

Interaction of Height and Flowering time QTL in oats and their effect on yield and grain quality

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Transgressive segregation is defined as the appearance of individuals in segregating populations that fall beyond their parental phenotypes and is often observed in breeding programmes. This is a valuable source of genetic variation as individuals identified are novel relative to their parents. The extensively phenotyped winter oat population derived from a cross between the conventional height cultivar Tardis with the dwarf oat Buffalo displays transgressive segregation for both height and flowering time. QTL analysis has revealed how the complementary action of genes from the two parents contributes to these traits. Although plant height in this population is conditioned by the major gene, *dw6*, a strong interaction was observed with flowering time QTL which also influenced extension growth. Three main QTL associated with flowering time were identified which displayed additive gene action. Buffalo and Tardis differ in their response to vernalisation and to photoperiod and distinct QTL for flowering time were obtained depending on the time of year the population was grown.

A series of QTL- near isogenic lines have been developed in which contrasting haplotypes for specific major QTL have been fixed in either a Buffalo or Tardis background using marker-assisted backcrossing. These are being used to dissect the effect of the genes controlling these traits in more detail and to develop tools to breed for improved adaptation, yield potential and grain quality. Gaining a better understanding of the genetic basis of wide-cross transgression is not only desirable from an academic view point, but also because of its practical implications.