

## Review of: "Transcriptome based identification and validation of heat stress transcription factors in wheat progenitor species Aegilops speltoides"

HARCHARAN DHALIWAL

Potential competing interests: The author(s) declared that no potential competing interests exist.

Aegilops speltoides, a closely related species to the B genome donor to durum and bread wheat and the G genome donor to Timopheevi wheat is a cross pollinating species with very high heat tolerance during grain filling period. In a very comprehensive comparative transcriptome study of Ae. speltoides with tetraploid and hexaploid wheat reported in this article, a number of HSFs over expressing in Ae. speltoides under higher temperature at seedling stage as compared to polyploid wheat have been identified and validated which could be introgressed and used for developing wheat cultivars with terminal heat tolerance. The voluminous transcriptome data has been thoroughly presented, interpreted, compared and discussed using the available software beyond my up to date knowledge. It is intriguing that the transcriptome analysis has almost similar number of transcripts in all the three species irrespective of their ploidy level and two to three time higher genome size. Some efforts have been made to explain that similarity but it does not seem to be convincing. Ae. speltoides has terminal heat tolerance and hence such comparative transcriptome analysis should have been done during anthesis and grain filling period in various tissues to identify the transcription factors, regulatory and candidate genes for heat tolerance. Some of the authors from Punjab Agricultural University, Ludhiana have already introgressed variability for heat tolerance from Ae. speltoides into durum and bread wheat as claimed in the introduction. These introgressed lines with heat tolerance should have been used to validate the HSF identified in this study so that these HSFs could be exploited individually or in combinations for developing terminal heat tolerant wheat cultivars. The article is beautifully written in very good scientific English but there are still some grammatical and punctuation mistakes and incomplete sentences which could have been taken care of.