Adaptation to the same environment can result in loss or gain of a character based on different population sizes

Saumil Shah (20151179)
Guide: Dr. Sutirth Dey

Introduction

- Classical descriptions of the fitness of an individual are related to its reproductive output in a given environment (Patten 2010).
- Fitness can also be defined for higher or lower biological units such as the population or the gene.
- Due to the interactions between various genes, fitness of a gene depends on the available genetic background, which leads to epistasis (Weinreich 2005).
- The environment can also have a major role in the determination of fitness.

  For example, white morph of the peppered moth was more fit before industrialization, black morph was more fit after industrialization.

Utility of the character is expected to determine its fate

- If the increase in the expression of a character increases the fitness in a given environment, then that character will be selected for in the population.
- On the other hand, if a character is disadvantageous in a given environment then it will get selected against in that environment.
- In an environment a trait can either be useful or disadvantageous, hence it either gets selected for or against in the population, **BUT NOT BOTH!**
- Please note that drift is not being invoked to explain character evolution here.

Gain and loss of a character in the same environment? Even when all the populations end up adapting?

- A population can gain or lose a trait in a given environment just by varying population size.
- *E. coli* cultures were grown in a cocktail of 3 antibiotics
- Cultures with smaller population size enhanced efflux activity compared to ancestors whereas Cultures with larger population size lost efflux activity as compared against the ancestors

Reference: *E. coli* experiments

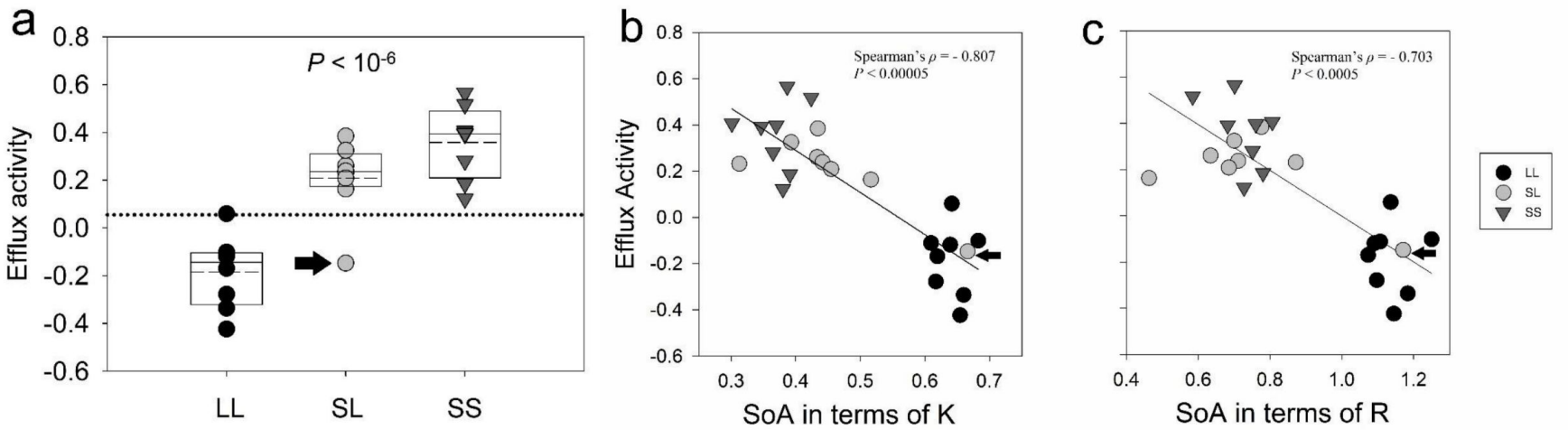


Figure: Evolved efflux activity and its correlation with the speed of adaptation. (a) EA in the three population-types after evolution in the presence of the antibiotic cocktail. The solid lines in the box-plots mark the 25th, 50th, and 75th percentiles; the dashed lines within the box plots represent means (N=8). The black dotted line represents the ancestral efflux activity. Each data point represents the average of two independent efflux measurements. The grey data point marked with an arrow in each of the three panels represents the only non-LL population that lost the ancestral efflux activity (see the text for details), and is the same replicate that was an outlier in Fig 1. EA had a strong negative correlation with SoA, expressed in terms of (b) carrying capacity (K) and (c) maximum growth rate respectively.

