

Optimizing Root Characters and Grain Yield in Wheat

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Abstract: Plant breeders rarely study root characters, which may not be efficient. Recent studies with isogenic lines for the rye 1RS (Kavkaz) translocation in spring bread wheat Pavon 76 indicated 1RS increased root biomass, with 1RS.1AL translocation having 28% more roots than Pavon in sand cultures. In field studies, 1RS.1AL had 35% more grain yield than Pavon with irrigation. These results, and similar ones with 1RS.1AL translocation in winter wheat Karl 92 in Colorado, suggest the root systems of some US wheats are not large enough to support maximum grain yield. US wheats are influenced by germplasm from the CIMMYT program, where stems are dwarfed by the reduced height (*Rht*) alleles. These alleles may also proportionally dwarf the roots. The 1RS translocation may reverse the effect of *Rht* alleles on roots, less so on shoots. Many modern wheat cultivars have small root systems relative to landraces. Increased root biomass may allow for increased water and fertilizer uptake. Wheat breeders should select directly for root size and branching to increase grain yield under irrigation.

Keywords: bread wheat; durum wheat; root biomass; root branching; root depth; grain yield

Wheat breeders rarely select directly for root characters, which may hinder progress towards increased grain yield. Wheat-rye translocations, particularly those involving the short arm of rye (*Secale cereale* L.) chromosome 1R (1RS), have been widely used in wheat breeding programs world wide (LUKASZEWSKI 1990). Recent studies with near-isogenic lines for the 1RS translocation in spring and winter bread wheat (*Triticum aestivum* L.) grown in California (EHDAIE *et al.* 2003) and Colorado (OWUCHE *et al.* 2003) suggest the small root system of some semi-dwarf US and Mexican wheat cultivars may limit expression of maximum grain yield. Compared with isogenic series for above ground plant characters, there are few reports of the effect of root biomass and branching on grain yield in bread wheat. The 1RS arm has been used extensively in wheat breeding. On average the 1RS.1BL translocation confers a 7% grain yield increase world-wide (RAJARAM *et al.* 1983). While the morphological basis of the 1RS-translocation effect was not understood, it was initially thought to involve disease and pest resistance (ZELLER & HSAM 1983) and finally "improved adaptation". The

field studies of MANSKE and VLEK (2002) suggested bread wheat lines with and without the 1RS.1BL translocation might differ for root characters in acid soils, but the authors did not find root differences in neutral or alkaline soils. Recent studies with a near isogenic series for the 1RS translocation from Kavkaz wheat, in Pavon 76 spring wheat, in sand cultures indicated that the 1RS_K translocation always codes for increased root biomass and branching in Pavon. There was a marked location effect on root biomass depending on which homoeologous group 1 chromosome the 1RS arm was translocated to, with 1RS.1AL > 1RS.1DL > 1RS.1BL > Pavon. The 1RS.1AL translocation had 28% more root biomass than Pavon, and this was associated with 35% more grain yield in field studies with irrigation in California (EHDAIE *et al.* 2003). A similar 1RS.1AL translocation effect in winter wheat Karl 92 was reported from irrigated field studies in Colorado (OWUCHE *et al.* 2003) who found a 24% difference in grain yield between lines with and without a rye translocation. The 1RS.1AL translocation present in Karl 92 is thought to be the same as that found in the southeastern USA bread

Table 1. Grain yield of spring wheat Pavon 76 and winter wheat Karl 92 and their 1RS translocations under well-watered and droughted field conditions

Genotype	Grain yield (t/ha)		
	mean	droughted	well-watered
Pavon 76 ¹	4.1	2.9	5.2
1RS.1AL	4.9 (20%)	2.8	7.0 (35%)
Karl 92 ²			–
1RS.1AL			– (24%)

¹EHDAIE *et al.* (2003); ²OWUCHE *et al.* (2003)

wheat Amigo (SEBESTA & WOOD 1978). OWUCHE *et al.* (2003) did not look at the root system of their near-isogenic lines, but their results suggest the 1RS.1AL translocation effect on root biomass is expressed in both winter and spring wheats, and that depending on background, it is capable of increasing grain yield from 24 to 35% with irrigation. The objective of this paper is to determine if the 1RS.1AL translocation from Amigo also affects root size in spring wheat Pavon and to present a working hypothesis of how the 1RS translocation might alter root and shoot morphology.

MATERIALS AND METHODS

The 1RS_A.1AL_A translocation from Amigo was transferred to Pavon 76 spring bread wheat by Dr. A. J. Lukaszewski, from whom we obtained seed. The effect of the 1RS_A.1AL_A translocation in Pavon 76 was compared with the 1RS_K.1AL_P translocation in Pavon and the Pavon check at Riverside in sand cultures in an unheated, air-conditioned glasshouse from October 15, 2003 to January 15, 2004, in an experimental design similar to that used by EHDAIE *et al.* (2003). Seeds of the three test lines were germinated in Petri dishes and seedlings of similar size were transplanted to sand cultures containing 6.5 kg silica sand in polyethylene bags in plastic pots. The sand was brought to water holding capacity with 1755 ml half strength Hoagland solution. A small hole was put in the bottom of the bag that allowed water to drain freely from the bag, but not sand. One seedling was planted per pot. There were four replicates of the experimental materials. Plants were watered as needed, or at daily intervals with half strength Hoagland solution. At anthesis no more water was applied to the experimental plants, which were allowed to dry down. The number of tillers with

and without spikes was recorded and the height of the tallest spike. Culms were cut from the roots at sand level. Roots were carefully washed free of sand and the length of the longest root measured. Roots and stems were dried in a hot air oven for 10 days and the biomass recorded.

The 1RS arm from Kavkaz was translocated into three locations in Pavon 76, namely 1RS.1AL, 1RS.1BL and 1RS.1DL, creating, with Pavon 76, 4 near-isogenic lines (LUKASZEWSKI 1993). These lines were grown in sand cultures in a glasshouse, and in field studies at Moreno Valley, each over two seasons, in well watered and drought stressed conditions (EHDAIE *et al.* 2003). A similar contrast between Karl 92 and 1RS.1AL Karl 92 was conducted in field plots in Colorado (OWUCHE *et al.* 2003).

RESULTS AND DISCUSSION

In the experiment reported here, the 1RS_A.1AL_A translocation (from Amigo) and 1RS_K.1AL_P trans-

Table 2. Root biomass of landraces and commercial wheat cultivars measured in sand culture pot experiments under well-watered conditions

Genotype	Root biomass (g/plant)
Landraces	
Chinese Spring	4.38
Iran No. 14	3.25
Iran No. 49	6.43
Commercial	
Ramona 50	2.70
Sholeh	2.30
Chenab 70	2.43
Anza	2.35
Yecora Rojo	2.00
Pavon 76	2.50

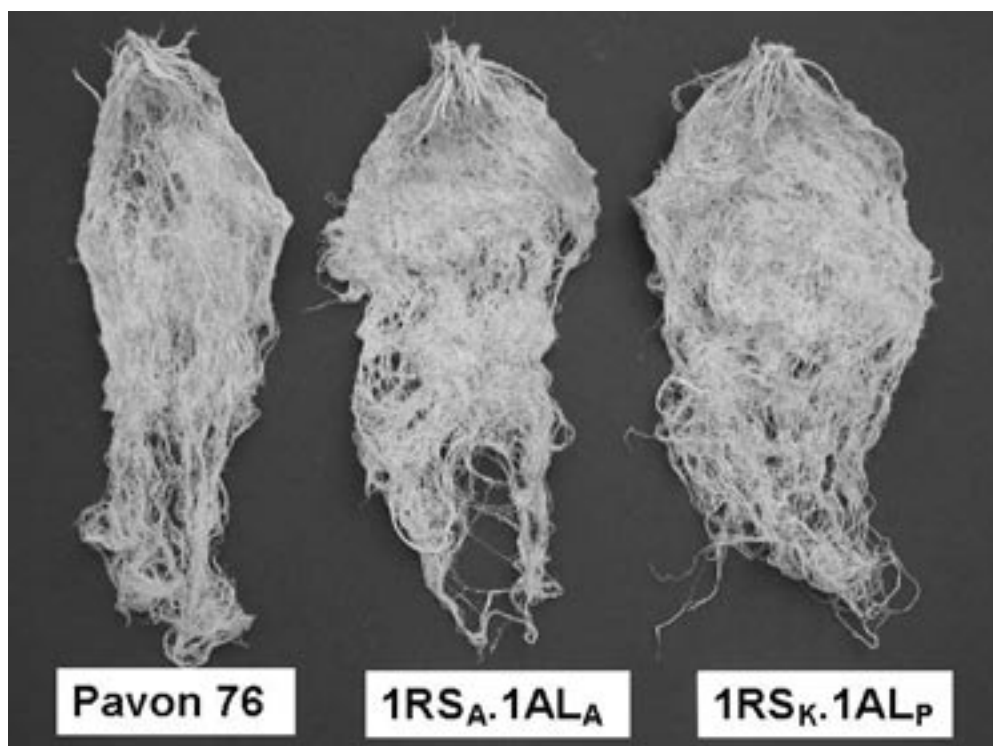


Figure 1. Root biomass of Pavon and two 1RS translocations grown in sand culture pot experiment under well-watered conditions

location lines in Pavon also showed more root biomass than Pavon 76 by 9% and 31%, respectively (Figure 1). That the 1RS translocations from Kavkaz and Amigo both increased root biomass, may explain why the 1RS.1AL translocations lines from Kavkaz and Amigo also may produced more grain yield in irrigated field studies relative to their check cultivars (Table 1) (EHDAIE *et al.* 2003; OWUOCHE *et al.* 2003). The 1RS arm from Kavkaz always increased root biomass in Pavon, depending on which homoeologous chromosome 1 it was translocated to (Figure 2) (EHDAIE *et al.* 2003). There was a marked location effect with 1RS_K.1AL_P having 28%, 1RS_K.1DL_P having 22%, and 1RS_K.1BL_P having 11% more root biomass than Pavon 76 in sand cultures. Many USA and Mexican wheats have small root systems similar to Pavon, and in contrast to the larger root systems of landraces (Table 2).

