

PROJECT TITLE

Root phenotypes of flowering time alleles

CONSORTIUM

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SUMMARY OF THE REPORT

Variation in flowering time is a key feature in many higher plant species that allows adaptation to local conditions, such as seasonal variation in day length at different latitudes. However, many of the flowering time control genes encode highly conserved functions that are phylogenetically conserved across eukaryotes, suggesting that they may be intimately involved in several other basic cellular and developmental processes. If this is indeed the case, then selection for particular flowering time alleles may necessitate trade-offs and understanding these could provide useful insights for crop breeding. This study will use the rapid cycling annual grass, *Brachypodium*, as a

model to evaluate the interaction between flowering time and root development. We have noted that there seems to be a link between variation in flowering time and in root functions such as water use and root length, and aim to combine natural variation, genetics and phenotyping to test the correlation.

Material used for these experiments included two biparental mapping populations and a set of specific mutant lines with characterized changes in known flowering time genes.

Access to the small plant platform at Aberystwyth University allowed characterization of these diverse lines, using variation in water use and root imaging to relate phenotypic variation with genetic variation, thereby addressing the hypothesis that one or more flowering time alleles also affect root function.