

Identifying the genomic evolution of obesity in starvation-selected

Drosophila

Tyler Peters^{1,2}, Austin McKenna², Allen Gibbs²

Department of Mathematics, Fort Valley State University, Fort Valley GA, 31030¹, School of Life Sciences, University of Las Vegas, Nevada, NV, 89154²

UNLV

Abstract

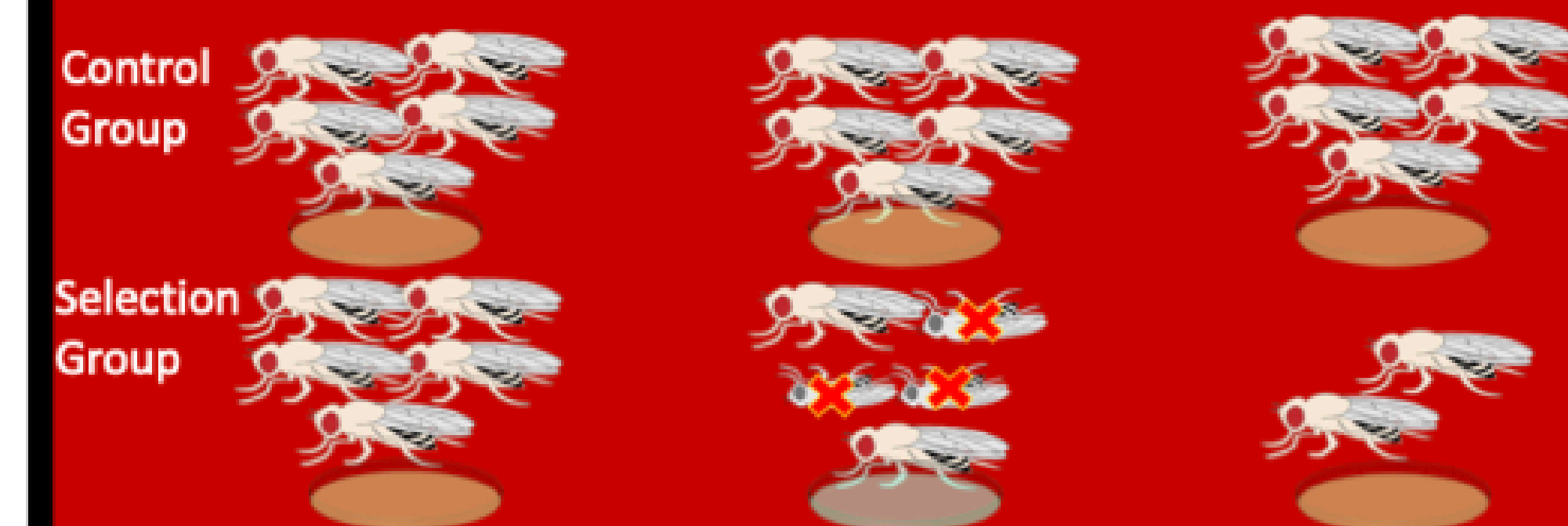
Drosophila melanogaster is a model species for studying physiological and genomic processes commonly found in humans. Previous studies have evolved obese phenotypes in *Drosophila* through starvation selection. We carried out starvation selection on five distinct populations of *Drosophila melanogaster*. DNA samples were collected from each selected population of flies to conduct a genome-wide association study (GWAS). A total of 814,408 single nucleotide polymorphisms (SNPs) were identified across the genome at 120X coverage. Using Principal component analysis (PCA) we determined that after only one generation of starvation selection, the five selected populations cluster together away from the founding control population. To pinpoint SNPs at different frequencies between the founding population and our generation, we determined that about 10,000 were significantly different in allele frequency. We observed thirteen shared candidate genes between the five populations. Of the thirteen candidate genes, seven of them were clustered on the 3L chromosome. Results indicate rapid genomic evolution in response to starvation selection. With these results and the association between the genotype and phenotype of *Drosophila melanogaster*, we hope to eventually compare similar genes within humans to make a connection between the human genome and obesity.

