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Editorial: Aegilops: Promising Genesources to Improve Agronomical and Quality Traits of Wheat

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Editorial on the Research Topic

Aegilops: Promising Genesources to Improve Agronomical and Quality Traits of Wheat

INTRODUCTION OF AEGILOPS

Aegilops species have contributed significantly to wheat improvement despite the challenges in exploiting wild species, such as crossability and incompatibility (Börner et al., 2015; Fedak, 2015). They have been used in particular as sources of genes conferring resistance to biotic stresses, but also for more complex traits such as abiotic stress and yield.

The genus Aegilops consists of 22 species with the C, D, M, N, S, T and U genomes, which have high allelic diversity relative to wheat. Aegilops tauschii, the D-genome donor of bread wheat, has been most widely used for wheat breeding, followed by A. speltoides and A. ventricosa. However, because most Aegilops species are in the secondary and tertiary gene pools of wheat they are difficult to utilize due to recombination barriers and useful variation from these species is only available in the form of translocation/introgression lines.

IDENTIFICATION OF DIVERSITY IN TRAITS FOR WHEAT IMPROVEMENT

As sources of tolerance to biotic stresses, 20% of the total number (over 75) resistance gene loci identified in cereals are present in Aegilops species (Ponce-Molina et al., 2018). These include two thirds of the 54 loci for resistance to powdery mildew (Tang et al., 2018), and the 12 resistance loci for Cereal Cyst Nematodes (Ali et al., 2019). In the present topic, the addition of A. markgrafii chromosomes to wheat increased the resistance to 19 of 20 powdery mildew isolates in addition line AV(E) (Niu et al.).

New stem rust resistance genes have also been identified in Aegilops, such as Sr46, Sr47, Sr51 and Sr53 (in A. tauschii, A. triuncialis, A. searsii and A. geniculata respectively; Liu et al., 2011a; Liu et al., 2011b; Klindworth et al., 2012; Yu et al., 2015) and three additional genes in A. tauschii (Rouse et al., 2011), three genes in Ae. sharonensis (Singh et al., 2015; Yu et al., 2017) and one gene in A. umbellulata (Edae et al., 2016). In addition, it has been reported that 81% of accesses of A.
Aegilops species are also a resource for novel genes and alleles providing tolerance to abiotic stresses. In this topic Suneja et al. provide a good example of the identification of several A. tauschii accessions as potential donors of adaptive plasticity to stress.

Aegilops species also serve as a resource for introducing useful genetic variation in grain processing and nutritional quality in wheat (Triticum aestivum). Seed storage proteins are the major determinants of end product quality and mainly consist of glutenins and gliadins. A large number of allelic forms of these proteins have been identified in Aegilops species and in some Aegilops species such as A. searsii, A. geniculata and A. longissima this variation has been linked with improved breadmaking quality. Aegilops species has also been explored for diversity in the grain texture-related proteins, called puroindolins (Pins) and grain softness proteins (GSP). In particular, studies carried out in a number of countries have identified almost 100 alleles of Pin a, Pin b and GSP across 200 lines/accessions. This allelic variation could be utilized in breeding programs to extend the textural characteristics of wheat (Kumar et al.).

Aegilops has attracted further attention in relation to increasing the grain mineral content of wheat. In particular, to produce biofortified wheat with higher the contents of iron and zinc in order to alleviate deficiencies in these minerals which currently affect more than 2 billion people worldwide (Cakmak, 2017; Black et al., 2013; Velu et al., 2018b). Some Aegilops species have been reported to contain three to four-fold higher concentrations of Zn and Fe grain content than wheat, having been reported to contain three to four-fold higher concentrations of Zn and Fe grain content than wheat, indicating that they are promising resources to improve wheat composition. Velu et al. developed translocation lines with rye and different Aegilops species in a wheat genetic background to increase the Zn content. Although the potential health benefits of Aegilops species by increased minerals in wheat have not yet been realized, they should have an impact in the future (Kishii).

