

Positive selection alone is sufficient for whole genome differentiation at the early stage of speciation process in the fall armyworm

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Abstract

Background: The process of speciation inherently involves the transition from genetic to genomic differentiation. In the absence of a geographic barrier, the whole genome differentiation may occur only when the homogenizing effect of recombination is overcome across the whole genome. The fall armyworm is observed as two sympatric strains with different host-plant preferences across the entire habitat. These two strains exhibit a very low level of genetic differentiation across the whole genome, suggesting that whole genome differentiation occurred at an early stage of speciation. In this study, we aim at identifying critical evolutionary forces responsible for the whole genome differentiation in the fall armyworm.

Results: We found that these two strains exhibit a low level of genomic differentiation ($F_{st} = 0.0176$), while 91.3% of 10kb windows have genetically differentiated sequences ($F_{st} > 0$). We observed that a genomic reduction in migration rate due to combined effects of mild positive selection and genetic linkages to selectively targeted loci are responsible for the whole genome differentiation.

Phylogenetic analysis shows that positive selection generates the whole genome differentiation by sub-setting of variants in one strain from the other.

Conclusions: From these results, we concluded that positive selection alone is sufficient for whole genome differentiation during the process of speciation. This study demonstrates that the propensity of adaptation alone determines the speciation events, suggesting that adaptive evolution is a single critical driving force for species diversity.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Figures

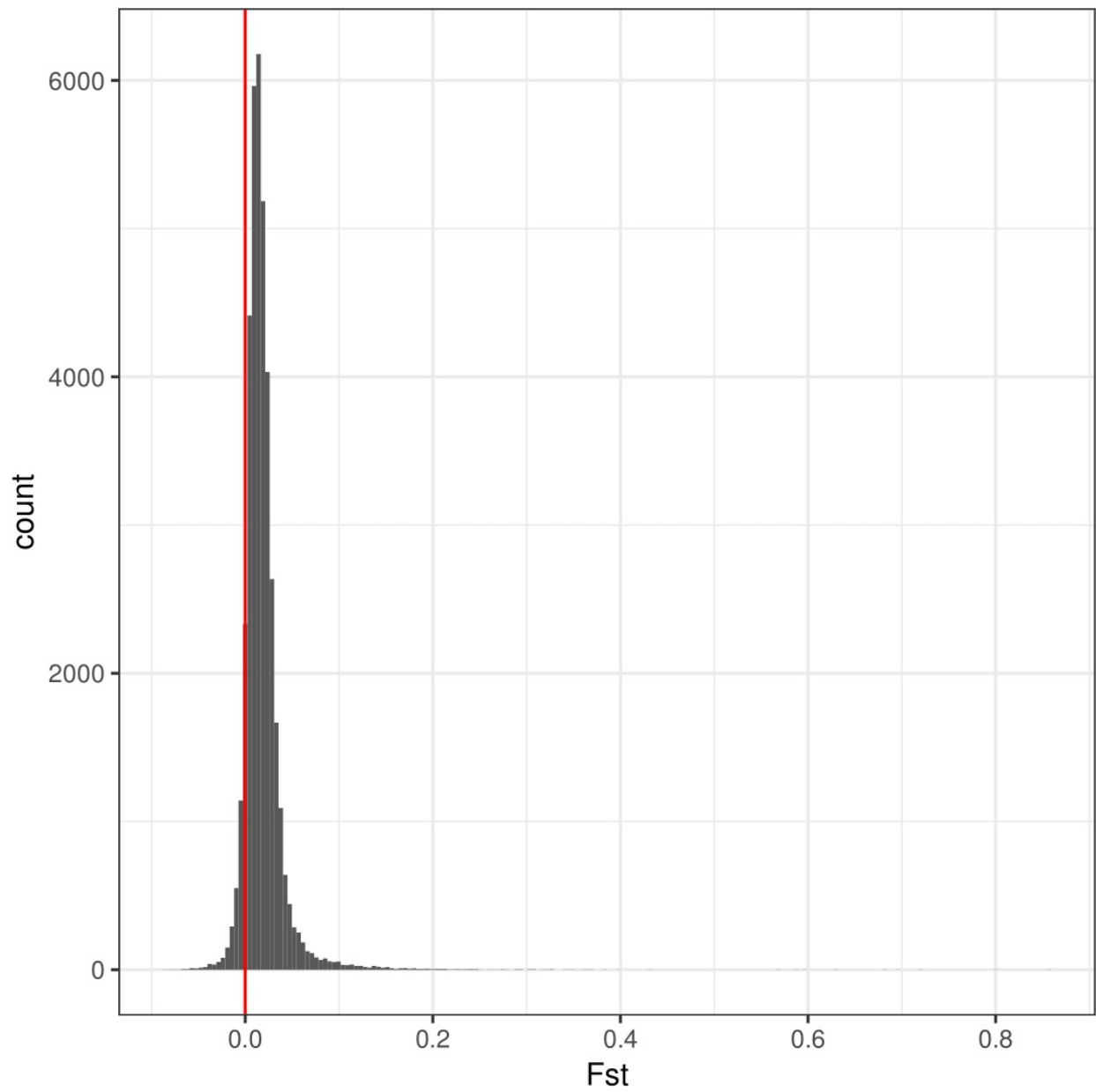


Figure 1

Whole genome differentiation between strains The histogram was made from F_{st} calculated in 10kb windows. The red vertical bar indicates $F_{st} = 0$.

