Phenotyping for physiological breeding and gene discovery in wheat.

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Approaches that can be used to increase rates of genetic gains in stress breeding include (i) strategic, trait-based crossing to combine complementary traits in progeny, (ii) high-throughput phenotyping and genotyping to enrich for desirable alleles in early generations, and (iii) exploring genetic resources to broaden the genetic base. Using a combination of the above approaches, CIMMYT has released drought-adapted germ plasm that shows superior expression of a range of complementary physiological traits deriving from both conventional sources and landraces and wild relatives. New genetic technologies are expected to further accelerate the potential for genetic gains, however, one of the current bottlenecks is precision phenotyping. For gene discovery within mapping populations, high-throughput phenotyping techniques such as thermal imaging for canopy temperature and spectral reflectance for ground cover and stem carbohydrates permit large numbers of genotypes to be screened with high efficiency. Confounding factors still need to be resolved in studies where genes of major effect are not controlled. Major genes not only affect the crop's morphology but also may lead to interactions between phenology and, for example, availability of soil water at key growth stages. These factors may cause QTL to be falsely identified and complice the already difficult challenge of dissecting 'genotype x environment' interaction. New generations of mapping populations are being developed that contrast in drought-adaptive traits but not in flowering time or height. However, progeny of bi-parental crosses still encompass the problem that transgressive segregation of parental alleles usually result in some agronomically inferior genotypes and, therefore, alleles long since excluded in plant breeding may mask more subtle effects. Association genetics provides a potential alternative where genetically diverse but elite cultivars can be used for gene discovery.

Evolution of wheat genomes.

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The DNA sequences of wheat A, B, and D *Acc* homoeoloci were analyzed with a view to understanding the evolution of the *Acc-1* and *Acc-2* genes and the origin and evolution of the three genomes in modern hexaploid wheat. The 2.3–2.4 million years ago (MYA) divergence time calculated for the three homoeologous chromosomes, based on coding and intron sequences of the *Acc-1* genes, is at the low end of other estimates. Our clock was calibrated using 60 MYA for the divergence between wheat and maize. On the same time scale, wheat diverged from barley and rice 11.6 MYA and 50 MYA, respectively, based on sequences of *Acc* and other genes. The regions flanking the *Acc* genes are not conserved between the A, B, and D genomes, but they are conserved among them. Substitution rates in intergenic regions consisting primarily of repetitive sequences vary substantially along the loci and are, on average, 3.5-fold higher than the *Acc* intron substitution rates. The composition of the *Acc* homoeoloci suggests haplotype divergence exceeding 0.5 MYA, in some cases. Such variation might result in a significant overestimate of the time since tetraploid wheat formation, which occurred no more than 0.5 MYA.