

The Population Genetics of Foraging Behavior

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Acknowledgement



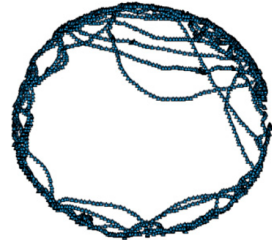
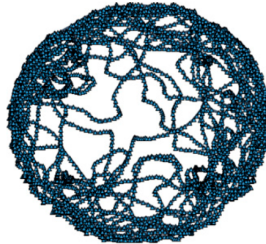
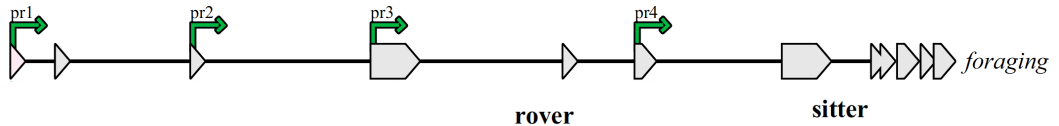
Joaquin Nunez

Introduction:

The foraging-mode paradigm

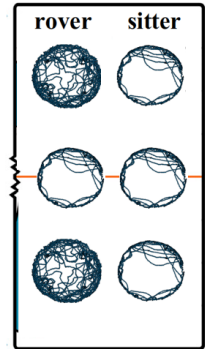
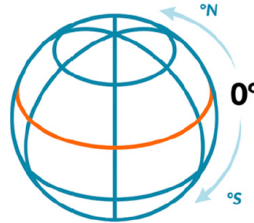


Drosophila melanogaster foraging behavior



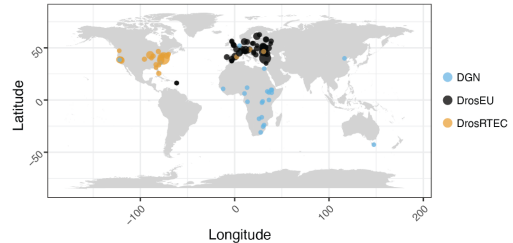
The *Drosophila foraging* gene provides an opportunity to understand the mechanisms underlying evolutionary responses to environmental variation

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



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

2. The DEST dataset enables one to study genetic variation accross populations spanning America and Europe



Materials and Methods:

Analyses

- ▶ Genetic differentiation among populations according to Weir and Cockerham (1984)



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Analyses

- ▶ Genetic differentiation among populations according to Weir and Cockerham (1984)
- ▶ Population structure based on admixture proportions



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- ▶ Population structure based on admixture proportions
- ▶ Genotype–environment association analysis based on LFMMs with a ridge penalty (Jumentier et al., 2022)



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- ▶ Genetic differentiation among populations according to Weir and Cockerham (1984)
- ▶ Population structure based on admixture proportions
- ▶ Genotype–environment association analysis based on LFMMs with a ridge penalty (Jumentier et al., 2022)
- ▶ Isolation by environment and isolation by distance

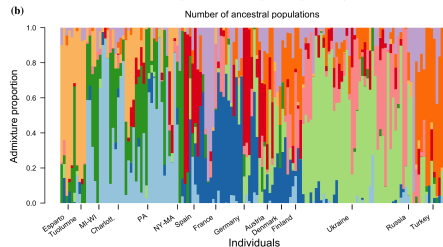
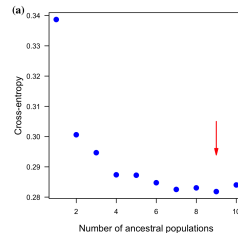
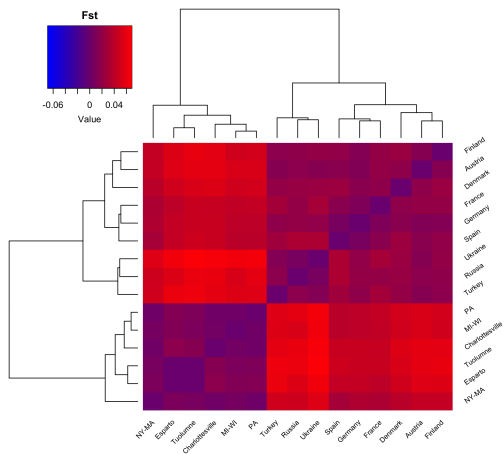


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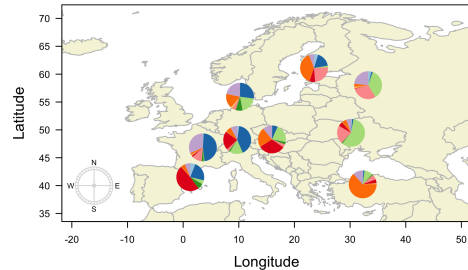
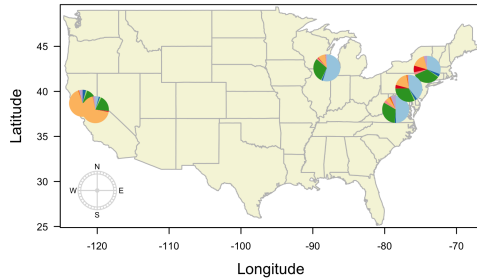
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Results and Discussion:

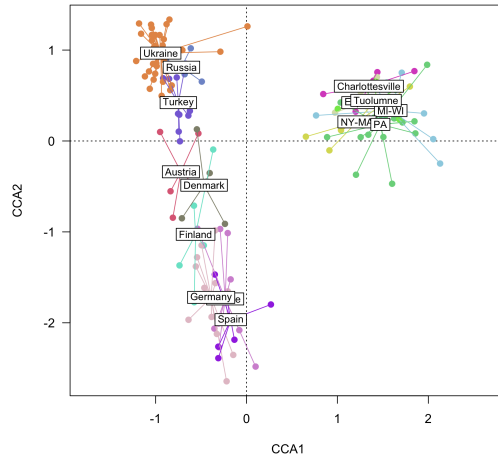
A genetic differentiation test, and an analysis of population structure revealed an east-west gradient in allele frequency



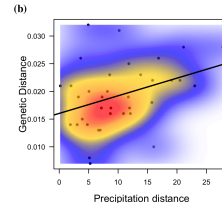
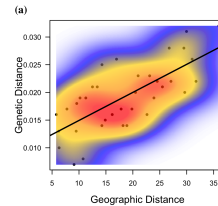
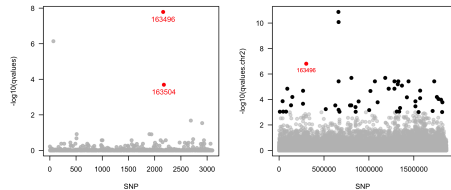
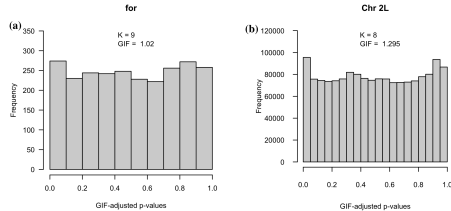
Stronger structure in populations collected in America than those collected in Europe, although the structure of pools from Ukraine, Turkey, and Russia stands out



Spatially varying selection driven by the seasonality of net primary production



Models of isolation by environment and isolation by distance are likely driving genetic differentiation among populations



Concluding remarks

- East–west gradient in allele frequency across populations

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Concluding remarks

- ▶ East–west gradient in allele frequency across populations
- ▶ Dmel populations are genetically differentiated resulting from spatially varying selection driven by the seasonality of precipitation

Scan the qr-code below for access to the paper:

