Understanding the Rapid Evolution of Pigmentation in D.melanogaster Liam Flatley (CAS '24) with mentorship from Dr. Paul Schmidt (Penn Department of Biology)

Aims

Aim #1: Determine whether the genetic basis for rapid evolution of pigmentation exhibits parallelism.

Throughout the yearly seasonal cycle, we identify alleles that are responsible for both midpoint and extreme shifts changes in pigmentation phenotypes. We can test whether the same alleles change frequency in response to seasonal evolution at different latitudes.

Aim #2: Test the adaptive significance of pigmentation in rapidly evolving populations.

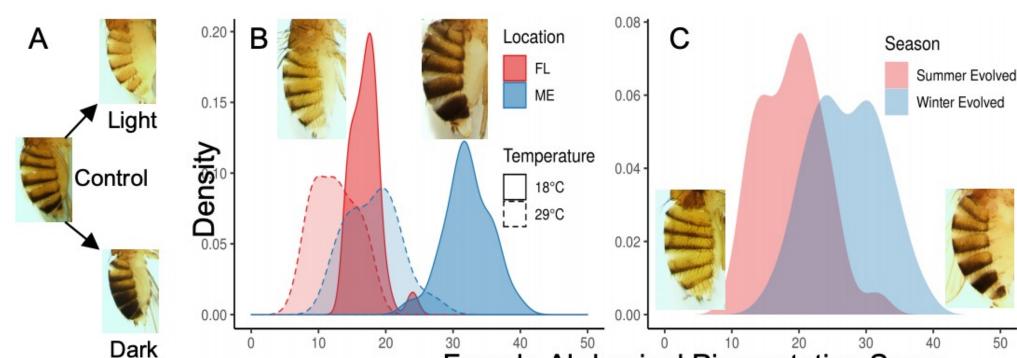
We test the hypothesis that natural selection acts on the pigmentation phenotype.

• Aim #3: Cisregulatory variation and the genetics of pigmentation.

We use allelic imbalance to reveal variation in cis regulatory sequences that influence pigmentation and respond to natural selection. We test if flies from different areas with similar pigmentation patterns have similar cisregulation patterns, identify cisregulatory loci, and test whether changes in pigmentation show cis variation in the same loci as comparisons in extreme phenotypes.

