

Root architecture of wheat and barley is affected by expression of reduced height genes

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Most modern temperate cereal cultivars contain major dwarfing genes, but there are conflicting reports in the literature about their effects on root growth. Near-isogenic lines were used to characterise the effects of semi-dwarfing and dwarfing alleles on root growth of *Triticum aestivum* cv Mercia and cv Maris Widgeon. These NILs (*Rht*-B1b, *Rht*-D1b, *Rht*-B1c, *Rht*8, *Rht*-D1c and *Rht*-12) were grown in gel chambers, soil-filled columns and in the field.

Total root length of the dwarf lines (*Rht*-B1c, *Rht*-D1c, and *Rht*12) was significantly different to that of the control although the effect was dependent on the experimental methodology; in gel chambers root length of dwarfing lines was increased by about 40% while in both soil media it was decreased (by 24-33 %). Root dry mass was 22% to 30% of the total dry mass in the soil-filled column and field experiments. However, no significant differences in root length were found between semi-dwarfing lines and the control line in any experiment, nor was there a significant difference between the root lengths of the two cultivars grown in the field. Although total root length was altered by dwarf alleles at the reduced height genes, root architecture (average root diameter, lateral root: total root ratio) was not affected by height reducing alleles. A direct effect of dwarfing alleles on root growth, rather than a secondary partitioning effect, was suggested by these experiments.

A barley mutant (*sln1.d*), orthologous to *Rht*-B1b and *Rht*-D1b had a comparable phenotype to *Rht*-B1c and *Rht*-D1c and was used to explore differences in genes expression between the control and the GA mutant. Microarray data and microscopy of *Hordeum vulgare* cv Himalaya were used to identify putative target genes of the gibberellic acid pathway in roots and to give new insights into the interdependence of root and shoot growth.