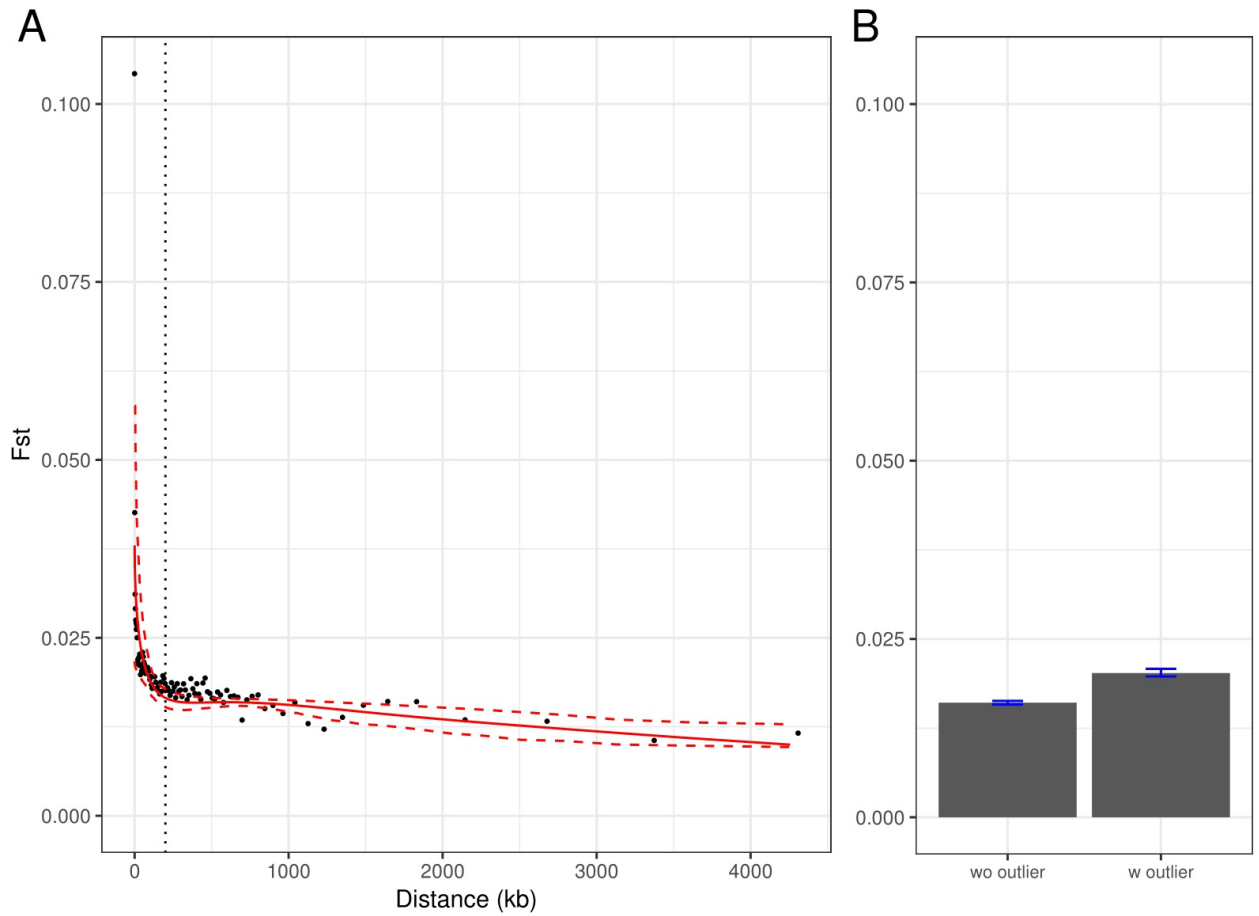


Figure 2

The effect of genetic linkage to selectively targeted loci on Fst A. Fst calculated according to the distance from the nearest outlier of genetic differentiation. The left-most point corresponds to Fst from the outliers. The solid red curve is fitted smooth-spline with $df = 5$, and the red dotted curves are 95% confidence intervals with 1,000 bootstrapping. The vertical dotted line indicates the distance equal to 200kb. B. The barplot shows Fst from the scaffolds with outliers and without outliers.

