

**GENOTYPIC VARIABILITY OF ROOT AND SHOOT TRAITS OF BREAD WHEAT
(*Triticum aestivum* L.) AT SEEDLING STAGE**

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The evaluation of the embryonic root and stem of bread wheat (*Triticum aestivum* L.) in the early stage of development (seedling stage) can be a powerful tool in wheat breeding aimed at obtaining progenies with a greater early vigour. It is revealed that genotypes with faster early vigour have produced higher biomass and grain yield. In this study, the evaluation of traits of the embryonic root and the embryonic stem of 101 bread wheat genotypes was performed at the 10-day old seedlings. The following eight morphological traits of roots and stems were analysed: primary root length, branching interval, the number of roots, total length of lateral roots, angle of seminal roots, stem length, root dry weight and the stem dry weight. Analysed lateral roots included seminal roots. The greatest, i.e. the smallest variability of observed traits was detected in the branching interval, i.e. the stem length, respectively. The highest positive correlation was determined between the primary root length and the total length of lateral roots. The cluster analysis, based on observed traits, shows that genotypes were clearly divided into two main clusters, A and B. The two clusters essentially differed from each other in the values of the following traits: primary root length, total length of lateral roots, root dry weight, stem dry weight and the stem length. Genotypes with shorter primary and lateral

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roots, lower root and stem dry weight and a shorter stem were grouped in the cluster B. On the other hand, the cluster A encompassed genotypes with values of these traits above or around the average. The values of the remaining analysed traits: the angle of seminal roots, the number of lateral roots and the branching interval varied greatly between obtained clusters. The cluster analysis showed the homogeneity of genotypes originating from Serbia and the region; their values of the root and stem length and weight were mostly around and below the average. However, the values of the angle of seminal roots, number of lateral roots and the branching interval were above average.

Keyword: wheat, root, stem, correlations, cluster analysis

INTRODUCTION

Wheat is one of the most important field crops. It satisfies half of the calorie and protein needs of one third of the world's population (MUJEEB-KAZI and RAJARAM, 2002). The global wheat demand is projected to increase to 750 million tonnes by 2025 (AHMAD *et al.*, 2013). Therefore, increasing wheat production in the world is much needed to ensure food security for the human population. In the era of global climate changes and the growth of the human population, the main goals in wheat breeding are to develop varieties with higher yields, quality and resistance to abiotic and biotic factors (AHMED *et al.*, 2019).

Research has shown the importance of the trait designated as early vigour or germination power of seedlings in the small grains breeding programmes. It has also been shown that genotypes with greater early vigour produced higher biomass and grain yield both under optimal and drought conditions (DODIG *et al.*, 2008; KANDIĆ *et al.*, 2009; ZHAO *et al.*, 2019). Early vigour - the size of leaves and stem developed in the early developmental stages - is an important property of crops, because increased early vigour is associated with the greater water-use efficiency (BOTWRIGHT *et al.*, 2002). Greater early vigour will reduce water evaporation from the soil under the plant leaf canopy, thus conserving moisture for later stages of development. On the other hand, a strongly developed root system provides water intake from deeper, more moisture soil layers later in the season when drought occurs. Furthermore, a faster development of the leaf surface improves the ability of crops to compete with weeds, and thus can help reduce the use of herbicides (COLEMAN *et al.*, 2001). Early vigour is also associated with a greater nitrogen uptake capacity (MAIDUP *et al.*, 2012). Research performed in Australia has shown that wheat with high early vigour could maintain a strong growth of the root and the stem under early seasonal water deficits and could recover faster with subsequent rain than wheat with low early vigour (FRENCH and PALTA, 2014). Moreover, studies carried out on wheat have shown a close association of drought tolerance in the seedling stage and the reproductive stage (MOUD and MAGHSOUDI, 2008; DODIG *et al.*, 2015). Early vigour can be estimated by easily measurable parameters, and this can be a useful tool in wheat breeding programmes in which a large number of genotypes have to be analysed (MAIDUP *et al.*, 2012).

