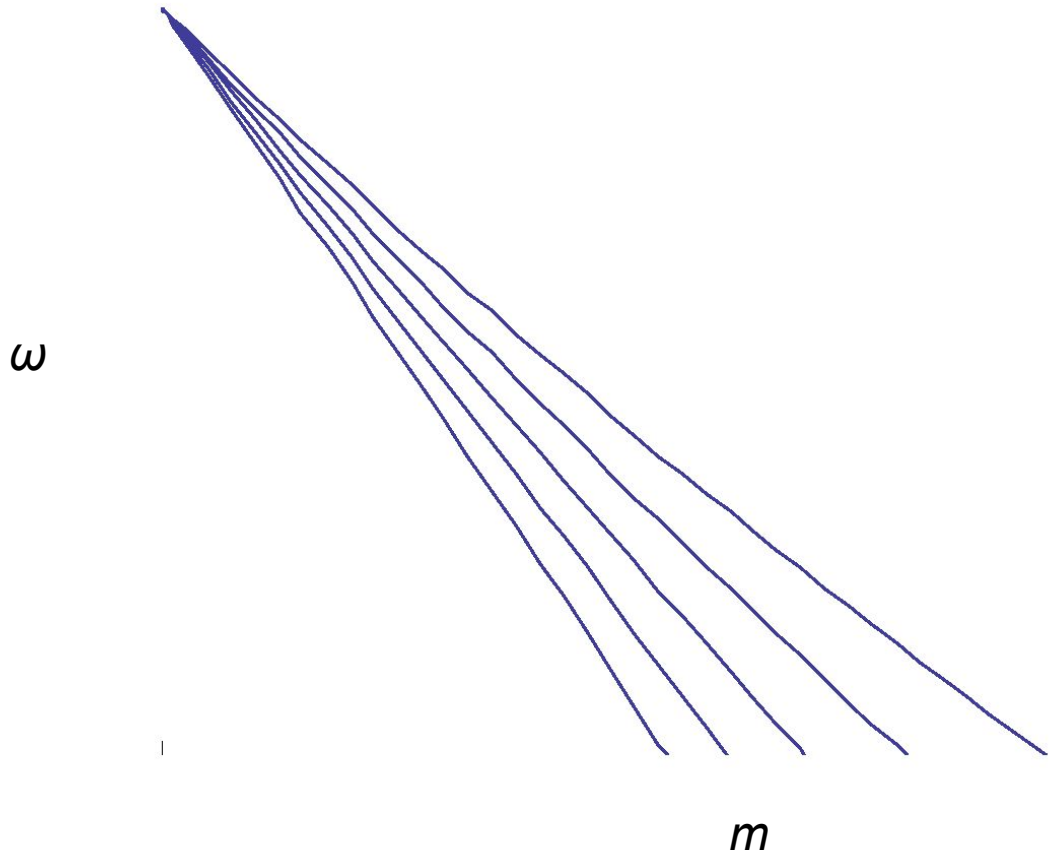


*p*2

*p*1

*m*=0.2

Mating prior to migration has a destabilizing effect.



The G-test (or likelihood ratio or maximum likelihood test) is similar to the chi-square test.

