

GENETIC VARIATION FOR ROOT DEVELOPMENTAL TRAITS IN *BRASSICA NAPUS* SEEDLINGS

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The importance of root architecture in plant production stems from the fact that many soil resources are unequally distributed, or are subject to localized depletion, so that the spatial arrangement of the root system will in large measure determine the ability of a plant to exploit those resources. In soil due to the low mobility of some plant nutrients, their acquisition is dependent on the spatial exploration by plant roots. Soil exploration by plant roots is a function of root growth and architecture. Root architectural characters in crop plants are important for nutrient acquisition, which includes basal root whorl number, adventitious rooting, root hair length, density, branching etc. under genetic control of the plant species/genotypes.

Root morphology, architecture, root hair density, ability to modify the rhizosphere and mycorrhizal symbiosis strongly influence the nutrient acquisition by plants (Ma et al. 2001; Wissuwa and Ae 2001; Schweiger et al. 2007). Root development plays a significant role in seedling establishment and vigour after germination. Root vigour and architecture have a significant influence on the ability of the plant to access soil water; hence root traits play a key role in plant growth and ultimately yield.

Despite the importance of the roots, few studies have systematically investigated the extent of genetic variation for root vigour and architecture in *Brassica napus*. In this study we are investigating root developmental traits in a large *B. napus* diversity set comprising more than 500 inbred lines representing winter, spring and semi-winter type oilseed, fodder, vegetable and re-synthesized rapeseed (ERANET-ASSYST diversity set) along with the segregating, doubled haploid winter oilseed rape mapping population from the cross 'Express 617' x 'V8' (ExV8-DH).

To digitalize the root developmental parameters in large numbers of genotypes under controlled conditions an *in vitro* rhizotron system was used. Seeds were surface sterilized by washing with 6% NaOCl and were sown on the plates containing growth medium (standard MS medium in Gelrite). Plates were then placed vertically in the growth chamber for seed germination. Plants root development was estimated at 3, 5 and 7 days after sowing by scanning with a flatbed scanner (Scanjet 5400C, Hewlett-Packard). Images of the growing root systems (e.g. Figure 1) were obtained by digitizing plates from the bottom and were analysed by using image analysis software ImageJ NIH Images (Abramoff et al, 2004). On day 7, each visible secondary root was given a registration number. The lengths of both primary and secondary roots were recorded on that image and later on images corresponding to earlier days.



Figure 1. Example for assessment of root development in the *in vitro* rhizotron system. Five plants each from three different inbred lines showing clear differences in seedling and root development are shown. Plates are digitalized on a flatbed scanner at 3, 5 and 7 days after sowing and mean values for primary and secondary root development are calculated from differential root length measurements of each genotype over time.

Data from primary and lateral root length and number of lateral roots will be used for quantitative trait locus (QTL) mapping and association analysis using genome-wide SNP data. Identification of genomic sequence regions linked to QTL controlling variation for root traits is a first step towards marker-assisted selection for improved root vigour, and could eventually lead to the identification of genes involved in regulation of root developmental traits.

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