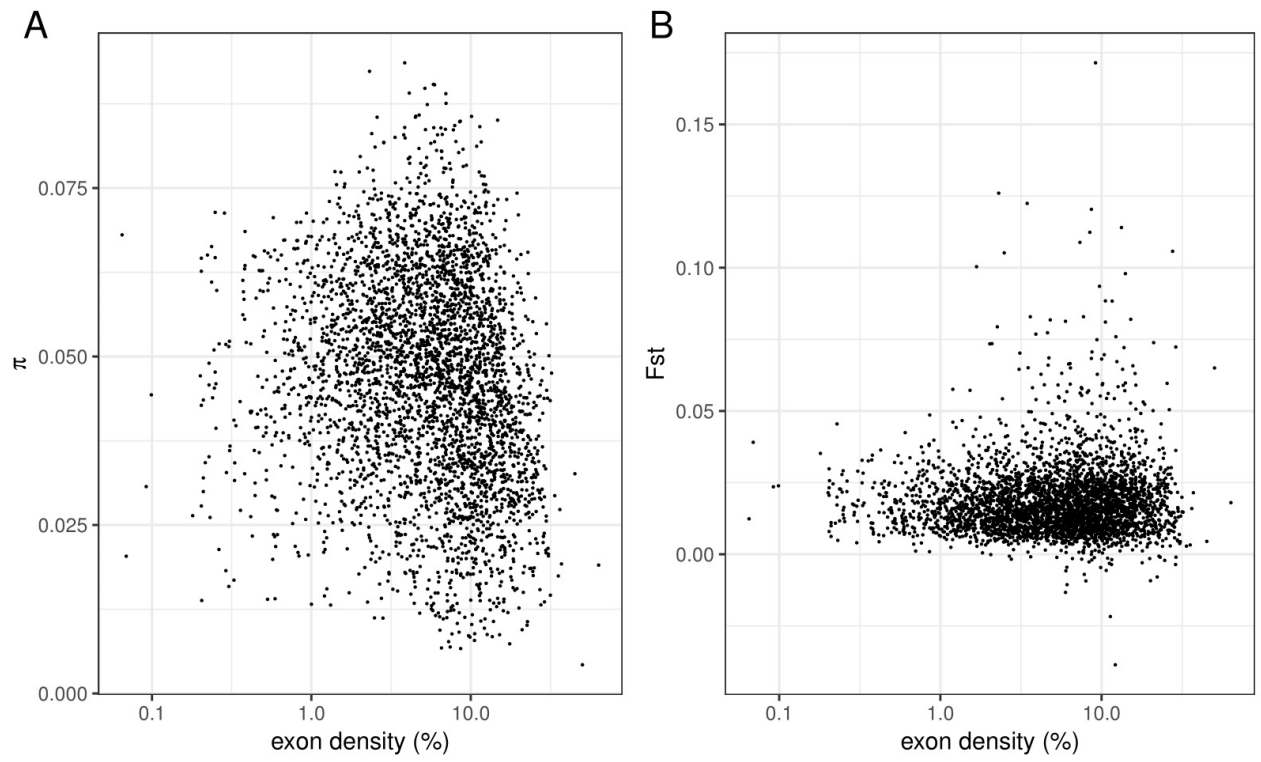


Figure 3

Testing background selection The relationship of exon density with π (A) and F_{st} (B).

