Supporting Information: Demographic history and patterns of selection in maize during and since domestication

Timothy M. Beissinger, Li Wang, Arun Durvasula, Kate Crosby, Matthew Hufford, Jeffrey Ross-Ibarra

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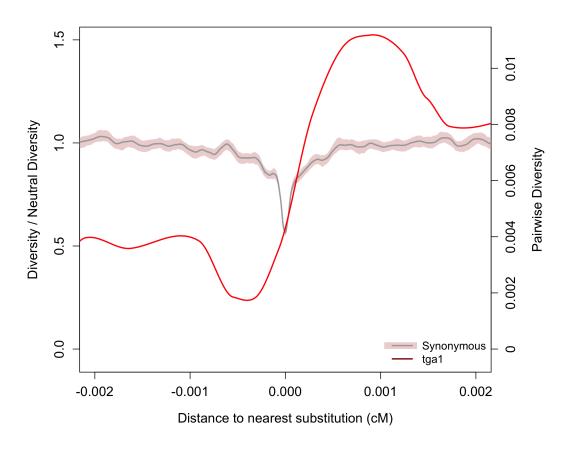


Figure S1: Diversity surrounding the causitive polymorphism at the *tga1* locus is plotted. Since this is only one gene, the large amount of noise compared to our average plots is expected. However, notice that diversity precisely at the causitive polymorphism is reduced and a recovery of diversity is observed away from that site.

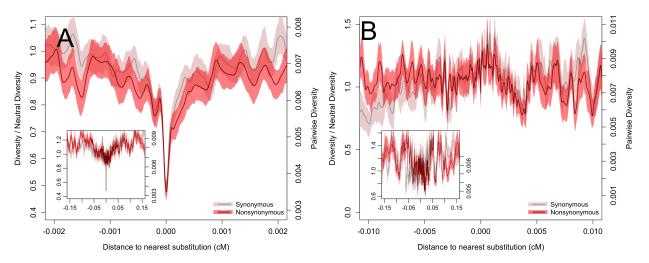


Figure S2: Pairwise diversity surrounding synonymous and nonsynonymous substitutions in maize at highly conserved (A) or unconserved (B) sites. Bootstrap-based 95% confidence intervals are depicted via shading. Inset plots depict a larger range on the x-axis.

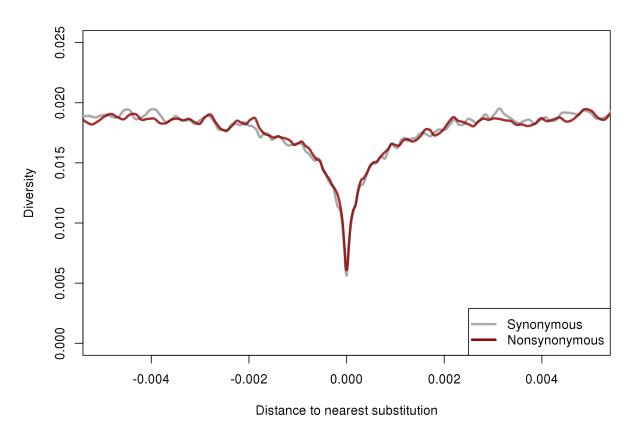


Figure S3: Singleton diversity surrounding synonymous and nonsynonymous substitutions in maize.

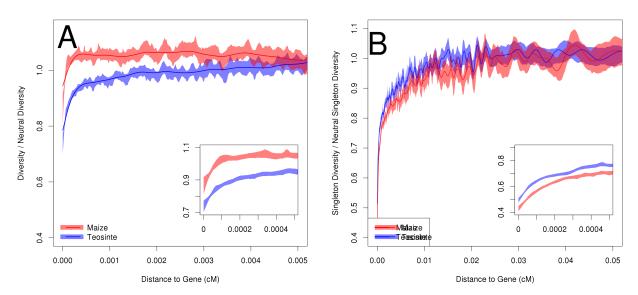


Figure S4: Relative level of diversity versus distance to the nearest gene, in maize and teosinte, based on only sites that do not show evidence of hard or soft sweeps according to H12. Two measures of diversity were investigated. **A** displays pairwise diversity, which is most influenced by intermediate frequency alleles and therefore depicts more ancient evolutionary patterns, and **B** depicts singleton diversity, influenced by rare alleles and thus depicting evolutionary patterns in the recent past. Bootstrap-based 95% confidence intervals are depicted via shading. Inset plots depict a smaller range on the x-axis.

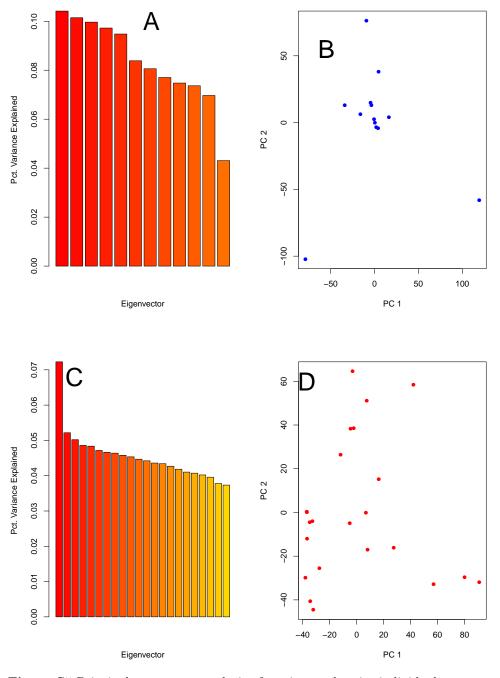


Figure S5:Principal component analysis of teosinte and maize individuals to ensure that no close relatives were inadvertantly included in our study. Plots are based on a random sample of 10,000 SNPs. **A:** Percentage of total variance explained by each principal component for teosinte. **B:** PC1 vs PC2 for all 13 teosinte individuals. **C:** Percentage of total variance explained by each principal component for maize. **D:** PC1 vs PC2 for all 23 maize individuals.

Maize	Teosinte
BKN009	TIL01
BKN010	TIL02
BKN011	TIL03
BKN014	TIL04-TIP454
BKN015	TIL07
BKN016	TIL09
BKN017	TIL10
BKN018	TIL11
BKN019	TIL12
BKN020	TIL14-TIP498
BKN022	TIL15
BKN023	TIL16
BKN025	TIL17
BKN026	
BKN027	
BKN029	
BKN030	
BKN031	
BKN032	
BKN033	
BKN034	
BKN035	
BKN040	

Table S1: A list of maize and teosinte individuals included in this study. Sequencing and details were previously described by Chia et al (2012).