Longitudinal sequencing reveals polygenic and epistatic nature of genomic response to selection

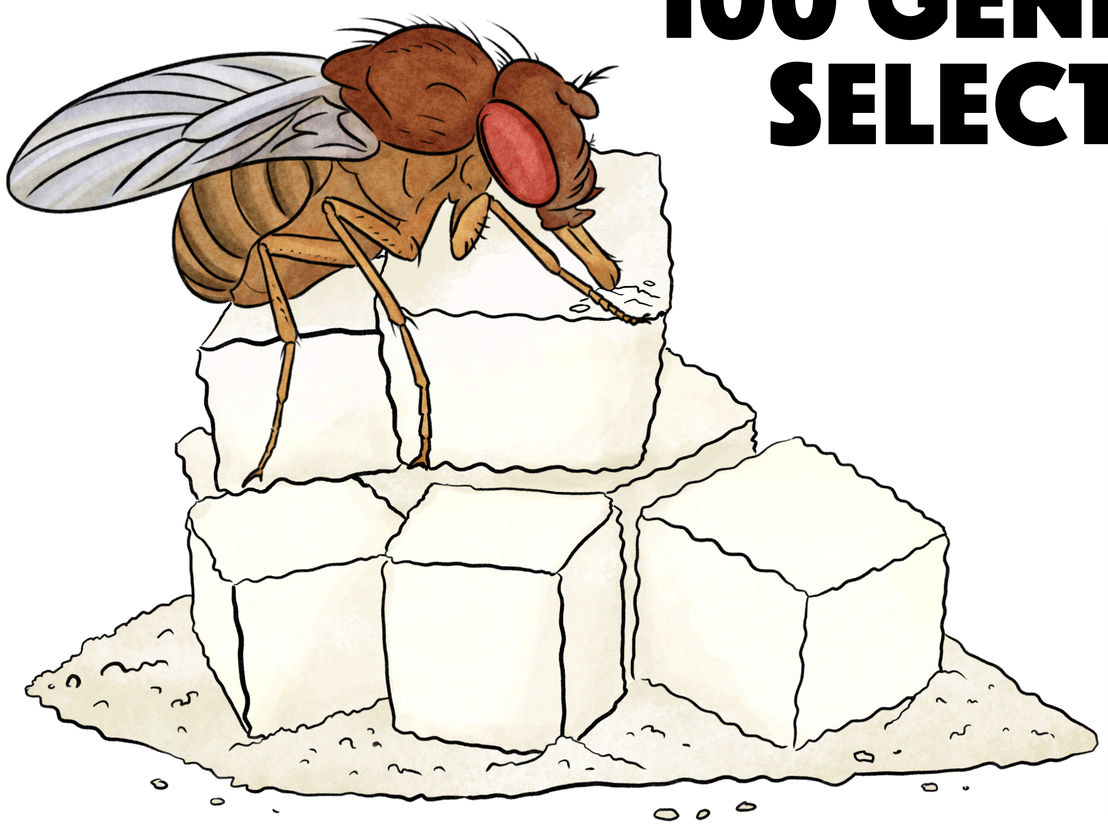
Simon K. G. Forsberg[*,1,2,5], **Diogo Melo**[*,1,2,6], Scott Wolf[1,2], Jennifer K. Grenier[4], Minjia Tang[1,2], Lucas P. Henry[1,2], Luisa F. Pallares[3], Andrew G. Clark[4], and Julien F. Ayroles[1,2]

[*] These authors contributed equally to this work.

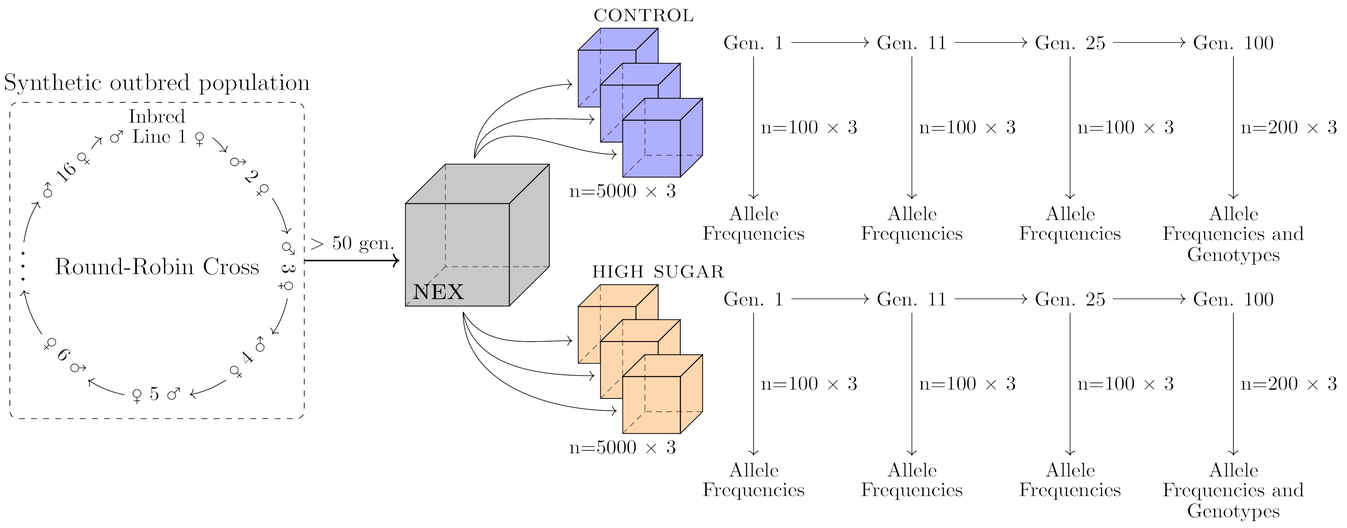
[1] Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ [2] Department of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ
[3] Friedrich Miescher Laboratory of the Max Planck Society, Tübingen, Germany [4] Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY, USA
[5] Department of Medical Biochemistry and Microbiology, Uppsala University, Sweden [6] Departamento de Genética e Biologia Evolutiva, Intituto de Biociências, Universidade de São Paulo