Water deficiency mostly affects roots in wheat plants (AHMED *et al.*, 2019). The size of the root system is a key trait for more efficient water and nitrogen uptake in wheat (FIGUEROA-BUSTOS *et al.*, 2018). The root system traits are of essential importance because they provide information about the soil and resources contained in the soil. The root system architecture (RSA) and morphology are factors used to define the root system traits. Root morphology refers

to the traits of the main root axis, including root hairs, root diameter and cortical ageing, while RSA refers to the entire root system or a large part of it (STANGOULIS and NGUYEN, 2019). The root system traits are often associated with drought resistance, such as the rooting depth, the root distribution in the soil and the density (HAMMER *et al.*, 2007). There is ample evidence of genotypic variability of the root system traits of many crop species. In wheat, these traits include the rooting depth, root elongation rate, root distribution by depth, xylem elements diameter, as well as the stem dry weight to root dry weight ratio. Numerous RSA studies have shown significant differences between high-yielding drought-resistant genotypes and standard wheat varieties that are characterised by smaller lateral branching and greater uniformity and the smaller depth of roots in the post-flowering stage (HAMMER *et al.*, 2007). A study carried out by NAKAMOTO and OYONAGI (1994) have shown significant genotypic variability in the growth angle of wheat lateral roots. They averred that deep-rooted genotypes had a narrower growth angle of lateral roots, while genotypes with shallower root systems had lateral roots that grew wider.

Considering the difficulties in wheat breeding for common root traits due to its inaccessibility in the soil, high phenotypic plasticity of root traits as a response to various soil conditions and the lack of fast and economic methods, RSA traits expressed in early developmental stages that also determine the growth and functioning of a mature root system can be a much better criterion for selection within wheat breeding programmes (MANSCHADI *et al.*, 2008). Various methods have been developed for screening wheat genotypes in the seedling developmental stage with the aim to derive drought-resistant varieties (BOTWRIGHT *et al.* 2007; MANSCHADI *et al.* 2008; WATT *et al.*, 2013). These methods also include the hydroponic technique (AYALEW *et al.*, 2015). Some of the proposed methods included the following as good selection criteria: relative amount of water in leaves, early vigour of seedlings, length of both roots and stems (HAMEED *et al.*, 2010). Root phenotyping requires a growth system, image processing and software tools. Root images can be obtained with or without the destruction of the root system depending on the cultivation method and the root image processing technique (STANGOULIS and NGUYEN, 2019). Selection of wheat genotypes based on seedling traits is easier, cheaper and less demanding than selection in later stages of the plant development. Furthermore, seedling traits show moderate to high variability of additive gene effects under different environmental conditions (AHMED *et al.*, 2019).

The aim of the present study was to observe the correlation and genetic variability of 101 bread wheat genotypes in terms of traits of embryonic roots and embryonic stems for the purpose of selection of parental genotypes for further crosses in order to develop progenies with increased early vigour of roots and stems.

MATERIAL AND METHODES

Plant material

A hundred one bread wheat genotypes (*Triticum aestivum* L.) selected from the collection of the Maize Research Institute, Zemun Polje were used in the trial. The observed genotypes originated from Serbia, the region and different parts of the world. Names/designations of the genotypes and the countries of their origin are presented in Table 1.

Table 1. Names/designations and the country of origin of observed genotypes (designation according to www.fao.org/countryprofiles)

