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Title: *Unraveling the ecological and genetic basis of adaptive variation in plants: the value of dense regional collections of populations*

Summary: Adaptive variation in phenotypic traits enhances the viability of populations in changing environments and accounts for the establishment of new populations in novel environments. In the long run, natural selection determines the distribution range of any organism whose populations may eventually occur in contrasting environments and displaying broad phenotypic variation. Acquiring an in-depth understanding of the ecological and genetic basis underlying adaptive variation is not a straightforward task, given the multiple combinations of environmental cues and genetic regulatory pathways that plants can use to adjust their phenotypes to the environment. *Arabidopsis thaliana* represents an outstanding model plant to conduct evolutionary studies and disentangle the process of adaptive variation in plants. The reason is the powerful combination of dense regional collections of natural populations from diverse environments across the distribution range, detailed phenotypic characterization of life-history traits in controlled conditions but also in field experiments, the detailed functional knowledge of several key genes, and in the last few years the availability of complete genome sequences. In this communication, we present some major findings from a long-term research conducted on *A. thaliana* from SW Mediterranean Basin (Spain, Portugal and Morocco), characterized by the diversity of environments where *A. thaliana* occurs, to unravel the evolutionary ecology of the species across the region and the genetic basis of adaptive variation in life-cycle traits. We focus on three major aspects of our research that overall highlight the relevance of dense regional collections of natural populations to achieve our goals. First, we stress the fact that adaptive variation shapes the life cycle by acting on traits in a hierarchical manner, although the intensity and sign of natural variation on the same traits need not to be constant over space and time. Second, we show that dense collections of natural populations also allow the detection of low-frequency functional alleles of key flowering time genes from different genetic regulatory pathways and their relationship with environmental variables, illustrating the spatial complexity of the genetic basis of adaptive variation at a regional scale. And third, we demonstrate the importance of phenotyping a large number of naturally occurring accessions in field experiments to better depict genome-wide signatures of adaptive variation in flowering time. Finally, we wrap up the communication by outlining ongoing and future research lines, identifying the potentiality but also the caveats of the approach, and providing hints on the importance of model systems, such as *A. thaliana*, to better understand the response of plants to global climate change in these challenging times.

Bio Sketch: As a plant population biologist, I am interested in understanding the processes that govern the performance, dynamics and adaptive variation of plant populations. To that end, I mostly work with natural populations of the annual plant *Arabidopsis thaliana* across the SW Mediterranean Basin, which is the area of the species' distribution range harboring the greatest genomic diversity. Besides, *A. thaliana* is the only plant model system that also allows the thorough study of the genetic basis of ecologically and evolutionarily important life-cycle traits, opening the door to the mechanistic understanding of trait variation in nature. My multidisciplinary research integrates data from field studies, common garden experiments, and whole-genome sequencing through multiple international research collaborations.

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