

Reverse Genetics (Objective 4, March 2007)

This will involve

- a) access to ca. 5000 pea cDNA sequences (ESTs).
- b) annotating sequences and identifying targets for TILLING, based on database mining and identity of orthologous genes involved in plant shoot architecture
- c) designing primers based on candidate genes, derived from a) and b) and from databases developed within the EU project (Grain Legumes)
- d) TILLING for mutants in these genes, using the platform developed within the EU project (Grain Legumes) and assessing phenotypes of mutants.

Progress:

- a) Access to ca. 5000 pea cDNA sequences (ESTs).**

Reported in year 1 (see PCGIN annual report 2005/06).

- b) annotating sequences and identifying targets for TILLING, based on database mining and identity of orthologous genes involved in plant shoot architecture**

Preliminary BLAST studies were undertaken in year 1.

- c) designing primers based on candidate genes, derived from a) and b) and from databases developed within the EU project (Grain Legumes)**

See (d), but further targets could be identified.

- d) TILLING for mutants in these genes, using the platform developed within the EU project (Grain Legumes) and assessing phenotypes of mutants.**

Sequences identified in Objective 5c have been used for TILLING in conjunction with the EU FP6 project 'Grain Legumes' and a set of 19 lines identified as carrying distinct alleles are being grown at JIC. Similarly, three lines corresponding to TILLED mutants affecting a protein involved in seed digestibility (Objective 6) have been obtained.