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THE SMART-BREED PROJECT: INNOVATIVE MOLECULAR TECHNOLOGIES FOR THE ADAPTATION OF HORTICULTURAL SPECIES TO CLIMATE CHANGE THROUGH PRECISION BREEDING

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Climate change is affecting the ecological balance of the planet, and its impact on agriculture risks to neutralize all the domestication efforts exerted by the breeders to adapt the genetics of plant species to the cultivation environment, threatening the national and regional agricultural production.

The SMART-BREED project aims to develop innovative molecular technologies to study the effects of genetic variability and use this information to accelerate the breeding of new resilient varieties that maintain their productive and typical characteristics in more variable and extreme environmental conditions.

In living organisms, the process of adaptation to the environment involves the accumulation of random mutations in the DNA that can be fixed /selected in the population if they confer an evolutionary advantage. Genetic diversity, in natural or domesticated populations, constitutes a source of allelic variants "tested" naturally in the field of evolution, and are therefore an important resource for genetic improvement. More than 60% of adaptive mutations are associated with genes encoding transcription factors (TF), proteins that bind to specific DNA sequences to increase, decrease or

modulate the level of gene expression in response to the environment and developmental signals. TF therefore constitute the main target genes on which the processes of adaptation of the genotype to the environment in wild populations and in domesticated species naturally act.

As a "proof of concept", the project focuses on three transcription factors, SOC1, STM and ATHB2, with a proven role in two agronomic traits that are important for the production and adaptation to the environment of horticultural species: flowering time and shade avoidance, as examples for the development of molecular and genomic strategies in precision breeding. These traits and TFs are studied in three plant species: *Arabidopsis thaliana* (model species for genetics and Brassicaeae), *Lactuca sativa* (model agricultural species for Asteraceae) and *Solanum lycopersicum* (model agricultural species for Solanaceae).

Around these key TFs, three technological platforms (biodiversity, genome editing and gene co-expression networks) are being developed that will be integrated to design new strategies for the development of advanced molecular markers. The molecular design strategies that are being developed will be valid for all transcription factors, and therefore extended to the genetic improvement of agronomic traits for which transcriptional networks and key transcription factors are known.