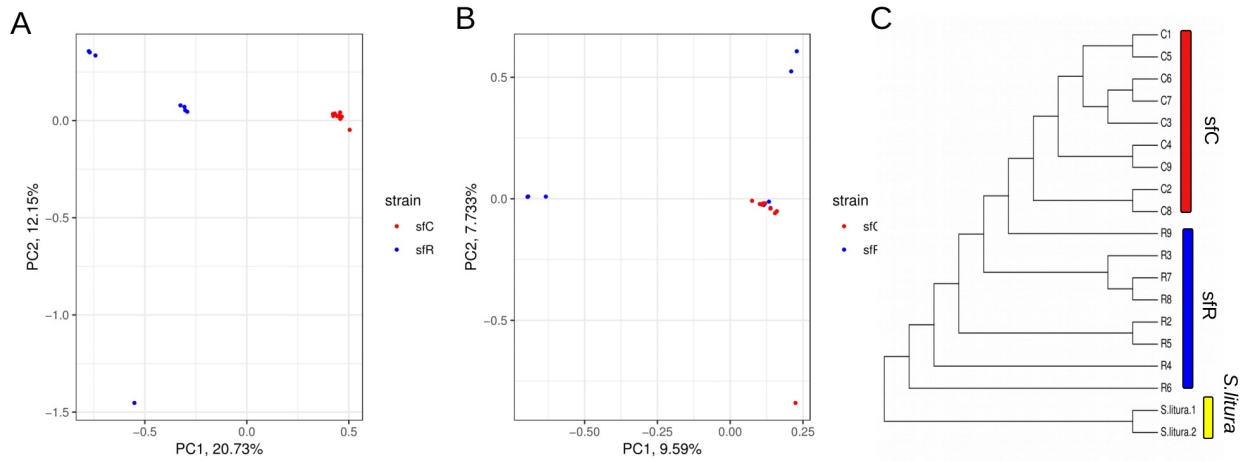


Figure 4

Subsetting of sfC variants from ancestral sfR variants Principal component analysis from the outliers (A) and from the whole genome (B). The red and blue dots represent sfC and sfR, respectively. C. A phylogenetic tree reconstructed from the whole genome.

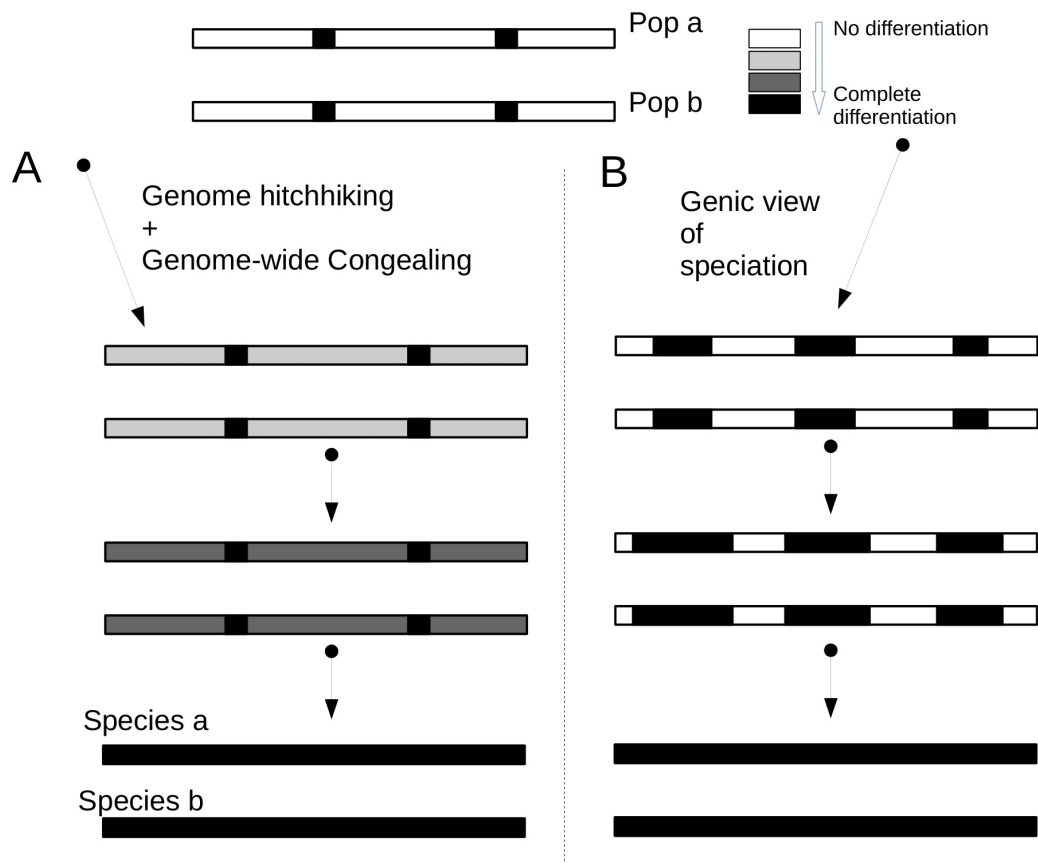


Figure 5

Speciation models concerning whole genome differentiation. The process of speciation initiates from genetic differentiation between population a and population b, and finishes when these two populations are evolved to species a and species b with completely differentiated genomes. A. According to genome hitchhiking[9, 10] and genome-wide congealing model[39, 40], positive selection targeting many loci cause whole genome differentiation with a low extent by the combined effect of mild positive selection. Following positive selection rapidly accelerate the rate of whole genome differentiation by the synergistic effect of linkage disequilibrium across the whole genome until whole genome sequences are completely differentiated. In this model, whole genome differentiation is generated at the early stage of a speciation process. B. According to the genic view of speciation[1], the fully differentiated loci are progressively enlarged or additional fully differentiate loci are generated until whole genome sequences are differentiated. In this

model, whole genome differentiation is generated at the end of a speciation process.

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