Genomic balancing selection is key to the invasive success of the fall armyworm

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Abstract

A successful biological invasion involves survival in a newly occupied environment. If a population bottleneck occurs during an invasion, the resulting depletion of genetic variants could increase inbreeding depression and decreased adaptive potential, potentially resulting in the extinction. How invasive populations survive and thrive in a newly occupied environment and how, in many cases, they maintain moderate levels of heterozygosity are still contentious issues. The pest Fall armyworm (FAW; Lepidoptera: Spodoptera frugiperda) is native to the Western hemisphere. Its invasion in the Eastern hemisphere was first reported from West Africa in early 2016, and in less than four years, it swept sub-Saharan Africa and Asia, finally reaching Australia. In this study, we used population genomics approaches to investigate the factors explaining the invasive success of the FAW. We observe a drastic loss of mitochondrial polymorphisms in invasive populations, whereas nuclear heterozygosity exhibits a mild reduction. The population from Benin in West Africa has the lowest length of linkage disequilibrium amongst all invasive and native populations despite its reduced population size. This result supports that balancing selection increased heterozygosity by facilitating the admixture of invasive populations from distinct origins and that, once heterozygosity was sufficiently high, the FAW started spreading globally in the Eastern hemisphere. As comparable heterozygosity levels between invasive and native populations are commonly observed, we postulate that heterozygosity restoration through balancing selection could be widespread among successful cases of biological invasions.

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