

Patterns of Demography and Selection During and Since Maize Domestication

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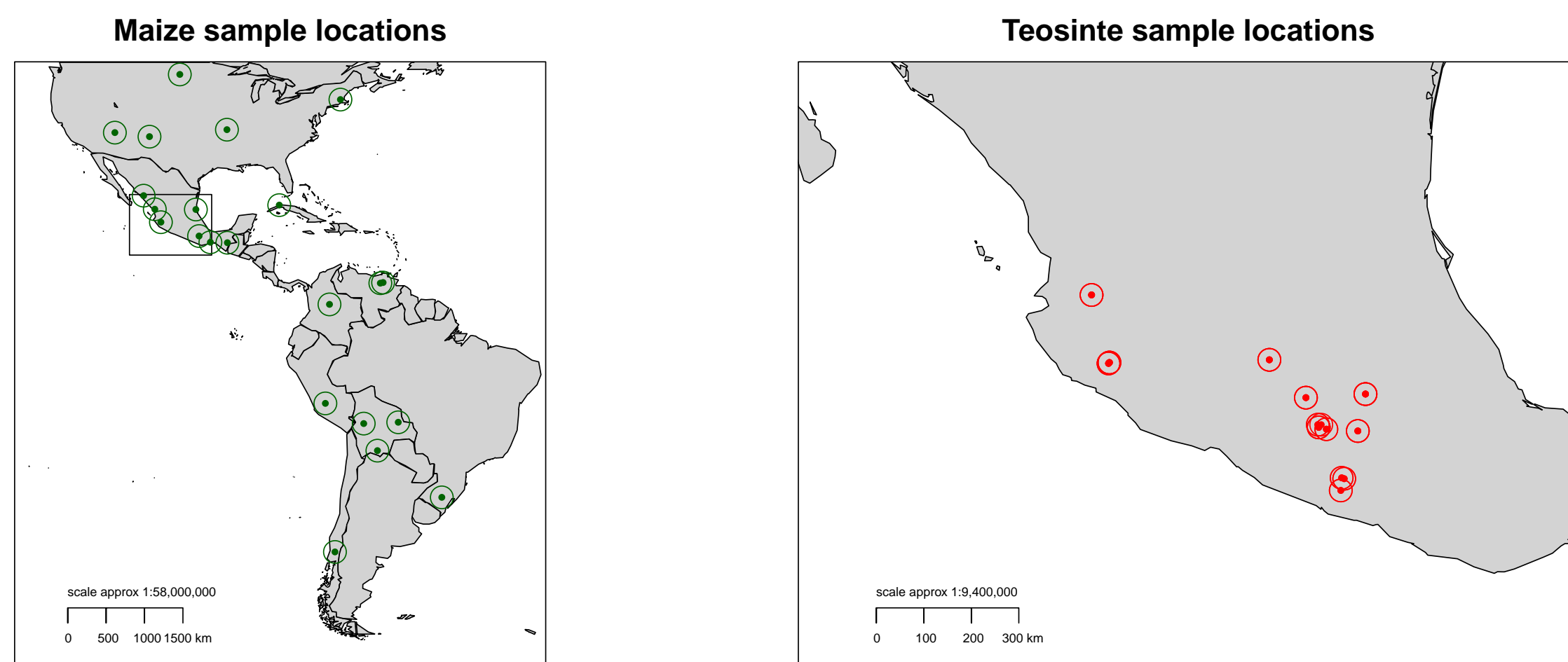
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Introduction

