**ABSTRACT OF RESEARCH LINE**

The scientific interest of our laboratory is to understand the genetic, molecular and evolutionary mechanisms involved in plant adaptation to different environments through developmental modifications. To address this question we are mainly exploiting the enormous amount of genetic variation that exists in nature within the wild, annual, and model plants *Arabidopsis thaliana* and *Cardamine hirsuta* Most of the adaptive variation affects the so-called quantitative traits owing to the continuous patterns of variation determined by the combined effect of numerous genes and the environment. Given the complexity of the quantitative variation, for long time we focus our research in a model and classical trait, flowering initiation, which is a major developmental transition in the life cycle of plants (El-Assal *et al.*, 2001; Ausín *et al.*, 2004; Abe *et al.*, 2015). Nevertheless, we have also studied other complex traits, such as growth, seed dormancy, stress tolerances and, currently, trichome patterning.

This general objective has been the topic of our research as independent laboratory at the CNB-CSIC since 2005, aiming to find the genes and nucleotide polymorphisms that are responsible for adaptive natural variation. In this respect, in the past few years we have identified several new genes such as *SVP* (Mendez-Vigo *et al.*, 2013), *AtARQ1* (Sanchez-Bermejo *et al.*, 2014), *ICARUS1* (Zhu *et al.*, 2015) and *ICARUS2* (Mendez-Vigo *et al.*, 2019), as well as novel functional mutations of previously known genes like *FRI*, *FLC, DOG1*, *GL1*, *TCL1* and *TRY* (Arteaga et al., 2021, 2022). In addition, to understand the evolutionary mechanisms of plant adaptation we are also investigating the environmental factors that contribute to maintain the genetic variation in nature. Specially, given the relevance of the current global climate change, we have addressed the role of climatic factors, showing that temperature is affecting the plasticity and geographic distribution of multiple adaptive traits (Mendez-Vigo *et al.*, 2011, 2016, 2019; Vidigal *et al.*, 2016; Tabas-Madrid *et al.*, 2018; Castilla et al., 2020; Arteaga et al., 2021).

In the past years we have also focused our research on the study of the natural variation of *A. thaliana* and *C. hirsuta* at a regional scale in the Iberian Peninsula. We have shown that this region is an ideal scenario to study plant adaptation because it contains wide climatic and ecological variation, and it is the Eurasian region with the larges genetic diversity of *A. thaliana* and *C. hirsuta* Cao *et al.*, 2011; Baumgarten et al., 2023). To study this genetic variation we have developed unique collections of ~125-250 *A. thaliana* and *C. hirsuta* Iberian populations (Picó et al., 2008; Vidigal *et al.*, 2016; Castilla et al. 2020), which have become an essential component of the 1001 Genomes project of Arabidopsis and Cardamine (1001 Genomes Consortium, 2016; Durvasula *et al.*, 2017; Baumgarten et al., 2023). In addition, we have developed several RIL and GWAS mapping populations involving Iberian accessions (Mendez-Vigo *et al.*, 2010, 2016; Sanchez-Bermejo *et al.*, 2012; Tabas-Madrid *et al.*,2018; Arteaga et al., 2021), as well as an international TILLING service in the reference strain L*er* (Martin *et al.*, 2009).