



## **ABSTRACT**

### *“Genetic dissection of drought tolerance in wheat”*

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Tolerance to drought is a quantitative trait, with a complex phenotype, often confounded by plant phenology. Breeding for drought tolerance is further complicated since several types of abiotic stress, such as high temperatures, high irradiance and nutrient toxicities or deficiencies can challenge crop plants simultaneously. There are additional problems in investigating the genomics of drought tolerance in wheat: most pathways and candidate genes are unknown and progress in genomics and gene cloning has been slowed due to the size (16,000 Mb) and the complexity of the genome (hexaploid). A research program for increasing drought tolerance of wheat should tackle the problem in a multi-disciplinary approach, considering interaction between multiple stresses and plant phenology, and integrating the physiological dissection of drought tolerance traits and the genetic and genomics tools, such as quantitative trait loci (QTL), microarrays and transgenic crops. The strategy developed at the ACPFG targets a specific environment and selects appropriate germplasms adapted to the chosen environment based on extensive definition of the morpho-physiological and molecular mechanisms of tolerance of the parents. Traditional genetics and recent omics tools are used to create structured populations and develop models for QTL analysis and positional cloning.