Objective & Methods

- Create a model and simulate the phenomenon adaptation to the same environment can result in loss or gain of a character based on different population sizes.
- Find the minimal set of conditions (for this model) to reproduce the above phenomenon.
- We conducted Wright-Fisher simulations for haploid asexual individuals with discrete generations at several different population sizes.
- Our model had two loci: locus A and locus B.
- Each locus could be expressed at three levels: Low (L), intermediate (O) and high (H). Each level represented an allele.
- Fitness values represent number of offsprings produced per generation per individual.

Sign Epistasis

- In sign epistasis, a gene can be deleterious on one genetic background and beneficial on others in the same environment (Weinreich 2005).
- In our model, Gene A exhibits sign epistasis on Gene B backgrounds.
- Total 9 genotypes (i.e., A_OB_L, A_OB_O, etc.)
- The wild-type genotype is A_OB_O.

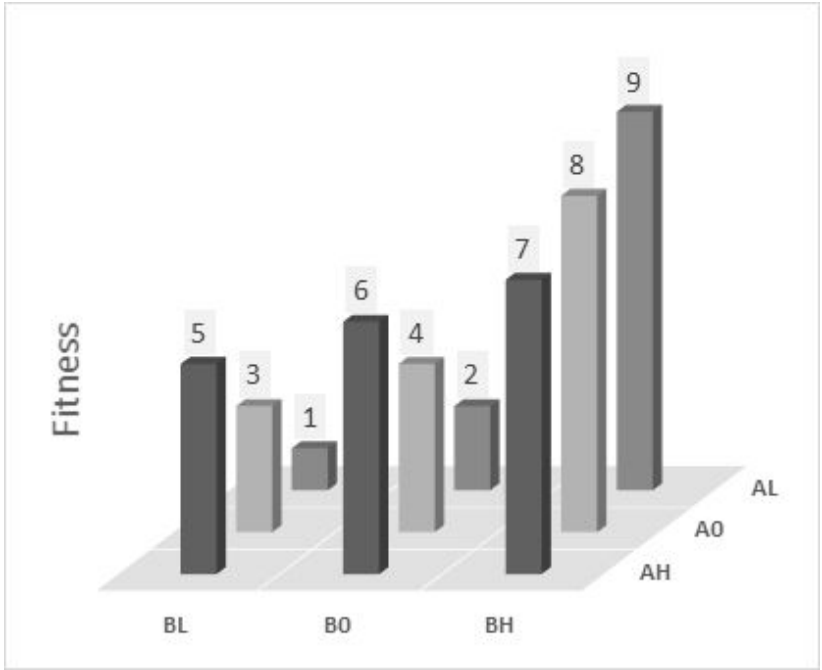
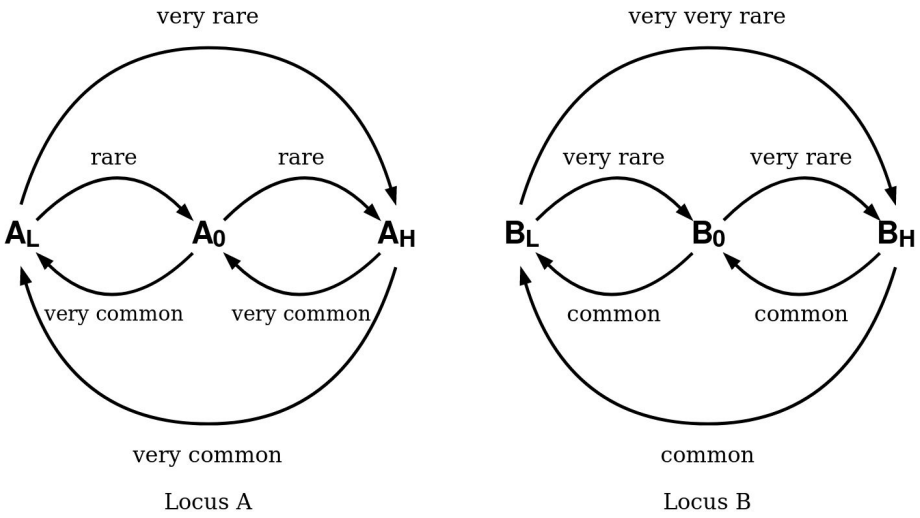


