Universität Basel

Research Project

Understanding the genotype-phenotype-fitness maps at species' range limits

Third-party funded project

Project title Understanding the genotype-phenotype-fitness maps at species' range limits
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Background: The causes of geographic range limits are unresolved. What we know so far is that roughly half of current range limits are due to dispersal limitation while the other half are due to constraints on adaptation to environmental conditions at range edges. Simple evolutionary principles suggest that limits to adaptation must stem from either the shape of environmental gradients imposing selection or the genetics of traits on which selection acts. Hence, natural selection is the link between the two types of limitation. This is the focus of this research proposal; the goal is to study the selection regime at range edges, the shape of change in the selection regime from within the range to beyond the range edge, and the targets of selection: the traits, pathways and genes involved.

Hypotheses: Theory is not specific about the shape of environmental change causing range limits, but all models agree that steep changes in environmental gradients can attract range limits. The main hypothesis to be tested is that steep environmental gradients, known from niche modelling, translate into selection intensity on the genome and on traits at the current range limit. For genetic limits to adaptation, theory predicts that genetic variation for key traits is low throughout the distribution or that multiple traits are strongly correlated in specific ways. Therefore, the hypotheses for genetic limitations are that selection at the edge acts on traits with generally low genetic variation or that multivariate selection is antagonistic to the genetic correlation matrix.

Procedure: I propose a large scale selection experiment and assessment of phenotype, genotype and fitness at four range edges of the North American Arabidopsis lyrata. At all edges, three sites on a transect will be included – one within the range but close to the edge, one at the edge and one beyond the edge. Previous work shows that these edges are characterized by steep climatic gradients. The plant material will stem from one large outcrossing population from the current center of distribution, which will first be propagated in the greenhouse for one generation to produce seeds of 300 unrelated families. I will profile the genotype of each family by whole-genome sequencing of both parental plants, revealing family allele frequencies for each single-nucleotide polymorphism (SNP) site. In the greenhouse (N = 300 seed families . 5 stress treatments . 6 plants) and at each selection site (N = 12 sites . 300 seed families . 8 tubs), we will collect data on growth trajectory, phenology, survival and reproductive output. We will (1) estimate G-matrices of growth and phenology under different niche-relevant stress factors (greenhouse study and outdoors), (2) associate tolerance traits assessed in the greenhouse and performance outdoors with SNPs – producing genotype-phenotype-fitness maps, (3) link selection intensities with environmental conditions outdoors and (4) study antagonistic genetic interactions in traits and in selection.

Importance: Although natural selection is a key process in all areas of evolutionary ecology, few studies have estimated how selection varies along environmental gradients. Changes in selection at range limits have never been investigated in nature. This project will address these major gaps. Important answers can be expected in regard to the relation between environmental gradients and selection, the relative importance of selection versus genetic constraints in adaptive evolution, and why adaptation to environmental change can fail.

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