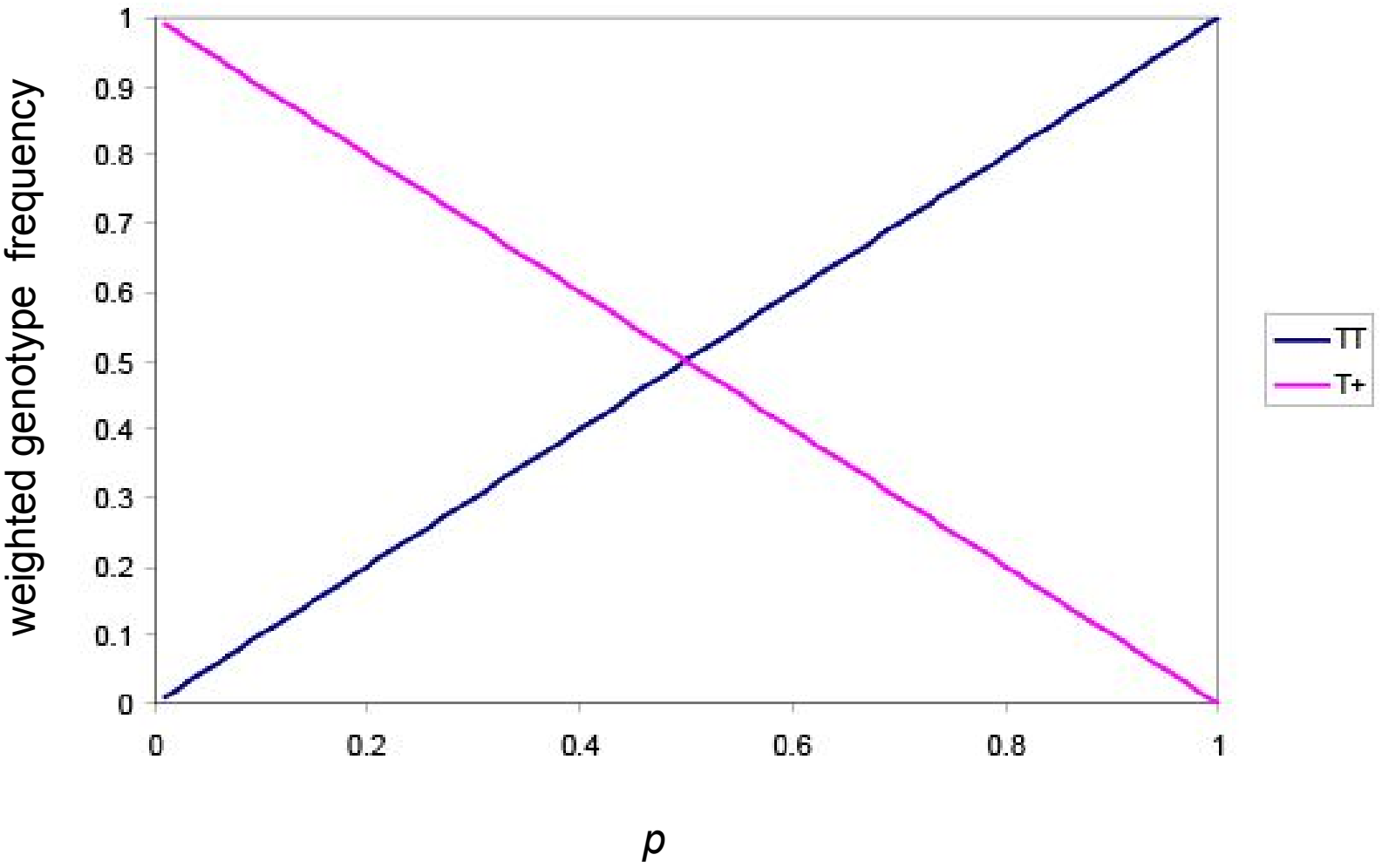
$$\chi^2 = \sum_{ij} \frac{\left(O_{ij} - E_{ij}\right)^2}{E_{ij}}$$

