Universität Basel

Research Project

The genetic basis of evolutionary constraints

Third-party funded project

Project title The genetic basis of evolutionary constraints
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Background: A major question in evolutionary biology and ecology is why species have spatially and ecologically restricted distributions. Why do species not evolve the ability to occur everywhere? In this proposal, I argue that the most plausible answer is that the capacity to tolerate or resist stress can evolve only at the cost of reduced fitness or enhanced susceptibility to other kinds of stress. These trade-offs arise because the fitness and tolerance/resistance traits have a common genetic basis; this prevents selection from breaking the trade-off, and results in limits to distributions. This project will be the first to describe the genomic basis of key genetic correlations that define the trade-offs involved in distribution limits.

Hypothesis: The fact that the southern and northern edges of plant distributions often follow climate isoclines suggests that climate factors are an important determinant of distributions. I hypothesize that tolerance or physiological resistance to abiotic stress constrains species distributions because of genetic trade-offs among tolerance/resistance traits – or between them and fitness – caused by pleiotropic effects of genes or physical linkage. This implies that such genetic correlations are robust across populations and environmental conditions. Our work will focus on Arabidopsis lyrata, a plant for which the full range of genomic tools is available.

Procedure: We currently have seed and maternal DNA from 50+ populations of A. lyrata covering most of the species distribution in North America (14ř latitude, from North Carolina to Canada). A first step is to link single nucleotide polymorphisms with climate conditions across all populations, using RAD-tag sequencing. This will detect the functional genes associated with climate variation, suggest traits undergoing adaptation, and highlight genetic correlations (trade-offs) that potentially constrain the distribution. Next, an association study will reveal the genes and genomic regions linked to traits identified by the first step, and especially those responsible for traits involved in trade-offs. I expect that genetic correlations will be determined by pleiotropy and tight linkage with suppressed recombination.

Importance: This study will integrate phenotypic and physiological approaches to abiotic stress resistance with genomic analysis of resistance traits and their genetic correlations. The results will address fundamental questions in ecology (What determines species distributions?), in evolutionary biology (How do trade-offs limit evolution?), in evo-devo (Are there general constraints on development?), and in physiology (Which resistance traits are independent?). Plant and animal breeders are also keenly interested in trade-offs, how they function, how they can be overcome, and at what cost.

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