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COMPONENTS OF PHENOTYPIC VARIANCE AND HERITABILITY OF EARLY VIGOUR TRAITS OF BREAD WHEAT UNDER CONTRASTING WATER REGIMES

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Abstract: Exploring drought-tolerance potential and phenotypic plasticity at early stages of development in root system architecture could be crucial in regard to breeding for drought resistance and for selecting wheat ideotypes under climate change conditions. A total of 11 genotypes from the collection of 101 bread wheat genotypes, with desirable traits related to increased drought tolerance, were selected as parents and eight crosses were performed. The genotypes of the P and F1 generations were grown in hydroponic cultivation under polyethylene glycol 6000-induced osmotic stress. The objective of this research was to assess components of phenotypic variance and broad-sense heritability of early vigour traits (nine root and shoot traits) of bread wheat genotypes under induced drought stress compared to the control, in order to choose appropriate traits for breeding for drought resistance. The effect of the genotype on the variability of the tested root traits was higher (46.6%), compared to the tested shoot traits (25.5%), meaning that the root traits can be taken as a more reliable criterion for selection for drought tolerance compared to the investigated shoot traits. Broad-sense heritability was high (> 82%) for most of the tested traits (primary root length, number of seminal roots, total seminal root length, angle of seminal roots, shoot length, the ratio of root dry mass to shoot dry mass), with low genotype × environment interaction (< 20% of total variation) and breeding for drought tolerance should be focused on these traits.

Key words: *Triticum aestivum* L., drought stress, root system architecture, shoot traits, seedlings, broad-sense heritability, components of phenotypic variance.

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Introduction

Drought can lead to a 50–90% reduction in wheat yield, and genotypes displaying strong early seedling establishment (vigour) in challenging conditions can be identified and selected by screening diverse plant materials on a large scale (Bhandari et al., 2024; Ahmed et al., 2025). Early vigour is a genetically complex trait (Moore and Rebetzke, 2015). Despite the moderate heritability, all the contributing traits are influenced by strong environmental covariates through the maternal effect as well as a potentially significant genotype × environment (GE) interaction (Rebetzke et al., 2022). Experimental approaches aimed at understanding the GE interaction as well as the management of environmental processes is expensive and time-consuming due to the time required for studying climatic factors over a long period of time. There is an opportunity to investigate the effect of early vigour through crop process modelling that integrates crop physiology, climate and soil conditions and their impacts on crop growth and yield. Such approaches enable a rapid assessment of the importance of early vigour under different climatic, edaphic and agro-technical conditions (Zhao et al., 2019).

Manschadi et al. (2006) estimated that each additional millimetre of water extracted during grain filling generated an additional 55 kg ha^{-1} of wheat grain yield. Root system architecture (RSA) broadly describes the development and growth of root systems targeted to explore and exploit available water and nutrients while anchoring shoots prior to, and during, canopy development (Rebetzke et al., 2022). Wheat develops seminal roots first. These roots remain active throughout the life of the plant and play an important role in early vigour and water uptake from deep soil strata (Rossi et al., 2024). Manschadi et al. (2008) found that RSA is closely linked to the angle of seminal root growth at the seedling stage and that selection for the growth angle and the number of seminal roots may identify drought-tolerant genotypes. Typically, wheats adapted to regions with limited rainfall had a high number of seminal roots descending with a narrow gravitropic angle and deeper root systems, whereas wheats adapted to environments with higher rainfall and/or irrigation tend to have wide seminal root angles, presumably facilitating water and nutrient acquisition from a wider sub-surface area (Hohn and Bektas, 2020).

Progress has been made in screening for drought resistance and evaluating root traits. Selection of wheat genotypes with larger roots and extended seminal and adventitious roots shows promise for improved grain yields, especially in arid and semi-arid regions, indicating substantial genetic heterogeneity in osmotic stress tolerance (Afzal et al., 2017). Several high-throughput phenotyping methods have been used to evaluate roots, including hydroponic systems using growth pouches (or germination paper), aeroponic and agar-plate systems, soil-filled rhizotron, gel-filled chambers with transparent walls, compressed soil columns with X-rays to detect roots, paper-based “cigar roll” system and deep column techniques (Colombo et al., 2022). Current studies on wheat root phenotyping are limited to the very early seedling stage, with only a few phenotyping platforms used for measuring whole root systems in wheat, such as the germination paper technique and clear pots (Chen et al., 2020). The RSA ideotypes used to optimise agronomic performances are different from one environment to another, and the relationships between root traits measured in controlled environments and agronomic performances are inconsistent across locations and/or years (Roselló et al., 2019).

PEG molecules with a molecular weight of more than 3000 cannot penetrate the cell wall, and PEG6000, a commonly used variant, with a molecular weight of approximately around 6,000 g/mol, can simulate drought stress as a non-permeating osmotic agent without causing direct physical damage to the plants (Ahmed et al., 2025). PEG6000 restricts water availability in the growth medium, mimicking drought conditions, and often is used to assess drought-resistance during early growth stages due to its capacity to induce severe water stress (Mustamu et al., 2023). The PEG6000 treatment in the hydroponic experiment has been used in many studies to determine the effects of drought on the root phenotype of wheat seedlings, in order to determine the drought tolerance potential of genotypes and traits contributing to drought tolerance and are valuable for breeding (Tang et al., 2024; Sallam et al., 2024; Li et al., 2024; Kou et al., 2022; Azab et al., 2021).