$$G = 2\sum_{ij} O_{ij} \ln\left(\frac{O_{ij}}{E_{ij}}\right)$$

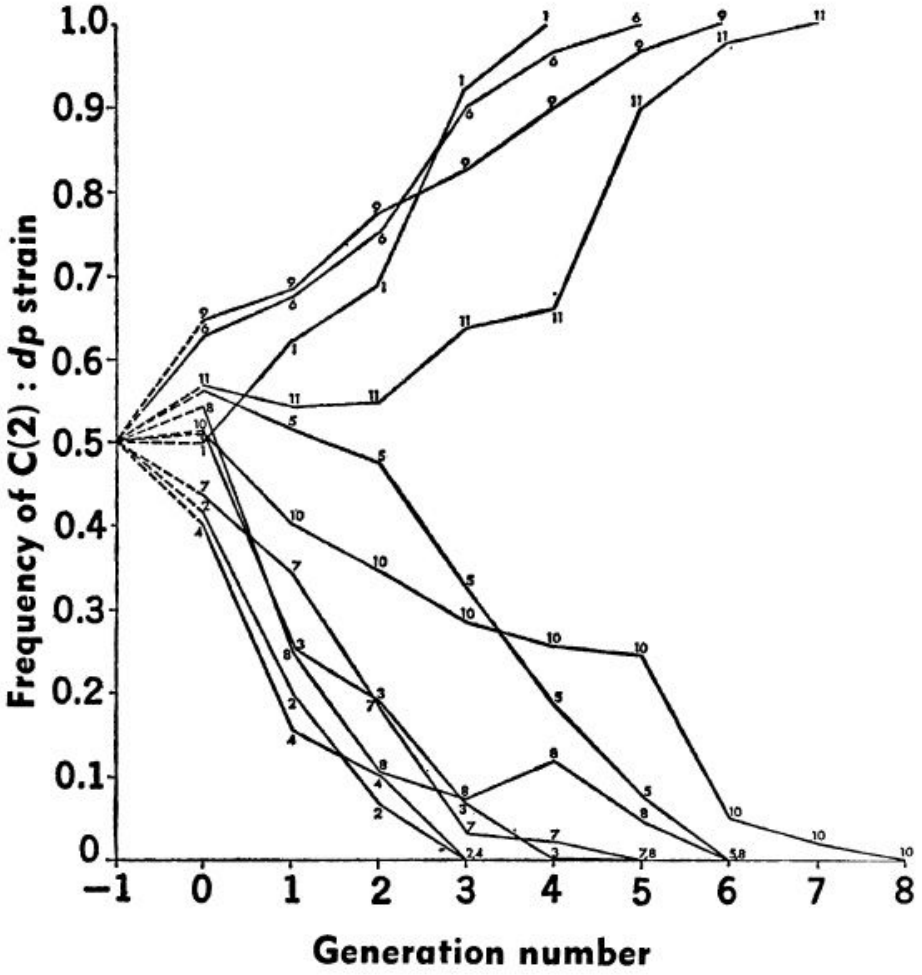
Expected values can be generated according to the Wright-Fisher model. Stochastic drift is not included in the model but is not expected to bias results (however the more data the better to average this out). G is expected to the Chi-square distributed.

Suggested/used for population bottle data by Clark *et al*. 1989

# Weighted by number of alleles in each genotype



# Early work failed to achieve underdominance with wildtype heterozygotes.



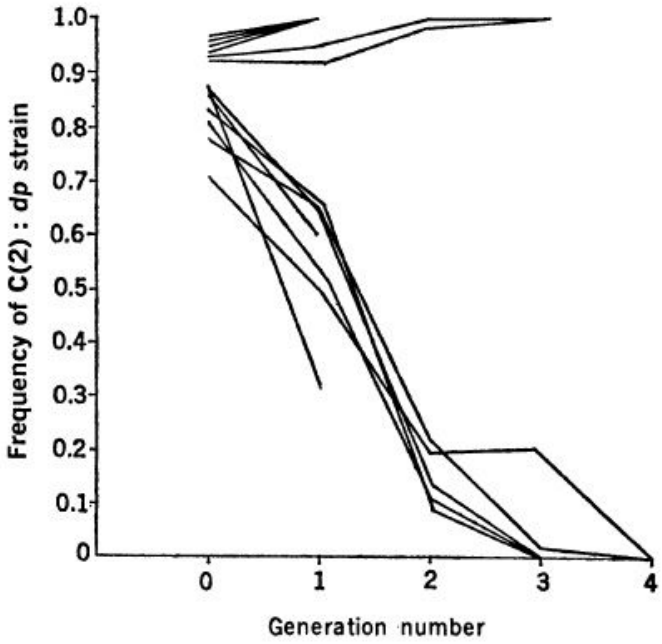




Fig. 6 (left). Change in frequency of C(2) : *dp* strain in competition with C(3) : *ri* strain. The unstable point is about 0.5. Fig. 7 (right). Change in frequency of C(2) : *dp* strain in competition with structurally wild-type strain. The unstable point is about 0.9.

Foster et al. (1972)