

Influence of the mutation load on the genomic composition of hybrids between outcrossing and self-fertilizing species

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June 1, 2023

Abstract

Hybridization is a natural process whereby two diverging evolutionary lineages reproduce and create offspring of mixed ancestry. Differences in mating systems (e.g., self-fertilization and outcrossing) are expected to affect the direction and extent of hybridization and introgression in hybrid zones. Among other factors, selfers and outcrossers are expected to differ in their mutation loads. This has been studied both theoretically and empirically; however, conflicting predictions have been made on the effects mutation loads of parental species with different mating systems can have on the genomic composition of hybrids. Here we develop a multi-locus, selective model to study how the different mutation load built up in selfers and outcrossers as a result of selective interference and homozygosity impact the long-term genetic composition of hybrid populations. Notably, our results emphasize that genes from the parental population with lesser mutation load get rapidly over-represented in hybrid genomes, regardless of the hybrids own mating system. When recombination tends to be more important than mutation, outcrossers' genomes tend to be of higher quality and prevail. When recombination is small, however, selfers' genomes may reach higher quality than outcrossers' genomes and prevail. Taken together these results provide concrete insights into one of the multiple factors influencing hybrid genome composition and introgression patterns in hybrid zones with species containing species with different mating systems.

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