In the past, there have been four basic approaches to breeding for improved drought tolerance (Dhanda et al., 2004). The first approach was to breed conventionally for high yield and to assume that this will provide a yield advantage under suboptimal conditions. The second approach was to breed for maximum yield in the water-limited environment, but the obstacle was the great temporal variability, which slowed down breeding progress. The third approach encompasses creation of cultivars for water-limited environments by selecting physiological and morphological mechanisms for drought resistance through traditional breeding programmes. Secondary traits have been successfully used to enhance the rate of genetic improvement for wheat under drought stress: early flowering, early vigour, plant height controlled with Rht1, Rht2 and Rht8 dwarfing genes, canopy temperature, osmotic adjustment, water uptake, root system, water use efficiency, and carbon isotope discrimination (Abdolshahi et al., 2015). The fourth approach for breeding under water-limited conditions aims to determine single drought-resistant traits as breeding targets.

The aim of this research was to assess the components of phenotypic variance and broad-sense heritability of early vigour traits of bread wheat genotypes in the hydroponic experiment-polyethylene glycol (PEG) induced osmotic stress vs. the control, in order to choose appropriate traits for breeding for drought resistance.

Material and Methods

Based on previous extensive studies (Blažić et al., 2021) that deeply analysed a total of 101 bread wheat genotypes from Serbia and 16 other countries, 11 genotypes with desirable drought tolerance traits were selected for the current research. A total of 11 genotypes from this collection were chosen as parents with selection criteria aimed at achieving drought tolerance and eight crosses were performed: 1. Euclid (FRA) x CHI 4 (CHN); 2. Dika (SRB) x Ingenio (FRA); 3. Pobeda (SRB) x Donska semi-dwarf (RUS); 4. Phoenix (USA) x NS 40S (SRB); 5. Pobeda (SRB) x Brigant (GBR); 6. Dika (SRB) x Donska semi-dwarf (RUS); 7. Zemunska rosa (SRB) x Ingenio (FRA); 8. WWBMC2 (USA) x Ingenio (FRA). The criteria for choosing parents in the crosses were related traits to increased drought tolerance: longer stem length, longer primary root, large number of seminal roots, large root dry mass and stem dry mass, beginning of root branching at the greatest possible distance from the beginning of the root. Contrasting genotypes that had the widest or narrowest angle between the outermost seminal roots were selected. The crosses were made with plants grown in pots under controlled greenhouse conditions.

The F1 offspring from eight crosses and 11 parental genotypes were grown simultaneously in a hydroponic experiment (induced osmotic stress vs. control) in the laboratory of the Plant GeneBank of the Directorate for the National Reference Laboratories of the Ministry of Agriculture, Forestry and Water Management of the Republic of Serbia in 2020. The seedlings were grown in a phytotron (KBW 720, Binder GmbH) under controlled conditions. The seeds of the parental and F1 generation for all crosses were germinated on the filter paper soaked in distilled water at 20˚C for four days. Fifteen uniformly germinated seeds per genotype per treatment and per control were placed on the perforated lid of the plastic box divided in the middle by a plastic partition to create control conditions and conditions for applying stress treatment with two control genotypes (NS 40S, Zemunska Rosa) chosen based on a difference in their reaction to osmotic stress. In the second half of the box, after setting up the experiment, the genotypes were first grown in nutrient culture only for three days, and then polyethylene glycol 6000 (PEG-6000, ACROS OrganicsTM) was added. Osmotic stress represents a surrogate for drought stress in the plant (Li et al., 2019). Wheat seedlings of different genotypes were grown in a completely randomised design with three replicates in both growth conditions. The hydroponic culture consisted of a modified Knop's solution (Blažić et al., 2024). The mode of operation of the phytotron was set as described in Blažić et al. (2021). The relative air humidity was 75%. The cycle was completed after 24 hours and repeated. The mode of operation lasted a further 7 days after PEG treatment, after which the plants were removed from the growth chamber. After 10 days of cultivation in the phytotron, 10 representative seedlings per genotype were selected, washed under running water, scanned, and the photographs were processed using the Image J programme (Rasband, 2020).

The following traits were measured: primary root length (PRL), distance to the first branch on the primary root (DFBR), number of seminal roots (NSR), total seminal root length (TSRL), angle of seminal roots (ASR), and shoot length (SL). After drying the samples for 24 h at a temperature of 80 °C, root dry mass (RDM) and shoot dry mass (SDM) were measured, and RDM/SDM was calculated.

