
Parallel and non-parallel patterns of divergence underlie the reproductive barriers in *L. fabalis*

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Résumé

Speciation proceeds by accumulating reproductive barriers, which gradually limit the ability of individuals from different groups to reproduce together. Strong reproductive isolation generally results from the association of different barriers. These associations can be facilitated by specific architecture of reproductive barriers, notably when the underlying barrier loci are found within regions of low recombination, such as chromosomal rearrangements. Chromosomal rearrangements also facilitate the spread of environmentally linked barriers, such as locally adapted loci, during the recolonisation of new favourable habitat. Geographically replicated hybrid zones established along environmental gradients represent an interesting opportunity to study the effect of the spread of chromosomal rearrangements on the evolution of reproductive barriers. Marine snails of the *Littorina fabalis* species are separated in two locally adapted ecotypes (dwarf vs large) that are repeatedly found along wave exposure gradients in Europe. Previous studies found that the two ecotypes show strong genetic differences mainly clustered in 12 putative chromosomal inversions on 9 out of their 17 chromosomes. Here, we studied two transects across ecotype hybrid zones located in two phylogeographic contexts. Surprisingly, we found the distribution of shell size along the wave exposure gradient is reversed between these two hybrid zones: small individuals are in the sheltered part in Sweden but in the exposed part in France. Using whole-genome sequencing, we found that the overall genetic differentiation between ecotypes was similar in both locations. Cline analyses showed that the vast majority of highly differentiated markers between ecotypes fall within inversions and present parallel patterns of allelic frequency gradients, i.e. the same association of alleles with environmental gradients. Interestingly, some of the remaining strongly differentiated SNPs, which showed reversed cline patterns, were also found within inversions. The sharpest of these anti-parallel clines clustered in a genomic region found to be associated with shell size. This calls for analyses of adaptive and demographic processes that could produce these surprising results.

Mots-Clés: Speciation, Populations Genomics, Coupling, Hybrid Zones, Chromosomal Inversions, Ecotypes

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