

## The genetic basis of *Fusarium* root rot tolerance in the 'Afghanistan' pea

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In 2003, Grünwald et al. found in their screen of the *Pisum* core collection a number of accessions that displayed significant tolerance to *Fusarium* root rot (1). Of the ten accessions exhibiting the highest tolerance to *Fusarium* root rot, six were determined to have originated from Afghanistan. Interestingly, not only were these six accessions collected from the same region of the world, but they also all possessed a genotype, including a set of allozyme markers, tall stature (*Le*), violet flowers (*A*), round seed (*R*), brown mottle on testa (*M*), and clear hilum (*pl*) that is unique to this region (3). Although not all of the six accessions have been tested, at least some are known to exhibit strain-specific nodulation with *Rhizobium leguminosarum*, conditioned by the *sym2* gene (2). In the study described here, we examined the genetic basis of this tolerance and were particularly interested in whether the brown mottle on the testa or the *sym2* gene might be contributing to the tolerant phenotype.

Two recombinant inbred (RI) populations were used in the analysis. One was very small (19 lines or RILs) and was used only for initial work. It was derived from the cross 'Afghanistan' (*sym2*) × A1078-239. The other, derived from CMG × PI 220174 consisted of 225 RILs (but only 35 completely scored). Screening for tolerance was performed in pots using 50 seeds from each RIL. Plants were harvested 25 days post-inoculation and rated on a 1-5 scale, with plants showing only minor lesions given a score of 1 and dead or dying plants scored as 5.

Results from the 'Afghanistan' × A1078-239 population indicated that the tolerance was not linked to either *M* or *sym2*. A more extensive QTL analysis of the CMG × PI 220174 RI population identified three regions of the genome that appeared to be influencing tolerance to *Fusarium* root rot. The region displaying the greatest effect on tolerance overlapped the *A* locus on linkage group (LG) II. The other two mapped to regions on LG IV and LG VII, with the QTL on LG VII showing the weakest effect. Accession PI 220174 had an average tolerance score of 1.2, whereas CMG averaged 3.3. A susceptible control, Dark Skin Perfection, averaged 3.45. Plants with the PI 220174 marker at all three QTL exhibited an average score of 1.2, matching that of the tolerant parent.

There appeared to be a strong interaction between the QTL on LG II and that on LG IV, in which the tolerance allele from PI 220174 on LG IV did not have an effect on tolerance unless the LG II QTL from PI 220174 was also present. These observations suggested a model of gene interaction that we propose for further study. We suggest that the QTL on LG II is *A*, a gene already known to be involved in the susceptibility of pea to *Phytophthora* and other soil-based pathogens. The QTL on LG IV might then represent a gene acting downstream from *A* in the anthocyanin/polyphenol/flavanoid pathways. The QTL on LG VII acts independently of these pathways, but is a relatively weak gene for defense against *Fusarium* root rot. In support of this model is the observation that all of the ten most tolerant accessions identified by Grünwald et al. (1) had violet flowers, and thus were wild-type for *A*.

If this model is accurate, there is some concern regarding the practicality of using the Afghanistan source of tolerance when breeding varieties for human consumption. As nearly all commercial types being grown for human consumption are white-flowered (homozygous *a*), neither the QTL on LG II nor that on LG IV will be applicable to improvement of such varieties. The flavors and pigments produced in the seed of pea plants with the dominant *A* gene are not appreciated by consumers, and without this allele the QTL on LG IV does not appear to be expressed. Only the QTL on LG VII would be available, and this gene has the weakest effect.

1. Grünwald, N. J., Coffman, V. A. and Kraft, J. M. 2003. *Plant Disease* 87: 1197-1200.
2. Lie, T.A. 1984. *Plant Soil* 82: 415-425.

3. Weeden, N.F. and Wolko, B., 1988. Measurement of genetic diversity in pea accessions collected near the center of origin of domesticated pea. IPBGR final report, Rome, 20 pp.