To determine the significance of genotype and environment (treatment) as sources of variation in the examined root and shoot traits, a two-way analysis of variance (ANOVA) was used following a randomised complete block design, where the environment meant growing wheat seedlings without and with osmotic stress by applying treatment with PEG:

$$X_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijk}$$

X_{ijk} – analysed trait value of the *i*-th genotype $(i = 1, \dots, 19)$, in the *j*-th environment $(j = 1, 2)$ and the *k*-th replication $(k = 1, .., 3)$ (μ – mean average; α_i – main effect of the *i*-th genotype; β_j – mean effect of the *j*-th environment; $(\alpha\beta)_{ij}$ – effect of the interaction of the *i*-th genotype and the *j*-th environment; ε_{ijk} – error. The model of a two-way ANOVA is presented in the general table (Table 1).

Table 1. The general model of a two-way ANOVA.

Source of variation	Sum of squares (SS)	DF	Mean squares (MS)	F
Genotype (G)	SS_G	i-1	$MS_G=SS_G/i\text{-}1$	$F_G=MS_G/MS_{Er}$
Environment (E)	SS_E	j-1	$MS_E=SS_E/j\text{-}1$	$F_E=MS_E/MS_{Er}$
G × E	SS_{GE}	(i-1) (j-1)	$MS_{GE}=SS_{GE}/(i\text{-}1)\ (j\text{-}1)$	$F_{GE}=MS_{GE}/MS_{Er}$
Error	SS_{Er}	ij (k-1)	$MS_{Er}=SS_{Er}/ij(n\text{-}1)$	
Total	SS_T	ik-1		

**i* – number of genotypes, *j* – number of environments, *k* – number of replications.

The variance components were estimated based on the combined two-way ANOVA according to Falconer (1981) as follows:

$$V_g = \frac{MS_g - MS_{ge}}{re}$$

$$V_{ge} = \frac{MS_{ge} - MS_{er}}{r}$$

$$V_{er} = MS_{er}$$

$$V_p = V_g + \frac{V_{ge}}{e} + \frac{V_{er}}{re}$$

where V_g, V_{ge}, V_{er} and V_p are the variances due to genotypes, genotype × environment interaction, experimental error and phenotypes, respectively. MS_g, MS_{ge}, MS_{er} are the mean squares of genotypes, genotype × environment interaction and pooled error with e being the number of environments and r – the number of replications. Broad-sense heritability h^2_{BS} (%) is expressed as:

$$h^2_{BS} = \frac{V_G}{V_P} \times 100$$

The genotypic coefficient of variation CV_G (%) is calculated as follows:

$$CV_G = \frac{\sqrt{V_G}}{\bar{x}} \cdot 100$$

The phenotypic coefficient of variation CV_P (%) is calculated as follows:

$$CV_P = \frac{\sqrt{V_P}}{\bar{x}} \cdot 100$$

where V_G is the genetic variance, V_P is the phenotypic variance, and $\bar{x}$ is the average value of the trait of interest.

All statistical analyses were performed in the MINITAB V. 16 programme (Minitab Inc., 2021).

Results and Discussion

Using a two-way analysis of variance, the significance of the sources of variation for nine investigated root traits and shoot traits of 19 wheat genotypes seedlings grown under PEG-induced osmotic stress and under control conditions is shown (Table 2). Statistically significant (P < 0.01) F-test values were determined for both main factors (genotype, environment) for all investigated traits. The GE interaction had a statistically significant (P < 0.01) effect on the variation of most investigated root traits and shoot traits, except for TSRL, where the effect was statistically significant (P < 0.05) and for NSR, where it had no statistically significant effect. Many authors (Dhanda et al., 2004; Rauf et al., 2007; Bayoumi et al., 2008) determined a significant effect of PEG treatment on the wheat seedling morphology, as well as a significant differential response of the genotypes to the simulated drought stress. For all the traits analysed, genotype had on average the greatest influence (42.51%) on the total variation of the tested traits expressed as percent of the total sum of squares (SS) (Table 2). The environment contributed 17.06% of total sum of squares to the total variation of the studied traits, and the GE interaction contributed 13.79% (Table 2). The genotype had the greatest influence on the ASR (87.12% of total SS) and on the PRL (60.97% of total SS), while it had the least impact on the SDM (17.26% of total SS). The environment had the greatest effect on the SL (43.23% of the total SS) and on the SDM (40.09% of the total SS), and the least influence on the ASR (0.28% of the total SS).

Table 2. Two-way ANOVA for root traits and shoot traits of 19 wheat genotypes under two contrasting water regimes.

Trait		Genotype (G)	Environment (E)	G × E interaction
PRL	F	12438^{**}	167.42^{**}	17.31^{**}
	SS (%)	60.97	9.02	18.54
DFBR	F	97.55^{**}	757.86^{**}	46.39^{**}
	SS (%)	22.95	32.12	36.71
NSR	F	6.75^{**}	13.90^{**}	$1,16^{NZ}$
	SS (%)	20.04	4.45	1.11
TSRL	F	27.43^{**}	36.91^{**}	1.98^{*}
	SS (%)	49.81	7.18	3.84
ASR	F	287.79^{**}	19.50^{**}	10.95^{**}
	SS (%)	87.12	0.28	6.26
SL	F	53.88^{**}	577.60^{**}	6.97^{**}
	SS (%)	33.77	43.23	8.59
RDM	F	53.01^{**}	128.48^{**}	15.00^{**}
	SS (%)	38.48	12.37	28.86
SDM	F	17.18^{**}	264.39^{**}	5.48^{**}
	SS (%)	17.26	40.09	13.22
RDM/SDM	F	30.93^{**}	28.88^{**}	2.88^{**}
	SS (%)	52.17	4.78	6.96
Mean†	SS (%)	42.51	17.06	13.79

