Resistance to aphid and weevil in wild peas

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Pea (*Pisum sativum*) is a widely cultivated temperate grain legume whose production can be constrained by a number of stresses. In an attempt to address the need of resistant cultivars we started at Córdoba in 1996 a research program to support resistance breeding paying particular attention to enlarging genetic diversity by identifying and exploiting resistances available in wild relatives. Like this, we identified sources of resistance in *Pisum* spp. to the parasitic weed broomrape (*Orobanche crenata*), and to the fungal diseases ascochyta blight (*Didymella pinodes*), powdery mildew (*Erysiphe pisi*), rust (*Uromyces pisi*) and fusarium wilt (*Fusarium oxysporum* f.sp. *pisi*). These were successfully crossed with elite pea cultivars and submitted to breeding. We also advanced in the understanding of the resistances by studying genes or QTLs, and in the characterization of the resistance mechanisms (1,2).

This program was recently enlarged searching for resistance also to insect pests such as pea aphid (*Acyrthosiphon pisum*) (Figure 1) and to the pea weevil (*Bruchus pisorum*) (Figure 2). This included from the screening of germplasm to the assessment of the mechanisms involved in the resistance. A multi-environment field screening allowed the identification of a number of sources of incomplete resistance to weevil (3). Both antixenosis and antibiosis mechanisms were identified against both pests under controlled conditions (4,5).

As only intermediate levels of incomplete resistance were identified we approached quantitative genetic analysis in an attempt to unravel the genetic control of resistance and the identification of molecular markers to assist breeding. Genetic studies were performed using two recombinant inbred line (RIL) populations, one developed from a cross between two *P. fulvum* accessions, and a second one developed from the cross between *P. sativum* ssp. *syriacum* and *P. sativum*. Both RILs populations were genotyped by DArTseq, and the first one was phenotyped for aphid and the second for weevil resistance. This allowed the identification of a number of QTLs associated to reduced plant damage by aphid (6), as well as others associated with reduced seed infestation by weevil, and to reduced weevil larval development (7). These studies are being continued with the aim of developing of breeders friendly molecular markers to assist resistance breeding.

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Figure 1. Pea aphid

Figure 2. Pea weevil