Aleksandra – SRB	L 1 – HUN	Triple dirk S – AUS
Alinea – FRA	L. Inia – CHL	U-1 – HRV
Andino – FRA	L1/91 – SRB	UPI 301 – IND
Apache – FRA	Lepoklasa – SRB	Vesna – SRB
Aurelia – SRB	Levante – ITA	Viktorija – SRB
Avalon – GBR	Liangxing 66 – CHN	Vireo "S" – MEX
Benni multifloret – USA	Liangxing 77 – CHN	WWBMC2 – USA
Bezostaja – RUS	LM 30 – CHN	Yamhill – USA
BG Carica – SRB	LM 31 – CHN	Yannong 15 – CHN
BG Merkur – SRB	LM 33 – CHN	Yannong 24 – CHN
BG Vitka – SRB	LM 35 – CHN	Yecora – MEX
Brigant – GBR	LM 36 – CHN	Z. Rosa – SRB
Cajeme – MEX	LM 37 – CHN	ZG K T 159/82 – HRV
CHI-4 – CHN	Lt 6/1 – SVN	ZP AU 11 – MKD
Ching Chng 6 – CHN	Lumai 23 – CHN	ZP AU 12 – MKD
Chris – USA	Mexico 3 – MEX	ZP AU 13 – MKD
CT 62 – SVN	Mironovska 808 – RUS	ZP AU 19 – SVN
Ct 87 – SVN	MV-Ilona – HUN	ZP AU 20 (Balkania) – MKD
Donska semi-dwarf – RUS	NS 40S – SRB	ZP Belija – SRB
Esperia – ITA	NS 46/90 – SRB	ZP Oka – SRB
Euklid – FRA	NS 74/95 – SRB	ZP Xt 810.11 – SVN
Eurofit – AUT	Oasis – MEX	ZP Xt 85.1 – SVN
Evropa 90 – SRB	Peking 11 – CHN	ZP Xt 86.1/21 – SVN
Florida – USA	Phoenix – USA	ZP Xt 88.5/2 – SVN
Graindor – FRA	PKB Arena – SRB	ZP Xt 88.86 – SVN
Highbury – GBR	PKB Dika – SRB	ZP Xt 9.23 – SVN
Ingenio – FRA	PKB Mlinarka – SRB	ZP Xt 9.24 – SVN
Inia – MEX	PKB Ratarica – SRB	ZP Xt 9.26 – SVN
Jimai 22 – CHN	PKB Talas – SRB	ZP Xt 9.27 – SVN
Kazahstan 19 – KAZ	PKB Vizeljka – SRB	ZP Xt 9.28 – SVN
Kazahstan 20 – KAZ	Pobeda – SRB	ZP Zlatna – SRB
Kenong 199 – CHN	Renesansa – SRB	Zvezdana – SRB
KG-100 – SRB	Shannong 22 – CHN	3-hairy – SRB
Kite – AUS	Tainong 18 – CHN	

Growing conditions of wheat seedlings

The trial was performed in the Plant Gene Bank of the Directorate for National Reference Laboratories of the Ministry of Agriculture, Forestry and Water Management in the cooperation with the Maize Research Institute, Zemun Polje. Seedlings of wheat genotypes were grown in a chamber for growing plants under controlled conditions - growth chamber/phytotron,

model KBW 720, Binder GmbH, with a possibility of adjusting the following parameters: temperature, humidity and lightning.

Prior to placing genotypes into the growth chamber, seeds were germinated on the filter paper soaked in distilled water for three days. Then, 15 uniformly germinated seeds were placed on the perforated lid of the plastic box - rhizobox (38 x 29 x 11 cm - Photograph 1). The rhizobox contained an aqueous nutrient culture, including nitrogen and different types of salts. The purpose of adding nitrogen was to trigger the dispersive root growth. Prior to placing seedlings on the perforated lid, the primary roots were marked with a marker. The seedlings were placed in a way that the entire root system was immersed in an aqueous solution. The container with the aqueous solution was lined on all sides with dark crêpe paper and connected to an oxygen pump. The experiment was performed in time series: genotypes of the ordinal numbers 1-20, 21-40, 41-60, 61-70, 71-81, 81-94, and 95-101 were placed in the first, second, third, fourth, fifth, sixth and the last, seventh series, respectively. The same control genotype (NS 40S) was used for each series.



Photo 1. Appearance of the rhizobox prior to its placing into the growth chamber

After placing the rhizobox into the growth chamber, the following mode of operation was set: for the first 11h there was light in the chamber at the temperature of 20°C; for the next hour temperature dropped from 20°C to 16°C in the dark; for the next 11h the chamber was in the dark at the temperature of 16°C, and then for the next hour the temperature increased from 16°C to 20°C in the light. Relative air humidity was 75%. The cycle was completed after 24h and was repeated. The mode of operation lasted 7 days after which the plants were removed from the growth chamber (Photograph 2).