$^{*}P < 0.05$; $^{**}P < 0.01$; †residual of explained variance at 100% is error variance; PRL – primary root length, DFBR – distance to the first branch at the primary root, NSR – number of seminal roots, TSRL – total seminal root length, ASR – angle of seminal roots, SL – shoot length, RDM – root dry mass, SDM – shoot dry mass, RDM/SDM – the ratio of root dry mass to shoot dry mass.

Under different environmental conditions, with and without imposed osmotic stress, shoot traits exhibited greater variation in relation to the root traits, thus confirming the above-mentioned results that the examined shoot traits were more sensitive to the effect of the applied treatment. Ahmed et al. (2025) indicated substantial genotype effects (P < 0.01) in osmotic stress tolerance, among the 80 bread wheat genotypes and advanced lines from Iran. PEG treatments (TPEG) displayed statistically ($P < 0.01$) distinct effects on seedling traits (PRL, SL, RDM, SDM) compared to the control, and the statistically significant ($P < 0.01$) interaction between G × TPEG, highlighting the differential performance of various genotypes under different osmotic potentials. Jain et al. (2014) analysed 34 genotypes of bread wheat in three different water regimes, and found that the different osmotic potentials had the greatest effect on the SDM. In the same experiment, they showed that the effect of the environment was much stronger than the effect of the genotype and the GE interaction, with the 85.2% contribution to the total variation of the SDM trait. Baloch et al. (2012) also indicated a significant sensitivity of shoot traits under the conditions of PEG-induced osmotic stress. Boudiar et al. (2020) reported in their barley seedling experiment that imposed drought reduced shoot growth (SDM reduction of 43%) almost twice as much as root growth (RDM reduction of 23%).

In general, the effect of the genotype was on average higher on the variability of the tested root traits (46.6%), compared to the tested shoot traits (25.5%). This means that the root traits under investigation can be taken as a more reliable criterion for selection for drought tolerance compared to the investigated shoot traits, because their response to environmental variation will be more stable. Baloch et al. (2012) reported that the development of the root system under water deficit conditions is a very viable selection criterion for resistance to osmotic stress.

Table 3. Components of phenotypic variations, broad-sense heritability, coefficient of phenotypic variation and coefficient of genotypic variation for root traits and shoot traits of 19 wheat genotypes under two contrasting water regimes.

Trait	V_G	V_{GxE}	V_E	V_P	h^2_{BS} (%)	CV_G (%)	CV_P (%)
PRL	2.50	0.76	0.40	2.90	86.1	12.9	13.9
DFBR	0.05	0.08	0.04	0.09	52.4	16.2	22.3
NSR	0.09	0.005	0.02	0.11	82.9	10.5	11.6
TSRL	5.83	0.45	0.45	6.29	92.8	10.6	11.0
ASR	291.41	20.95	11.53	302.94	96.2	18.2	18.6
SL	4.64	1.18	0.69	5.33	87.1	9.5	10.2
RDM	0.28	0.21	0.11	0.39	71.7	8.5	10.1
SDM	1.58	1.21	0.74	2.32	68.1	5.8	7.0
RDM/SDM	0.0012	0.0002	0.0001	0.0013	90.7	11.8	12.4

V_G – genetic variance; V_{GxE} – variance of genotype × environment interaction; V_E – ecological variance; V_P – phenotypic variance; h^2_{BS} – broad-sense heritability; CV_G – coefficient of genotypic variation; CV_P – coefficient of phenotypic variation; PRL – primary root length, DFBR – distance to the first branch on the primary root, NSR – number of seminal roots, TSRL – total seminal root length, ASR – angle of seminal roots, SL – shoot length, RDM – root dry mass, SDM – shoot dry mass, RDM/SDM – the ratio of root dry mass to shoot dry mass.

Manschadi et al. (2008) stated that unlike RSA traits adapted to drought conditions, the use of shoot traits in wheat breeding programmes for drought tolerance was less successful.

GE interaction is defined as variation in the relative performance of genotypes in different environments (Cooper and Byth, 1996). In the absence of GE interaction, a superior genotype in one environment can be considered superior in all other environments, while the presence of GE interaction confirms that certain genotypes are superior in certain environments. Therefore, it is important to know the magnitude of this interaction in order to understand the response of different genotypes to different environments. If a GE interaction is present, breeders strive to identify stable genotypes with relatively consistent performance across a range of environments. Significant GE interaction values reduce the correlation between phenotypic and genotypic values, as well as selection progress (Amare et al., 2020). The term GE interaction is sometimes used as a synonym for plasticity. Phenotypic plasticity is defined as the ability of a genotype to produce different phenotypes under different environmental conditions. Accordingly, as the GE interaction had the greatest influence on the DFBR and the RDM with 36.7% and 28.9%, respectively, these traits were characterised by high plasticity.