✉ Correspondence: Julien Ayroles <jayroles@princeton.edu>

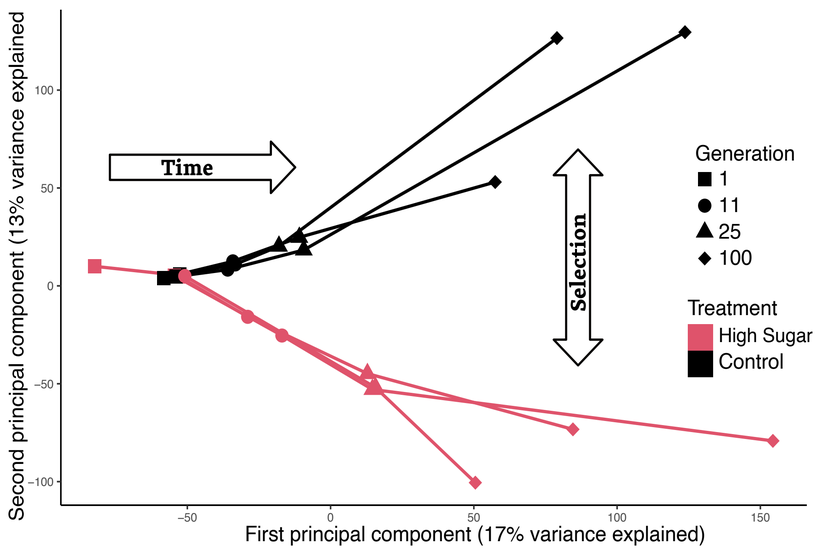
100 GENERATIONS OF HIGH-SUGAR SELECTION IN D. MELANOGASTER



Experimental design



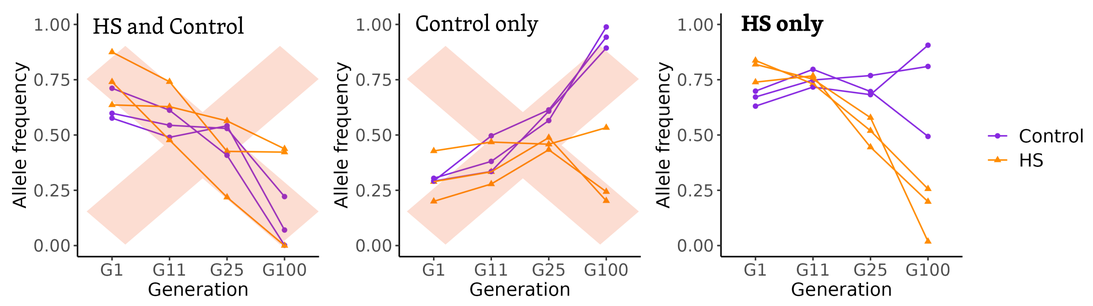
PCA across allele frequencies separates time and selection



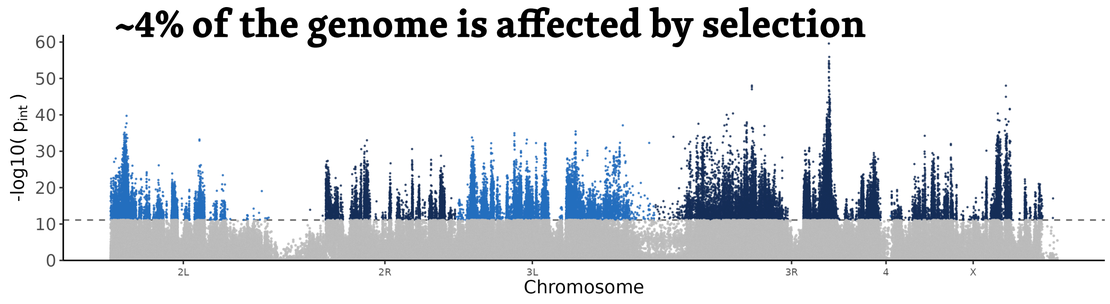
Detecting selected SNPs

Selected SNPs are detected using a linear model with an **interaction term** that identifies changes in allele frequency that are **exclusive** to the HS populations:

