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Mutation rate variation shapes genome-wide diversity in Drosophila melanogaster

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This article is a preprint and has not been certified by peer review [what does this mean?].

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Abstract

What shapes the distribution of nucleotide diversity along the genome? Attempts to answer this question have sparked debate about the roles of neutral stochastic processes and natural selection in molecular evolution. However, the mechanisms of evolution do not act in isolation, and integrative models that simultaneously consider the influence of multiple factors on diversity are lacking; without them, confounding factors lurk in the estimates. Here we present a new statistical method that jointly infers the genomic landscapes of genealogies, recombination rates and mutation rates. In doing so, our model captures the effects of genetic drift, linked selection and local mutation rates on patterns of genomic variation. We then formalise a causal model of how these micro-evolutionary forces interact, and cast it as a linear regression to estimate their individual contributions to levels of diversity along the genome. Our analyses reclaim the well-established signature of linked selection in Drosophila melanogaster, but we estimate that the mutation landscape is the major driver of the genome-wide distribution of diversity in this species. Furthermore, our simulation results suggest that in many evolutionary scenarios the mutation landscape will be a crucial factor shaping diversity, depending notably on the genomic window size. We argue that incorporating mutation rate variation into the null model of molecular evolution will lead to more robust inferences in population genomics.

Competing Interest Statement

The authors have declared no competing interest.

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