Figure 1: Epistasis and the fitness landscape.

Mutation Rates

- Individuals undergo mutations randomly, which results in inter-allelic changes.
- Locus A and B had different mutation rates, Mutation at locus A were more common than ones at locus B.



Mutation rate	Value*
very common	$1*10^{-3}$
common	$5*10^{-4}$
rare	$5*10^{-5}$
very rare	$5*10^{-8}$
very very rare	$1*10^{-9}$

Figure 2: Mutation rates on locus A and locus B.
*values are per individual per generation.

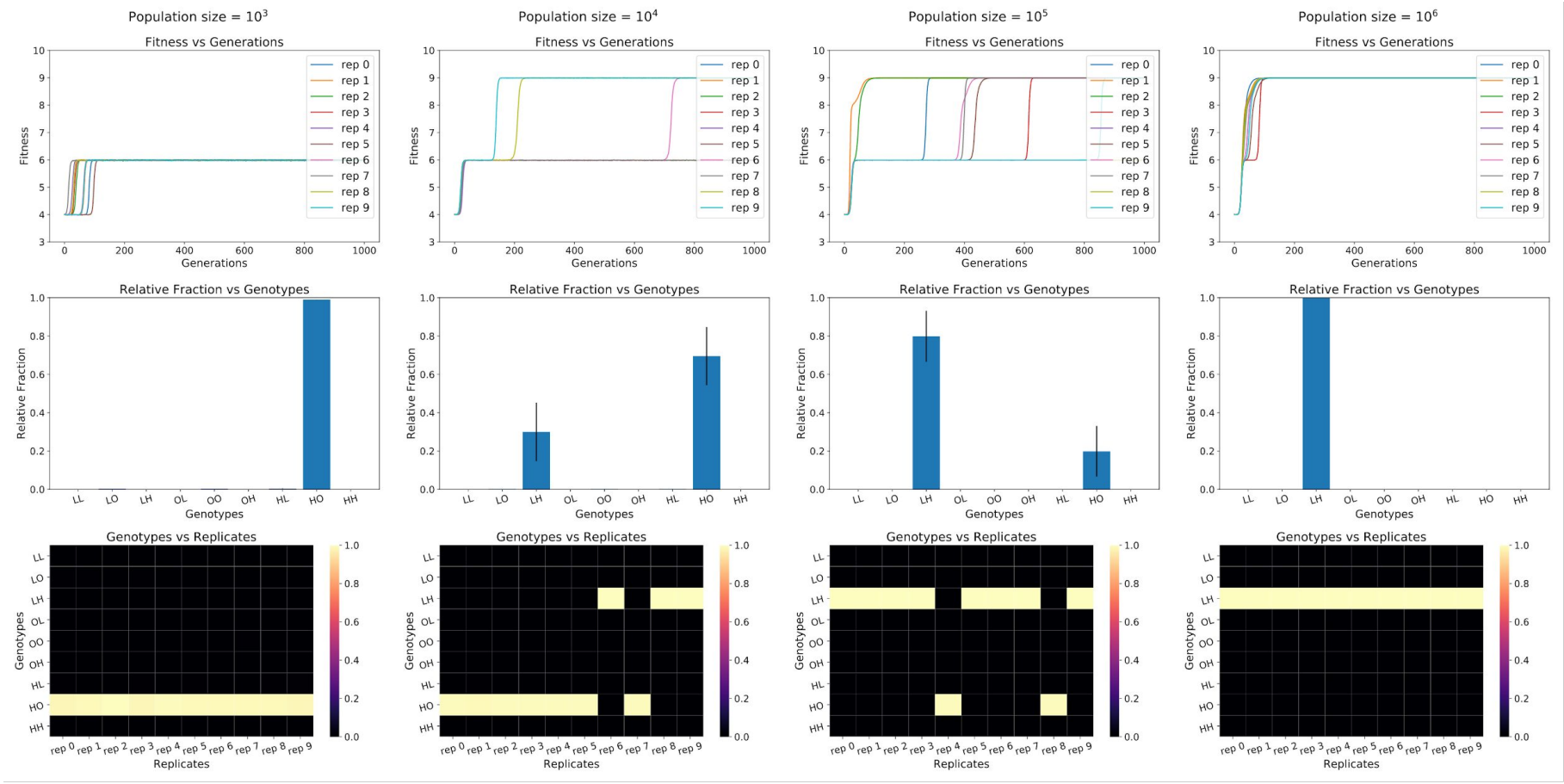


Figure 3: Comparison between different population sizes. Four columns are different population sizes 10^3, 10^4, 10^5 and 10^6, respectively. First row is fitness vs generation of all replicates. Second row is mean relative fraction (±SE) of all the genotypes. Third panel is replicate wise relative fraction of all the genotypes.

If there is no sign epistasis then the switch in phenotypes is not observed by changing population sizes

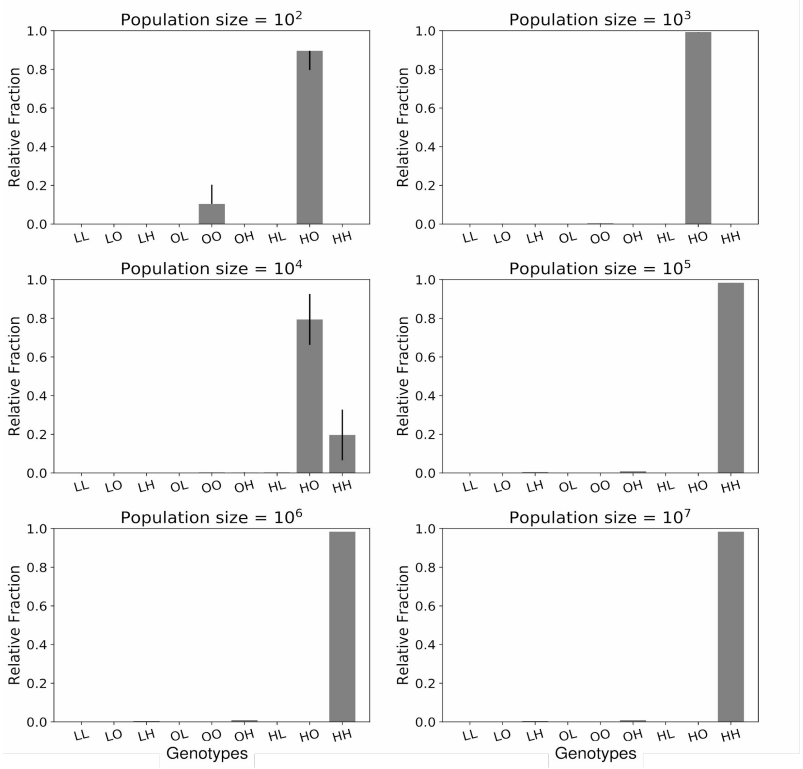


Figure 4: No epistasis control. Relative fractions (±SE) vs genotypes for different population size.

