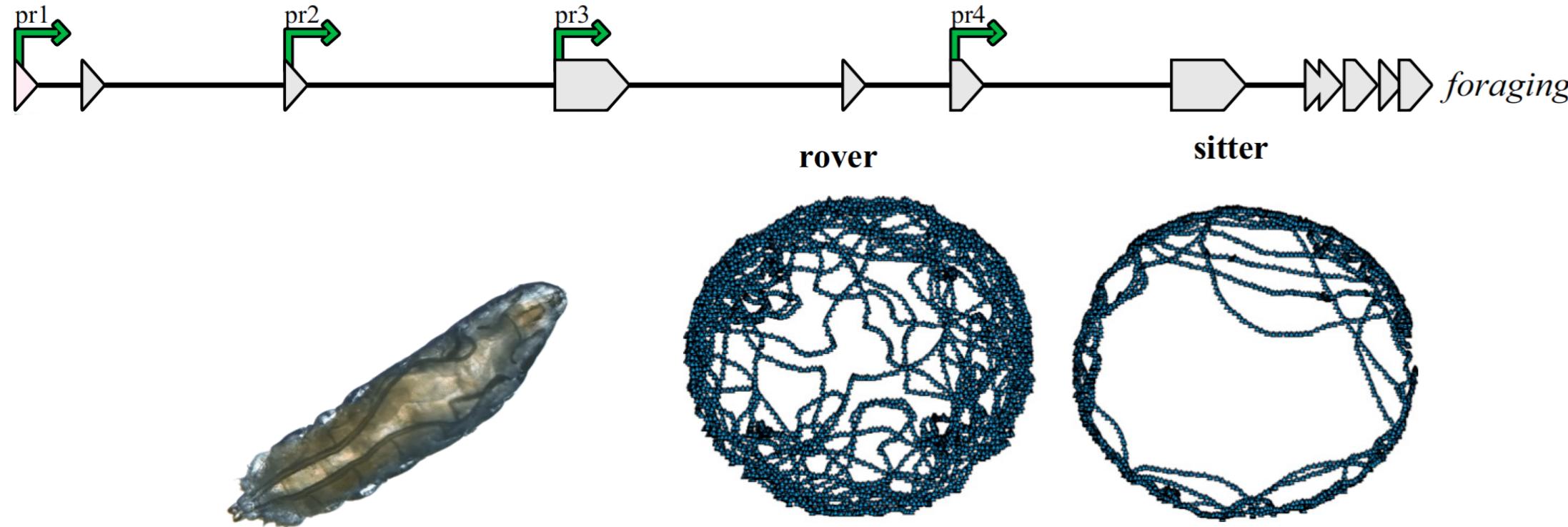


Dylan J. Padilla

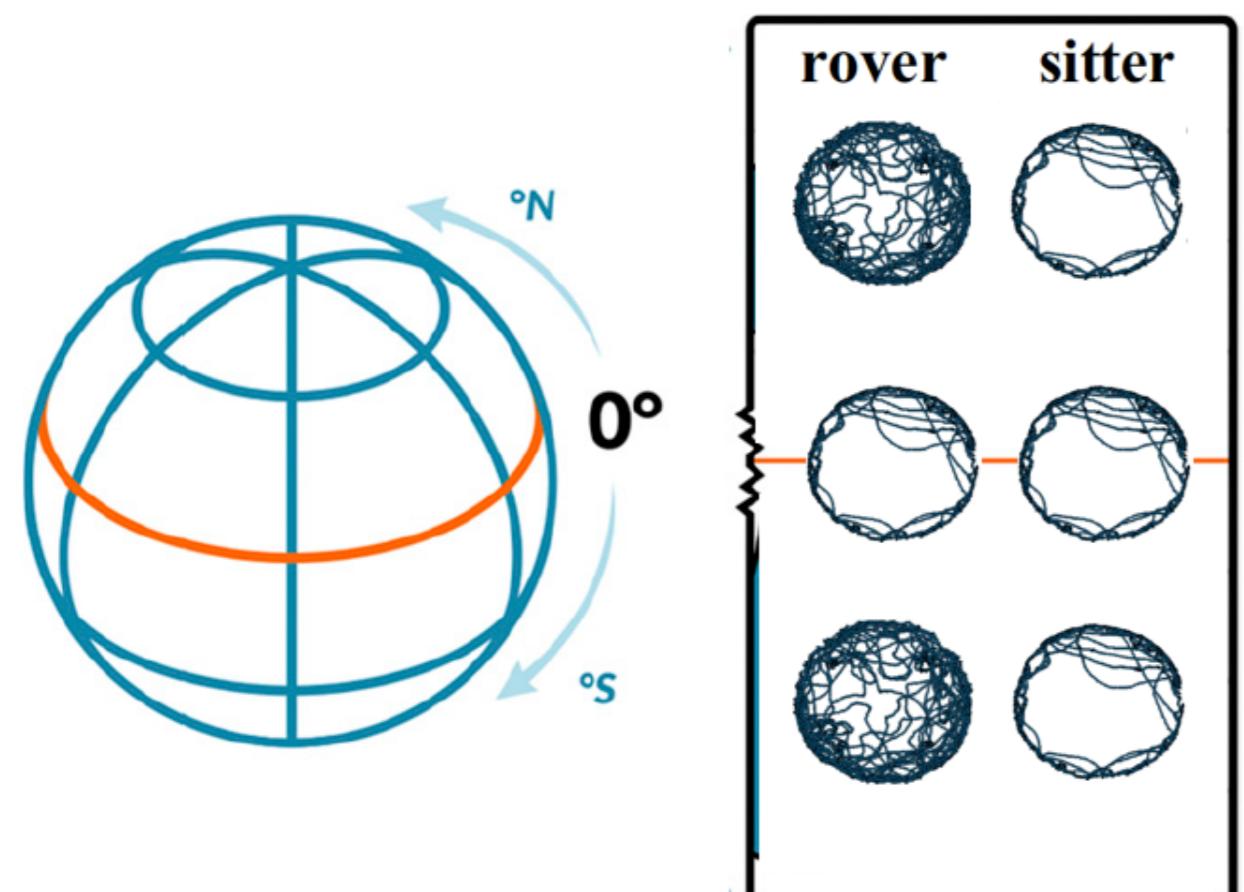
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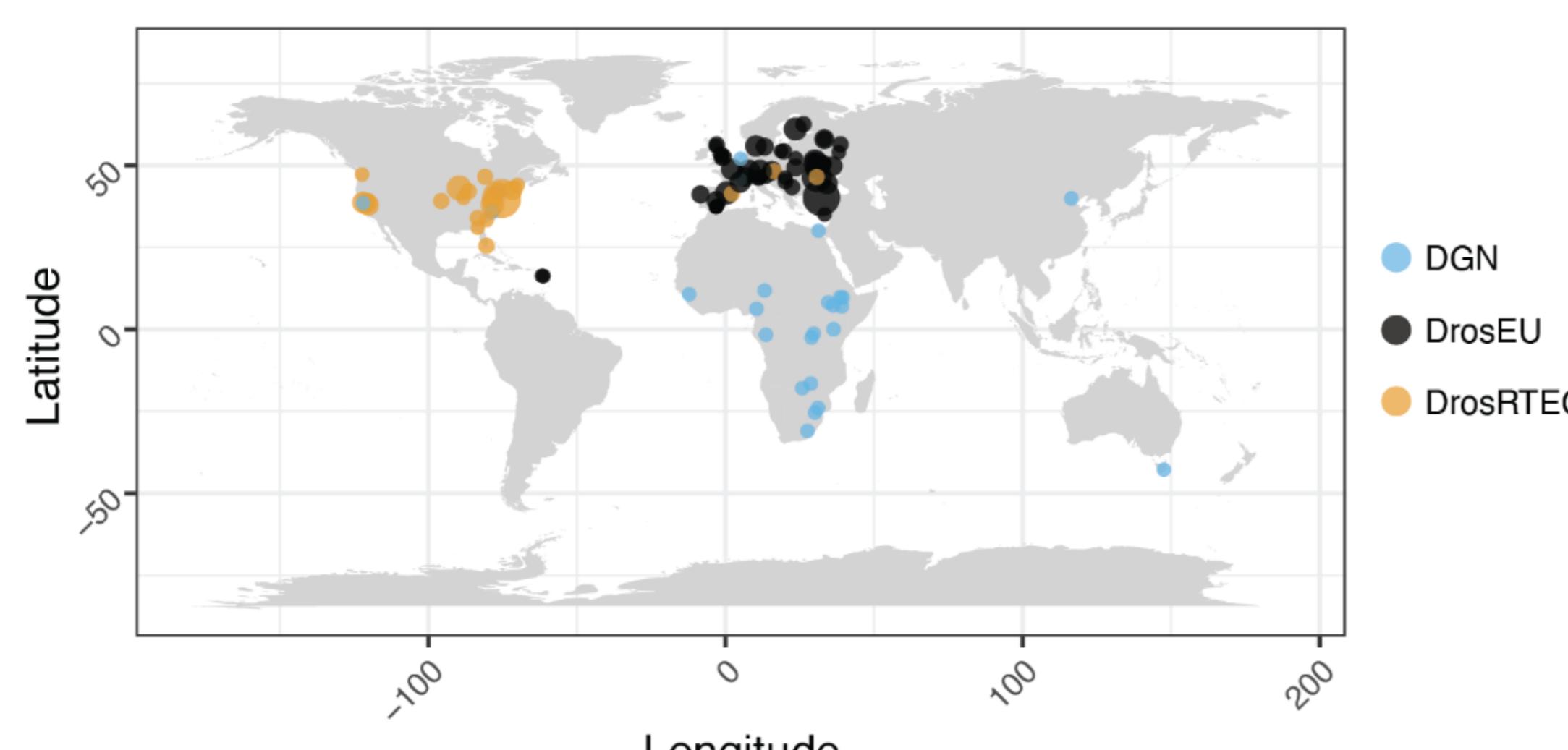
1. The *Drosophila foraging gene* provides an opportunity to understand the mechanisms underlying evolutionary responses to environmental variation



