Incipient allochronic speciation in the pine processionary moth: molecular analysis of a divergent population

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Sympatric speciation can occur by allochronic differentiation if genetic isolation is primarily due to a shift in the reproductive period. Such a process has been documented in a recently discovered pine processionary moth (PPM; Thaumetopoea pityocampa, Lepidoptera) population.

The PPM is a Mediterranean insect that reproduces in summer and whose larvae develop during winter (see Figure). In the pine forest of Leiria (Portugal), a PPM population with a “shifted” phenology (with larval development during summer) was discovered in 1997. This so-called “summer population” (SP) has been observed only in this region and occurs in sympathy with a population showing a “classic” phenology (hereby referred to as the “winter population” or WP). The sexual reproduction periods of the SP and the WP do not overlap.

What was the demo-genetic history of the two sympatric PPM populations?

17 microsatellites markers showed that:
- The SP and the WP are differentiated populations and remain stable over time
- Phenology is a key factor of the SP differentiation
- Possible gene flow between the SP and the WP
  - Some adults from the SP reproduce at the same time as WP (“Reverse SP”)
  - Plausible recent hybridization events between the SP and the WP

Mitochondrial DNA sequences of the COI gene (1500 bp) revealed:
- A local origin of the SP (shared haplotypes with the WP) for the maternal lineage
- A possible expansion of the SP (leading to singletons)
- That the SP and the WP are differentiated from the other Iberian populations

Conclusions and perspectives

The SP probably diverged from the sympatric WP and is now strongly differentiated from those with a “classical” phenology. Nevertheless, some genetically SP individuals came back to a WP life cycle (Reverse SP individuals). Hybridization seems to occur between the two divergent populations, suggesting the possibility of recent gene flow between the SP and the WP.

From these results, we elaborated scenarios describing the evolutionary history of the SP and the WP. We used a Bayesian inference method (Approximate Bayesian Computation) to explore these hypotheses, but the models tested did not allow reliable inference from the data and should still be improved. New, genome-wide genetic markers (SNPs) are being developed.

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