Conserved genetic architecture of morphological and life-history traits across four wild populations of Blue tit

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Abstract

How is the ecology of populations shaping their evolutionary potential? This question has both theoretical and applied interest as it allows to understand the interplay between selection and genetic architecture but also to assess whether genetic estimates of evolutionary potential can be devised. The genetic architecture of multiple traits is summarized in the genetic variance-covariance matrix (G-matrix). The G matrix has thus a central role in the understanding of phenotypic divergence and the quantification of the evolutionary potential of populations. Due to the very demanding nature of G-matrix estimations, the extent of its spatial variability among populations remains largely unknown, although laboratory experiments have shown that G-matrices can vary rapidly under divergent selection, e.g. in contrasted ecological contexts. In this study, we investigate spatial variation in G-matrices for morphological and life-history traits, using long-term datasets from four wild populations of Blue tit (*Cyanistes caeruleus*). These populations display marked phenotypic differences linked to contrasted habitat types, with two main ecotypes adapted to deciduous and evergreen forest habitats. Despite the remarkable phenotypic differences we found no difference in G-matrices among populations. Interestingly, the phenotypic variance-covariance matrices (P) were divergent across populations, suggesting that using P as a substitute for G may be invalid. Altogether, our results suggest that evolutionary potential can be remarkably stable across contrasted environments, in an ongoing study we are assessing the relative importance of selection and genetic architecture in population differentiation.

Keywords: Genetic architecture, spatial variation, evolutionary potential, selection, matrix

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