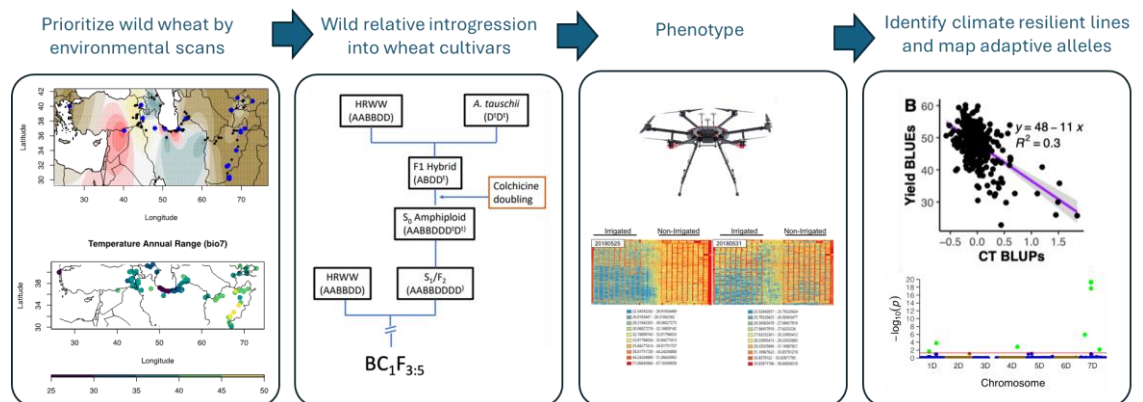


## Ecogeographic Genetics of Wheat's Wild Relatives Help Identify Beneficial Variants for Important Traits

It is widely accepted that one way to overcome the relatively low rates of gain in yield in wheat breeding programs is to introduce new genetic variation into breeding pools. This includes the option of introducing genetic variation from the wild ancestors of wheat, *Aegilops tauschii* and *Triticum turgidum* ssp. *dicoccoides* (wild emmer). Amongst the thousands of accessions of the wild relatives in collections today, which are most likely to carry combinations of alleles to introduce specific traits into cultivated wheat is an important issue, if strategies of more directed introgressions are to be adopted.

Nyine et. al. (<https://doi.org/10.1101/2024.03.20.585976>.) have undertaken the screening of a range of *Aegilops tauschii* accessions where data for the location and climatic adaptations of their origin are known. It was hypothesized that accessions adapted to drought stressed and/or heat stressed environments should carry alleles that aid resilience to these stresses, whereas accessions not adapted to such conditions will be much less likely to carry such alleles. Further, the particular *Aegilops tauschii* accessions contributing to the original formations of hexaploid wheat could not have contained all the alleles available in the wild species needed to provide high resilience to different climatic features and therefore were left behind and excluded from modern hexaploid germplasm pools.

An experiment was conducted that involved selecting a collection of *Aegilops tauschii* accessions taken from a range of climatic zones and sequencing segments of their genomes, determining the SNPs across the accessions and establishing statistical links between climatic (ecogeographic) zones and particular SNPs within the *Aegilops tauschii* collection. A diverse group of carefully selected 21 lines were then re-sequenced together with six recurrent hexaploid wheat lines using whole-genome sequencing approaches and crossed with elite winter wheat varieties to generate *Aegilops tauschii*-wheat amphiploids. The amphiploids were then crossed with six hard red winter wheat cultivars to develop *Aegilops tauschii*-wheat introgression lines. A total of 351 BC<sub>1</sub>F<sub>3</sub> introgression lines were then grown over three seasons and phenotyped in environments differing in amount of water stress. Significant correlations were found between the SNPs introduced from the *Aegilops tauschii* accessions adapted to drought conditions and the performance of the wheat introgression lines under drought conditions. The correlations showed that climatic gradients alone explain 57.8% of genomic variation in *Aegilops tauschii* with many alleles associated with climatic factors in *Aegilops tauschii* being linked with improved performance under water-limiting conditions. The most significant SNPs located on chromosome 4D and associated with temperature annual range in *Aegilops tauschii* accessions were linked with reduced canopy temperature in introgression lines, a phenotype known to be associated with drought tolerance.



These results, along with other studies, suggest that (i) introgression of climate-adaptive alleles from *Aegilops tauschii* has the potential to improve wheat performance under water-limiting conditions, (ii) variants controlling physiological processes responsible for maintaining leaf temperature are likely among the targets of adaptive selection in a wild relative and (iii) adaptive variation uncovered by GWAS in wild relatives has the potential to improve climate resilience of crop varieties.