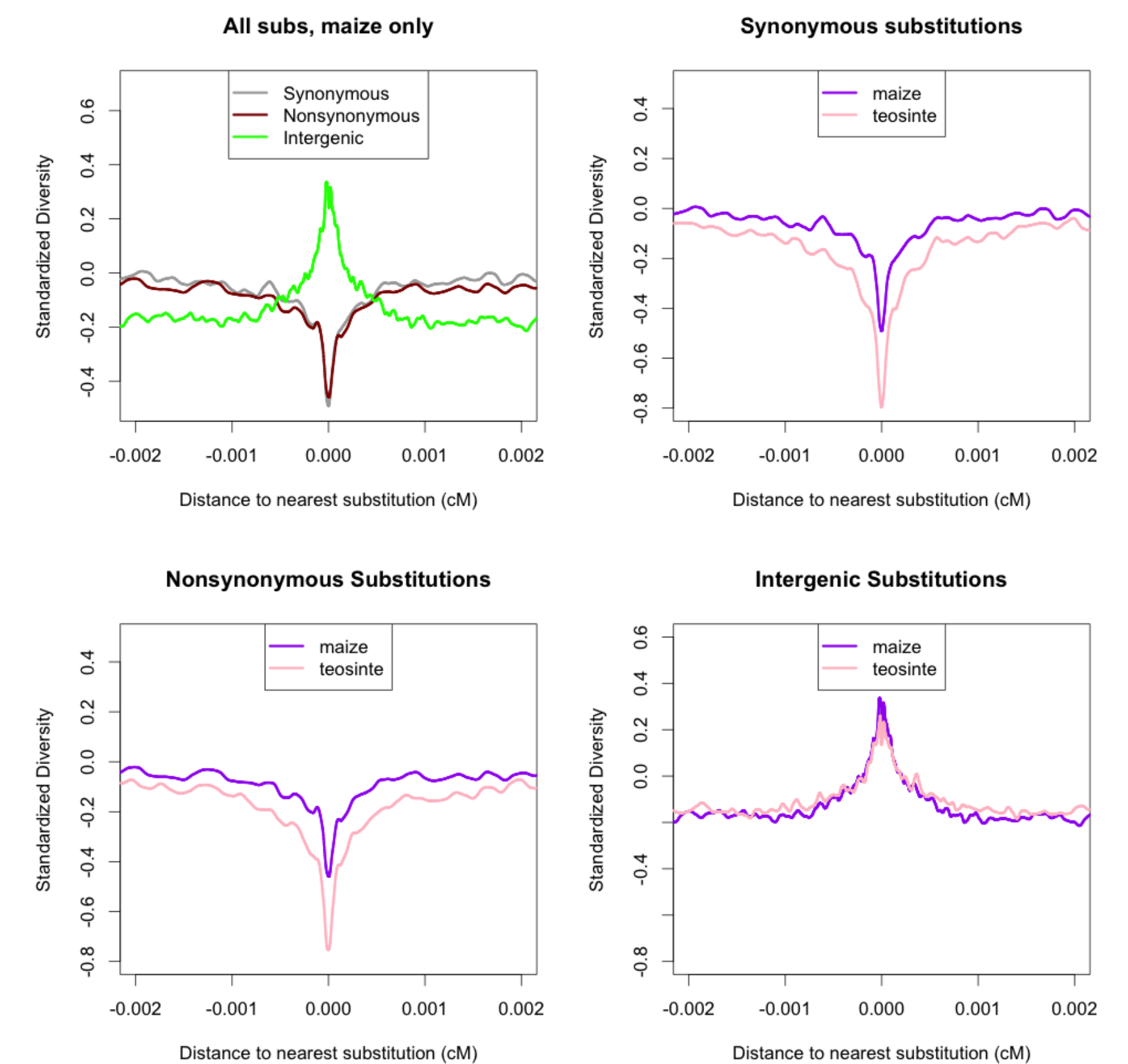
To better understand maize domestication, we employed whole genome sequence data from 23 maize and 13 teosinte samples from Maize HapMap2 [1] to investigate patterns of genetic variability resulting from the domestication process. Parameters of the domestication process were inferred from non-genic regions of the genome, for which selection is less likely to impact evolution. Next, diversity surrounding different classes of sites was evaluated to gauge the general selective forces governing domestication.



