

Physiological Responses of Wild and Cultivated Diploid Wheat Genotypes towards Salinity Stress

Mohd. Kamran Khan^{*1†}, Anamika Pandey¹, Mehmet Hamurcu¹, Zuhail Zeynep Avsaroglu¹, Ali Topal², Sait Gezgin¹

¹Department of Soil Science and Plant Nutrition, Faculty of Agriculture, Selcuk University, Konya 42150, Turkiye;

²Department of Field Crops, Faculty of Agriculture, Selcuk University, Konya 42150, Turkiye

*Corresponding author- mohdkamran.biotech@gmail.com, mkkhan@selcuk.edu.tr

INTRODUCTION AND AIM OF THE STUDY

- Wheat production is largely reduced by salinity stress around the world.
- High soil salinity that is likely to worsen with increasing climate change decreases the root-shoot growth, tissues, and eventually, leads to destruction of the wheat crops.
- Plants show substantial variation in salinity tolerance depending on the species and growth stages.
- As Triticum species is mostly sensitive to soil salinity, it is important to develop and grow salt tolerant wheat genotypes. However, modern hexaploid wheat holds less genetic variation lacking the potential alleles required for their adaptability towards high salinity.
- Bread wheat comprises A, B, and D sub genomes where *T. boeoticum*, *Triticum monococcum*, and *T. urartu* are considered as ancestral species of 'A' sub-genome. As 'A' genome of diploid wheat species share homology to 'A' sub-genome of hexaploid wheat, it can facilitate transfer of desirable traits in wheat breeding programs.
- Thus, the aim of this study was to assess genetic diversity of wheat germplasm with 'A' genome towards salinity stress (Figure 1).**



Figure 1. Growth of *T. monococcum* genotype, G16 under control and salinity stressed growth conditions.

RESULTS

- The studied genotypes showed significant diversity in salt tolerance within and among the species under 150 mM NaCl supply.
- While percentage change in shoot length of genotypes fluctuated between -45 to 5% under salinity stress as compared to control, root length spanned from -65 to 5%. Similarly, shoot fresh weight varied from -85 to 47 and root fresh weight from -86 to 88%. The percentage change in shoot and root dry weight shifted from -61 to 95% and -56 to 99% respectively (Table 1).
- Interestingly, most of the domesticated *T. monococcum* genotypes in the experiment showed higher tolerance to salinity stress as compared to genotypes of *T. aegilopoides*, *T. boeoticum*, and *T. urartu*.
- Salinity stress had similar diminishing effect on the root and shoot tissues of the studied species.

Table 1. Percentage Changes in Shoot length (SL), Root Length (RL), Shoot Fresh Weight (SFW), Root Fresh Weight (RFW), Shoot Dry Weight (SDW) and Root Dry Weight (RDW) of 31 diploid wheat genotypes under salinity stress as compared to control.

Genotype Code	Species	%SL	%RL	%SFW	%RFW	%SDW	%RDW
G.1	<i>T. aegilopoides</i>	-43	-49	-44	-41	-21	-21
G.2	<i>T. aegilopoides</i>	-30	-36	-24	-31	7	2
G.3	<i>T. aegilopoides</i>	-30	-45	-36	-45	-23	-6
G.4	<i>T. aegilopoides</i>	-31	-26	-54	-42	-18	-7
G.5	<i>T. aegilopoides</i>	-31	-34	-48	-61	-27	-43
G.6	<i>T. aegilopoides</i>	-29	-17	-31	-49	-6	-28
G.7	<i>T. aegilopoides</i>	-33	-23	-16	40	11	-10
G.8	<i>T. aegilopoides</i>	-30	-46	-28	-42	0	-35
G.9	<i>T. aegilopoides</i>	-35	-26	-48	-50	-35	-37
G.10	<i>T. aegilopoides</i>	-18	-65	-16	-5	14	-23
G.11	<i>T. aegilopoides</i>	5	-11	47	-27	95	99
G.12	<i>T. aegilopoides</i>	-35	-58	-46	-57	-5	-34
G.13	<i>T. monococcum</i>	-37	-27	-31	-35	14	-10
G.14	<i>T. monococcum</i>	-26	-45	-14	7	14	15
G.15	<i>T. monococcum</i>	-43	-62	-64	-86	-28	-49
G.16	<i>T. monococcum</i>	-7	-46	38	-20	55	30
G.17	<i>T. monococcum</i>	-10	-49	-9	-18	19	24
G.18	<i>T. monococcum</i>	-37	-59	-41	-59	-12	46
G.19	<i>T. monococcum</i>	-30	-19	-22	-11	-6	-4
G.20	<i>T. urartu</i>	-37	-48	-46	-46	-35	-11
G.21	<i>T. urartu</i>	-41	-61	-85	-77	-61	-56
G.22	<i>T. urartu</i>	-29	-29	-17	43	6	-17
G.23	<i>T. urartu</i>	-36	-44	-46	-32	-32	-34
G.24	<i>T. urartu</i>	-45	-46	-39	-10	-28	-27
G.25	<i>T. urartu</i>	2	5	24	88	-14	-34
G.26	<i>T. urartu</i>	-23	-48	-26	86	-32	-34
G.27	<i>T. urartu</i>	-28	-41	-2	49	-2	-38
G.28	<i>T. urartu</i>	-2	-40	-27	-59	6	87
G.29	<i>T. urartu</i>	-35	-35	-36	36	-28	-16
G.30	<i>T. boeoticum</i>	-36	-38	-38	-85	-27	-20
G.31	<i>T. boeoticum</i>	-6	-38	-26	-47	-4	5

METHOD

- Thirty one diploid 'A' genome wheat genotypes belonging to four species were screened under Control and Salinity stress (150 mM NaCl) growth conditions in hydroponic system.
- Growth parameters including root-shoot length, fresh weights, and dry weights were measured to assess the diversity in tolerance level of these genotypes against salt stress.

CONCLUSION

- There is a possibility of identifying a greater number of salt tolerant genetic resources on screening a larger number of genotypes from *T. monococcum* species.
- The tolerant genotypes identified in this study may serve as a good candidate to introgress the salinity tolerance trait in different wheat cultivars in breeding programs.