

Genetic and haplotype divergence between voltine ecotypes of the Asian corn borer (*Ostrinia furnacalis*)

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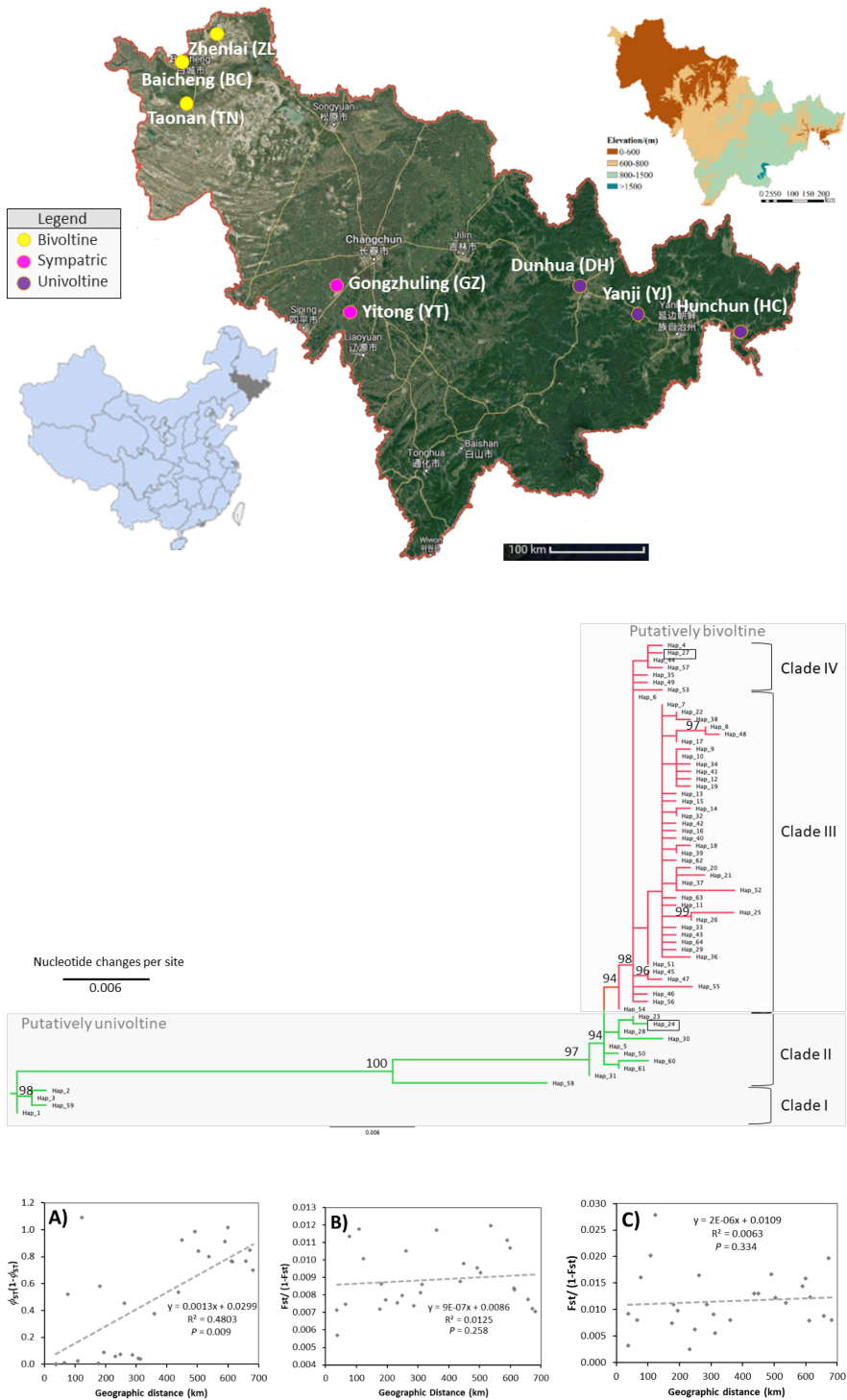
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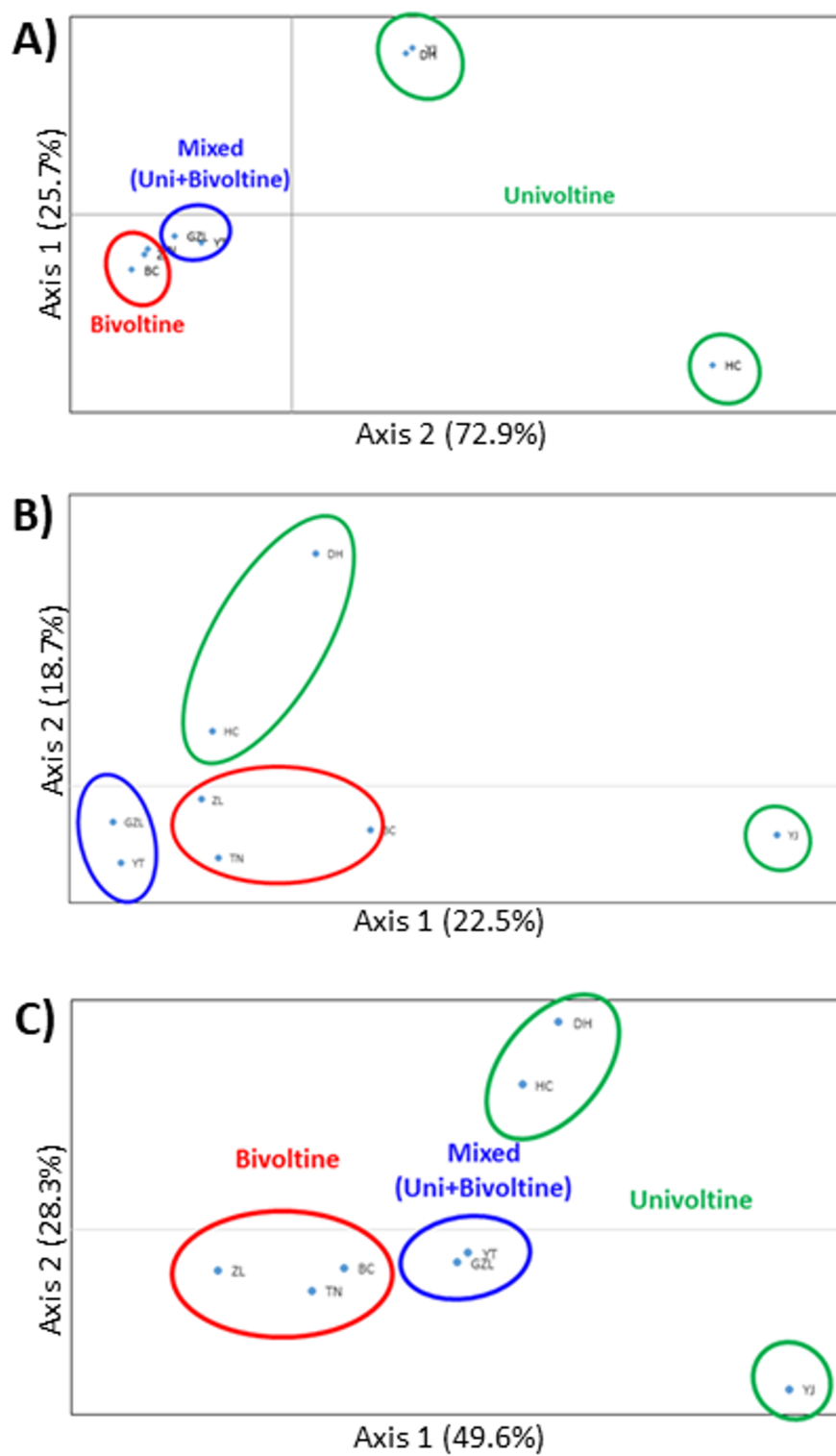
Abstract

