Genomics of the root-soil interphase

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Roots provide a dynamic interface between plants and the soil. Root systems anchor plants, enable them to acquire water and nutrients, generate and modify soil structure, and determine the distribution and quality of carbon fluxes into the soil microbial community. Root growth and distribution is determined both by plant genotype and the soil environment. For example, we have found previously that root growth is slowed by drought and salt stresses, but promoted by nitrogen deficiency – the extent of the response varying among barley lines tested. Mutants have provided insight into the genetic control of root traits such as the occurrence of root hairs. However, the study of metrical traits has lagged behind, because of the difficulty in screening large populations of root systems. Our aim is to study the genetic controls of root traits in barley, and to understand their functional significance. This work is integrated between the Plant-Soil Interface, Genome Dynamics and Gene Expression Programmes at SCRI.

We designed a rapid screening technique to select for root development during seedling establishment. Root length and depth, root number, and root angular spread were chosen as key parameters that determine the efficiency and rate at which root systems explore and exploit the soil volume. The two-dimensional seedling test consists of growing barley in the dark between two plates coated with thin layers of gel and recording root traits manually or using a desktop scanner with image analysis software (Fig. 1). A genetic mapping population of barley (Derkado x B83-12/21/5) has been subjected to this test and the loci affecting the 2-D root traits identified (Fig. 2) with, for example, loci affecting root length on four of the seven barley chromosomes: 2H, 4H, 5H and 7H. The only association with a known gene is that with decreased 2-D root length due to the *ari-e*.GP dwarfing gene on the short arm of chromosome 5H. In addition to 2-D root assays, data from several studies have also been mapped in this population e.g. salt tolerance in hydroponics, seedling response to gibberellic acid, field measurements of yield and laboratory assessment of grain nitrogen content[1]. From these studies we can say that the two dwarfing genes *sdw*1 and *ari-e*.GP affect many traits but are distinctive in their action as the *sdw*1 locus has fewer physiological

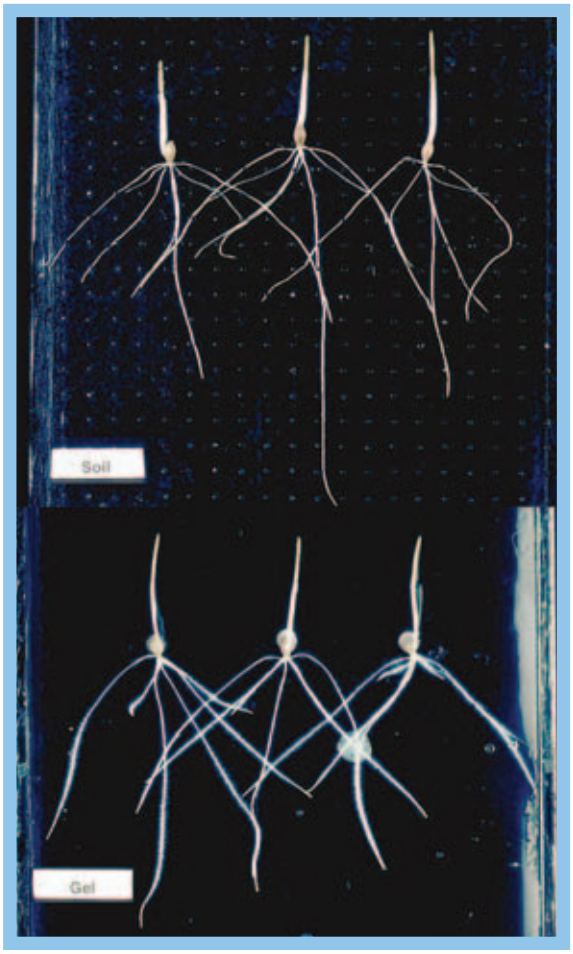

Figure 1 Barley seedlings growing in a 2-dimensional system to investigate root structure, the top panel shows the root system of the cultivar Chime after soil has been washed away, the bottom shows a similar developmental pattern when grown between gel coated plates.

effects. Field performance is only affected by the *ari-e*.GP locus which is association with a QTL x E effect for grain yield. Otherwise QTLs for seedling root traits, whether from hydroponic studies or from the 2-D test, show no association with yield QTLs. This is also the case for other seedling traits such as GS2 (the rate of leaf emergence) and TN2 (the rate of tiller emergence) and illustrates the lack of any direct relationship between early seedling development and yield in this population. There is, therefore, potential to alter root structure to improve root traits such as nutrient uptake without incurring a yield penalty.