Background

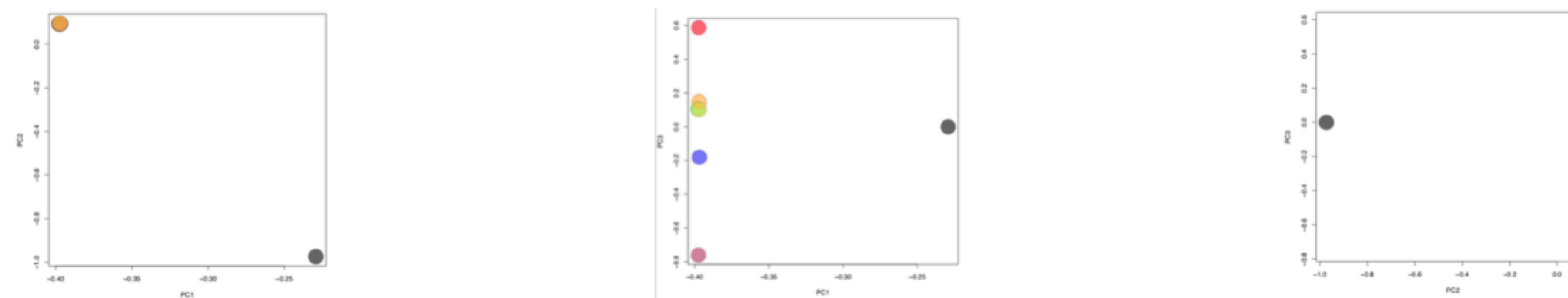
- Drosophila melanogaster* contains ~75% of all human disease causing genes, thus they provide a good model system for studying physiological disorders.
- Previous studies in the Gibbs lab have evolved obese flies through many generations of starvation selection.
- Recently, Hardy et al. 2018 performed a GWAS on starvation selected flies to link the obese phenotype to candidate loci in the genome. However it was difficult to make the connection since many other phenotypes had evolved in addition to obesity.

Methods

- Starvation selection was restarted for 10 generations on flies that had never been introduced to any selection pressures
- DNA samples were collected from each population to conduct a GWAS in order to determine the genomic impact of the fat phenotype
- Genomes from the founding population and Generation 1 were mapped to the reference genome using bwa
- Variants were called using gatk and snpEff.
- Downstream SNP analysis was conducted using R scripts used in Hardy et al., 2018

