

C. Moreau¹, H. Philpott², J. Thomas², L. Turner¹, M. Ambrose¹, C. Domoney¹ and N. Ellis¹
 1: John Innes Centre, Norwich NR4 7UH, UK
 2: NIAB, Huntingdon Road, Cambridge CB3 0LE, UK

There is an extensive set of genetic marker data for *Pisum* germplasm accessions, but the performance of these lines for the priority traits identified by breeders (yield, standing ability, protein content, disease resistance) is unknown. On the other hand, there is a wealth of phenotypic and performance data, but little genetic marker data, for cultivated lines. One of the objectives of the Defra-funded Pulse Crop Genetic Improvement Network is to associate performance with genotypic data for germplasm and cultivars.

Performance analysis of germplasm

A subset of JI lines was studied in triplicate micro-plots at three locations over 3 years. Two cultivars, Bilbo and Cooper, were included for the first year. Data relating to plant vigour, lodging components (Fig. 1), flowering time, canopy height (Fig. 2), maturation time, harvest index, vegetative and flowering nodes, are being collected.

In addition, disease trials are determining susceptibility of the same lines to *Peronospora viciae* (Fig. 3), *Mycosphaerella*, *Fusarium solani* f. sp. *pisi*, *Aphanomyces euteiches*, and *Phoma medicaginis*. The cross JI15XJI1194 is available, so it should be possible to map the resistance to downy mildew in this RIL population.



Fig. 1: Examples of specific scoring criteria for standing ability

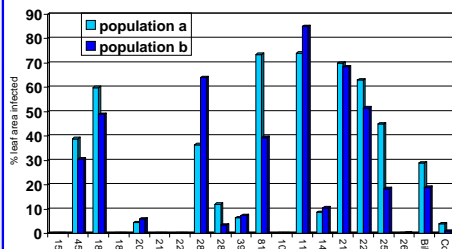


Fig. 3: Seedling reactions to two populations of downy mildew (*Peronospora viciae*)

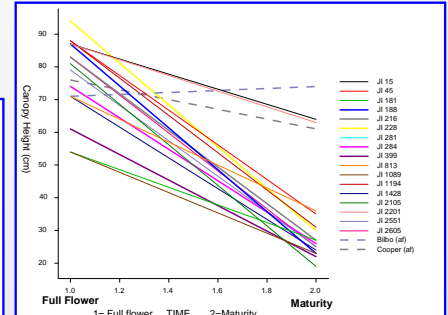


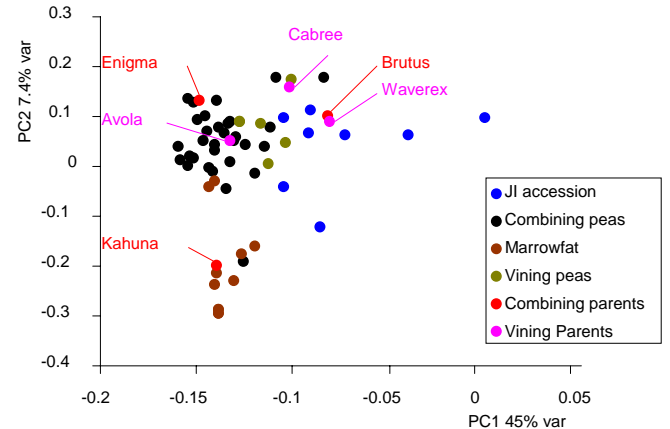
Fig. 2: Change in canopy height from full flower to maturity
 In bold are the lines carrying the beneficial allele of a lodging resistance marker (3).

Cultivar genotyping

A set of 48 cultivars, that are differential for breeders' priority traits, was selected for genotyping, using *PDR1* SSAP markers (1). JIC reference lines were included in this analysis. A principal components analysis (PCA), on 57 markers, showed that the cultivars could be distinguished genetically from the majority of the JIC lines that are the parents of existing recombinant inbred lines (Fig. 4). Crossing the three cultivars Waverex, Cabree and Avola will provide for genetic marker data relevant to the vining pea crop.