A sample of 10 representative seedlings of each genotype was drawn for scanning, drying and measuring. The following traits were measured: primary root length (PRL), the first branching interval on the primary root (FBPR), number of seminal roots (NSR), total length of seminal roots (TLSR), angle of seminal roots (ASR), stem length (SL), root dry weight (RDW) and stem dry weight (SDW). Initially, the stem was separated from the root in each seedling. The longest seedling leaf was measured with a ruler and recorded as the stem length. The root of each

seedling was scanned, after which photographs were processed and the following root system traits were measured: primary root length, the number of seminal roots, length of each seminal root using the computer-adapted program - ImageJ (Rasband, W.S., ImageJ, U. S. National Institutes of Health, Bethesda, Maryland, USA, <https://imagej.nih.gov/ij/>, 1997-2018). After roots were scanned and the stem lengths were measured, the plant material was placed into paper bags and dried in the thermostat at the temperature of 80°C for 24h. After 24h, dry weight of stems and roots was measured on an analytical balance.



Photo 2. Ten-day old seedlings after the growth in the growth chamber

Statistical analysis

Prior to the performance of statistical analyses, the correction of measured values for inter-series variations was done. Parameters of descriptive statistics, such as mean values, standard deviation, rank, and the coefficient of variations of observed traits were determined using the Microsoft Excel 2013 package. The coefficient of variation (CV) was calculated based on means and standard deviation. The visualisation of similarities of individual genotypes, in terms of observed traits (cluster analysis), as well as their mutual correlation were done in the software package MATLAB (R2018a). The cluster analysis was performed based on eight analysed traits, whereby the Euclidean distance was used as a measure of the similarity of individual genotypes. A clustergram was constructed based on the initial distance matrix. The initial data were standardised, which means that they were normalised to a zero mean and a unit standard deviation. The similarity of individual traits was obtained by subtracting the correlation coefficient from the unit. The Ward's method was used as a linkage method. Pearson's (simple) correlations were used for the interconnection of traits.

RESULTS AND DISCUSSION

Mean values and variability parameters of observed traits

Mean values and variability parameters of eight analysed traits are presented in Table 2. The least variation was observed in the stem length (CV=16.5%). The range of variation was from 11.25 cm (BG Carica) to 23.16 cm (Peking 11). The highest variation was in the branching interval on the primary root (CV= 36.2%). The range of variation was from 0.35 cm (Yecora) to 2.39 cm (CHI-4). The branching interval on the primary root is a trait that provides the information about the depth at which the system begins to branch. Root branching is important for plants because it anchors them to the soil and provides a supply of water, minerals and nutrients. It represents an important element of the adaptability of the root system to the environment in which it develops (ATKINSON *et al.*, 2014). The soil structure, cultivation and drainage have a key role in the root growth and distribution. Root systems with a greater depth of branching, deeply rooted, will improve the crop growth when water and N are limited (WASSON *et al.*, 2012). One of the possible reasons for high variability of branching trait could be very different soil conditions of the countries of origin of the observed genotypes to which the root systems have adapted over many years. In general, the variation of the majority of root traits such as FBPR (36.2%), PRL (30.1%), RDW (26.8%), TLSR (23.8%) and ASR (19.3%) was greater than the variation of the stem SDW (17.4%) and SL (16.4%). CHEN *et al.* (2020) analysed 41 traits of embryonic roots and stems in 184 genotypes of bread wheat and found out that the following morphological traits of roots: length, density, surface area and the volume contributed most to the variability among observed genotypes. Results obtained by HASAN *et al.* (2018) showed significant differences among observed bread wheat varieties mostly in root traits, at different soil depths and layers, as well as at different growth stages.