Broad-sense heritability was very high (over 90%) for the traits: ASR (96.2%), TSRL (92.8%) and RDM/SDM (90.7%). High h^2_{BS} (80–90%) was observed for: SL (87.1%), PRL (86.1%), and NSR (82.9%). Moderate h^2_{BS} (40–70%) was shown for SDM (68.1%) and for DFBR (52.4%). The assessment of heritability gives us an insight into the degree of genetic control of the expression of a certain trait and phenotypic reliability in predicting the success of selection (Ndukauba et al., 2015). The obtained results indicated that there was a high degree of h^2_{BS} of most of the tested traits and that for most of them consistent genotype performance can be expected in different environmental conditions, and that the selection of wheat genotypes for drought tolerance should focus on these traits. Since the DFBR showed the lowest h^2_{BS} of the examined traits, it should not be taken as a reliable selection criterion due to the greater influence of the external environment on its manifestation. Colombo et al. (2022) showed lower values for h^2_{BS} for NSR (66%), ASR (64%), SDM (67%), RDM/SDM (74%) for 715 bread wheat genotypes tested as seedlings in comparison to our results, by using a high-throughput phenotyping platform. Canè et al. (2014) also documented intermediate to high values for h^2_{BS} for ASR (73%) and for NSR (67%) for 183 durum wheat elite accessions tested as seedlings. Hohn and Bektas (2020) analysed the same traits in three doubled haploid populations of bread wheat and found intermediate values for h^2_{BS} for ASR, in the range 52.3%–70.2%, and for NSR in the range 47%–64%. Higher h^2_{BS} values for RDM (75%) and lower values for ASR (85%)

were found in an experiment with six independent replicates of 201 bread wheat genotypes evaluated as seedlings (Beyer et al., 2019). Abdolshahi et al. (2015) showed moderate h_{BS}^2 for PRL and RDW of 60% and 69%, respectively, and low h_{BS}^2 for NSR of 39% for 40 genotypes of bread wheat in a two-year glasshouse experiment under drought conditions in Iran. Christopher et al. (2013) estimated h_{BS}^2 for ASR with a value of 50% and for NSR with a value of 31% for bread wheat doubled haploid population. Dhanda et al. (2004) determined h_{BS}^2 values for RL (86.7% and 84.3%) and SL (87% and 68.5%) for 30 bread wheat genotypes, tested as seedlings under PEG-induced drought stress, under control and drought-induced stress conditions, respectively. Rajamanickam et al. (2024) showed intermediate to high values for h_{BS}^2 for TSRL, PRL, RDM, and SDM, of 71%, 72%, 86%, and 85%, respectively for 204 bread wheat genotypes tested as seedlings in the hydroponic experiment. Rebetzke et al. (2022) determined h_{BS}^2 values for TSRL, NSR, and SL, of 89%, 81%, and 73%, respectively, for 460 recombinant bread wheat inbred lines, similar to our study.

The genetic stability of a particular genotype for any studied trait is determined by a low coefficient of variation and a high heritability of the corresponding trait (Reddy et al., 2020). Sanguineti et al. (2007) and Canè et al. (2014) stated that the ASR in the seedling phase has two desirable characteristics that make it very suitable for genetic research: first, it does not require a great effort to measure it in a large number of genotypes, and second, it is precisely its high heritability. RSA traits related to root shape and spatial arrangement, such as the NSR and ASR, may provide growth and yield advantages under water deficit conditions (Rogers and Benfey, 2015). In addition to the ASR, among the other examined root traits, the PRL had a significant share of the variance of the genotype (61%) on the variation of this trait, confirming previous studies that selection for increased PRL can be expected to improve the breeding of wheat under drought conditions (Dhanda et al., 2004; Hameed et al., 2010; Shahbazi et al., 2012). The high broad-sense heritability of this trait indicates the possibility of successfully improving the PRL in the breeding efforts by using different germplasm (Ayalew et al., 2018). As the root geometry of adult plants is closely related to RSA (Manschadi et al., 2008), it can be assumed that genotypes that differ in root architecture at early stages of development could also differ in the field at later stages of growth, when water and nutrient uptake becomes critical for yield performance (Canè et al., 2014).

The value of the coefficient of genetic variation (CV_G) was the lowest for the SDM (5.8%), while it was the highest for the DFBR (16.2%). The coefficient of phenotypic variation (CV_P) had the lowest value for the SDM (7.0%), and the highest value for the DFBR (22.3%). The DFBR showed the highest values for both coefficients of variation, which is in accordance with the obtained results that this trait varied the most among all the examined traits, both in conditions without and with osmotic stress. The external environment, i.e. osmotic stress, contributed strongly to the variation of this trait. Abdolshahi et al. (2015) showed high values for CV_P for RDM and NSR, 41.3% and 22.9%, respectively, and medium value for PRL of 16.1%, with CV_G values significantly lower than CV_P, for 40 genotypes of bread wheat tested for two years in glasshouse experiment under drought conditions in Iran. The low values of CV_P and CV_G for SDM have indicated that the existing genetic variability is not sufficient to achieve a significant improvement of this trait under drought stress.