Few classical hard sweeps in *Zea mays*

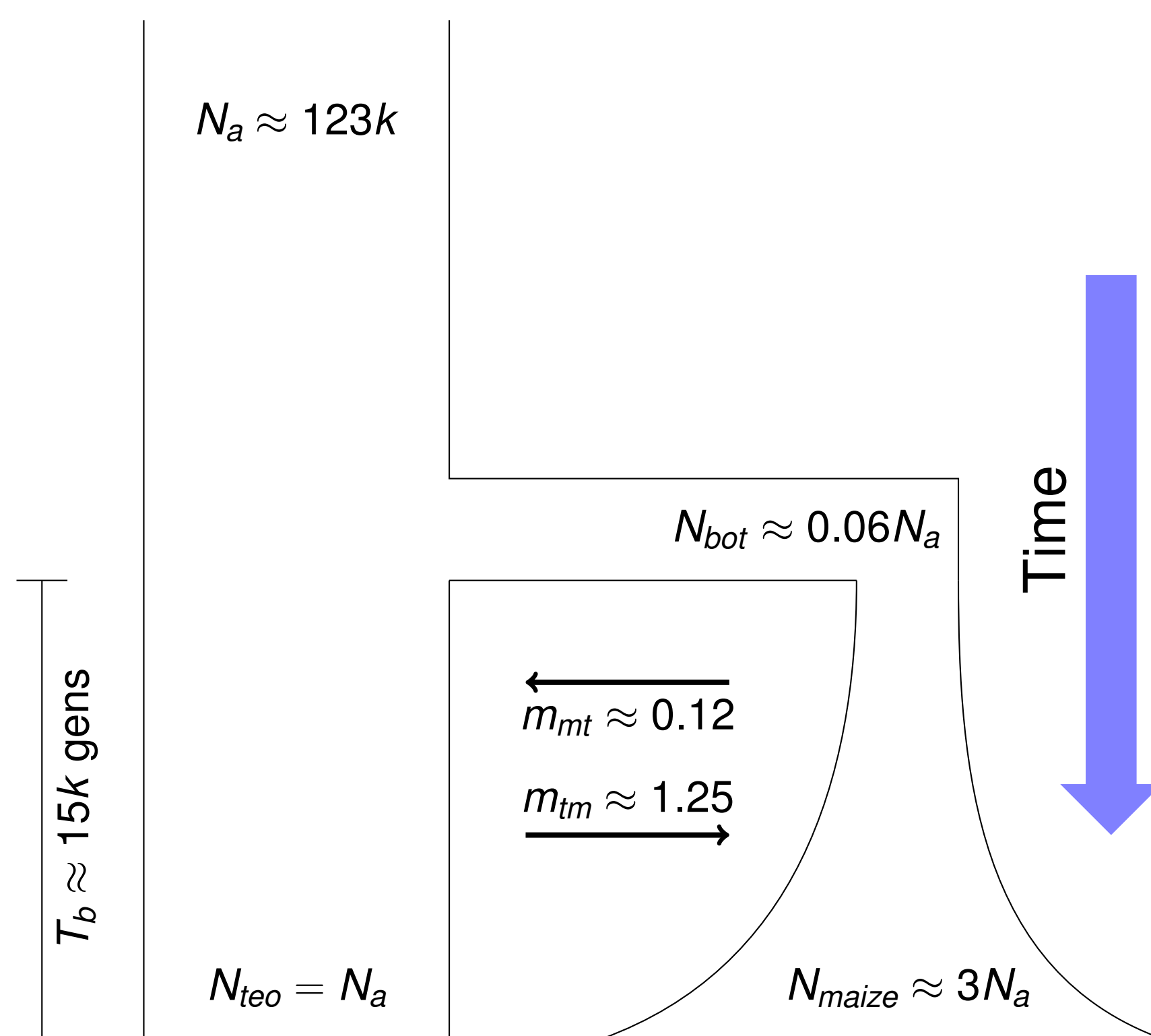
- Synonymous and nonsynonymous substitutions show similar reductions in diversity.

- Diversity around both classes of substitution shows greater reduction in teosinte than maize.