Table 2. Mean value, standard deviation, minimum, maximum, coefficient of variation (CV) for eight analysed traits

Trait	Mean value	Standard deviation	Minimum	Maximum	CV (%)
PRL (cm)	9.4	2.83	2.41	14.38	30.1
FBPR (cm)	1.27	0.46	0.35	2.39	36.2
NSR (#)	3.35	0.58	1.99	4.81	17.4
TLSR (cm)	19.12	4.56	10.32	29.99	23.8
ASR (°)	93.93	18.16	54.71	134.11	19.3
SL (cm)	17.5	2.88	11.25	23.16	16.5
RDW (mg)	4.47	1.2	1.42	7.7	26.8
SDW (mg)	16.43	2.86	10.53	24.62	17.4

Correlation analysis of observed traits

Correlation coefficients of the observed traits are shown in Table 3. The strongest, statistically positive correlation was recorded between PRL and TLSR ($r=0.794^{**}$). ZHU *et al.* (2018) stated that the primary root length reflected the total length of the lateral roots, and that these two traits were highly positively correlated. Similarity was also determined in the correlations among lateral (seminal) roots presented in the paper written by ZHU *et al.* (2018).

ASR was negatively correlated with TLSR, PRL and FBPR, but it was positively correlated with NSR. Furthermore, NSR was negatively correlated with PRL. This indicates that a smaller number of longer lateral roots with the narrower root growth angle resulted in the development of a longer, deeper root system of simpler architecture, which then overlapped less with neighbouring root systems in the soil, thus reducing the competition. At the same, the distribution of dry matter in the soil under agronomic conditions was improved (DE PARSEVAL *et al.*, 2017).

Table 3. Correlation coefficients among eight observed traits

	DPK	DPG	BBK	UDBK	USK	DS	SMK	SMS
PRL	1	-0.008	-0.245*	0.794**	-0.127	0.392**	0.642**	0.475**
FBPR		1	0.197*	0.112	-0.112	-0.359**	-0.305**	-0.283**
NSR			1	0.054	0.052	-0.364**	-0.298**	-0.361**
TLSR				1	-0.14	0.280**	0.579**	0.483**
ASR					1	0.077	-0.089	0.098
SL						1	0.520**	0.726**
RDW							1	0.716**
SDW								1

*, ** statistically significant at the 0.05 and 0.01 probability levels, respectively

Statistically positive correlations were also observed between SL and SDW ($r=0.726^{**}$), RDW and SDW ($r=0.716^{**}$), PRL and RDW ($r=0.642^{**}$), TLSR and RDW ($r=0.579^{**}$), SL and RDW ($r=0.520^{**}$), TLSR and SDW ($r=0.483^{**}$), PRL and SDW ($r=0.475^{**}$), PRL and SL ($r=0.392^{*}$), TLSR and SL ($r=0.280^{**}$) and FBPR and NSR ($r=0.197^{*}$). These results show that the root traits were highly positively correlated with the stem traits. The highest positive correlation between the root traits and the stem traits was detected between RDW and SDW. A significant positive correlation between these traits was also estimated by NARAYANAN *et al.* (2014), $r=0.64$. They stated that the increased intake of resources achieved by a larger root weight, could have contributed to the increase in the stem dry weight. Consequently, as a result of the increased stem growth, a larger number of photosynthetic assimilates reached the roots, which then increased their dry weight. BEKTAS *et al.* (2016) also pointed out to a positive correlation between the root traits and the stem traits. These authors determined a high positive correlation of root biomass and stem biomass, $r=0.78$. Furthermore, CHEN *et al.* (2020) have also established the strong correlation between these two traits, $r=0.85$.

Genotypes with a strongly developed root system in this study had a more abundant growth of the above-ground plant parts. This conclusion is consistent with the results obtained by FIGUEROA-BUSTOS *et al.* (2018). These authors indicated that the genotypes with better developed root systems (longer roots, greater root biomass, stronger root branching and thicker roots) had produced the leaf area and leaf biomass greater by 25%, compared to genotypes with less developed root systems. This was probably due to the higher level of photosynthesis in order

to provide the root system with necessary photosynthetic assimilates. The size of wheat root system is probably related to the amounts of photosynthetic assimilates that reach the root (FIGUEROA-BUSTOS *et al.*, 2018). Thus, by selecting plants with a better above-ground growth it is possible to predict a better development of the root system. This indirect selection of root traits through analysed stem properties has also been indicated by LIANG *et al.* (2011). These authors determined high positive correlations among 7 root traits and 10 stem traits of rice (*Oryza sativa* L.). All stem traits were significantly correlated with all root traits except the root diameter.

