

Relationship Among Seedling and Adult Plant Root System in Wheat¹

S. Kuruvadi*, T.F. Townely Smith**

ABSTRACT

Sixteen wheat (*Triticum durum*) genotypes were evaluated in the greenhouse for root development at four different dates ($D_1 = 15$, $D_2 = 30$, $D_3 = 45$ and $D_4 = 60$ days from seeding). The analysis of variance at each date and overall estimates of cultivar performance indicated highly significant differences among the genotypes studied for the total dry matter of root and shoot. The root and shoot growth was slow in the first two dates (D_1 and D_2) and increased rapidly in the last two dates (D_3 and D_4). Root dry matter increased 3.6 to 129.9 mg per day from 15 to 60 days of root development. Pelissier (4.9 g), a drought-resistant tall spring wheat cultivar, recorded maximum root mass, followed by the two breeding lines 7466-CF3C (4.6 g) and DT 367 (4.2 g). DT367 recorded maximum top dry matter of 8.3 g at 60 days of growth. Semidwarfs yielded more root and shoot dry matter over tall at D_1 , while tall produced consistently higher root and top dry matter over dwarfs in the other three dates. A highly significant interaction between dates and root mass of genotypes caused a change in the ranking of genotypes for root mass at different dates. Positive and significant correlations were obtained between 30 to 45 ($r = 0.5488$) and a mild association ($r = 0.3648$) between 30 and 60 days of root development, suggesting the optimum time to screen for wheat root development is 30 days from seeding. No relationship was evident between seedling root length and root mass of adult plants.

INTRODUCTION

A genotype with a deep and extensive root system is very important for drought avoidance. The extent and pattern of root development are closely related to the ability of the plant to absorb water and hence are of great significance in drought resistance (10). Several researchers (1, 9, 11, 12) have reported that plant water stress generally decreases as the extent of the root system increases. Jordan *et al.* (5) stated that selection for desired root

COMPENDIO

Se evaluó el sistema radicular de dieciséis genotipos de trigo en cuatro diferentes fechas ($F_1 = 15$, $F_2 = 30$, $F_3 = 45$ y $F_4 = 60$) después de la siembra, con el objetivo de determinar el tiempo óptimo para estudiar el desarrollo del sistema radicular, así como las posibles correlaciones entre diferentes características de la plántula. El análisis de varianza de cada fecha individualmente y de todas, conjuntamente, indicaron diferencias altamente significativas entre los genotipos estudiados para peso seco de raíz y de vástago. El crecimiento de raíces y vástagos fue muy lento en la primera y segunda fecha y se incrementó rápidamente en las últimas dos fechas. El peso de masa radicular se aumentó de 3.55 a 129.89 mg por día, de los 15 a 60 días. Pelissier, una variedad resistente a la sequía, produjo la máxima masa de raíz (4.9 g), siguiéndole dos líneas; 7466-CF3C (4.6 g) y DT367 (4.2 g). DT 367 produjo la máxima cantidad de materia seca (8.3 g) a los 60 días de crecimiento. Los genotipos semienanos produjeron mayor peso de materia seca de raíces y de vástago, en la primera fecha mientras los genotipos altos consistentemente produjeron mayor materia seca de ambos caracteres, en las fechas restantes. Una interacción altamente significativa entre fechas y masa radicular de los genotipos produjo un cambio en la clasificación de orden de genotipos para sistema de raíz, en diferentes fechas. Existen correlaciones positivas y significativas entre 30 y 45 días y una ligera asociación positiva entre 30 y 60 días del desarrollo del sistema radicular, sugiriendo que el tiempo óptimo para seleccionar el desarrollo de raíz fue 30 días después de la siembra. No existe una relación evidente entre longitud de plántulas y masa de sistema de raíces de planta adulta.

characteristics is slow and expensive, primarily because of the labour-intensive nature of root recovery and quantitation, but also because of additional constraints posed by soils which may greatly modify expression of genetic potential. Studies on seedling root length may be the most simple and rapid method for assessing the genotypes for greater root potential if there is a positive relationship between seedling root lengths and the root mass of the mature plant. Several investigators (3, 7) reported an association between early root growth and amount of roots at maturity. Irvine (4) studied the barley root system and concluded that there was no relationship between root length of seedlings and the root mass of the mature plant.

Relatively few reports are available in the literature which compare seedling and adult root characteristics, since studies of adult root characteristics are very time consuming. The present investigations were

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* Professor, Department of Plant Breeding, Universidad Autónoma Agraria "Antonio Narro", Buenavista, Saltillo, Coahuila, México

** Head, Cereal Breeding Program, Agricultural Canada Research Station, Swift Current, Saskatchewan, Canada

undertaken to: a) examine the variability present for root mass at different intervals of growth; b) study the relationship of seedling roots to roots at different dates of development; c) identify the optimum time for screening for root development; and d) study the associations among different stages of root development with several traits of the seedling.

MATERIALS AND METHODS

These investigations were carried out at the Agriculture Canada Research Station, Swift Current, Saskatchewan. Sixteen wheat (*Triticum durum*) genotypes were selected from diverse genetic backgrounds comprising of six semidwarfs (DI 363, Cando, 7268-94A1, 7461-Q4A, 7562-P3C and 7562-HB5D) and ten normal statured cultivars and breeding lines (DI 367, Wascana, Pelissier, Lakota, 7264-67B5, 7272-AQ5C, 7465-CR2C, 7466-CF3C, 7561-EZ2E, and 7561-FK2C). All these genotypes were obtained from the Swift Current wheat breeding project. The treatment design consisted of a split plot, randomized complete block with four replications. Main plot treatments were four different dates ($D_1 = 15$, $D_2 = 30$, $D_3 = 45$ and $D_4 = 60$ days from seeding) of root media washing and sixteen genotypes on subplots. Each carton comprised three plants of the same genotype. Adequate water was

applied to the carton as required. The soil was washed from the roots 15, 30, 45 and 60 days from seeding. The plants were grown in environmentally controlled chambers with 16 hours of light and eight hours of dark. The temperatures during light and dark periods were 20°C and 16°C, respectively. The cartons on each date were removed from the greenhouse and the soil was gently washed with a spray of water and the root mass separated from the soil. The root and shoot portions were sectioned, oven dried at 70°C for 24 hours and weights were determined.

The same 16 genotypes were grown in a wooden flat containing sand for a period of seven days from seeding under the same light and temperature. On the eighth day, sand was washed from the seedlings of each genotypes and roots were separated. The following five traits were measured on ten seedlings of each genotype: 1) number of roots; 2) length of the longest root; 3) total root length; 4) coleoptile length; and 5) total shoot length.

Data were obtained by analysis of variance for root and shoot values. Phenotypic correlations were worked out among different dates of root development with seedling attributes and also with root mass of the same genotypes grown in dry rhizotrons until flowering.

Table 1. Means of oven-dried roots and shoots at different dates.

Variety	Root dry mass days from seeding (g)					Shoot dry matter days from seeding (g)				
	15	30	45	60	Mean	15	30	45	60	Mean
Dwarfs										
DI 363	0.069	0.513	1.570	3.390	1.386	0.157	1.240	3.118	6.793	2.827
Cando	0.042	0.450	1.163	3.395	1.262	0.117	1.020	2.942	6.795	2.719
7268-94A1	0.040	0.338	1.375	3.365	1.279	0.114	1.083	3.103	6.903	2.800
7461-Q4A	0.068	0.338	1.289	2.540	1.058	0.419	1.168	3.748	8.045	3.277
7562-P3C	0.065	0.473	1.743	3.338	1.405	0.146	1.148	3.398	6.888	2.895
7562-HB5D	0.053	0.455	1.840	2.890	1.309	0.115	1.190	3.773	6.395	2.866
Mean	0.056	0.428	1.496	3.153	1.283	0.178	1.141	3.345	6.970	2.897
Talls										
DI 367	0.054	0.618	1.295	4.255	1.555	0.144	1.273	3.065	8.315	3.199
Wascana	0.052	0.610	2.055	3.533	1.562	0.136	1.508	4.160	7.793	3.399
Pelissier	0.054	0.668	2.145	4.873	1.935	0.142	1.413	3.785	7.750	3.272
Lakota	0.057	0.413	1.710	3.806	1.497	0.123	1.235	3.470	7.096	2.981
7264-67B5	0.057	0.495	1.565	3.628	1.436	0.135	1.303	3.353	6.995	2.946
7272-AQ5C	0.048	0.530	1.768	3.633	1.495	0.131	1.115	3.423	7.208	2.969
7465-CR2C	0.051	0.488	1.970	3.910	1.605	0.132	1.245	3.733	7.435	3.136
7466-CF3C	0.049	0.410	1.510	4.613	1.645	0.113	1.253	3.723	8.028	3.279
7561-EZ2E	0.049	0.485	1.420	3.698	1.413	0.124	1.173	2.680	7.425	2.851
7561-FK2C	0.041	0.588	1.835	2.558	1.255	0.104	1.240	3.630	6.100	2.769
Mean	0.051	0.530	1.727	3.851	1.539	0.138	1.276	3.502	7.415	3.079
General mean	0.053	0.492	1.641	3.589	1.442	0.130	1.225	3.443	7.247	3.012

RESULTS AND DISCUSSION

The means of oven-dried root and shoot weights of genotypes at each date of root washing and overall performance of the genotypes is presented in Table 1. The analysis of variance (Table 2) at each date and overall estimate of cultivar performance indicated highly significant differences among the genotypes studied for root and top dry matter. A highly significant interaction was obtained between the root mass of genotypes and dates, indicating that the genotypes responded differently at each date of root washing. The relation between top dry matter of genotypes and dates was not significant (Table 2).

The root and shoot growth was slow on the first two dates (D_1 and D_2), while it increased rapidly in the last two dates (D_3 and D_4). The root dry matter increased from D_1 (3.6 mg per day) to D_4 (129.9 mg per day). Root growth per day averaged approximately 3.6, 29.2, 76.6 and 129.9 mg per day at D_1 , D_2 , D_3 and D_4 , respectively. The seasonal average rate of root growth was 59.8 mg per day. The greater production of root and shoot dry matter in D_3 and D_4 was apparently the result of an overall increase in plant size, growth, number of tillers, height and vigor. At 45 days of root development, all the genotypes produced spike initiation, while the breeding line 7461-Q4A was headed at 58 days from seeding and the rest of the genotypes were on short blade. Maximum root development occurred between 45 days to 60 days from seeding. Pinthus (7) and Sathyanarayanaiah (8) have noted highest root growth formation between spike initiation and heading.

Pelissier (4.9 g), a popular drought-resistant tall cultivar, recorded maximum root dry mass at D_4 , followed by the two breeding lines 7466-CF3C

(4.6 g) and DT 367 (4.2 g). The performance of Pelissier was in conformity with Hurd (3), and Sathyanarayanaiah (8) reported that Pelissier had a very vigorous and extensive root system. The experimental line 7465-CR2C, which ranked in third position in overall mean root performance, ranked fourth in D_4 (3.9 g). DT 367 ranked in third position for roots, and first in shoot dry matter (8.3 g). The semidwarf breeding line 7461-Q4A ranked lowest, with 2.5 g for root mass, but was in second position for top dry matter (8.1 g), followed by another breeding line 7466-CF3C (8.0 g) and Wascana (7.8 g). Even with the lowest quantity of roots, the genotype 7461-Q4A produced higher top growth than the cultivar Pelissier, which ranked first for root dry mass.

Among the six semidwarfs, the cultivars Cando (3.4 g) and DT 363 (3.4 g) recorded maximum root quantity, followed by 7268-94A1 (3.3 g). Surprisingly, the semidwarfs yielded 8.9 percent more root mass and 22.3 percent shoot growth compared to tall at 15 days of growth. The tall genotypes produced consistently higher root masses of 19.4, 13.4 and 18.1 percent and top dry masses of 10.5, 4.5 and 6.2 percent at 30, 45 and 60 days from seeding respectively over dwarfs.

A highly significant interaction between dates and genotypes caused a change in the rankings of genotypes from D_1 to D_4 in the production of root mass. For example, DT 363 ranked first in D_1 and secured sixth, ninth and eleventh positions in D_2 , D_3 and D_4 respectively. DT 367 ranked seventh in D_1 , and occupied second, fourteenth and third place in D_2 , D_3 and D_4 , respectively. The tall spring wheat cultivar Wascana obtained ninth place in D_1 and secured third, second and ninth places in D_2 , D_3 and D_4 respectively. Pelissier was sixth in D_1 and first from D_2 to D_4 .

Table 2. Analysis of variance for root and shoot characters in wheat.

Source of variation	d.f.	Mean sum of squares							
		Root				Shoot		Interaction	
		15th day	30th day	45th day	60th day	15th to 60th day	15th to 60th day	Root	Shoot
Replication	3	1 9854	0 3239	11 7444	5 7450	11 5716	8 3611	1 041 2171	1 848 7330
Genotypes	15	5 8142**	9 9491**	3 8133**	4 0797**	5 0589**	2 4476**	2 9701**	1 4120NS
Error	45	0 0005	0 0037	0 0883	0 4021	0 1281	0 3060	0 1533	0 3419

** Significant at 1 percent level.

NS Non-significant.

In addition to Pelissier, these studies identified three breeding lines -7466-CF3C, DT 367-CR2C, and one cultivar (Wascana) - possessing high root mass by weight. These genotypes may contribute to drought avoidance.

An examination of the relationship between different dates (Table 3) revealed a positive and significant relationship ($r = 0.5488$) between 30 and 45 days of root development and a mild association ($r = 0.3648$) between 30 to 60 days, suggesting that the optimum time for screening for wheat root development is 30 days from seeding. Hurd (2) and Sathyanarayanaiah (8) observed that root penetration slowed at about six weeks and ceased at eight weeks from seeding. Cessation of root penetration coincided with heading, 58 to 60 days from seeding. We observed that the growth of roots ceases at heading. Therefore, root development at 60 days from seeding will reflect the quantity at maturity. These studies further suggest that the plant breeder can screen large populations to identify potential genotypes for roots at 30 days from seeding and can approximately predict the amount of roots at maturity. He need not wait until maturity for screening for wheat root development.

Seedling root characteristics were studied on the same genotypes one week after seeding and correlations worked out with different dates of root

development (Table 3). Positive and significant correlations were obtained between 15 days of root development ($r = 0.5523$) with length of the longest root. The correlation between length of the longest root of the seedling with 30 days ($r = 0.1259$), 45 days ($r = 0.2159$) and 60 days ($r = 0.4135$) growth of root development was not significant, indicating that seedling root lengths have no relationship with root development at different growth stages. A study of seedling root length at one week from seeding may not predict the performance for roots at maturity. Our results contradict several researchers (2, 3, 7) who have reported an association between early root growth and quantity of roots at maturity. Our results agree with Irvine's (4) barley root studies, where there was no relationship between root length of seeding and the root mass at maturity. The root development at 60 days from seeding under irrigated conditions showed a positive and highly significant correlation with the root mass of the same genotypes grown in dry rhizotrons ($r = 0.699$). Seedling characters such as length of the longest root ($r = 0.5096$), total root length ($r = 0.8129$), total shoot length ($r = 0.6996$) and 1000 kernel weight ($r = 0.5273$) are strongly associated with number of roots per seedling. Longest root length of the seedling is positively and significantly correlated with total root length ($r = 0.7693$) and total shoot length ($r = 0.8322$). Total root length is strongly associated with total shoot length ($r = 0.8464$) of the seedling.

Table 3. Phenotypic correlations between different dates of root development and seedling characters.

Traits	30 days root growth	45 days root growth	60 days root growth	Number of roots/ seedling	Longest root length	Total root length	Coleoptile length	Shoot length	1000 kernel weight	Root mass in dry rhizotron
15 days root growth	-0.0651	0.0238	-0.0844	0.4591	0.5523*	0.4655	0.1481	0.4658	0.2531	0.0140
30 days root growth	--	0.5488*	0.3648	0.1335	-0.1259	-0.0507	-0.1862	-0.1720	0.1956	0.0535
45 days root growth	--	--	0.1905	-0.0402	0.2159	-0.1693	-0.1662	-0.1150	-0.1225	0.2157
60 days root growth	--	--	--	-0.5366*	-0.4135	-0.5483*	-0.0643	-0.5555*	-0.1842	0.6999
Number of roots/seedling	--	--	--	--	0.5096*	0.8129**	-0.1709	0.6996*	0.5273*	0.6999
Longest root length	--	--	--	--	--	0.7693**	-0.0027	0.8322**	0.0287	-0.0420
Total root length	--	--	--	--	--	--	0.0492	0.8466**	0.3568	-0.3947
Coleoptile length	--	--	--	--	--	--	--	-0.1986	0.0275	-0.3618
Shoot length	--	--	--	--	--	--	--	--	0.2245	-0.1452
1000 kernel weight	--	--	--	--	--	--	--	--	--	-0.1792

** Significant at 1 percent level

* Significant at 5 percent level

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Notas y Comentarios

El aceite de castor comparte su veneno con la bacteria de la disentería

En lo que se refiere a venenos, una proteína, la ricina, extraída del ricino, la planta que nos dio el aceite de castor, el terror de los niños de mi época, a quienes se nos daba una cucharada al menor signo de malestar, se considera ahora uno de los venenos más poderosos. Una sola molécula es capaz de matar una célula. Los científicos han sabido por mucho tiempo que la ricina, que no es la única sustancia extraída de la semilla (otras son la ricinina, un alcaloide, y la ricinoleína, la del efecto purgativo), actúa atacando a los ribosomas, que son parte de la maquinaria esencial de la célula para sintetizar proteínas, pero no sabían lo que hace al ribosoma. Tampoco han sido capaces de explicar el porqué podría ser útil a la planta misma un veneno tan fatal. Ciertamente, ofrece una buena protección, aunque demasiado fervorosa, contra los animales que comen sus semillas. Uno encuentra en los diccionarios de química como el de A. y E. Rose (Omega, Barcelona, 1959), una llamada de atención sobre su peligro, al indicarnos que el contacto de pequeñas partículas con erosiones en la piel, ojos o nariz de los laboratoristas, pueden resultar mortal.

Ahora, investigadores médicos del Colegio Médico de Yamanashi, Japón, han encontrado que la ricina es un tipo único de enzima, similar a una toxina producida por una bacteria que causa la disentería. Yacta Endoy y sus colegas informan que la ricina no va al interior de un ribosoma a destruir la proteína y los ácidos nucleicos que allí se hallan (*Journal of Biological Chemistry* vol. 262, p. 5908 y p. 8128). Por lo contrario, la ricina corta, con precisión, una adenina residual en una posición en una cadena de ácidos nucleicos que forman una molécula crítica dentro del ribosoma, el RNA ribosomal "28S". Al hacer esto, la ricina deja intactas las conexiones de azúcar a lo largo del eje o espinazo del RNA.

Además, los investigadores encontraron que la ricina no podía remover el residuo específico de adenina si la estructura tridimensional de la molécula de RNA era perturbada. La mortal toxina vegetal necesita encajar en el blanco como un guante, y realizar su treta solamente cuando el RNA 28S era parte del ribosoma total, o era por lo menos dejado en su forma normal. El área alrededor de la adenina-4324 es la misma a través de todo el reino animal, y no es sorprendente que la ricina es venenosa universalmente, excepto para las bacterias cuyo RNA adopta una forma diferente alrededor del objetivo.