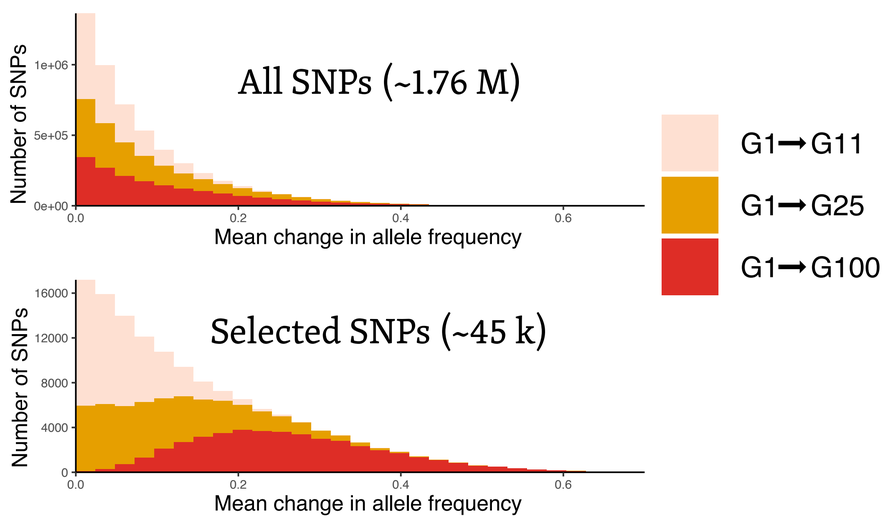
$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_t t_i + \beta_{\text{HS}}\text{HS}_i + \beta_{\text{HS*t}}\text{HS}_i t_i + e_i$$



~4% of the genome is affected by selection

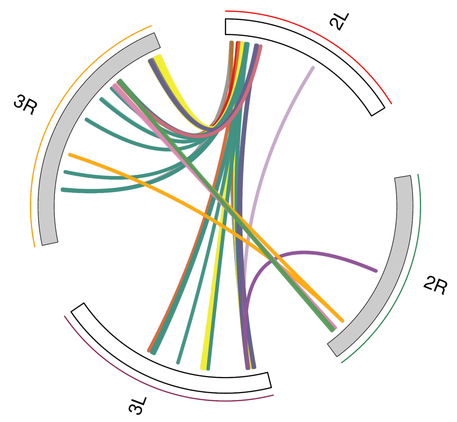


Allele frequency changes are larger at selected SNPs



Signatures of epistasis are visible in the adaptive architecture

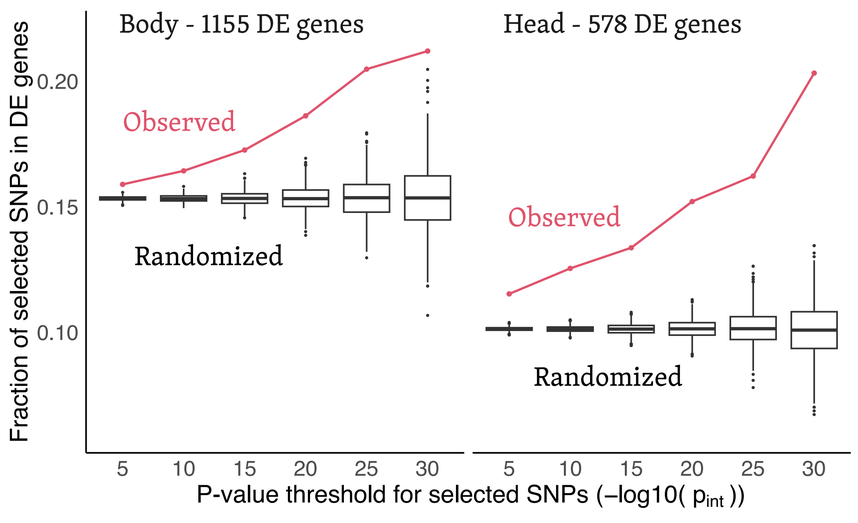
We find over 1000 SNP pairs with signatures of epistasis, and 11 SNP clusters with strong replicated signals:



SNP clusters are linked if they show:

1. Correlated allele frequency changes
2. Gametic disequilibrium across unlinked loci
3. Replicate signals across at least two selected populations
4. Both signals are exclusive to selected populations

Differentially expressed genes are enriched for selected SNPs



Simulations show that these signals are more likely in the presence of epistasis: