Do semi-dwarfing genes affect growth in temperate cereals?

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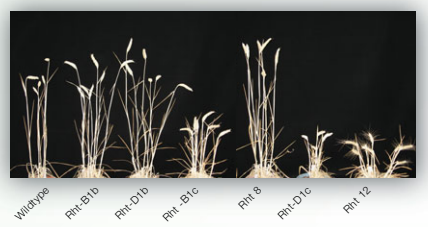
The aim of the project is to characterise the effect of semi-dwarfing and dwarfing genes on root development and growth in barley and wheat. Although reduced height genes (Rht) are associated with yield reduction and reduced early vigour, a few of the genes compensate for the reduced biomass with an increase in the harvest index or lodging resistance. About 90% of the semi-dwarf wheat cultivars grown currently contain Rht-B1b (formerly Rht1) and Rht-D1b (formerly Rht2) genes, which cause a moderate reduction in final crop height of approximately 15%.

The reduced height phenotype is mainly caused by reduced sensitivity to gibberellic acid (GA) by an interruption of GA biosynthesis or signal transduction. The effect of Rht genes on stem development and growth is well documented, but little is known about their effects on root growth. Whether and how Rht genes affect the root systems of temperate cereals is not clear, and there are conflicting reports about their effects on roots. The question is: Do semi-dwarfing and dwarfing genes affect root development and growth in temperate cereals?

To address the question, several near isogenic wheat lines (cv Mercia) were grown in gel chambers and soil. The root systems of these Rht lines were analysed with "Winrhizo" and Winrhizotron".



Method

Near isogenic lines of wheat (cv Mercia) containing semi-dwarfing genes (Rht-B1b, Rht-D1b, Rht-B1c, Rht8, Rht-D1c, and Rht12) were grown in gel chambers and in soil. Weighed seeds were individually surface sterilised, pre-germinated on filter paper and two seedlings planted in a gel chamber. The plants were grown at 15˚C for 10 d. The number of seminal root axes was counted and root length and diameter recorded by scanning with "Winrhizotron" at 2 d intervals. At final harvest, the plants were removed from the chambers and the dry weight of roots and shoots measured.

Seeds with a defined seed mass (40mg ± 1mg) were pre-germinated for the soil experiment. The seedlings of each genotype were grown in columns containing soil at either 27% or 18.5% volumetric water content. The water content of columns at 27% was kept constant while those at 18.5% were allowed to dry. After 26 days the root systems were washed and scanned with "Winrhizo" to measure total root length, average diameter and surface area.

Results

Gel chamber experiment

Figure 1 shows the increase of total root length with time (two days intervals)

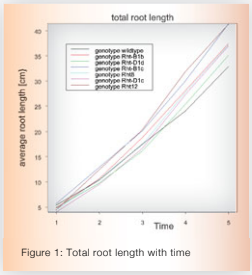


Figure 1: Total root length with time

Figure 2 shows the total root length at final harvest. The genotypes with least significant differences ($p < 0.05$) are marked (*). The genotypes (Rht-B1c, Rht-D1c, and Rht12) showed significant increase in total root length from the wildtype by 8 d.

The table highlights significant differences between the genotypes over time. The data were adjusted for the seed mass covariant, as the seed mass had a significant effect on root growth ($p < 0.01$).

Day	Wildtype	Rht-B1b	Rht-D1b	Rht -B1c	Rht 8	Rht-D1c	Rht 12	lsd (5%)
2	4.93	4.64	4.71	5.78	4.33	4.32	4.92	1.323
4	9.89	10.48	9.61	**12.93**	10.39	9.82	**12.97**	2.655
6	16.8	18.59	15.94	20.31	17.19	17.14	**21.12**	3.999
8	21.99	27.48	24.81	**30.61**	27.17	**28.76**	**34.13**	6.116
10	30.1	36.6	34.1	**42.2**	36.4	**39**	**44.5**	7.9

Table 1: Total root length with time

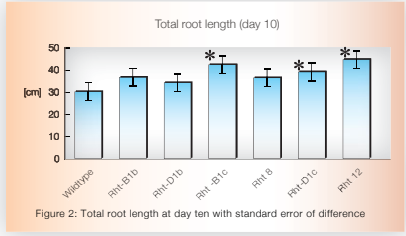
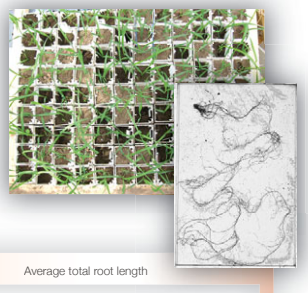


Figure 2: Total root length at day ten with standard error of difference

Soil experiment

Figure 3 shows total root length for each genotype at harvest (26 days). The genotypes compared to wildtype with a least significant difference ($p < 0.05$) are marked (*). The root systems of Rht-B1c, Rht-D1c, Rht12 differ from wildtype with the total root length significantly reduced.



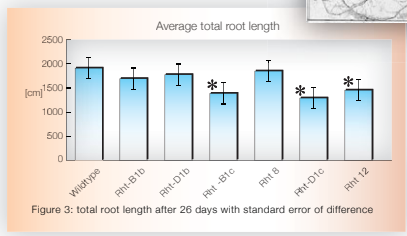


Figure 3: total root length after 26 days with standard error of difference

Conclusion

The following near isogenic lines in wheat showed significant differences in their total root length from the wildtype: Rht-B1c, Rht-D1c and Rht12. These genotypes had an increased total root length when grown in a gel chamber for 10 days but a shorter root system in the soil experiment after 26 days. Future work will test if root growth is influenced by the growth media or plant developmental stage. Expression studies of orthologous genes in barley should help to answer the question: how do these genes affect root growth?