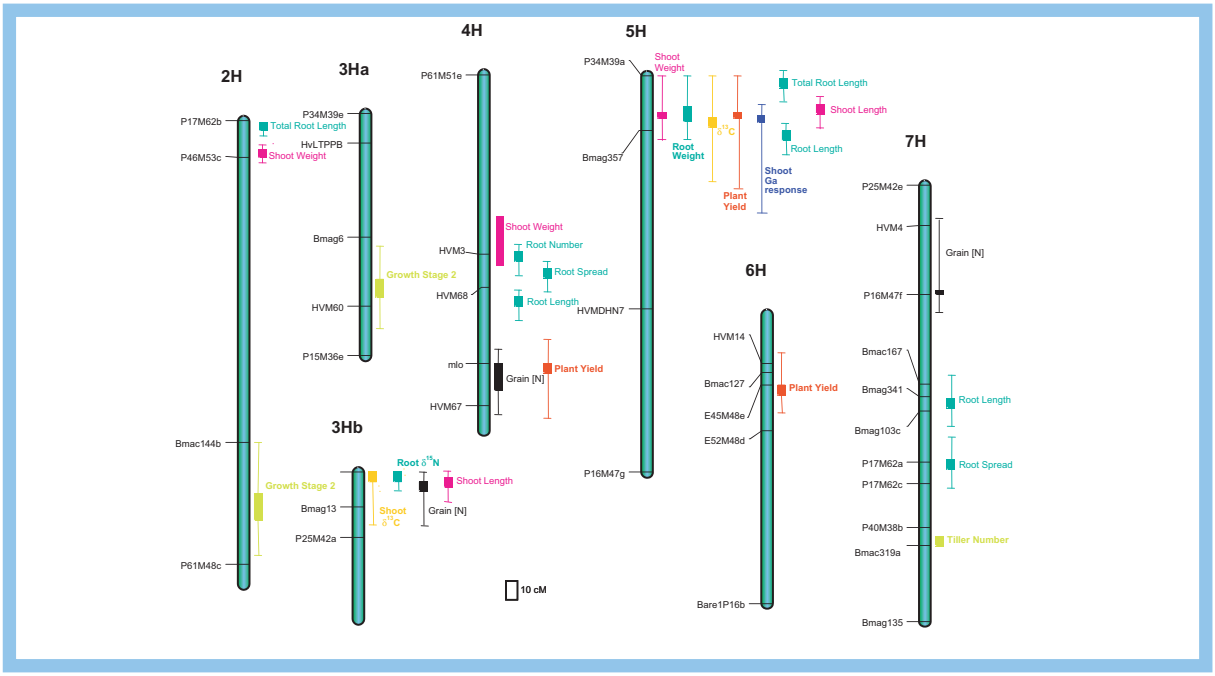

Figure 2 Genetic map of Derkado x B83-12/21/5 DH population. The position of QTLs is indicated by box and whisker plots. The box indicates 1 LOD distance and the whisker the map distance for which the QTL exceeds the threshold for SIM. No QTLs were located on chromosome 1H so it has been omitted.

In order to directly assay which genes may be of importance to abiotic stresses, gene expression in roots is being studied using expressed sequence tags (ESTs), cDNA-AFLPs and cDNA microarrays, as part of the Investigating Gene Function (IGF) programme (see article on Barley Transcriptome Resources). ESTs have been derived from root mRNAs of barley plants subjected to various hydroponic treatments (control, salt stress, nitrogen deprived, drought, waterlogging and etiolated) to identify common and specific responses. Over 1,000 ESTs from each treatment have been generated, allowing us to compare root gene expression among treatments. cDNA-AFLPs have been utilised to generate an independent comparison of expression (Fig. 3), and microarrays derived from unique root ESTs (~ 1,300) will be used to produce detailed expression profiles during root development and under stress. This will allow us to identify potential candidate genes for such stress responses in barley.

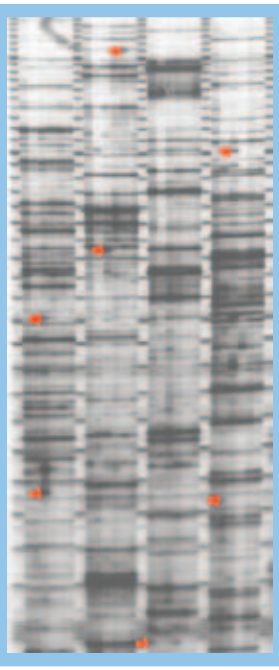

Figure 3 cDNA-AFLPs derived from barley root RNAs used to identify differentially expressed genes (examples highlighted) between different abiotic stresses.

Acknowledgements

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References

[1]Ellis, R.P., Forster, B.P., Gordon, D.C., Handley, L.L., Keith R.P., Lawrence, P., Meyer, R., Powell, W., Robinson, D., Scrimgeour, C.M., Young, G.R., Thomas, W.T.B. (2002). *Journal of Experimental Botany* 53, 1176-1176.