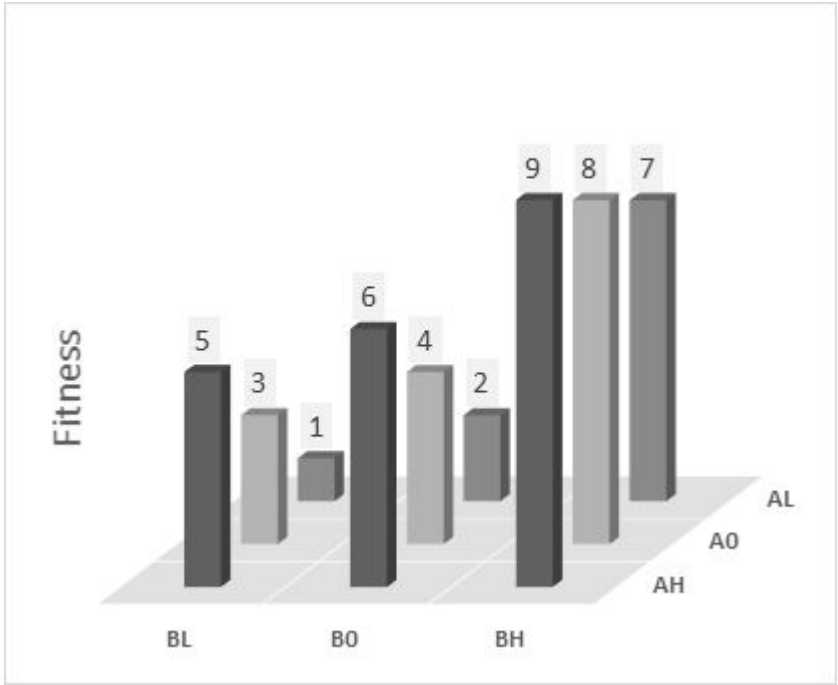


Figure 4b: Non-epistatic fitness landscape.

If mutation rates are the same across two loci then the switch in phenotypes is not observed by changing population sizes

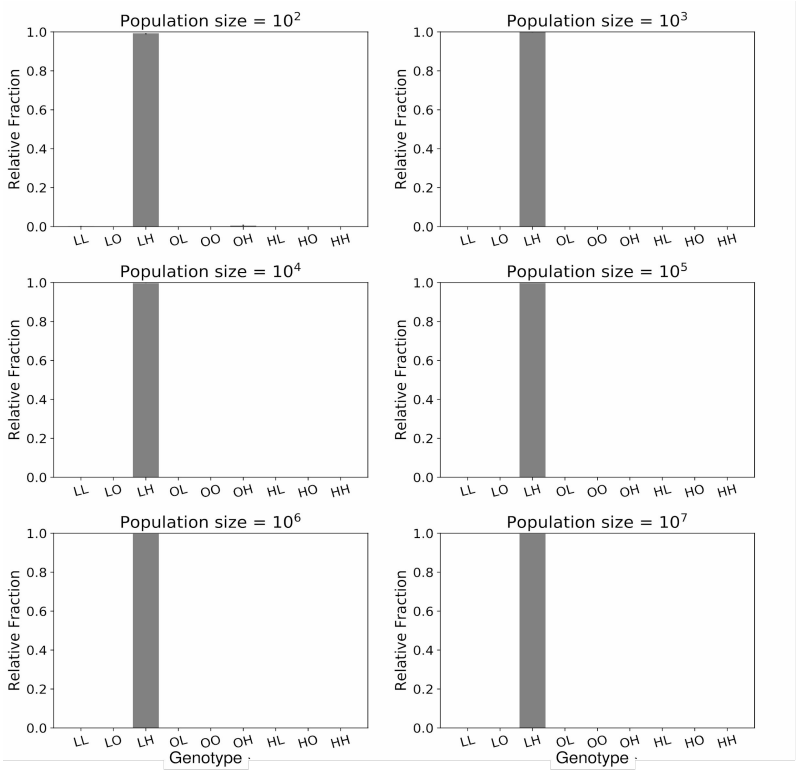


Figure 5: Locus A like mutation rate control. Relative fractions (±SE) vs genotypes for different population size.

