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Techniques to utilize Crop Wild Relatives in Agriculture

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Crop wild relatives (CWRs) are weedy and wild forms of domesticated and cultivated crops that typically occur in their centres of origin and are maintained in their natural forms. These include the ancestors or progenitors of all cultivated species and are abundant sources of diversity for many important plant breeding traits, including tolerance to abiotic and biotic stresses. In the coming decades, there will be a need to increase agricultural production in response to climate change, which necessitates the development of more resilient and resource-efficient crop varieties. CWRs can play an important role in broadening genetic bases and introducing economic traits into crops, but their direct use by breeders for varietal improvement programmes is typically not advantageous due to the presence of barriers to crossing or chromosome introgression with cultivated species and their high frequency of agronomically undesirable alleles. Therefore, pre-breeding is desirable for all activities that aim to transfer desirable, economically advantageous traits and genes from unadapted germplasms that cannot be used directly in breeding populations but can be used to develop a transitional set of materials that breeders can use to create new cultivars for farmers. Pre-breeding seeks to identify and isolate desirable genetic traits from CWR and incorporate them into breeding material that is readily hybridizable with contemporary elite varieties.

Techniques to utilize CWRs

Interspecific hybridization is considered as an essential evolutionary force for plant adaptation and speciation. Although CWRs have enormous potential for crop cultivar enhancement, they are underutilised due to significant limitations including cross-incompatibility, linkage drag, and inadequate adaptability. Furthermore, even with cross-compatible wild crop relatives within a species, hybridization is difficult due to linkage drag, which requires significant effort, time, and resources to minimise. Moreover, interspecific and intergeneric hybrids resulting from extensive crossbreeding are frequently afflicted with nonviability of offspring, sterility, or both. Plant tissue culture (embryo rescue, somatic hybridization, haploid and double haploid production, etc.) and genetic engineering have the potential to overcome these obstacles, as do other developing or relatively new techniques such as genome editing, genomic selection, targeting and modification of specific gene pathways and development of exotic introgression libraries.

Numerous genome-editing tools, including transcription activator-like effector nucleases (TALENs), zincfinger nucleases (ZFNs), and meganucleases (MNs), have allowed plant scientists to manipulate genes in cereal plants. However, these approaches are expensive and difficult, requiring complicated editing procedures. The CRISPR/Cas9 system has emerged in recent years as a cost-effective and potent instrument for targeted mutagenesis, including single base substitution, multiplex gene editing, gene knockouts, and regulation of gene transcription in plants. Thus, genome modification based on CRISPR/Cas9 has demonstrated tremendous potential for crop improvement. Recently, the concept of "speed breeding" has been developed, in which controlled growth chambers with light supplementation are used to reduce the life cycle of crops for research and commercial purposes.

"Introgressiomics" refers to the large-scale, systematic development of plant materials and populations carrying genome fragments obtained from (mostly wild) crop relatives into the genetic background of crops, which may permit the development of new generations of cultivars with enhanced properties. The goal of 'Introgressiomics' is the enormous production of introgression materials for future (anticipated and unanticipated) requirements; consequently, it may be considered an advanced form of pre-emptive breeding. Modern breeding experimental approaches (e.g., de novo domestication, genome editing and speed breeding) used in CWRs and the use of computational (e.g., machine learning) approaches that could accelerate the use of CWR species in breeding programmes for crop adaptation and yield improvement.

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