The role of traits in non-adaptive diversification: some insights from a continental archipelago.

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Abstract

The role of traits in diversification is primarily addressed within a macroevolutionary framework, where certain clade-specific traits are linked with increased diversification rates. Comparative phylogenetic tests can be very powerful for gaining an understanding of traitdependent diversification patterns, but do not provide explicit links with the underlying microevolutionary processes. Comparative population genomic studies under an appropriate study design have the potential to bridge this gap, providing insights into the role of traits in driving divergence at the microevolutionary level. Here we use a comparative phylogeographic/population genomic approach to provide insights into the role of ecological traits in driving non-adaptive diversification of darkling beetles (Coleoptera: Tenebrionidae) across the Aegean archipelago. Previous results of the presenting author identified habitat preference as a key trait determining diversification of flightless darkling beetle lineages across the Accean islands. Here we review the existing evidence, by re-analysing published and unpublished phylogenies of 15 darkling beetle genera. We delimit independently coalescing groups in each clade and estimate divergence times across the major geological barriers, which demonstrate that (a) stable-habitat specialist lineages are consistently deeply subdivided across the major geological barriers, (b) ephemeral-habitat specialists maintain species cohesion with shallow subdivision across the major geological barriers and (c) generalist lineages show intermediate levels of phylogeographic subdivision. We further examine more closely the microevolutionary processes at the early stages of diversification, by focusing on population divergence across an island group that has undergone cycles of fission-fusion during the Quaternary sea-level oscillations. We generate genome-wide SNP data (from ddRADseq) for five darkling beetle species sampled across nine present-day islands, which have been connected during low sea-level periods, and analyse them using coalescent-based demographic inference. The results show (a) deep divergence times and low levels of gene flow among populations of stable habitat specialists, (b) strong population bottlenecks in ephemeral-habitat specialists and (c) higher levels of gene flow among populations of habitat generalists. Our results highlight the importance of trait-mediated population persistence and gene flow in diversification and more generally the utility of combining micro- and macroevolutionary perspectives for a better understanding of the diversification process.

sciencesconf.org:ib2019:254521

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 ${\bf Keywords:} \ {\bf Aegean, \ Coleoptera, \ comparative \ phylogeography, \ demographic \ inference, \ habitat \ preference$