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“Filling gaps and removing traps
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***Triticum araraticum*: A Wild Tetraploid Wheat Species with Potential Implications in Crop Breeding Programs**

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Abstract

Wheat is one of the major crops, globally known since its early domestication in the Fertile Crescent 12000 years ago. Its evolutionary process and species diversification are of interest to many breeders. With the help of molecular markers, it became feasible to reveal the information about crop genomes and detect their genomic diversification. Our research aimed at characterising one of the least explored wheat species. This wild wheat species was first identified in the 1930s and given its botanical name *Triticum araraticum*, Jakubz in 1947 by Jakubziner, with a tetraploid genome (GGAuAu). Wheat Ararat is the wild progenitor of domesticated tetraploid *T. timopheevii* and it is included among the group of hulled wheat with tenacious glumes and disarticulated spikes. Our research was conducted on 79 different genotypes of *T. araraticum*, originated from Turkey, Iraq, Iran, Israeli, Syria, Azerbaijan, and Armenia. The genotypes were sampled from their natural habitat by H. Özkan and yet kept in the genebanks. With the implementation of a retrotransposon-based iPBS marker system, we could identify the genomic diversification among the 79 genotypes arranging them into two main clusters. Moreover, we estimated a number of phenotypic measurements, revealing that *T. araraticum* has an average plant height of 95 cm, spike length of 11.5 cm, peduncle length of 40 cm, spike weight of 1.25 gm, seed weight per spike of 0.4 gm, and a number of 30 seed grains per spike. Additionally, most of the plants required up to 115 days until starting the heading (spikes production). Our research revealed substantial phenotypic diversity in *T. araraticum*. Moreover, the nutrient analysis revealed wild wheat accessions had an average zinc content of 96 mg kg⁻¹, phosphate concentration of 5.5 g kg⁻¹, and phytate content of 15 g kg⁻¹. Hence, we concluded that *T. araraticum* accessions involved in our study showed diversification at the genomic, phenotypic, and nutritional levels ensuring the diversified genomic pool of Ararat that can help in enriching the genomic diversity of wheat cultivars if being implemented in breeding programs.

Keywords: Genomic diversification, iPBS retrotransposons-based markers, wheat evolution, wild relatives