

NEWS AND VIEWS

PERSPECTIVE

Rapid adaptation to climate change

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In recent years, amid growing concerns that changing climate is affecting species distributions and ecosystems, predicting responses to rapid environmental change has become a major goal. In this issue, Franks and colleagues take a first step towards this objective (Franks *et al.* 2016). They examine genomewide signatures of selection in populations of *Brassica rapa* after a severe multiyear drought. Together with other authors, Franks had previously shown that flowering time was reduced after this particular drought and that the reduction was genetically encoded. Now, the authors have sequenced previously stored samples to compare allele frequencies before and after the drought and identify the loci with the most extreme shifts in frequencies. The loci they identify largely differ between populations, suggesting that different genetic variants may be responsible for reduction in flowering time in the two populations.

Keywords: adaptation, climate change, ecological genetics, genomics/proteomics, molecular evolution, natural selection and contemporary evolution

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Response to severe drought

Relative to spatially varying selection, temporally varying selection is understudied mainly because it requires the foresight to collect well-documented samples and carefully store them over time. In this case, Franks and colleagues combined temporal sampling with genome sequencing to identify loci with allele frequency changes after a severe drought that lasted from 2000 until 2004. The authors collected seeds from *Brassica rapa* populations growing in two populations: 'Arboretum' and 'Back Bay', both before the drought (1997) and at the end of the drought (2004) (Fig. 1). In a previous publication, Franks and colleagues grew the pre- and postdrought samples together in a common garden and found flowering time was reduced in both postdrought populations relative to predrought

baselines (Franks *et al.* 2007). This was consistent with selection due to a shortened growing season and a drought-escape strategy. It was an important finding and has been highly cited as evidence that selection can act rapidly in natural populations.

Now, Franks and colleagues have followed up this previous finding by sequencing pools of the pre- and post-drought samples to identify loci where allele frequencies shifted following the drought (Franks *et al.* 2016). The main finding was that most of the loci identified differed between the two populations.

Additional mapping will be needed to determine whether the actual functional variants are shared between the populations, but the results suggest that the genetic variants responsible for flowering time shifts in the two populations are largely different.

Trait architecture and temporally varying selection

Populations may respond rapidly to climatic shifts if relevant polymorphisms are already present in the population. For example, in cases where the response trait is highly polygenic, underlain by many variants each with a small effect, standing variation can provide the raw material to mount a rapid response. Moreover, variation in the trait can be maintained by repeated bouts of similar selection pressures over time or space.

Consistent with this, Franks and colleagues find changes in allele frequencies across the genome, which fits with a model in which small effects across many loci are responsible for phenotypes under selection during evolutionary bouts. This is similar to findings in another recent published case of temporally varying selection (this time in *Drosophila*) in which many variants across the genome change seasonally, and these variants overlap with those implicated in spatially varying selection (Bergland *et al.* 2014). In contrast, a recent study of the genetics underlying changes in beak morphology in Darwin's finches implicated only a few regions across the genome (Lamichhaney *et al.* 2015).

As data from additional studies accumulate, it will be interesting to assess how these patterns compare across studies. A contrast between situations in which similar selection pressures are encountered regularly over time versus those that arise only rarely may underlie some of the differences in findings.

Future directions in genomics of environmental response

This work shows how combining resurrection experiments with genomewide sequencing can potentially reveal the

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Fig. 1 The figure shows inter-annual variation in *Brassica rapa* populations at the Back Bay site. The left panel shows plants in a normal year and the right shows the same site during a drought year.

basis of recent, rapid evolution. With growing interest in the effects of global climate change, this type of study will surely become more common in the coming years. While long-term ecological studies are challenging to organize and fund, they are necessary to uncover the temporal dynamics of selection pressures over time in natural environments. One impressive large-scale effort to collect seeds for comparison with future populations is Project Baseline (www.baselineseedbank.org) (Etterson *et al.* 2016), which has stored seeds from over 60 different plant species from over 250 locations to provide material for future resurrection studies as well as baseline allele frequencies at these locations. In general, studies that combine time series allele frequency data with trait mapping and functional validation will be necessary to provide in-depth information about the genetic architecture of the response to novel and extreme environmental stresses. The paper by Franks *et al.* (2016) in this issue of *Molecular Ecology* helps to pave the way towards this direction.

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