

PCGIN overview (March 2007)

We have held a number of stakeholder and network management meetings and extended the list of registered stakeholders through the PCGIN website, www.pcgin.org. Additional outreach activities, including talks and demonstrations, have been used to highlight and inform research within PCGIN. These are summarised below (Section 11a).

In objective 2, 'Phenotyping' data from the 2006 growing season at three locations are available for pea through the web-site. These data have been used to inform choices of lines selected for analysis in 2007, to complement the bean lines to be included in plot trials in the 2007 season.

Within objective 3 'Performance', collation of the relevant trial data from NIAB and consultation with the stakeholder group led to the selection of cultivars for genotyping. Genotyping of selected cultivars was used to choose three parents for crosses; the parent lines were chosen in consultation with industry to provide maximum information on the genetics of the characters of priority to breeders and crosses are underway. We have in addition undertaken an assessment of genetic variation within a set of vining pea cultivars and propose to progress these to develop a set of mapping populations for trait analysis. This additional project has been initiated in consultation with stakeholders.

For objective 4, an oligonucleotide array, based on 6000 EST (expressed sequence tag) sequences, is available to PCGIN through the GL-TTP. Information on primers from these (and other) sequences developed within the EU FP6 integrated project 'Grain Legumes' is available to the PCGIN in a similar manner. Preliminary studies undertaken within the 'Grain Legumes' project suggested that this oligonucleotide array would not provide a simplified method for identifying deleted segments within the framework of objective 5. A proposal to BBSRC to test the more extensive Affymetrix arrays of *Medicago truncatula* for this type of hybridisation assay was unsuccessful.

Objective 5A has led to the identification of a good candidate for a pea gene regulating a clear trait. This is a strong vindication of this approach as a way of defining pea genes. Thus we are confident that an ordered collection of Fast Neutron mutants can provide a systematic set of gene knock-outs for pea. For objective 5B further genetic mapping in pea is underway in order to refine the genetic map that aligns the pea and *Medicago truncatula* genomes. Our focus is to ensure the correct order of anchor markers placed by the 'Grain Legumes' consortium. For field bean, we have collected a set of diverse lines and selfing is underway to generate inbred parents. We will undertake a genetic diversity assessment in order to identify suitable parents for mapping populations in 2007/2008. For lupin we propose no experimental work, but maintain contact with the lupin mapping projects in Poland and Western Australia.

For objective 6 'Genetics of Seed Quality Traits', consultation with stakeholders and end-users led to the definition of priority traits for pulse vegetable (vining and export) markets, as well as for animal feed; further input was sought *via* the web-site (www.pcgin.org), to involve the industry further in the choice of lines and protocols. Quality traits have been targeted and variant lines identified for defining the role of candidate genes in determining these traits in pea. A major problem for seed quality in beans emerged during the year, as a result of unprecedented infestation by the bruchid beetle (*Bruchus rufimanus*). The network as a whole became involved in providing scientific information to various groups affected by this problem; this culminated in a LINK proposal being submitted by PGRO, together with a NIAB/JIC/PGRO proposal submitted to BBSRC/DFID. Both of these proposals have been accepted at the pre-proposal stage, and full proposals invited.