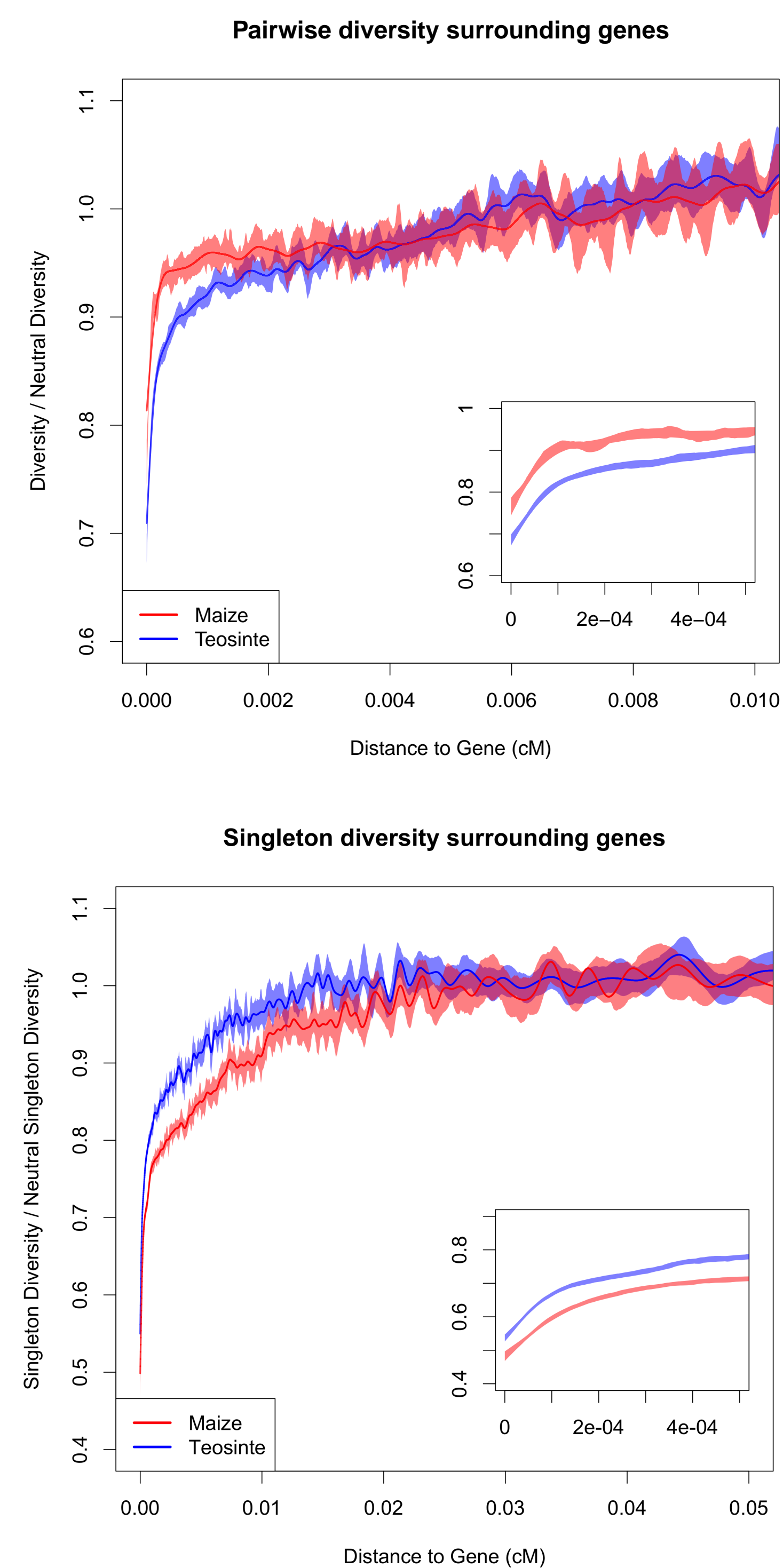


Demography of maize domestication

- Model estimated with $\delta a \delta i$ [2] using nongenic SNPs.
- Bottleneck involved N_e only $\sim 6\%$ of teosinte.
- Current maize N_e much larger than teosinte, and likely an underestimate.

