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GENOMIC APPROACHES TO DISSECT THE GENETIC BASES OF STRESS TOLERANCE IN CEREALS

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A large number of genomic-based strategies and tools are currently available to dissect the highly complex genetic basis of stress tolerance in plants, with the final aim of improving crops. On one side, high-throughput functional genomics are contributing to identify the main key loci and the network of physiological processes involved in stress perception, signal transduction and response at the cellular, organ and plant levels. On the other side, QTL mapping and the description of allelic and haplotypic diversity are moving at unprecedented speed to depict the genetic bases of stress tolerance in crops germplasm, in order to identify more desirable alleles. In the process to translate this knowledge to breeding, complicating factors are the co-occurrence of multiple stresses and the difficulty to properly phenotype the high number of plants usually required in order to tailor novel cultivars more resilient to abiotic stresses. Among these, drought is the most recalcitrant and difficult to work with, also due to its unpredictability. We will describe a number of examples from our work on drought-related traits in durum wheat, barley and maize where genomics has significantly contributed to acquire useful knowledge which could be translated in breeding applications by means of marker-assisted selection and genetic engineering.