The root dry weight is more correlated with the stem dry weight, in relation to the correlation of only lateral roots or only primary roots. It indicates that the growth of both primary and lateral roots is important for a better aboveground growth. Lateral roots are very important in the water uptake from the soil, as in such a way a larger amount of absorbed water reaches shoots, resulting in the better growth of the above-ground plant parts. A study by KNIPFER and FRICKE (2011), performed on barley (*Hordeum vulgare* L.), showed that lateral roots contributed 92% to the total plant water uptake. Our results indicate that the total length of lateral roots was more important for the stem growth than the number of lateral roots, because genotypes with a smaller number of lateral roots had greater values of the stem length ($r = -0.364^{**}$) and the stem weight ($r = -0.361^{**}$). Not only NSR, but also FBPR, which reflects the branching depth, was negatively correlated with the majority of other traits. The genotypes with a greater branching depth had shorter primary roots and narrower growth angles of seminal roots. Moreover, genotypes with a greater branching depth were narrower, while genotypes with shallower root systems grew wider. Such negative correlation was also obtained by OYANAGI *et al.* (1993), NAKAMOTO and OYANAGI (1994), ARAKI and IJIMA (2001).

Cluster analysis

A graphical representation of the genetic variability of 101 bread wheat genotypes based on eight observed traits is shown in a form of a clustergram in Figure 3. Each value from the initial distance matrix based on which the clustergram was constructed is represented by a differently coloured rectangle described in the colour bar, located on the left side of the clustergram. Each column on the clustergram represents a different trait. Each row represents a different genotype and provides information about all traits of a given genotype.

The clustergram shows that the observed genotypes are grouped into two main clusters, A and B. There are 85 and 16 genotypes in the larger cluster A and the smaller cluster B, respectively. The cluster A is divided into the following two subclusters: A1 and A2. The subcluster A1 is smaller and encompasses 35 genotypes, while the subcluster A2 is larger and contains 50 genotypes. The affiliation of genotypes to a certain cluster and a subcluster is presented in Table 4.

TLSR, PRL, RDW, SDW and SL are the traits that led to the division of genotypes into two main clusters (A and B). The cluster A encompasses genotypes with values of these traits above and around the average, while the cluster B contains genotypes with values of these traits below the average. TLSR, PRL, RDW and SDW are traits responsible for subclustering (A1 and A2). The subcluster A1 encompasses genotypes with above-average values of these traits, while the subcluster A2 mainly contains genotypes with the values of these traits around the average. Regarding the remaining three observed traits (ASR, FBPR and NSR), their values differed the

most among clusters and subclusters. The subcluster A1 includes genotypes with values of these traits below and above the average, while the subcluster A2 contains mostly genotypes with the values around average. The cluster B mainly contains genotypes with above-average values of these traits.

Thirty- five genotypes originating from 13 countries are grouped in the subcluster A1. The largest number (13) of genotypes was from China, while a very small number (4) of genotypes originated from Serbia, although they were the most represented among observed genotypes. On the other hand, 50 genotypes originating from 15 countries were grouped into the subcluster A2. The largest number of grouped genotypes (14) was from Serbia. Sixteen genotypes from four countries of origin were classified in the cluster B. The largest number of the genotypes (10) was from Serbia.