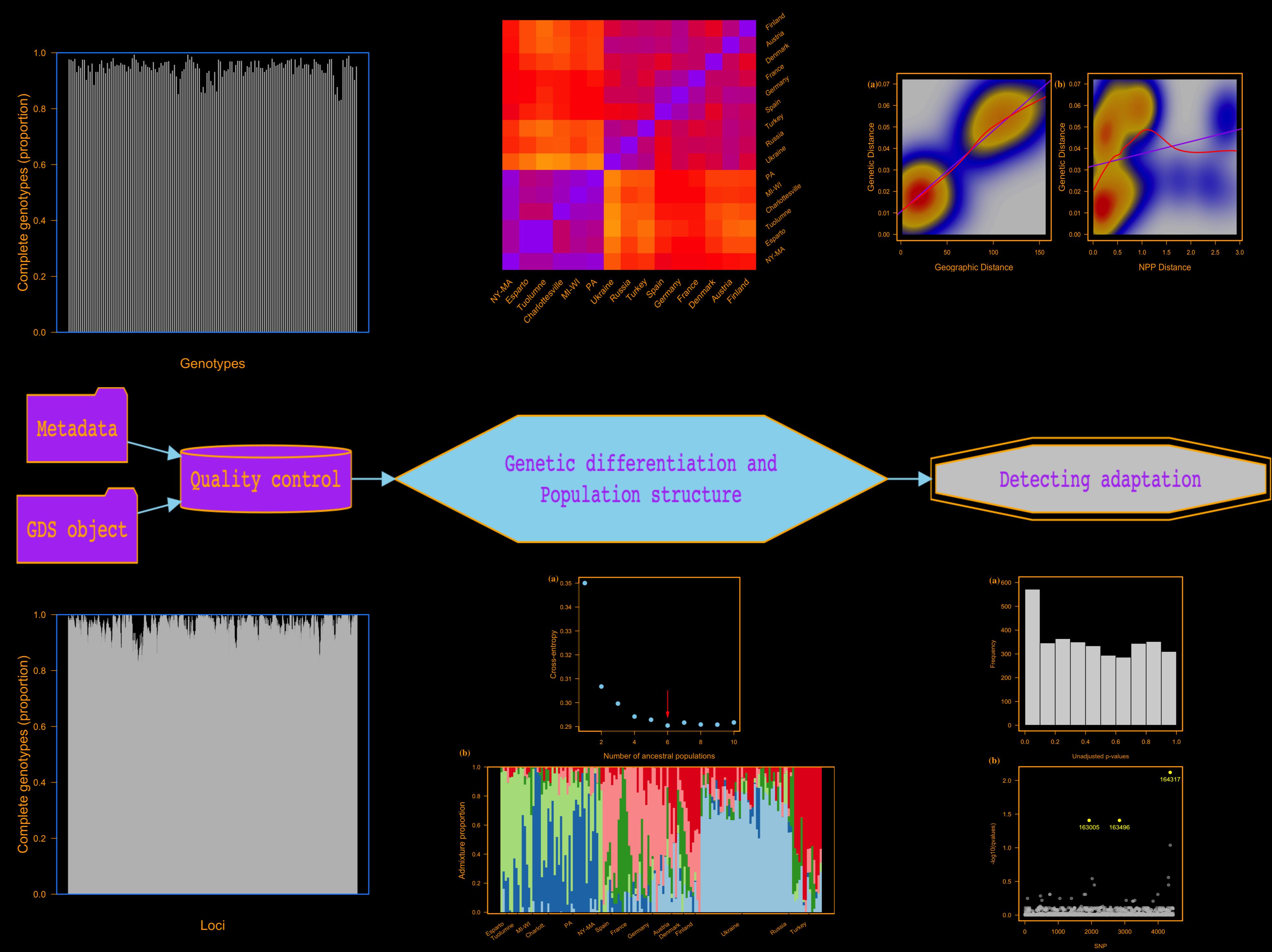
2. Given its allelic variants, one should expect geographic variation of the *for gene* among populations



3. The DEST dataset enables one to study genetic variation across populations spanning America and Europe



The population genetics of foraging behavior



An analysis of genetic differentiation based on Fst estimates revealed two major genetic clusters; one with all the American samples grouped together, and the other one grouping the European samples. Similarly, there is some degree of genetic differentiation among samples within each continent, suggesting a total of 6 ancestral populations k with unique patterns of allelic variation in the *for* gene. The results indicate that different patterns of gene flow as expected under models of isolation by environment (IBE) and isolation by distance (IBD) are likely driving the genetic differentiation among populations of *D. melanogaster*.