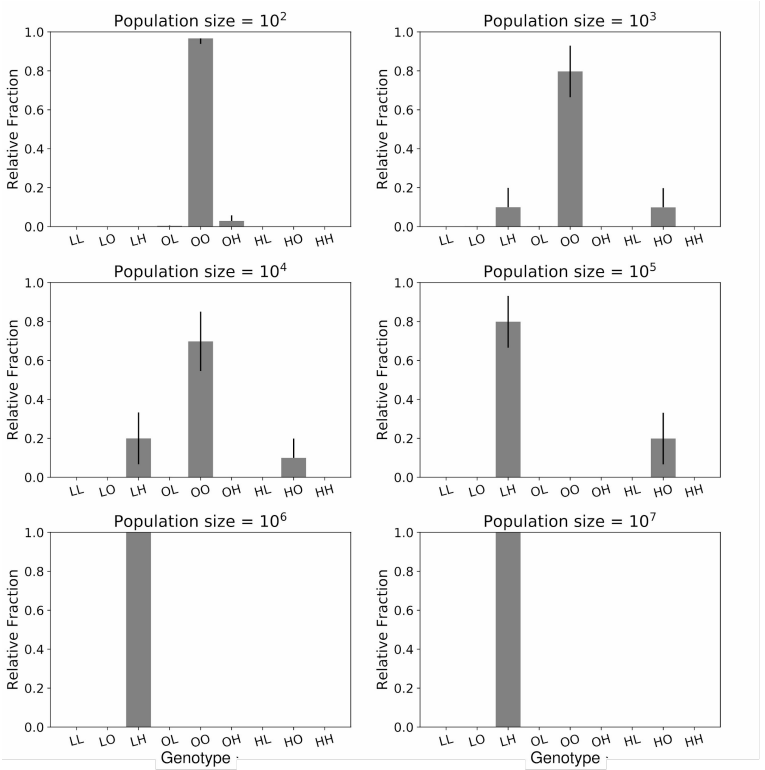


Figure 6: Locus B like mutation rate control. Relative fractions (±SE) vs genotypes for different population size.

If there is no epistasis and the mutation rates are identical across two loci then the switch in phenotypes is not observed by changing population sizes

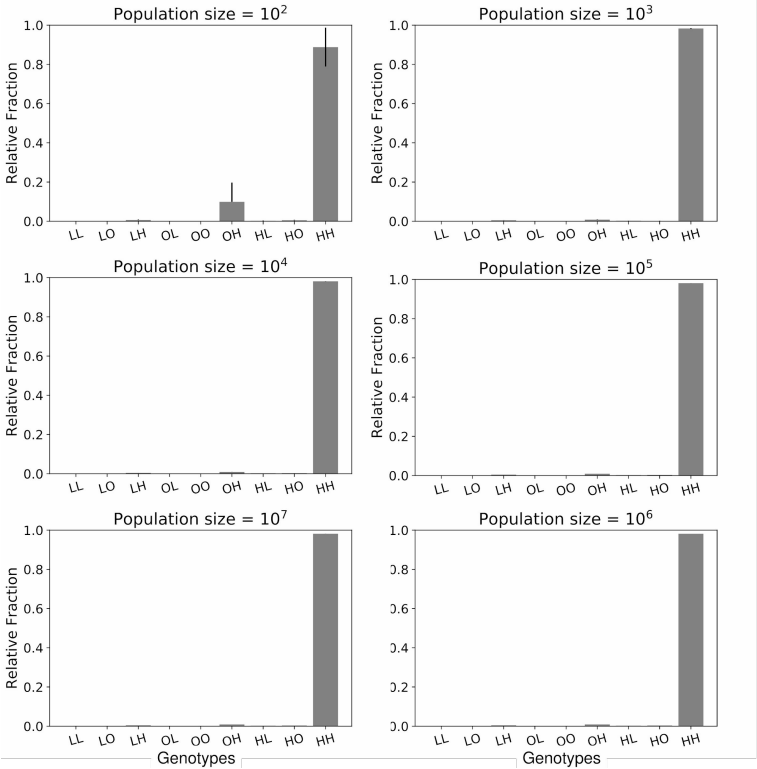


Figure 7: No epistasis with locus A like mutation rate control. Relative fractions (±SE) vs genotypes for different population size.