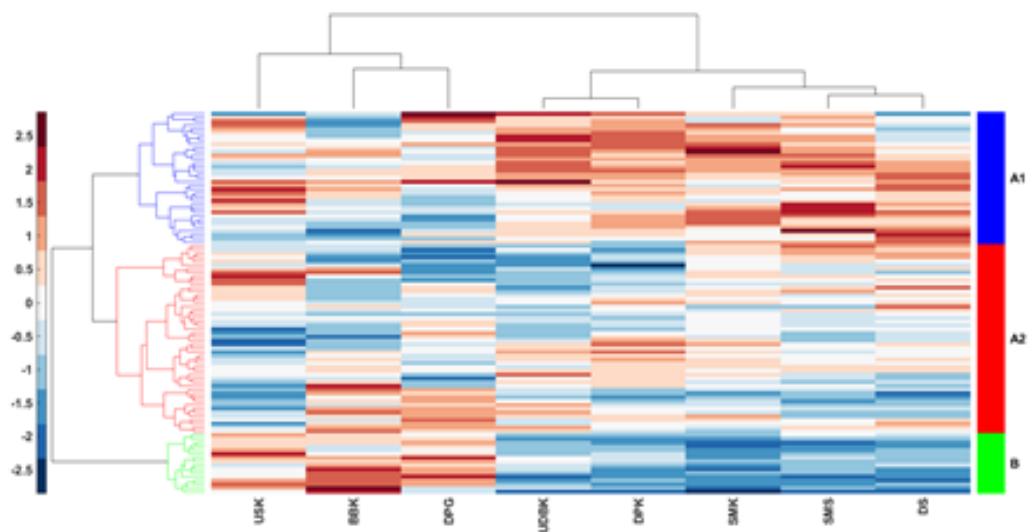


Figure 3. Cluster for 101 observed bread wheat genotypes obtained by the cluster analysis

The highest number of genotypes from Serbia was grouped within the cluster B and the subcluster A2. Using the cluster analysis, the majority of observed genotypes originating from the countries of the region (Slovenia, Croatia, North Macedonia and Hungary) were grouped into the subcluster A2 or the cluster B. These results indicate that genotypes originating from Serbia and the region had mostly average or below average values for the root and the stem length and weight, and the above-average values for the RSA traits: ASR, FBPR and NSR.

Table 4. *Belonging of observed genotypes to clusters*

SUBCLUSTER A1	CLUSTER A		CLUSTER B
	SUBCLUSTER A2		
CHI-4	ZGKT 159/82	PKB Vizeljka	
Yannong 24	Yecora	Lepoklasa	
Yannong 15	NS 46/90	KG-100	
Shannong 22	Grandor	Florida	
Tainong 18	Levante	ZP AU 11	
Lumai 23	Cajeme	Mexico 3	
Liangxing 77	Yamhill	Aleksandra	
Liangxing66	L1	PKB Talas	
Euklid	L1/91	PKB Ratarica	
Ingenio	Highbury	3-hairy	
Z. Rosa	Benni multifloret	PKB Arena	
Kazahstan 19	Chris	ZP AU 13	
ZP Xt 9.24	Avalon	BG Vitka	
Vesna	Kite	Oasis	
Jimai 22	Ct 87	ZP AU 12	
WWBMC2	Apache	ZP Oka	
Phoenix	LM 36		
U-1	Evropa 90		
PKB Dika	NS 74/95		
L.Inia	LM 35		
LM 30	Esperia		
Rebensansa	Alinea		
LM 33	Bezostaja		
LM 37	Aurelia		
Brigant	ZP Xt 9.28		
Donska semi-dwarf	ZP Xt 86.1/21		
Kazahstan 20	NS 40S		
ZP Xt 9.26	Lt 6/1		
ZP Xt 9.27	Viktorija		
ZP Xt 85.1	LM 31		
MV-Ilona	ZP Xt 88.5/2		
Triple dirk S	ZP Xt 810.11		
Peking 11	ZP Xt 9.23		
CT 62	Eurofit		
Inia	Andino		
	ZP Xt 88.86		
	ZP AU 20 (Balkania)		
	Kenong 199		
	PKB Mlinarka		
	BG Carica		

BG Merkur
Vireo S
Ching Chang 6
ZP Zlatna
Zvezdana
UPI 301
Pobeda
ZP Belija
ZP AU 19
Mironovska 808