A similar analysis (with 153 markers) for the combining cultivars alone shows inter-varietal differences (Fig. 5). On the basis of this plot, together with NIAB phenotypic data (Fig. 6), distinct cultivars: Brutus (large blue), Enigma (white) and Kahuna (marrowfat), were chosen as parents for the development of RIL populations.

Fig. 4: PCA of selected accessions and cultivars



Analysis of the parental marker data, using the population genetics programme 'Structure' (2), has facilitated an analysis of the genetic distinctness of the chosen parents with respect to their relationship to the cultivars as a whole (Fig. 7). Mapping populations based on three-way reciprocal crosses between the cultivars Brutus, Enigma and Kahuna will provide genetic markers relevant to the broad groups of the combining/marrowfat pea crop.

Fig. 5: PCA of Combining peas

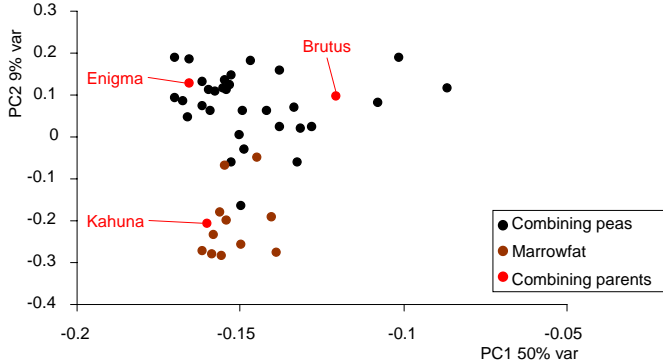


Fig. 6: Linking traits and markers: NIAB performance scores

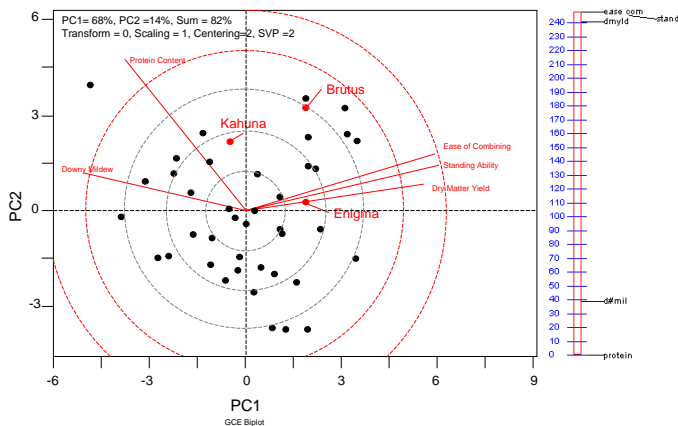
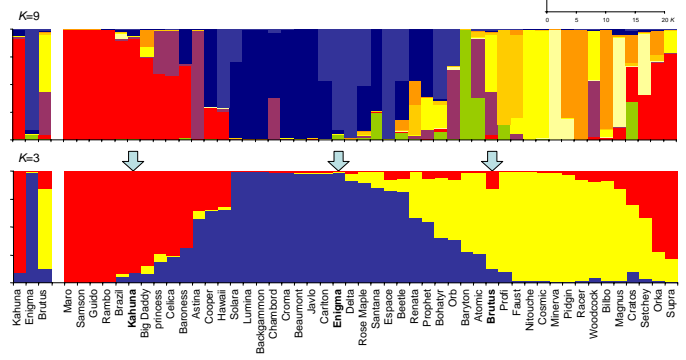


Fig. 7: Population structure and the parents (blue arrows) for PCGIN mapping populations.



References:

- Jing R *et al.* (2005) *Genetics* 171: 741-752.
- Pritchard J.K *et al.* (2000) *Genetics* 155: 945-959.
- Tar'an *et al.* (2003) *TAG* 107:1482-1491.