Conclusion

The genetic analysis of the appropriateness of using root system architecture traits and shoot traits of bread wheat seedlings configuring early vigour under simulated drought stress indicated that broad-sense heritability was very high and high (> 82%) for most of the tested traits (primary root length, number of seminal roots, total seminal root length, angle of seminal roots, shoot length, the ratio of root dry mass to shoot dry mass), with low genotype × environment interaction (< 20% of total variation) and that the breeding for drought tolerance should be focused on these traits. Since the distance to the first branch on the primary root showed the lowest value for broad-sense heritability, and the greatest extent of genotype × environment interaction, it should not be considered as a reliable selection criterion due to the greater environmental influence on its manifestation.

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References

Abdolshahi, R., Nazari, M., Safarian, A., Sadathossini, T., Salarpour, M., & Amiri, H. (2015). Integrated selection criteria for drought tolerance in wheat (*Triticum aestivum* L.) breeding programs using discriminant analysis. *Field Crops Research*, *174*, 20-29.

Afzal, F., Reddy, B., Gul, A., Khalid, M., Subhani, A., Shazadi, K., & Rasheed, A. (2017). Physiological, biochemical and agronomic traits associated with drought tolerance in a synthetic-derived wheat diversity panel. *Crop and Pasture Science*, *68* (3), 213-224.

Ahmed, K., Shabbir, G., & Ahmed, M. (2025). Exploring drought tolerance for germination traits of diverse wheat genotypes at seedling stage: a multivariate analysis approach. *BMC Plant Biology*, *25*, 390.

Amare, A., Mekbib, F., Tadesse, W., & Tesfaye, K. (2020). Genotype x environmental interaction and stability of drought tolerant bread wheat (*Triticum aestivum* L.) genotypes in Ethiopia. *International Journal of research Studies in Agricultural Sciences*, *6* (3), 26-35.

Ayalew, H., Liu, H., Börner, A., Kobiljski, B., Liu, C., & Yan, G. (2018). Genome-wide association mapping of major root length QTLs under PEG induced water stress in wheat. *Frontiers in Plant Science*, *9*, 1759.

Azab, O., Al-Doss, A., Alshahrani, T., El-Hendawy, S., Zakri, A.M., & Abd-ElGawad, A.M. (2021). Root system architecture plasticity of bread wheat in response to oxidative burst under extended osmotic stress. *Plants*, *10* (5), 939.

Baloch, M.J., Dunwell, J., Khakwani, A.A., Dennett, M., Jatoi, W.A., & Channa, S.A. (2012). Assessment of wheat cultivars for drought tolerance via osmotic stress imposed at early seedling growth stages. *Journal of Agricultural Research*, *50*, 299-310.

Bayoumi, T.Y., Eid, M.H., & Metwali, E.M. (2008). Application of physiological and biochemical indices as a screening technique for drought tolerance in wheat genotypes. *African Journal of Biotechnology*, *7* (14), 2341-2352.

Beyer, S., Daba, S., Tyagi, P., Bockelman, H., Brown-Guedira, G., I.W.G.S.C., & Mohammadi, M. (2019). Loci and candidate genes controlling root traits in wheat seedlings-a wheat root GWAS. *Functional & Integrative Genomics*, *19*, 91-107.

Bhandari, R., Paudel, H., Nyaupane, S., & Poudel, M.R. (2024). Climate resilient breeding for high yields and stable wheat (*Triticum aestivum* L.) lines under irrigated and abiotic stress environments, *Plant Stress*, *11*, 100352.

Blažić, M., Dodig, D., Kandić, V., Đokić, D., & Živanović, T. (2021). Genotypic variability of root and shoot traits of bread wheat (*Triticum aestivum* L.) at seedling stage. *Genetika-Belgrade*, *53*, 687-702.

Blažić, M., Dodig, D., Kandić, V., Branković, G., & Živanović, T. (2024). The impact of PEG-induced drought stress on early vigour traits of bread wheat. *New Zealand Journal of Crop and Horticultural Science*, 1-13. https://doi.org/10.1080/01140671.2024.2304766

Boudiar, R., Casas, A.M., Gioia, T., Fiorani, F., Nagel, K.A., & Igartua, E. (2020). Effects of low water awailability on root placement and shoot development in landraces and modern barley cultivars. *Agronomy*, *10* (1), 134.

Canè, M.A., Maccaferri, M., Nazemi, G., Salvi, S., Francia, R., Colalongo, C., & Tuberosa, R. (2014). Association mapping for root architectural traits in durum wheat seedlings as related to agronomic performance. *Molecular Breeding*, *34*, 1629-1645.

Chen, Y., Palta, J., Prasad, P.V.V., & Siddique, K.H.M. (2020). Phenotypic variability in bread wheat root systems at the early vegetative stage. *BMC Plant Biology, 20* (1), 185.