Observed genotypes originating from the region had shorter primary roots, shorter lateral roots, lower root weight, shorter stems and the lower stem weight. At the same time, they had broader growth angles of lateral roots (wider branching), greater branching depth and a higher number of lateral roots. Thus, their root systems were shorter but wider. Such a root system could be an adaptation to the climatic conditions that occur in the area of South-Eastern Europe. The shallow and wide root system provides a water intake from the shallower layers of the soil at the time when there is occasional rain in the spring part of the growing season. The deep but narrow root system occurs under conditions of very little rainfall during the growing season. Such a root system provides a water intake from deeper soil layers where water was accumulated during the winter period or during the period with increased precipitation. According to DODIG *et al.* (2008), genotypes originating from Serbia and the countries of the region have high yields but poor drought tolerance. The maximum possible root length provides the water/moisture availability from deeper layers of the soil when there is no precipitation during the season (AHMED *et al.*, 2019). The root length during the seedling growth phase is a key trait for increasing adaptability to drought conditions (SHAHBAZI *et al.*, 2012), hence the above described traits of the root system of genotypes from Serbia could be one of the reasons for their poor drought tolerance.

Increasing yields in arid environments has becoming a progressively more important goal in wheat breeding, because of the increasing frequency and severity of drought consequences. Developmental traits, such as a deeper root system and early vigour, can help a crop to use more water (DODIG, 2010). Taking into account the obtained results, one of the possible solutions to achieve this goal would be to cross genotypes within the subcluster A1 (with above-average values of the root length and weight) to genotypes within the cluster B (with a broader branching angle and a greater branching depth), originating from Serbia or the region, with the greatest possible yield potential.

CONCLUSION

The observed root traits showed greater genetic variability compared to the stem traits. The greatest variability among observed genotypes was detected for the branching interval on the primary root, while the smallest variability was established for the stem length. Root and stem traits were highly positively correlated. The highest positive correlation of root and stem traits was established between the root dry weight and the stem dry weight. Genotypes with more

developed root systems also had the enhanced above-ground growth. Thus, based on more abundant above-ground growth, genotypes with improved root traits could be selected, which could facilitate selection in the field. The cluster analysis showed the homogeneity of genotypes originating from Serbia and the region; they usually had average or below-average values of the root and stem length and weight. However, they generally had above-average values of traits related to root architecture: the broader growth angle of lateral roots, greater branching depth and the higher number of lateral roots. In order to develop progenies with a greater early vigour of roots and stems, regional genotypes, from the cluster B, with higher values of the traits related to root architecture, and genotypes from more distant parts of the world (subcluster A1) with higher values of the root and stem length and weight, should be selected as parental genotypes for further crosses.

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**GENOTIPSKA VARIJABILNOST SVOJSTAVA KORENA I STABLA KLIJANCA
HLEBNE PŠENICE (*Triticum aestivum* L.)**

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Izvod

Ocena svojstava korena i stabla hlebne pšenice (*Triticum aestivum* L.) u ranoj fazi razvića, na stupnju klijanaca, može biti moćan alat u oplemenjivanju pšenice sa ciljem dobijanja potomstva sa bržim ranim porastom. Pokazano je da su genotipovi sa bržim ranim porastom proizveli veću biomasu i prinos zrna. U ovoj studiji izvršena je ocena svojstava korena i stabla 101 genotipa hlebne pšenice u fazi klijanaca starosti 10 dana. Analizirano je 8 morfoloških svojstava korena i stabla: dužina primarnog korena, distanca do prve grane na primarnom korenu, broj bočnih korenova, ukupna dužina bočnih korenova, ugao seminalnih korenova, dužina stabla, suva masa korena i suva masa stabla. Analizirani bočni korenovi podrazumevali su seminalne korenove. Najveću varijabilnost od ispitivanih osobina imala je distanca do prve grane na primarnom korenu, a najmanju dužina stabla. Najveća pozitivna korelacija je utvrđena između dužine primarnog korena i ukupne dužine bočnih korenova. Klaster analiza pokazala je homogenost genotipova poreklom iz Srbije i regiona; njihove vrednosti dužine i težine korena i stabla bile su uglavnom oko i ispod proseka. Međutim, vrednosti za osobine: ugao seminalnih korenova, broj bočnih korenova i distanca do prve grane na primarnom korenu, bile su iznad proseka.

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