

“Genomics 2 Breeding”- A New Frontier for Wheat Improvement

IWYP, its partners and associated scientists are continuously searching for breakthroughs and new platforms/frameworks that can accelerate wheat improvement. Whole genome sequencing is one of them, but only in the last few years has the number of complete sequences started to increase, enabling wheat breeding to enter this new frontier of science. Critical to capitalize on this new knowledge are the bioinformatic tools necessary to decipher the enormous amounts of sequence data generated and make them breeder-friendly and easy to use. Of note are the results from the large consortium, “Watkins Worldwide Wheat Genomics to Breeding” (<https://www.wg2b.com/>), formed and led by the Agricultural Genomics Institute at Shenzhen (AGIS) in China and the John Innes Centre (JIC) in the UK that has recently shown the way for sequencing, analyzing, comparing and dissecting large numbers of wheat genomes. By resequencing, analyzing, comparing and dissecting 827 genomes from landraces in use around the world in the 1920’s (“The Watkins Collection”) and from over 200 recent, diverse wheat cultivars the consortium concluded that only 2 of the 7 ancestral major groups of genome sequences have been incorporated into modern wheats (<https://doi.org/10.1101/2023.10.04.560903>), leaving behind many novel loci from the remaining ancestral groups that were proven to be functional and beneficial candidates for improvements in traits, e.g., yield, NUE, pathogen resistance, and climate resilience. This sets new goals and options for wheat breeding, i.e., to inject and evaluate the lost/unused genetic variation that includes over 44,000 haplotype segments in just the Watkins collection alone, some of which could surely bring wanted gains and important traits into modern wheat varieties, as shown by the consortium.

Formation of a new Consortium

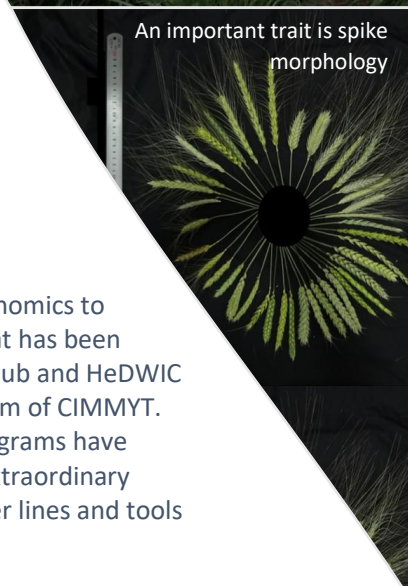
Building on this, AGIS, CIMMYT, JIC and IWYP have created a new consortium, “Global Wheat Genomics to Breeding” (GlobalWheatG2B), to characterize and interpret the genomes in a) the germplasm that has been used extensively to select physiological yield, drought and heat trait improvements in the IWYP Hub and HeDWIC programs at CIMMYT and b) the long-established extensive Global Spring Wheat Breeding Program of CIMMYT. The genomes of about ~1000 carefully selected and extensively phenotyped lines from these programs have already been sequenced in AGIS and the sequence polymorphisms between them defined - an extraordinary achievement - in order to usher in a new era in wheat breeding and to initiate the design of better lines and tools for breeders across the world.

What Will be Gained?

The new program will 1) reveal the haplotypic segments in these IWYP, HeDWIC and CIMMYT spring wheat lines compared with those of other varieties and landraces, including the well-defined Watkins collection, 2) define the insertions of DNA segments from wild relatives that provide part of the novelty of the germplasm used in the IWYP Hub to select improved traits, 3) define what sequences/haplotypes/genes have been selected that correlate with and are responsible for the performance/traits of lines in the many environments in the Global CIMMYT testing programs. A very large number of polymorphic DNA markers will be defined to aid precise selection regimes, thus optimizing genotyping platforms for low or high coverage, as required. Toolkits of markers purposely defined will be built to enable any chromosome segment to be tracked precisely in wheat breeding programs around the world. These and the many other outputs and resources shared worldwide from G2B will generate new understanding of both the successes and limitations of current wheat genetics and open up a new frontier for community-based wheat breeding. The global impact will be large.



Growing lines for DNA collection and pure seed multiplication at CIMMYT



An important trait is spike morphology