
Ancient versus recent invasion: two genetic signatures in colonization history of a freshwater selfing snail *Galba cubensis*

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Abstract

The distribution of genetic variability within species depends not only on currently acting forces but also on species history. Phylogeographic patterns, colonization events or biological invasions can leave distinct genetic signatures. Recently established populations harbour population reduced genetic diversity due to founder effect while ancient established populations belong to deeper phylogenetic clades and harbour higher genetic diversity. We focus on *Galba cubensis*, an hermaphroditic freshwater snail and intermediate host of *Fasciola hepatica*, the causative agent of fascioliasis in the Neotropics. We evaluate the distribution of genetic diversity over its distribution range using 15 nuclear microsatellite markers and rDNA ITS-2 and mtCOI sequences in order to infer its demographic dynamics and colonization history. We detected a large selfing rate in most populations with a strong populations structure. The presence of high number of multi locus genotypes (MLG) and haplotypes in North American samples argues for a North American origin. An ancient introduction in Cuba probably occurred from South USA since we found high number of MLG but only one ITS-2 haplotype on this island. Another interesting result is the ancient divergence between Northern and Southern American populations showing few gene flows between the both sides of the Amazon River. Finally newly established populations showed diminished genetic diversity. These results are discussed in the light of (1) phylogeographic patterns at the Neotropic scale, (2) human activities resulting in recurrent introductions and bioinvasions and (3) implications for the expansion of fascioliasis.

Keywords: Phylogeography, Neotropic, freshwater snails, *Fasciola hepatica*, fascioliasis, *Galba cubensis*

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