Genomic causes and consequences of sympatric allochronic differentiation in a defoliating insect

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Résumé

What are the genetic mechanisms implicated in allochronic differentiation and how allochrony may affect the demography and the genetic features of populations is an important question both in evolutionary biology and conservation genetics. In particular, allochronic divergence of populations may reduce effective population size and gene flow and increase inbreeding and genetic load. In the Leiria National Park in Portugal, a population of the pine processionary moth Thaumetopoea pityocampa has undergone allochronic differentiation, resulting in a shifted phenology, a reproductive isolation and a strong genetic differentiation. The objectives of this study are (1) to reconstruct the recent demographic history of the shifted population (SP) compared to unshifted ones, notably to infer the age of the split between these populations and the extent of bottlenecks, (2) to measure the extent of inbreeding and genetic load and its potential purge, and (3) to identify regions potentially involved in the phenological shift and increased genetic differentiation. To achieve these goals, we resequenced individuals and pools of individuals for SP and 7 unshifted portuguese populations. We found a strong genetic differentiation between SP and other populations (Fst ranged from 0.225 to 0.351), and a reduced heterozygosity in SP (on average by 16%). Using msprime and ABCRF, we identified a relatively recent bottleneck in SP and neighboring populations but showed that the split of SP was likely more ancient (_˜3500 generations). Using GONe, we confirmed that the SP population had a relatively small effective size and that most of the Portuguese populations showed a recent decline. Using RZooRoH we found that SP and neighboring populations had relatively high inbreeding compared to other populations, with a 3 times larger fraction of the genomes included in ROH, that were likely

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generated between 50 to 100 generations ago. We estimated piN/piS and Rxy to evaluate the potential accumulation and purging of deleterious alleles. Finally, using genome scans, we identified several regions and genes potentially involved in allochrony, the differentiated regions being located on the Z chromosome and leading to its over-differentiation in SP.

Mots-Clés: Genetic load, Population genomics, Allochronic isolation, Demographic history, Inbreeding, Sex chromosome