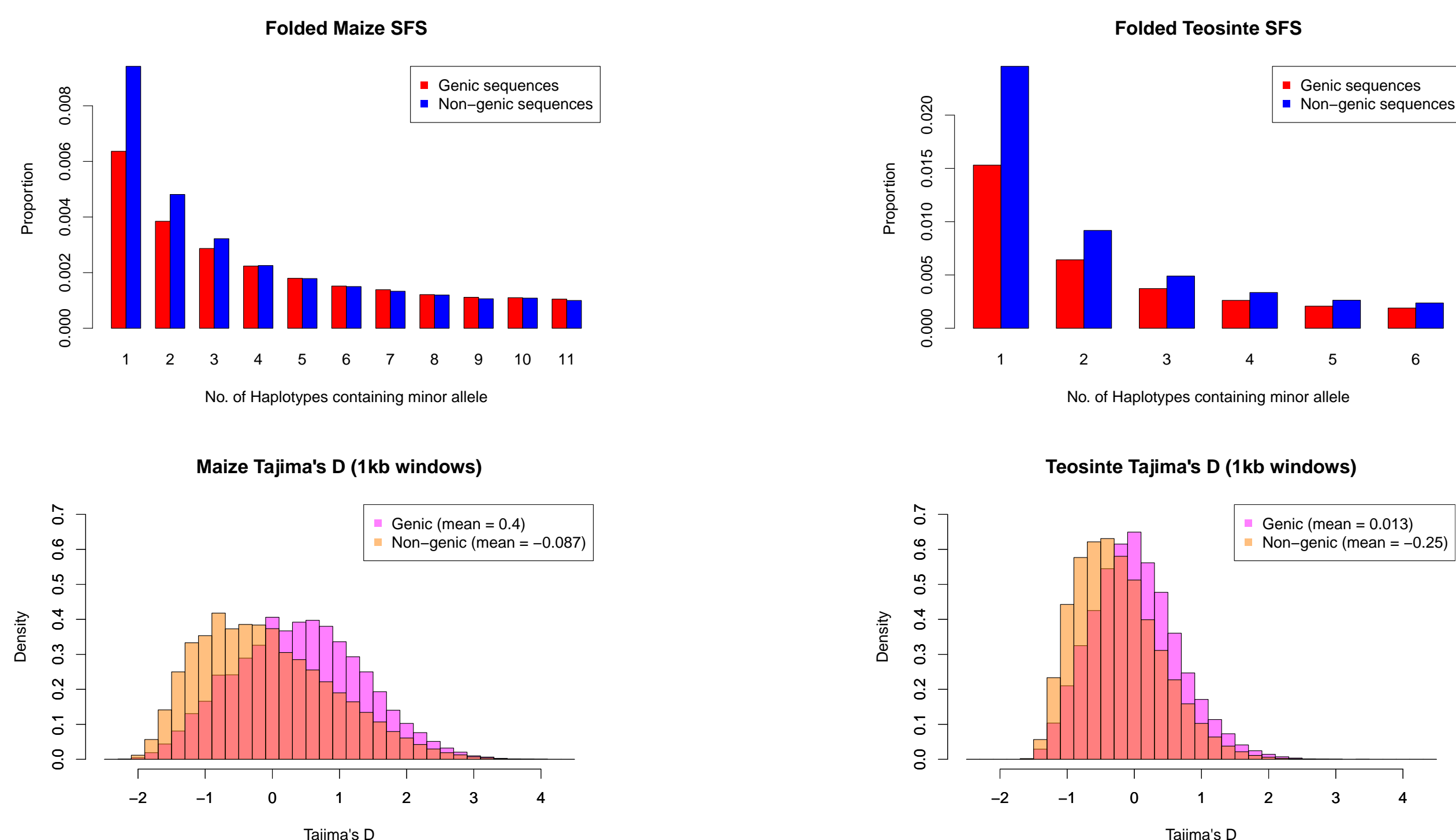


Demography changes strength of purifying selection.



- Purifying selection reduces genetic diversity in and near genes.
- Teosinte displays a greater reduction of pairwise diversity near genes than does maize (top), reflecting long-term differences in N_e .
- Maize displays a greater reduction in singleton diversity near genes than does teosinte (bottom), reflecting larger recent N_e in maize.
- Maize domestication bottleneck reduced efficacy of purifying selection, but large N_e post-expansion leads to stronger purifying selection on recent mutations.

Genes are not evolving neutrally



Genome-wide site frequency spectra show a paucity of low frequency alleles in genes compared to nongenic regions. Because demographic processes should impact the whole genome similarly, this suggest the action of purifying selection removing diversity in genes.

References and acknowledgements

- [1] Chia et al., Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012.
- [2] Gutenkunst et al., Inferring the joint demographic history of multiple populations from multidimensional SNP data. PLoS Genetics, 2009.

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