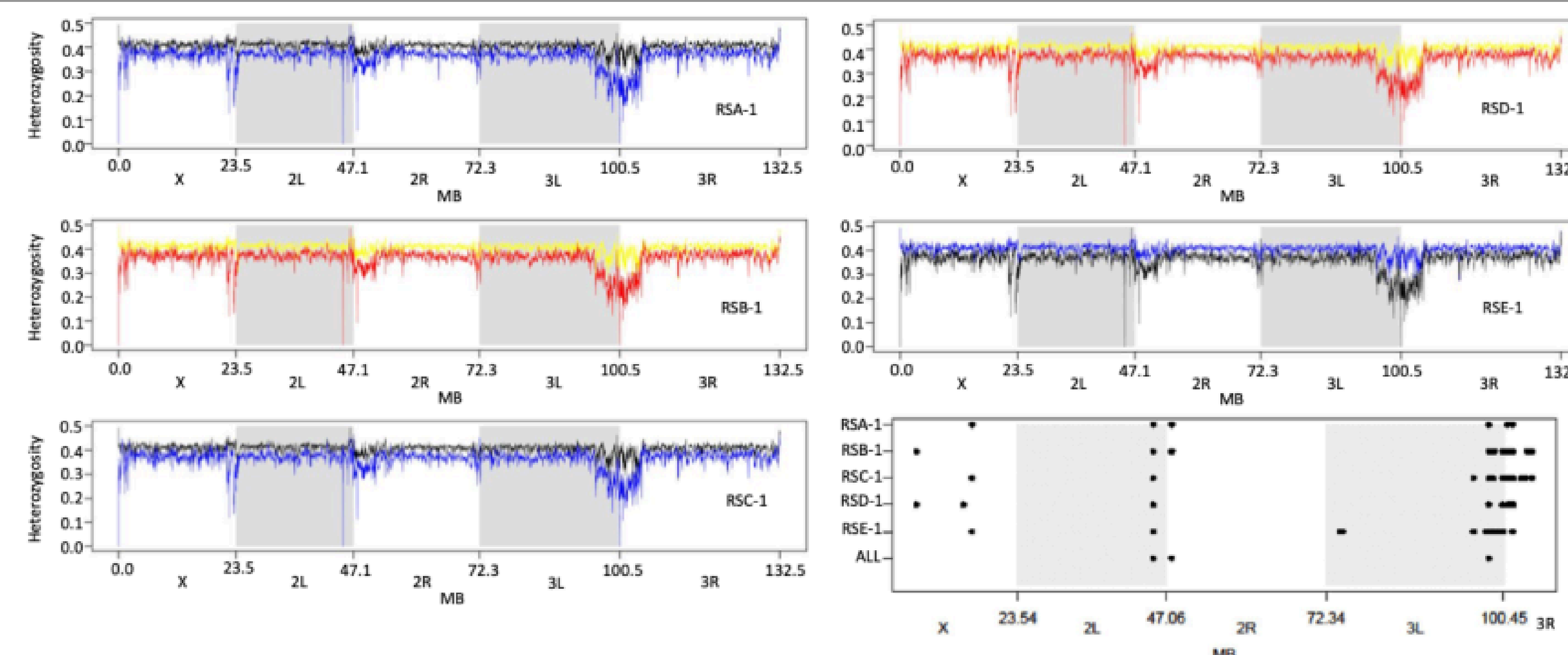


GENOMIC VARIATION GENERATION 1



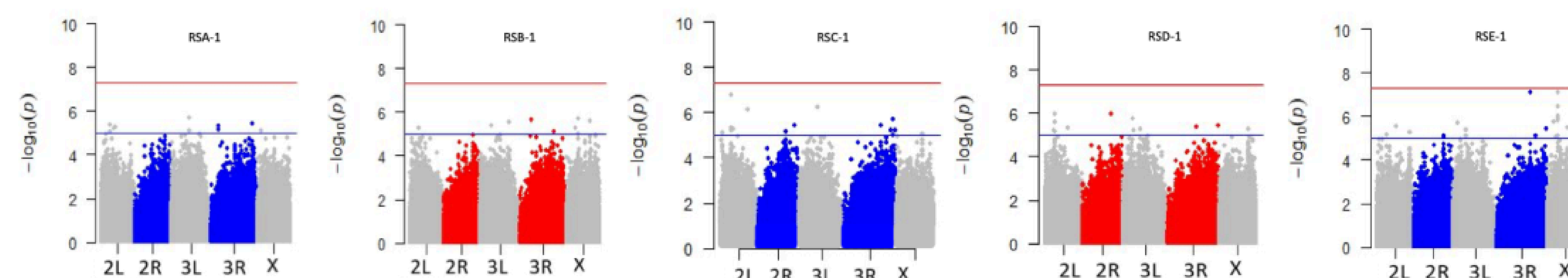
- Principal Component Analysis- Used to reduce the number of variables and differentiate between data sets
- After only one generation of starvation selection, the selected populations cluster together away from the founding control population
 - This indicates that after only one generation of selection, noticeable differences appeared within the genomes of starvation-selected flies

GENOMIC HETEROZYGOSITY



- Heterozygosity Plot- Shows level of heterozygosity across entire genome
- Heterozygosity is slightly higher in the founding population compared to the selected populations
 - Blocks of low heterozygosity (<0.1) are few, but seem to be consistent across populations