The positive association between root biomass and grain yield in the Pavon 76 near-isogenic series in glasshouse sand-cultures, and root biomass in the glasshouse and grain yield in field studies, suggests the root system of Pavon is not large enough to take up sufficient water and nutrients to support maximum grain yield in irrigated fields (Figure 2). The root system of wheat cultivars should be

optimized as well as the shoot system to support maximum grain yield (EHDAIE & WAINES 1994). MACKEY (1973) noted the root system of European wheats had decreased in size during the last 100 years due to neglect of direct selection for root characters, and to use of *Rht* stem dwarfing genes that are pleiotropic and also proportionately dwarf the roots. The same may be true for other US wheats than Pavon, which were strongly influenced by Mexican green-revolution germplasm (BORLAUG 1968) that also has small roots, relative to landrace wheats. However, the reduction in root size in USA bread wheats was evident before introduction of Mexican wheats since Ramona 50 released in California in 1950 also has a relatively small root system (Table 2). The effect of the 1RS translocations from Kavkaz and Amigo in sand culture, which increase the size of the root system, may allow uptake of more water and nutrients, which in turn supports increased grain yield.

We hypothesize genes on 1RS may interact with genes in the gibberellin synthetic pathway in wheat (SPIELMAYER *et al.* 2004) and reverse the effect of reduced height genes (*Rht*) on root size. A gene in this pathway is located on chromosome arms 1AL, 1BL and 1DL. Gene(s) on chromosome 1A were reported to control root biomass independently of

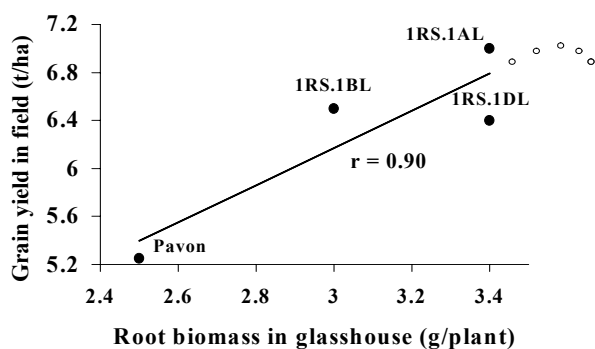


Figure 2. Relationship between root biomass in the glasshouse and grain yield in well-watered field experiments and the possibility of increasing grain yield by optimizing root biomass.

shoot biomass in cultivar chromosome substitution lines for Hope in Chinese Spring (TROUGHTON & WHITTINGTON 1968). MIRALLES *et al.* (1997) concluded wheat with a semi-dwarf stem, but with a root system that can continue to grow after anthesis is desirable. A recent model for root characters in winter wheat in the UK suggests root length should extend to 2 m and there should be many fine roots at depth to more efficiently mine the complete soil profile for water and nutrients, rather than only the top 30 cm (KING *et al.* 2003). This model also predicts there will be more grain yield from increased water uptake than from increased nitrogen uptake. The recent model (KING *et al.* 2003) contrasts with that of PASSIOURA (1984) and RICHARDS and PASSIOURA (1989) for rainfed conditions in Australia, where a wheat plant with a small root system, which conserves water use until grain filling later in the season, is postulated as ideal. Clearly, there is considerable scope for genetic manipulation of the size and characteristics of the wheat root system and for hypothesis testing in conjunction with variation in uptake of water and nutrients, and their effect on grain yield. In addition, the optimum root size of modern European wheat cultivars needs to be determined, similar to that for stem height (FLINTHAM *et al.* 1997).

The literature is sparse for isogenic studies with wheat roots, in part due to a general lack of interest in roots by geneticists and breeders, and partly because of the small number of near isogenic series available, and the time it takes to make isogenic lines. Germplasm curators may help and characterize differences in root morphology in wheat cultivars, landraces and in related species and genera, so that we have a thorough knowledge

of the variation available to breeders. Wheat geneticists may make many more isogenic series, both for individual loci, or for larger groups of loci including arm translocations. Wheat breeders should experiment with direct selection for improved root characters in breeding programs to test if these affect grain yield. Several methods to observe root systems in parental lines are available, though all involve assumptions and considerable labor (POLOMKSI & KUHN 2002). Once the differences among contrasting parents are understood, selection in a segregating population will be less difficult, and generation time may be lessened by use of molecular markers.

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