Christopher, J., Christopher, M., Jennings, R., Jones, S., Fletcher, S., Borrel, A., Manschadi, A.M., Jordan, D., Mace, E., & Hammer, G. (2013). QTL for root angle and number in a population developed from bread wheat (*Triticum aestivum* L.) with contrasting adaptation to water-limited environments. *Theoretical and Applied Genetics*, *126*, 1563-1574.

Colombo, M., Roumet, P., Salon, C., Jeudy, C., Lamboeuf, M., Lafarge, S., Dumas, A.V., Dubreuil, P., Ngo, W., Derepas, B., Beauchêne, K., Allard, V., Le Gouis, J., & Rincent, R. (2022). Genetic analysis of platform-phenotyped root system architecture of bread and durum wheat in relation to agronomic traits. *Frontiers in Plant Science*, *25* (13), 853601.

Cooper, M., & Byth, D.E. (1996). Understanding plant adaptation to achieve systematic applied crop improvement-a fundamental challenge. In M. Cooper & G.L. Hammer (Eds.), *Plant adaptation and crop improvement*. (pp. 5-23). Wallingford: CABI Publishing.

Dhanda, S.S, Sethi, G.S., & Behl, R.K. (2004). Indices of drought tolerance in wheat genotypes at early stages of plant growth. *Journal of Agronomy and Crop Science*, *190* (1), 6-12.

Falconer, D.S. (1981). *Introduction to quantitative genetics.* London and New York: Longman.

Hameed, A., Goher, M., & Iqubal, N. (2010). Evaluation of seedling survivability and growth response as selection criteria for breeding drought tolerance in wheat. *Cereal Research Communications*, *38* (2), 193-202.

Hohn, C.E., & Bektas, H. (2020). Genetic mapping of quantitative trait loci (QTLs) associated with seminal root angle and number in three populations of bread wheat (*Triticum aestivum* L.) with common parents. *Plant Molecular Biology Reporter*, *38*, 572-585.

Jain, N., Singh, G.P., Yadav, R., Pandey, R., Ramya, P., Shine, M.B., Pandey, V.C., Rai, N., Jha, J., & Prabhu, K.V. (2014). Root trait characteristics and genotypic response in wheat under different water regimes. *Cereal Research Communications*, *42* (3), 426-438.

Kou, X., Han, W., & Kang, J. (2022). Responses of root system architecture to water stress at multiple levels: A meta-analysis of trials under controlled conditions. *Frontiers in Plant Science*, *13*, 1085409.

Li, X., Ingvordsen, C.H., Weiss, M., Rebetzke, G.J., Condon, A.G., James, R.A., & Richards, R.A. (2019). Deeper roots associated with cooler canopies higher normalized difference vegetation index, and greater yield in three wheat populations grown on stored soil water. *Journal of Experimental Botany*, *70*, 4963-4974.

Li, X., Chen, Y., Xu, Y., Sun, H., Gao, Y., Yan, P., Song, Q., Li, S., & Zhan, A. (2024). Genotypic variability in root morphology in a diverse wheat genotypes under drought and low phosphorus stress. *Plants*, *13* (23), 3361.

Manschadi, A.M., Christopher, J., deVoil, P., & Hammer, G.L. (2006). The role of root architectural traits in adaptation of wheat to water-limited environments. *Functional Plant Biology*, *33*, 823-837.

Manschadi, A.M., Hammer, G.L., Christopher, J.T., & deVoil, P. (2008). Genotypic variation in seedling root architectural traits and implications for drought adaptation in wheat (*Triticum aestivum* L.). *Plant and Soil*, *303*, 115-129.

Minitab, (2021). Statistical Software, version *16*. *Minitab Incorporation*. Retrieved January 11, 2020, from https://www.minitab.com/en-us/products/minitab/

Moore, C., & Rebetzke, G.J. (2015). Genomic regions for embryo size and early vigour in multiple wheat (*Triticum aestivum* L.) populations. *Agronomy*, *5*, 152.

Mustamu, N.E., Tampubolon, K., Basyuni, M., Al-Taey, D.K., Janabi, H.J.K.A, & Mehdizadeh, M. (2023). Drought stress induced by polyethylene glycol (PEG) in local maize at the early seedling stage. *Heliyon*, *9* (9), e20209.

Ndukauba, J., Nwofia, G.E., Okocha, P.I., & Ene-Obong, E.E. (2015). Variability in egusi-melon genotypes (*Citrullus lanatus* [Thumb] Matsum and Nakai) in derived savannah environment in South-Eastern Nigeria. *International Journal of Plant Research*, *5* (1), 19-26.

Rajamanickam, V., Vinod, K.K., Vengavasi, K., Kumar, T., Chinnusamy, V., & Pandey, R. (2024). Root architectural adaptations to phosphorus deficiency: unraveling genotypic variability in wheat seedlings. *Agriculture*, *14* (3), 447.

Rasband, W.S. (2020). ImageJ. *National Institutes of Health*. Retrieved on January 01, 2020, from https://imagej.nih.gov/ij/

Rauf, M., Munir, M.M., Hassan, M., Ahmad, M., & Afzal, M. (2007). Performance of wheat genotypes under osmotic stress at germination and early seedling growth stage. *African Journal of Biotechology*, *6*, 971-975.