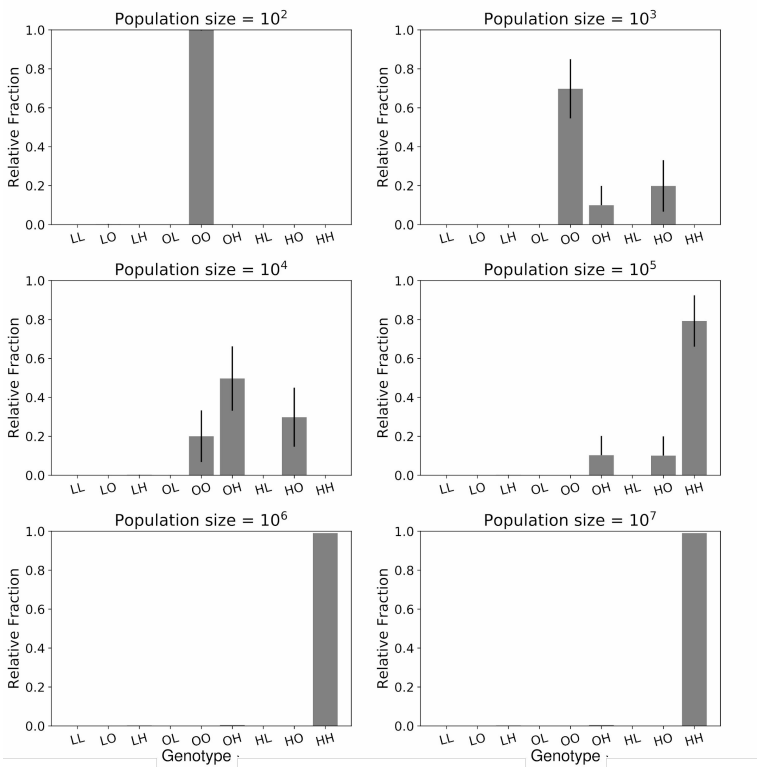


Figure 8: No epistasis with locus B like mutation rate control. Relative fractions (±SE) vs genotypes for different population size.

Have we indeed simulated the experimental results?

- It is possible to gain or lose a trait in an environment independent of the utility of the trait provided a special configuration of genome.
- We know that at least two interacting genes are required to give rise to such phenomenon.
- However, the fitness of the *E. coli* cultures with small and large population sizes was the same when the character of interest was assayed.
- This can’t be achieved with two-locus setup.
- We also tested if adding another A-like locus makes this possible.

