The expression of phenotypic plasticity of different fitness related traits in multi-dimensional environments

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Abstract

Understanding the way individuals react to new environmental pressures has become crucial to assess the impacts of global change. Phenotypic plasticity is recognized as a central factor in mediating individual fitness, by allowing organisms to rapidly adjust to a wide array of new environments. Yet, understanding the role of environmental drivers in determining phenotypic plasticity remains largely unclear, especially in natural populations. Indeed, the phenotypic expression of traits results from the influence of multiple environmental gradients in interaction with individual genotype. In this study, we aimed at disentangling the effects of two environmental variables (temperature and nutrient level) and the genotype, as well as their interactions, on the expression of phenotypic plasticity. In microcosms, we submitted 15 distinct, clonally reproducing genotypes of ciliate protists (*Tetrahymena thermophila*), to a combination of 5 temperature and 5 nutrient levels, and quantified phenotypic traits linked to the demography (growth rate), the morphology (size and shape) and the movement (speed and linearity) of the individuals. Statistical models including these factors explained more than 70% of the variance in the phenotypic response and allowed us to compute three-dimensional reaction norms representing the overall impact of both environmental factors. The mean plastic responses to temperature and nutrients were consistent with the literature, but their impacts were largely independent, and their interaction was systematically negligible. However, their respective interaction with genotype was significant for several traits, indicating that phenotypic plasticity was indeed variable. We also found that the response of traits linked to movement varied greatly with genotype, while those of traits linked to demography or morphology, which are subject to stronger selection pressures, were more consistent across all genotypes.

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