Rebetzke, G.J., Zhang, H., Ingvordsen, C.H., Condon, A.G., Rich, S.M., & Ellis, M.H. (2022). Genotypic variation and covariation in wheat seedling seminal root architecture and grain yield under field conditions. *Theoretical and Applied Genetics*, *135* (9), 3247-3264.

Reddy, V.R.P., Aski, M.S., Mishra, G.P., Dikshit, H.K., Singh, A., Pandey, R., Singh, M.P., Gayacharan, Ramtekey, V., Priti, Rai, N., & Nair, R.M. (2020). Genetic variation for root architectural traits in response to phosphorus deficiency in mungbean at the seedling stage. *PLoS One*, *15* (6), e0221008.

Rogers, E.D., & Benfey, P.N. (2015). Regulation of plant root system architecture: implications for crop advancement. *Current Opinion in Biotechnology*, *32*, 93-98.

Roselló, M., Royo, C., Sanchez-Garcia, M., & Soriano, J.M. (2019). Genetic dissection of the seminal root system architecture in mediterranean durum wheat landraces by genome-wide association study. *Agronomy*, *9*, 364.

Rossi, R., Bochicchio, R., Labella, R., Amato, M., & De Vita, P. (2024). Phenotyping seedling root biometry of two contrasting bread wheat cultivars under nutrient deficiency and drought stress. *Agronomy*, *14*, 775.

Sallam, A., Awadalla, R.A., Elshamy, M.M., Börner, A., & Heikal, Y.M. (2024). Genome-wide analysis for root and leaf architecture traits associated with drought tolerance at the seedling stage in a highly ecologically diverse wheat population. *Computational and Structural Biotechnology Journal*, *23*, 870-882.

Sanguineti, M.C., Li, S., Maccaferri, M., Corneti, S., Rotondo, F., Chiari, T., & Tuberosa, R. (2007). Genetics dissection of seminal root architecture in elite durum wheat germplasm. *Annals of Applied Biology*, *151*, 291-305.

Shahbazi, H., Bihamta, M.R., Taeb, M., & Darvish, F. (2012). Germination characters of wheat under osmotic stress: Heritability and relation with drought tolerance. *International Journal of Agriculture: Research and Review*, *2*, 689-698.

Tang, K., An, C., Li, L., Sun, T., Song, J., & Zhao, J. (2024), Effects of drought and salt stress on the root phenotype of wheat seedlings and underlying gene expression analysis. *Frontiers in Plant Science*, *15*,1475500.

Zhao, Z., Rebetzke, G.J., Zheng, B., Chapman, S.C., & Wang, E. (2019). Modelling impact of early vigour on wheat yield in dryland regions. *Journal of Experimental Botany*, *70* (9), 2535-2548.

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KOMPONENTE FENOTIPSKE VARIJANSE I HERITABILNOST OSOBINA RANOG PORASTA HLEBNE PŠENICE POD KONTRASTNIM SNABDEVANJEM VODOM

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Rezime

Istraživanje potencijala za toleranciju na sušu i fenotipske plastičnosti arhitekture korenovog sistema u ranim fazama razvoja moglo bi biti ključno u pogledu oplemenjivanja na otpornost na sušu i za selekciju ideotipova pšenice u uslovima klimatskih promena. Ukupno 11 genotipova iz kolekcije od 101 genotipa hlebne pšenice, poreklom iz Srbije i 16 različitih zemalja sveta, sa poželjnim osobinama u smislu povećane tolerancije na sušu, odabrano je za roditelje i izvršeno je osam ukrštanja. Genotipovi iz P i F1 generacija gajeni su u hidroponskoj kultivaciji u osmotskom stresu izazvanom polietilen glikolom 6000. Cilj ovog istraživanja je bio da se procene komponente fenotipske varijanse i heritabilnosti u širem smislu osobina ranog porasta za devet osobina korena i izdanka genotipova hlebne pšenice u indukovanom vodnom stresu i u kontrolnim uslovima, kako bi se izabrale prikladne osobine za oplemenjivanje na otpornost na sušu. Uticaj genotipa bio je veći na varijabilnost testiranih osobina korena (46,6%), u poređenju sa testiranim osobinama izdanka (25,5%), što znači da se osobine korena mogu uzeti kao pouzdaniji kriterijum za selekciju na toleranciju na sušu u poređenju sa ispitivanim osobinama izdanka. Heritabilnost u širem smislu bila je visoka (> 82%) za većinu ispitivanih osobina (dužina primarnog korena, broj seminalnih korenova, ukupna dužina seminalnih korenova, ugao seminalnih korenova, dužina izdanka, odnos suve mase korena i suve mase izdanka), a malom interakcijom genotip × sredina (< 20% ukupne varijacije) i oplemenjivanje na toleranciju na sušu trebalo bi da bude usmereno na ove osobine.

Ključne reči: *Triticum aestivum* L., sušni stres, arhitektura korenovog sistema, osobine izdanka, heritabilnost u širem smislu, komponente fenotipske varijanse.

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