Diapause is an adaptive dormancy strategy by which arthropods endure extended periods of adverse climatic conditions. Seasonal variation in larval diapause initiation and duration in the Asian corn borer, *Ostrinia furnacalis*, influences adult mating generation number (voltinism) across local environmental conditions. Degree of mating period overlap between sympatric voltine ecotypes influence hybridization level, but impact on *O. furnacalis* population genetic structure and evolution of divergent adaptive phenotypes remains uncertain. Genetic differentiation was estimated between voltine ecotypes collected from 8 locations in Jilin Province, China [3 single generation (univoltine), 3 two generation (bivoltine), and 2 sympatric locations] in 2014. Mitochondrial cytochrome c oxidase subunit I (COI) haplotypes were partitioned into groups corresponding to historically allopatric univoltine or bivoltine population origins using Bayesian and phylogenetic clustering methods. Haplotypes from sympatric locations were clustered more-closely to bivoltine locations, but influenced by local demographics. Despite this COI haplotype divergence between ecotypes, results were confounded by significant adherence to an isolation-by-distance model. Additionally, analyses of single nucleotide polymorphism (SNP) genotype data implicate voltinism, as opposed to geographic distance, as contributing to low but significant levels of variation among locations. Regardless, only 11 of 257 SNP loci were predicted to be under selection, suggesting population genetic homogenization except at loci proximal to factors putatively responsible for locally adaptive or voltinism-specific traits. These findings provide evidence that divergent voltine ecotypes may be maintained in allopatric and sympatric areas despite relatively high rates of nuclear gene flow, yet influence of voltinism on maintaining observed haplotype divergence remains unresolved.

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