Background Information

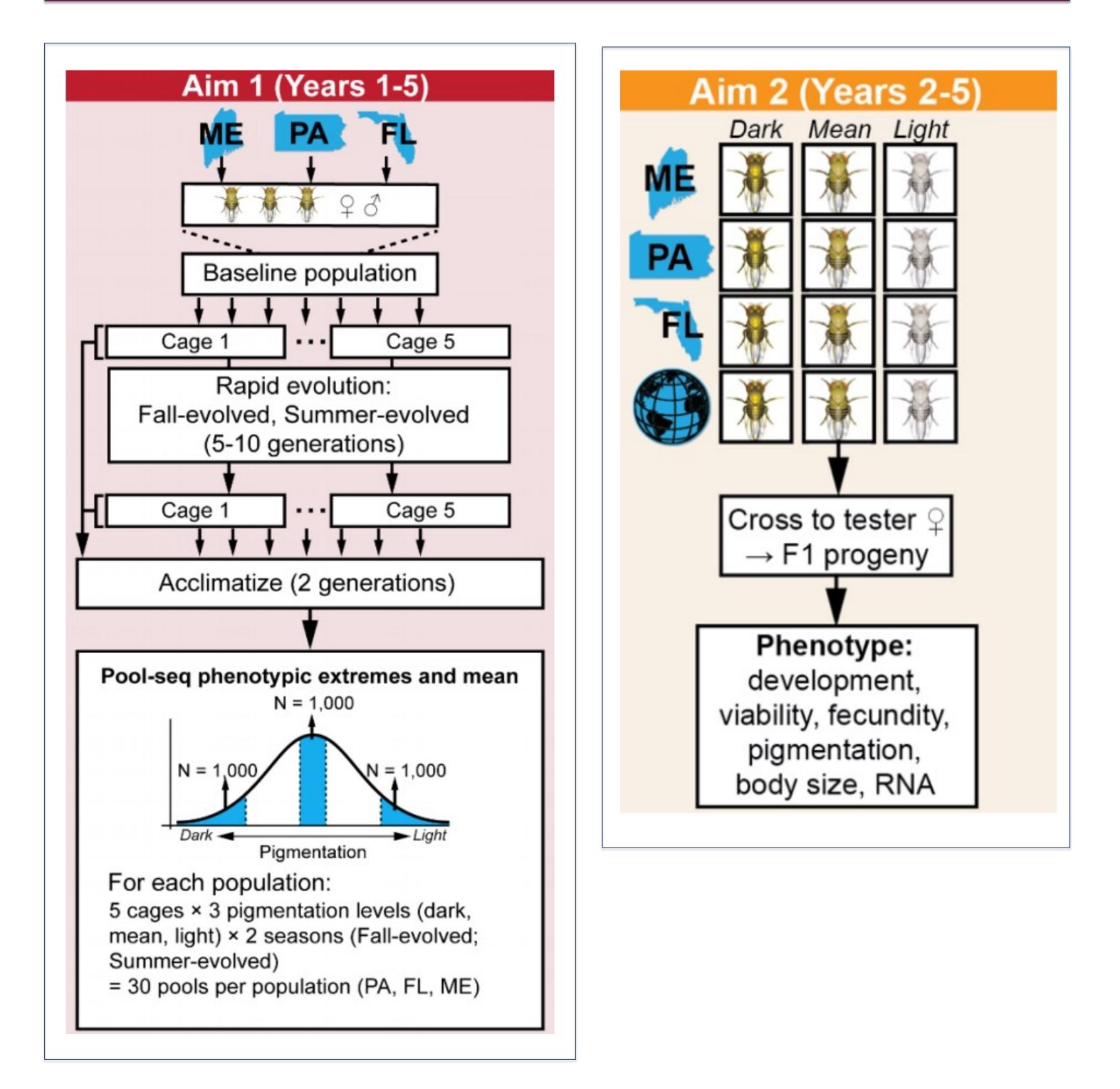
Pigmentation has evolved cyclically with season: flies are dark at the end of winter and light at the end of the summer. This seasonal evolutionary cycle repeats annually. These patterns reflect changes in the genetic composition of the populations, not plasticity due to environmental effects, as phenotyping is conducted after three generations of culture under standard laboratory conditions.