**ESTABLISHMENT AND EXPLOITATION OF GENOMIC RESOURCES IN AEGILOPS SPP.**

A high-throughput genotyping platform has been specifically designed for screening species related to wheat and used to screen multiple accessions representing all species in the genus Aegilops. This application was useful for identifying diversity and determining the relationships within and between Aegilops species (Przewieslik-Allen et al.). Genome adaptability to environmental changes, especially to rapid climatic fluctuations, underlies the survival and evolution of species. In wild species, genetic and epigenetic changes are accompanied by significant alterations in the complex nuclear repetitive DNA fraction. Perpetual intra-organismal reshuffling of repetitive DNA mirrors the structural plasticity of the A. speltoides genome, which is related to genetic diversity through the distribution of the species in contrasting ecogeographical environments (Pollak et al.). Ruban and Badaeva proposed a model for the evolution of the S-genome of A. speltoides. The genomes of allopolyploid wheats have evolved by different species-specific chromosome translocations, sequence amplification, and elimination and re-patterning of repetitive DNA sequences. These events occurred independently in different wheat species and in A. speltoides. The 5S rDNA locus of chromosome 1S was probably lost in ancient A. speltoides prior to formation of cultivated Triticum timopheevi (AAGG genomes), but after the emergence of ancient emmer (AABB genomes). rDNA profiling and distribution was used to divide diploid Aegilops species into two groups corresponding to the Emarginata and Triticata sub-sections. It was found that the evolution of Emarginata species was associated with an increase of C-banding and heterochromatin, amplification of Spelt-52, re-patterning of the pAesp_SAT86, and a gradual decrease in the amount of the D-genome-specific repeats pAs1, pTα-535, and pTα-s33.

A. tauschii (2n = 2x = 14, genome DD), also known as Tausch’s goatgrass, is the D genome donor of hexaploid bread wheat (T. aestivum, 2n = 2x = 42, AABBD genome). It is a rich source for tolerance to biotic and abiotic stresses. A TILLING (Targeting Induced Local Lesions In Genomes) population of A. tauschii (TILL-D) was developed using ethyl methanesulphonate (EMS) as a mutagen which, together with the newly published A. tauschii reference genome sequence, will facilitate the discovery and validation of genes for agronomically important traits and their transfer into bread wheat (Rawat et al.). Population structure analysis based on high quality SNPs confirmed the differentiation of A. tauschii into two lineages (L1 and L2). A MiniCore collection consisting of 29 L1 and 11 L2 accessions was identified based on genotypic, phenotypic and geographical...
data. This captures 84% of the total allelic diversity in the whole collection, showing that it is possible to reduce the number of accessions which need to be screened by 90% (Singh et al.). A genome wide association study (GWAS) of the grain Fe, Zn, Cu and Mn contents also indicated that A. tauschii lineage 2 had higher Fe and Cu concentration than lineage 1 (Arora et al.). The associations were related to genes encoding transcription factor regulators, mineral transporters and phytosiderophore synthesis.

The stability of translocation or alien introgression lines is always of concern. King et al. developed homozygous wheat/A. muticum disomic introgression lines and characterized their stability using genomic in situ hybridization and SNP analysis (King et al.). Zhang et al. studied the efficiency of transferring A. tauschii segments to wheat using a synthetic octaploid (AABBDDDDDD, 2n = 8x = 56) and used bridge crosses to mapped QTL for agronomically important traits.

Wheat/A. markgrafii disomic addition lines carrying the chromosomes B, C, D, E, F and G, respectively, were screened with SSR markers showing that they corresponded to wheat homoeologous groups 2, 5, 6, 7, 3, and 4, respectively. Useful markers were also identified for chromosome engineering of wheat (Niu et al.).

The papers brought together in this topic therefore illustrate the range of current research on the characterisation of Aegilops species and identification of important traits for exploitation in wheat improvement.

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**Conflict of Interest:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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