# **Triticum araraticum:** a wild tetraploid wheat species with potential implications in crop breeding programs

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#### BACKGROUND

Wheat evolution and diversification has been the spot of many ongoing researches. Studies indicated that genus *Triticum* was exposed to a series of polyploidization led to the raise of diploid,

#### **METHODOLOGY**

Screening on agarose gel "Gel Electrophoresis". Red arrows refer to the position of polymorphic bands recorded



PCR using eight iPBS primers

DNA isolation from fresh leaves

### **GENOMIC ANALYSIS**



Hierarchical clustering depending on "Ward" using the iPBS binary recorded data of polymorphic bands for 79 accessions for

tetraploid, and hexaploid wheat species, all with a basic chromosome number x = 7. Evolution of tetraploid genomes BBA<sup>u</sup>A<sup>u</sup> and GGA<sup>u</sup>A<sup>u</sup> returns to the occurrence of independent allopolyploidization events resulting from the outcrossing between the two diploid wild grasses of *Aegilops speltoides* (SS), believed to be the female parent and the wild wheat *Triticum urartu* as the male parent. Among the tetraploid wheat, *T. araraticum* whose discovery occurred during the 1930s, and yet given its scientific name by Jakubziner in 1947.



Plants of *Triticum araraticum* after five months of transferring the seedlings to field trials, under rainfed conditions in Adana, Turkey within the research station of Cukurova University. The left picture shows spikes of different wheat species where *Araraticum* is identified with the blue arrow.

*T. araraticum* morphologically resembles wild emmer wheat *T. dicoccoides*, though their genetic constitution is varied. Wild *Araraticum* was shown to possess fragile rachis and tenacious glumes enclosing the grains. It is subdivided into two subspecies encompassing *T. araraticum ssp. kurdistanicum* Dorof. et Migiusch and *ssp. araraticum Jakubz.*, depending on the morphological variation. This research was conducted to identify the diversity among various *T. araraticum* accessions in order to uncover some of its mysteries for understanding its potential implementation in wheat breeding programs.



Seeds grinding for measuring the nutrient content of zinc, phosphorous, and phytate

Nutrient Genomic Content analysis

> Phenotypic analysis

Encompassed field parameters of heading days, plant height, peduncle length, and spike length, along with harvest data of spike weight, seed number per spike, seed weight per spike, and grain parameters using SmartGrain software.

Identifying the genomic diversity was done using Retrotransposon-based Marker Analysis of single primers (iPBS Amplification) (Table). Polymorphic bands were recorded as binary data where (0) refers to the absence of polymorphic band and (1) refers to its existence. Analysis were done using software R.

iPBS Primer Name	Sequence	Nr. Polymorphic bands recorded	Tm (°C)	CG Content (%)	Optimal Annealing Ta (°C)
2239	ACCTAGGCTCGGATGCCA	3	60.4	61.1	55.0
2252	TCATGGCTCATGATACCA	1	52.7	44.4	51.6
2373	GAACTTGCTCCGATGCCA	10	57.9	55.6	51.0

 Image: Second Second

determining the genomic diversification among Ararat accessions. Applied distance method was that of "Euclidean". Three identified clades, blue clade encompassed accessions of *T. dicoccoides*, while both red and black clades were that of *T. araraticum* accessions. Depending on the data acquired from eight primers, giving 60 dominant markers (loci), the clustering analysis was conducted to reveal the existence of two main clades of the Ararat accessions.



N8.2400 N12.235 N12.2391 N12.235 N12.2391 N12.2393 N12.2393 N12.2393 N12.2394 N12.2373 N12.2374 N12.23

Heatmap developed by implementing distance method Euclidean showing data

•	CCCAGCAAACCA	9	47.1	00.0	55.5
5	TCGCATCAACCA	10	45.1	50.0	52.5
	ATCTGTCAGCCA	13	43.6	50.0	52.6
3	GAACCCTTGCCGATACCA	6	57.1	55.6	51.0
)	CCCCTCCTTCTAGCGCCA	8	61.6	66.7	51.0

structure where Tara2599/3 was separately grouped from other accessions clustered in two main groups. M = Marker resulted from the amplification using primers (polymorphic band). Vertical axis encompasses the accessions names. Colored scale reflects the values of correlation distance.

#### PHENOTYPIC ANALYSIS



The observations within recent study were recorded for nine phenotypic traits, encompassing field observations and harvest data. Histograms visualize the allocation of recorded data among the accessions where the average plant height recorded 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 seeds per spike of 30 grains.



Correlation matrix (correlogram) clarifying the relationships within recorded data for both field and harvest parameters. Color intensity and the size of the oval shape are proportional to the correlation coefficients between each pair of variables. PH states for plant height, PL for peduncle length, SL for spike length, HD for heading days, SVV for spike weight, SVVS for seed weight per single spike, and SNS for seed number per single spike.

#### **NUTRIENT CONTENT**



Histograms visualize the data allocation of nutrient content measured for the 79 wheat accessions. Analysis were done by a rate of two analytical replicates per accession. the average content of zinc recorded was 96 mg/kg, phosphorus of 5.5 g/kg, and phytate of 17.8 g/kg.



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hytate content d/k

Boxplots visualizing nutrient content in Ararat accessions. The central line is the middle of the data (median value). The ends of the whiskers represent both minimum and maximum measurements for nutrient content.





Scatterplots matrix visualising pairwise correlations. The value of linear regression model coefficient (R<sup>2</sup>) is attached per each correlation to determine the linear model being fit with recorded data, along with P-values to reflect the correlation significance.

#### CONCLUSION

- The survival of *T. araraticum* in wildness up to our date and for thousands of years makes it a source of attraction to be involved in breeding programs concerning the implementation of wild relatives in enhancing the genomic pools of domesticated crop cultivars.
  The wild *Araraticum* accessions involved in this study showed diversity at the genomic, phenotypic, and nutritional levels.
- Resembling to the unpublished work of Kilian et al, Araraticum accessions were arranged into two clusters depending on the genomic analysis. However, the findings of this research shall be further confirmed by conducting genomic analysis using SSR and SNPs marker systems.
- Wheat accessions showed to possess high content of Zn, P, and Phytate which we believe they need further investigation to confirm such results.

#### **References:**

**S**ubtropics

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