EXPLOITING UNTAPPED WILD GENETIC DIVERSITY FOR CIMMYT WHEAT IMPROVEMENT

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Over the past century, the development and successful application of plant breeding methodologies has produced high-yielding wheat varieties. However, many potentially beneficial alleles have been lost due to bottlenecks imposed by the domestication of wheat coupled with intensive selection in modern breeding. Allelic variations of genes present in wild relatives can be recovered only by going back to the ancestors of cultivated wheat. One way to do this is the reconstitution of hexaploid wheat by interspecific crosses. Since the early 1990s, the International Maize and Wheat Improvement Center (CIMMYT) has focused largely on the creation of synthetic hexaploid wheats and backcrossing them to elite bread wheat cultivars producing synthetic derived lines that incorporate new, useful alleles. To date, CIMMYT has produced more than 1,000 synthetic hexaploid wheats using various durum wheat (AB genome) and *Aegilops tauschii* (D genome) resources. At the molecular level these synthetic hexaploid wheats and their derivatives are genetically diverse and distant from traditional bread wheat cultivars. Other wheat relatives can also be used as AB genome donors to generate new synthetics, thus providing access to new sources of diversity, alleles and traits. Diversity within AB genome species was analysed using microsatellite markers (SSRs), which showed that durum wheat accessions cluster together and are closely related to most of the *Triticum turgidum* subsp. *polonicum* and subsp. *turgidum* accessions. *Triticum turgidum* subsp *dicoccum* and subsp. *dicoccoides* accessions are less related to durum wheat and possessed higher genetic diversity and allelic richness. The use of *T. turgidum* subsp. *dicoccum* and subsp. *dicoccoides* accessions to develop new synthetic hexaploid wheats may better exploit the untapped genetic diversity of wild species for wheat improvement.