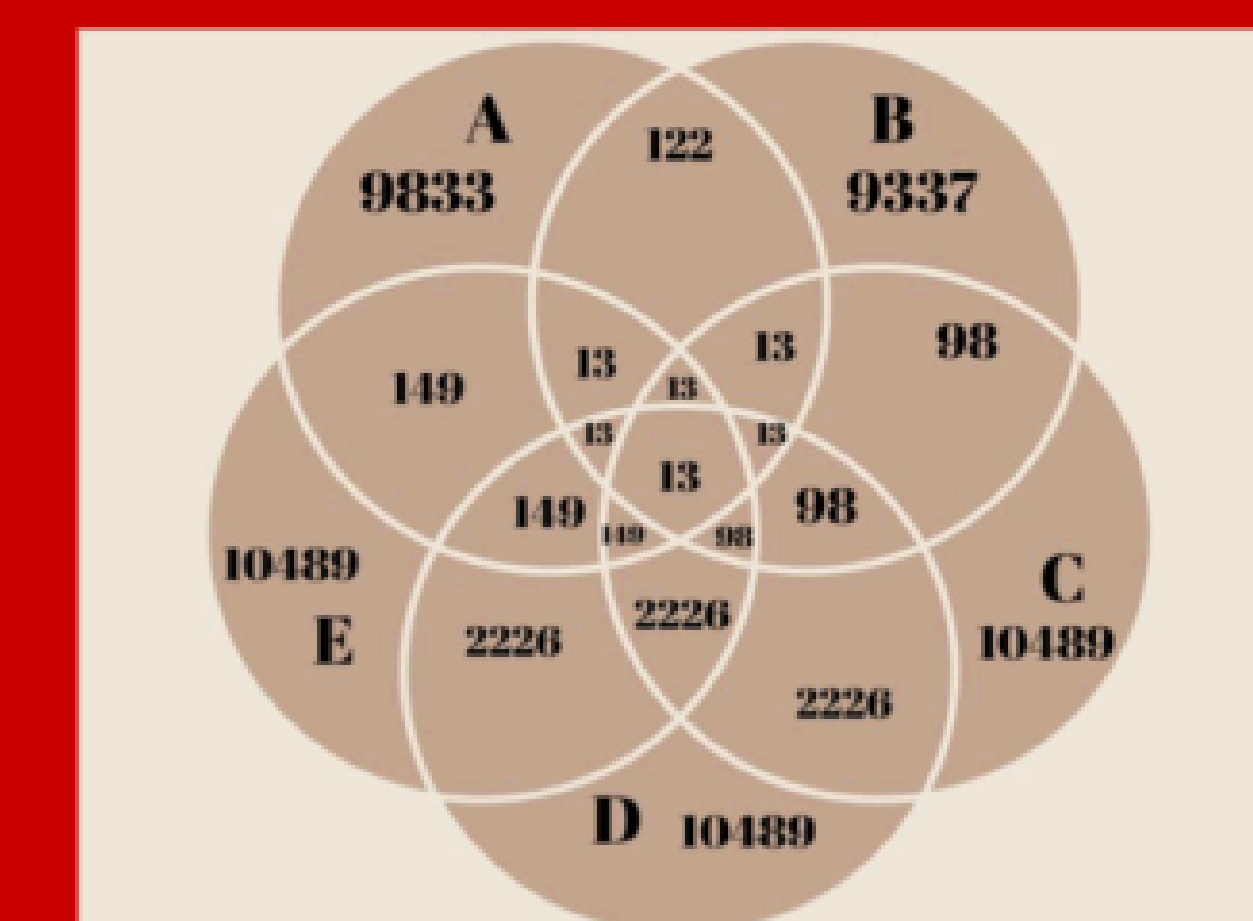
CANDIDATE SNPs



- Manhattan Plot- Displays SNPs with p-values across genome
- All data points above line have a significantly different frequency in genome compared to the founding population
 - Significant data points could be candidate genes

RESULTS

- In each of our five selected populations, we discovered about 10,000 SNPs with significantly different allele frequencies compared to the control population
- Thirteen candidate loci were shared among the five populations
- Seven of these candidate loci were on the 3L chromosome



	Chromosome	position
1	2L	11194966
2	2L	1415137
3	2L	1909638
4	2R	19593010
5	3L	1043009
6	3L	17316652
7	3L	19434760
8	3L	19486845
9	3L	20004498
10	3L	20159034
11	3L	20924637
12	3R	13319003
13	3R	26117502

CONCLUSIONS

- Starvation selection can lead to rapid genomic evolution as early as one generation.
- Starvation resistance seems to evolve in different ways, but some changes are shared across the populations.
- Through analysis of these results in *Drosophila melanogaster*, we hope to identify similar genes in humans to gain a better understanding of the genomic basis of obesity.

Acknowledgements

This project was funded by the Mechanisms of Evolution REU program on the campus of University of Las Vegas, Nevada

Additional funding for this project was provided by the National Science Foundation

Special thanks for aid in project
Austin McKenna