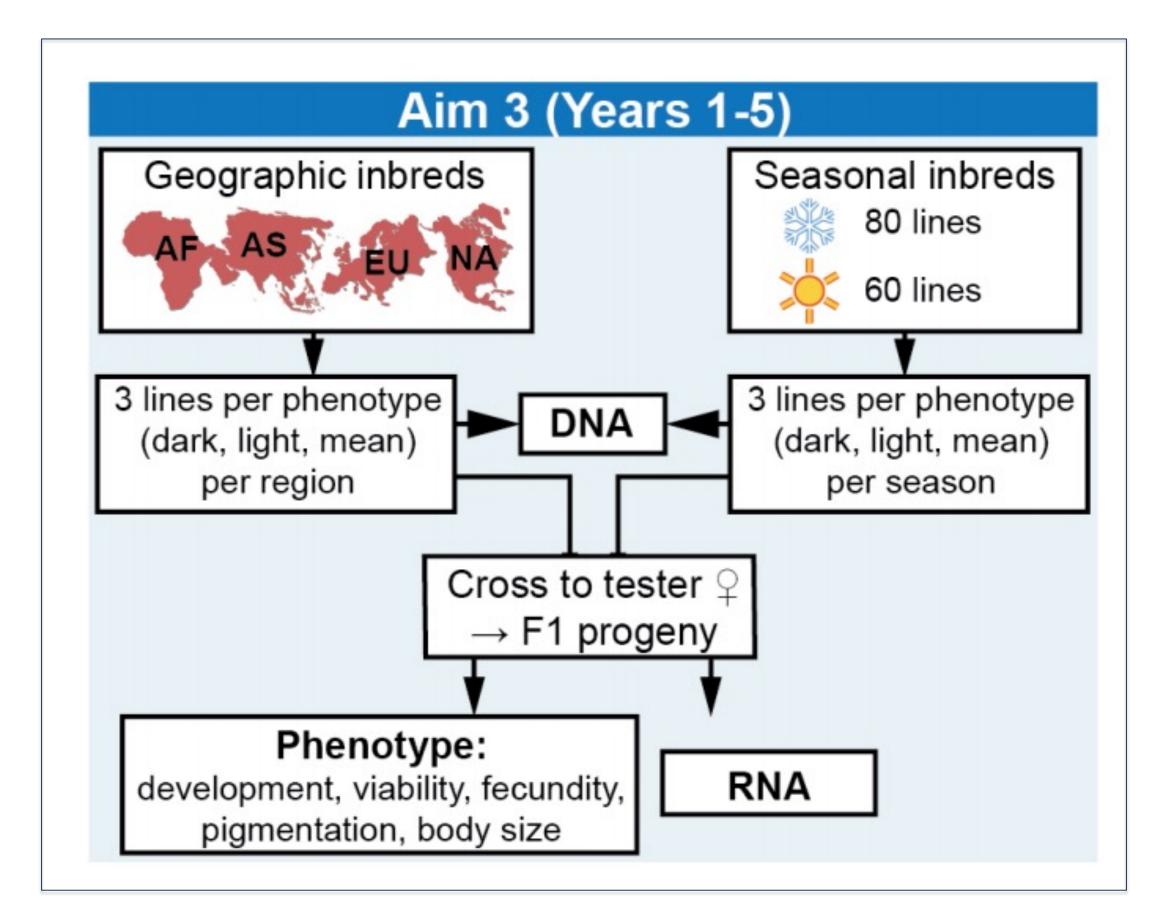


Female Abdominal Pigmentation Score

Pigmentation in natural populations of D. melanogaster is due to many loci. There are more than twenty major effect pigmentation loci in D. melanogaster that have been functionally verified and many more that have been associated in QTL studies. Large effect loci such as ebony, tan, yellow, bric-a-brac1, and bric-a-brac2 have been identified as important in pigmentation in the context of natural populations.

Approach







This is an ongoing study, and the only data that has been collected is from preliminary studies. The three main products of the completed experiment include an understanding of:

1) genetic architecture and dynamics of rapid evolution of complex traits in natural populations exposed to complex environments

2) parallelism and generality in the evolutionary process at multiple scales -among experimental replicates, among populations from distinct latitudes, among lines derived from four continents, between the outcomes of natural and artificial selection, among light/midpoint/dark pigmentation phenotypes, and among genetic variants that determine mean/median phenotype vs. those that result in extreme trait values

3) means vs. extremes, and how complex traits evolve rapidly and predictably in complex environments

4) the constraints of pleiotropy on rapid evolution, and how this ultimately impacts the translation between genetic variation and complex phenotype

Sources & Acknowledgements

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Sources: Schmidt, P. (2021). PDF. Philadelphia; Schmidt Lab.



Significance

Rapid evolution is central to a number of biological phenomena of fundamental **significance:** adaptation to the environment and evolutionary rescue, vectorborne disease, drug resistance, and dynamics of cancer, to name a few.

Pigmentation offers an ideal system in which to examine adaptive dynamics over space and time. Pigmentation is of broad adaptive significance in a variety of taxa and intraspecific patterns of pigmentation can reflect local adaptation.

• Rapid evolution of pigmentation offers a distinct window into evolution and an important opportunity to improve scientific knowledge.

Conclusion