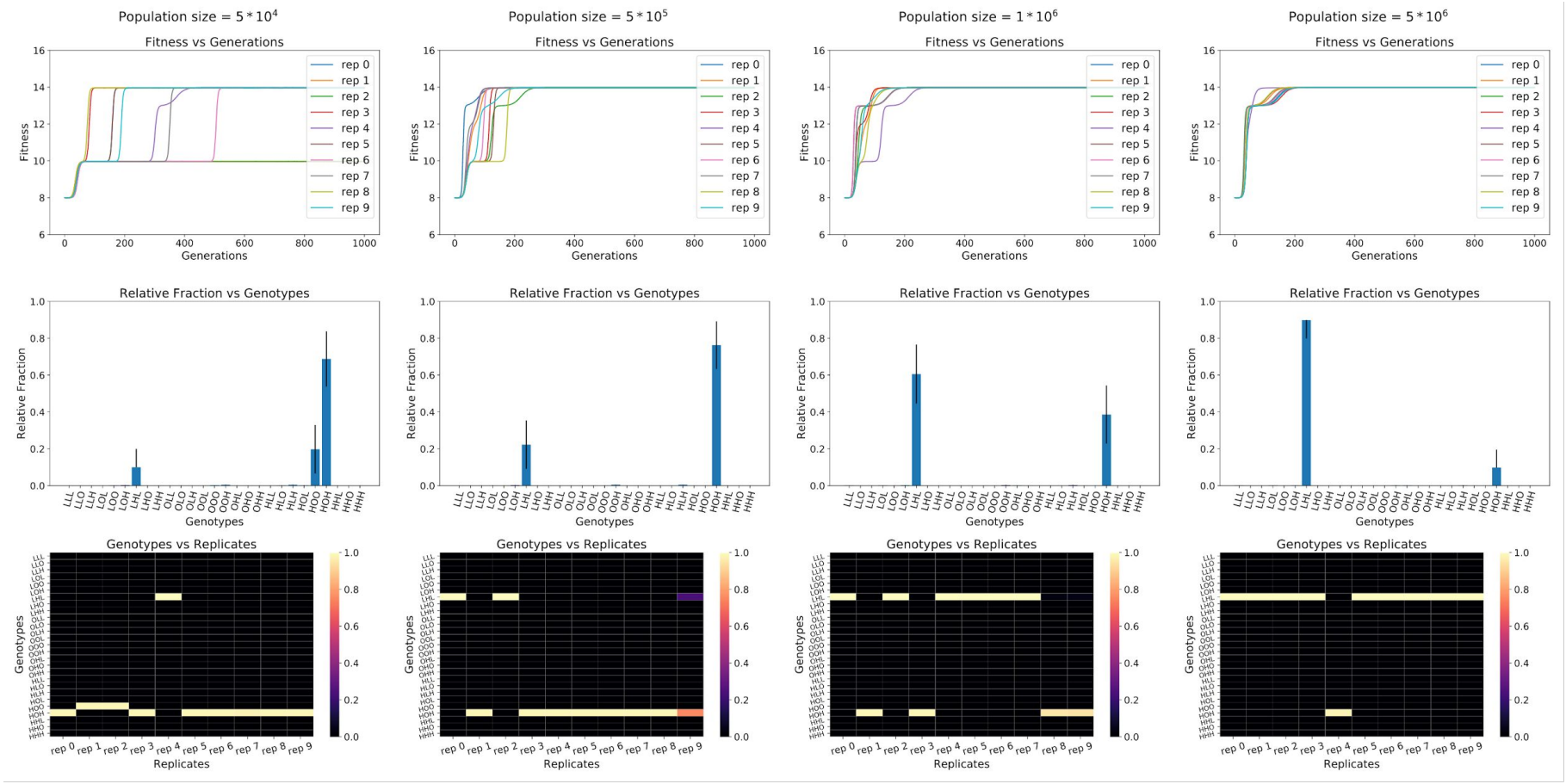


Figure 9: Comparison between different population sizes with three loci. Four columns are different population sizes $5*10^4$, $5*10^5$, 10^6 and $5*10^6$, respectively. First row is fitness vs generation of all replicates. Second row is mean relative fraction (±SE) of all the genotypes. Third panel is replicate wise relative fraction of all the genotypes.

Conclusions and Future Direction

- A trait getting selected for and against in the same environment is a striking phenomenon
- Changes in a **quantitative** parameter (population size) can lead to **qualitative** changes in character fates.
- The developed model uses very basic tools and it is intuitive.
- Once the fitness landscape and mutation rates are defined, the output is predictable.
- The *E. coli* genome can be searched for such interacting genes.

References

1. Patten, M. (2010). Levels of Selection. Encyclopedia of Animal Behavior, 272-276. doi:10.1016/B978-0-08-045337-8.00112-1.
2. Raynes, Y., Gazzara, M. R., & Sniegowski, P. D. (2012, 03). Contrasting Dynamics Of A Mutator Allele In Asexual Populations Of Differing Size. Evolution, 66(7), 2329-2334. doi:10.1111/j.1558-5646.2011.01577.x
3. Weinreich, D. M., Watson, R. A., & Chao, L. (2005, 06). Perspective: Sign Epistasis And Genetic Constraint On Evolutionary Trajectories. Evolution, 59(6), 1165-1174. doi:10.1111/j.0014-3820.2005.tb01768.x
4. Chavhan, Y., Karve, S., & Dey, S. (Under review). Adapting in larger numbers can make populations more vulnerable to environmental changes.