Review of: "Exotic alleles contribute to heat tolerance in wheat under field conditions"

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Modern wheat breeding process has seriously reduced wheat's genetic variation, particularly in the D genome. As the ancestral donor of the D genome, *Aegilops tauschii* is one of important resources to break the bottleneck. A ideal strategy to increase the genetic diversity of wheat is to develop a series of synthetic hexaploid wheat by crossing *Aegilops tauschii* with durum wheat, or synthetic octaploid wheat by crossing *Aegilops tauschii* with bread wheat.

This paper used 149 spring wheat lines including both elite cultivars and exotic-derived stocks and evaluated yield and related physiological traits. GWAS was used to anchor marker trait association (MTA). Comparative genomic analysis was conducted in a 1.49Mbp region and a novel *Ae. tauschii* MAPK gene was speculated to be one key candidate gene.

This paper did show solid evidence that wheat wild relatives are of great value for useful gene mining.

However, there still several concerns with this study:

1. The pedigree of synthetic hexaploid wheats was lacking and the stability of the derived stocks was not clear as well.
2. GWAS from several environments could help identify stable QTL while no replicates provided.
3. For the candidate gene analysis, it showed that great difference existed in different *Aegilops tauschii* assembles. A clear haplotype analysis was recommended to find the closest sublineae and reference genome.
4. Forward genetic population or transgene analysis were suggested to confirm the candidate gene(s).