Mapping water-soluble carbohydrate content in perennial ryegrass

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Introduction Perennial ryegrass (*Lolium perenne* L.) is the main species used in UK agriculture and shows considerable genetic variation for water-soluble carbohydrate (WSC) content (Humphreys, 1989, Turner *et al.,* 2001, 2002). High-sugar grasses have already proved useful in UK livestock production (Miller *et al.,* 2001), but can be unpredictable in the field. Increased understanding of carbon partitioning in ryegrass would benefit future breeding programmes.

Materials and methods A perennial ryegrass mapping family derived from a high WSC x low WSC cross was used to map components of WSC comprising fructan polymers, fructan oligomers, sucrose, glucose and fructose. In order to identify regions of the genome which control basic carbohydrate metabolism, a strategy to maximise G-effects and minimise GxE and E-effects was employed. Data were replicated over years (ie one replicate was collected each year for several years), and QTL reproducible over years were characterised. In this way confounding effects from short-term environmental variation were minimised. Two different tissues (leaves and tiller bases) and two sampling times (spring and autumn) were included to give some information on tissues with different roles and carbon status. Carbohydrates were measured by HPLC. Interval and composite mapping were carried out with MapQTL.

Results Most traits showed considerable variation within the family. Tiller bases always had higher WSC than leaves and autumn samples had more WSC than spring samples. In most of the tissues analysed high molecular weight fructan constituted the major part of the WSC pool. Correlations between traits didn't always lead to corresponding clusters of QTL and some traits had no reproducible QTL. Many QTL were observed in only one year's data and were disregarded. Reproducible QTL were found in only a few regions of the genome and tended to form clusters. Leaf and tiller base QTL did not coincide; tiller base QTL were identified on linkage groups 1 and 5 and leaf QTL on linkage groups 2 and 6. The QTL explained between 8 and 59% of the variation in the traits. The QTL do not currently overlie the positions of those fructosyltransferases that have been mapped. These have been located to linkage groups 3 and 7. However, some of the QTL on linkage group 6 do overlie invertase genes.

Conclusions Environment has a strong influence on carbohydrate content, but some QTL are reproducible over years. These QTL are located in regions that have previously been identified as important in analyses of single replicates (Humphreys *et al.,* 2003). However the QTL do not currently correspond with mapped candidate genes for fructan synthesis. Although fructan breakdown genes could be involved, it is also possible that these QTL are determined by regulatory genes.

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