SCREENING FOR ROOT BIOMASS DISTRIBUTION OF DIFFERENT WHEAT AND WILD GENOTYPES

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Abstract

Significant amount of root biomass was present in the top layer of soil. According to this, average root biomasses of 39 genotypes were 50.3% in 30 cm, 62.0% in 60 cm and 73.8% in 90 cm. Wheat genotypes and wild relatives showed apparent genetic variability for root biomass distribution (RBD). In 30, 60 and 90 cm root lengths, maximum values were obtained from Yellowstone with 73.7% in 0-30 cm, Tamaroi with 85.4% in 0-60 cm and 92.1% in 0-90 cm, respectively, while minimum values were taken from Iza with 25.9% in 0-30 cm, Ribasa 1 with 44.5 and 58.5% in 0-60 cm and 0-90 cm, respectively. Cultivars grown in a large area generally indicated large RBD in top soil, while genotypes such as *T. monococcum* (Kelycras, Iza), landraces (Ribasa 1, Ribasa 2) and cultivars (Gerek 79, Kunduru 1149) grown in decreasing harvested area showed small RBD.

Many factors affect root growth, development and distribution. The principal soil physical factors affecting root growth include soil water status, mechanical impedance, temperature, and aeration. Also, root growth is affected by soil chemical and biological factors, available water and nutrition. Root growth also depends on varieties, so tall varieties have deep root system (Barraclough 1991). Root growth is also affected by the source-sink relationships that exist within the plant (Willaume and Pagès 2006, Zhang and Hu 2013).

Total root length density and root biomass (Waines and Ehdaie 2007 and Ehdaie *et al.* 2010) are indicators of the size of a root system. A vigorous root system which has large biomass, length and root length density is then considered as a large root system.

There is a balance between root and shoot traits. Therefore it is suggested that selection could be deep and small root system in dry land, adversely large root system in irrigated land. Palta *et al.* (2011) indicated that large root system contributed to increasing the capture of water and nitrogen early in the season, and facilitates the capture of additional water for grain filling. On the other hand, Passioura (1983) suggested that small root systems could provide benefits in water-limited situations through improved water use efficiency.

Roots in the subsoil have potential value in feeding the plant, provided plant nutrients and water are available (Lotfollahi 2010). Borg and Grimes (1986) indicated 150 - 290 cm for barley root and 150 - 300 cm for wheat root under favorable environment conditions. Akman and Topal (2014) showed that root length of wheat reached above 240 cm and root biomass was accumulated to top of soil. Differences in distribution of root length and root dry-weight through the soil profile among lines were largely confined to the upper soil layers (i.e. the top 30 cm). Increases in root mass per unit root length associated with Rht alleles are evidencing a surplus of photoassimilates during stem elongation which are used for thickening the roots due to the lack of alternative sinks (Miralles *et al.* 1997). Approximately 65% of the total root dry weight was in the 0 - 30 cm layer

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(Gregory *et al.* 1978). Morita *et al.* (1993) revealed that approximately 50% of the winter wheat root system was in the top 20 cm of soil layer and approximately 80% was in 60 cm. This study aimed to investigate genotypic differences in root length and biomass distribution in 39 wheat genotypes and the wild relatives.

Parameter	Unit	Results	
PH		6.02	Slight acidic
EC	mhos/^m	1.53	Non-saline
CaCO ₃	CaCO3%	1.20	Calcareous
Organic matter	%	4.51	High
Texture	ml	46.20	Loam
Total salts	%	0.05	Non-saline
$P(P_2O_5)$	kg/da	73.66	Very high
Potasyum (K ₂ O)	"	412.01	Edequate
Ca	mg/kg	10465.00	Very high
Mg	"	728.00	High
Zn	"	63.48	Edequate
Mn	"	19.08	Very high
Cu	"	16.84	Edequate

Table	1.	Physico-chemical	pro	perties of	peat used	as soil	in the study.

Table 2. Average temperature and precipitation including 1980 - 2013 and 2013 - 2014 in Konya.

Months												
Years	9	10	11	12	1	2	3	4	5	6	7 Total M	Mean
2013 - 2014*	3.0	12.1	15.0	10.3	95.3	21.9	25.9	14.1	33.3	29.0	41.2 301.1	
1980 - 2013	10.2	30.8	37.3	42.1	33.1	25.0	25.7	37.3	40.9	21.4	7.1 310.9	
2013 - 2014**	18.6	10.8	8.0	-2.2	2.5	4.7	7.6	13.1	16.1	20.2	20.2 1	12.5
1980 - 2013	18.6	12.5	5.5	1.4	-0.4	0.7	5.2	10.9	15.5	20.2	23.5 1	0.3

* = Precipitation (mm), ** = Temperature (°C).

This study was conducted to investigate distribution of wheat root biomass in full grain maturity (GS 92) of 39 wheat genotypes under field conditions at Konya, Turkey during the 2013 - 2014 growing season. In the study, 39 genotypes of *Triticum aestivum*, *T. durum*, other *Triticum* and *Haynaldia* wild species were studied (Table 3). The experiment design was laid down "in randomized completed block design" with three replications. Each cultivar was sown in cylindrical PVC tube that was 200 cm height and 12 cm diameter, previously replaced to soil. The soil medium was a mixture of peat (70%) and perlite (30%). Soil properties are shown in Table 1. After the emergence, a seedling per tube was allowed to grow. At sowing, fertilizer DAP (18% N, 46% P₂O₅) 130 kg/ha, was applied as topdressed to all plots and at the stem elongation stage (GS 31) and completing of flowering (GS 69), a solution including 37.5 g urea (46% N), 64 g microelements (Cu, Fe, Mn and Zn), 11.8 cc humic acid for 200 tubes was used with drip irrigation system. Plants were watered once again at tillering stage. Weeds were manually eradicated. Plant roots were washed and cleaned in July and cut in segments in length of 0 - 30

cm, 30 - 60 cm, 60 - 90 cm, 90 cm above. Total root biomass and root biomass per root length was recorded after drying at 80°C for 48 h. The obtained values were transformed to percentages.

Genotypes	Taxonomy	Origin
TR062	Triticum turgidum subsp. durum	Line in Turkey
Konya 2002	T. aestivum subsp. aestivum	Turkey
Bayraktar 2000	T. aestivum subsp. aestivum	"
Harmankaya	T. aestivum subsp. aestivum	"
Tosunbey	T. aestivum subsp. aestivum	"
Karahan 99	T. aestivum subsp. aestivum	"
Çeşit 1252	T. turgidum subsp. durum	"
Kamut	T. turgidum subsp. durum	"
Kamçı	T. aestivum subsp. aestivum	Landrace in Turkey
Gır	T. turgidum subsp. durum	"
Sönmez 2001	T. aestivum subsp. aestivum	Turkey
Vanlı	T. aestivum subsp. aestivum	Landrace in Turkey
Ahmetağa	T. aestivum subsp. aestivum	Turkey
Berkmen	T. aestivum subsp. aestivum	Landrace in Turkey
Bezostaja 1	T. aestivum subsp. aestivum	Registered in Turkey
Kirik	T. aestivum subsp. aestivum	Turkey
Kızaltan 91	T. turgidum subsp. durum	"
Gerek 79	T. aestivum subsp. aestivum	"
Kunduru 1149	T. turgidum subsp. durum	"
Iza	T. monococcum subsp. monococcum	Landrace in Turkey
Esperya	T. aestivum subsp. aestivum	Registered in Turkey
PahaNIL (vrn4)	T. aestivum subsp. compactum	United States, Washington
Yellowstone	T. aestivum subsp. aestivum	United States, Montana
Tamaroi	T. turgidum subsp. durum	Australia
ARS - Amber	T. aestivum subsp. aestivum	United States, Washington
Pseudo-Boeticum	T. monococcum subsp. aegilopodies	Asia Minor
Daws High PPO	T. aestivum subsp. aestivum	United States, Washington
Rufum	T. turgidum subsp. dicoccon	Ethiopia
Rampart	T. aestivum subsp. aestivum	United States, Montana
Asturie H4	T. turgidum subsp. turgidum	Spain, Oviedo
WIR 29576	T. aestivum subsp. macha	Georgia
Westonia	T. aestivum subsp. aestivum	Australia
Vizir	T. aestivum subsp. aestivum	France
G 3081	T. turgidum subsp. dicoccoides	Lebanon, El Beqaa
Spelta 46	T. aestivum subsp. spelta	Belgium, Namur
Ribasa - 2	T. aestivum subsp. aestivum	Landrace in Turkey
Haynaldia villosa	Dasypyrum villosum	Taken from Bulgaria
Ribasa -1	Triticum aestivum subsp. aestivum	Landrace in Turkey
Kelcyras	T. monococcum subsp. monococcum	Albania

Table 3. Properties of wheat genotypes and wild relatives used in the study.

The statistical significance among means was determined by analysis of variance using statistical packages - MSTAT-C and Minitab - followed pair wise comparisons by LSD test. Meteorological data in a long-term and growing season of Konya are given in Table 2.

Statistically significant differences were found between wheat genotypes and wild relatives in terms of root biomass per unit length in 0 - 30, 0 - 60 and 0 - 90 cm (p < 0.01). Wheat genotypes and the wild relatives showed the highest root intensities in the topsoil. Root biomass distribution significantly decreased from deep in root length.

Source	DF	SS	MS	F	SS	MS	F	SS	MS	F
		() - 30 cm			0 - 60 cr	n		0 - 90 cr	n
Cultivar	38	14976.46	394.12	8.66**	11647.26	6 306.51	6.90**	7989.74	210.26	5.37**
Blok	2	142.56	71.28	1.57	51.32	25.66	0.58	33.00	16.50	0.42
Error	76	3458.95	45.51		3375.42	44.41		2973.52	39.13	
Total	116	18577.98			15074.00)		10996.25	5	

Table 4. Analysis of variance of biomass distribution in 0 - 30, 0 - 60 and 0 - 90 cm root lengths.



Fig. 1. Root biomass distribution in different root lengths of wheat genotypes.

According to our results, average root biomasses of genotypes were 50.3% in 30 cm, 62.0% in 60 cm and 73.8% in 90 cm. At the early stage of growth, over 90% of the root biomass of winter wheat was accumulated in the upper 40 cm of soil. At maturity, however, roots below 1 m constituted only about 10% of the total root length (Zhang *et al.* 2004). There is a widely accepted evidence for genotypic diversity in the root characteristics of many crop species (O'Toole and Bland 1987 and Ford *et al.* 2006). In the study, wheat genotypes and wild relatives showed apparent genetic diversity in root biomass distribution. In 30 cm root length, maximum and minimum root biomass distributions were obtained from Yellowstone with 73.7% and Iza with 25.9%. In 60 and 90 cm root length, maximum values were obtained in Tamaroi with 85.4 and 92.1%, respectively, while minimum values obtained in Ribasa 1 with 44.5 and 58.5%, respectively.

0 - 30	cm	0 - 60 c	0 - 60 cm		em
Cultivars	RBD (%)	Cultivars	RDB (%)	Cultivars	RBD (%)
Yellowstone	73.7 A	Tamaroi	84.5 A	Tamaroi	92.1 A
Tamaroi	70.2 AB	Yellowstone	81.4 AB	TR062	89.9 AB
TR062	69.0 AB	TR062	79.2 ABC	Yellowstone	88.6 ABC
Esperya	68.7 ABC	Esperya	77.5 A-D	Konya 2002	84.5 A-D
Konya 2002	67.3 A-D	Konya 2002	76.4 A-E	Tosunbey	83.4 A-E
Bayraktar 2000	66.7 A-E	Bayraktar 2000	74.8 A-F	Esperya	82.6 A-F
PahaNIL (vrn4)	62.5 A-F	Tosunbey	72.1 A-G	Bayraktar 2000	82.3 A-F
Harmankaya	62.3 A-F	Harmankaya	71.1 A-G	Gır	81.9 A-G
Tosunbey	60.0 A-G	PahaNIL (vrn4)	70.2 A-H	Rufum	81.6 A-G
Karahan 99	56.0 B-H	Gır	67.8 B-I	Harmankaya	79.0 A-H
Çeşit 1252	54.4 C-I	Karahan 99	66.7 C-J	PahaNIL (vrn4)	78.7 A - H
ARS-Amber	54.2 C-I	Rufum	66.5 C-J	Rampart	78.1 B-H
Kamut	53.9 D - J	Kamçı	65.2 C-K	Karahan 99	78.0 B-H
Pseudo-Boeticum	53.3 D-J	Rampart	64.4 D-L	Kamçı	77.5 B-H
Kamçı	53.2 D-J	Kamut	64.2 D-L	Kamut	77.0 B-I
Daws High PPO	52.4 E-J	Çeşit 1252	64.1 D-M	Ahmetağa	75.8 C-J
Gır	51.2 F-K	ARS-Amber	62.2 E-M	Çeşit 1252	74.3 D-K
Rufum	50.0 F-K	Pseudo-Boeticum	62.0 F-M	G 3081	74.2 D-K
Rampart	49.9 F - K	Daws High PPO	61.4 F-N	Daws High PPO	73.6 D - L
Sönmez 2001	49.4 F-K	Ahmetağa	60.5 G-N	WIR 295675	72.8 D-L
Asturie H4	49.3 F-K	WIR 295675	60.3 G-N	ARS-Amber	71.9 D-L
WIR 295675	49.3 F - K	Sönmez 2001	59.5 G-N	Vizir	70.9 E-M
Westonia	48.5 F-K	G 3081	58.4 G-O	Iza	70.5 E-M
Vizir	46.4 G - L	Asturie H4	58.3 G-O	Vanlı	70.3 E-M
G 3081	43.8 H-M	Westonia	57.8 G-O	Pseudo-Boeticum	69.8 F-M
Vanlı	43.7 H-M	Vanlı	56.6 H-O	Asturie H4	69.6 F-M
Ahmetağa	43.1 H-M	Vizir	55.4 I-O	Sönmez 2001	69.4 F-M
Berkmen	43.1 H - M	Gerek 79	55.3 I-O	Westonia	68.8 G-M
Bezostaja 1	42.5 H-M	Haynaldia	54.0 I-O	Kirik	67.3 H-M
Kirik	41.1 I-M	Berkmen	53.9 I-O	Haynaldia	66.5 H-M
Kızaltan 91	40.8 I-M	Kirik	53.4 J-O	Berkmen	66.5 H-M
Spelta 46	40.6 I-M	Bezostaja 1	52.8 J-O	Gerek 79	66.3 H - M
Gerek 79	40.5 I-M	Ribasa-2	52.4 J-O	Kızaltan 91	66.1 H - M
Kunduru 1149	39.4 J-N	Kızaltan 91	51.8 K-O	Kunduru 1149	64.0 I-M
Ribasa-2	39.4 J-N	Spelta 46	50.2 L -O	Ribasa-2	63.8 I-M
Haynaldia	37.2 K-N	Kunduru 1149	49.8 MNO	Spelta 46	62.7 J-M
Ribasa-1	32.9 LMN	Kelcyras	46.5 NO	Bezostaja 1	61.9 KLM
Kelcyras	31.0 MN	Iza	46.2 NO	Kelcyras	60.6 LM
Iza	25.9 N	Ribasa-1	44.5 O	Ribasa-1	58.4 M

Table 5. Root biomass distribution per unit length of wheat genotypes and wild relatives.

Large differences in root biomass distribution were observed among the wheat genotypes and the wild relatives. In central Anatolian conditions, where most of wheat cultivars such as Esperya, Konya 2002, Bayraktar 2000, Tosunbey, Karahan 99, Çeşit 1252 were grown in a large area had

more root biomass distribution in top of soil (Table 5). Furthermore, Yellowstone in Montana and Tamaroi in Australia that has a large adaptation potential and harvested area showed large root biomass distribution in top soil. However, cultivars such as Gerek 79, Kunduru 1149, Bezostaja 1 with decreasing harvested area in the region, wild wheat, *T. monococcum* (Kelcyras, Iza), wheat land races (Ribasa1, Ribasa 2) had little root biomass distribution. According to results, it could be a significant relation between yield and root biomass distribution in top of soil.

In conclusion, ten wheat genotypes, Tamaroi, Yellowstone, TR0 - 62, Esperya, Konya 2002 with large root biomass distribution in top soil, unlike genotypes Kelycras, Ribasa - 1, Ribasa - 2, Iza, Spelta 46 with small root biomass distribution can be used in QTL work for finding new genes to detect root biomass distribution.

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