Construction and evaluation of Near-Isogenic Lines for resistance to Aphanomyces euteiches in pea
Clément Lavaud, Angélique Lesné, Jean-Philippe Rivière, Pierre Mangin, Guillaume Roullet, Jean-François Herbommez, Philippe Declerck, Gilles Furet, Gilles Boutet, Alain Baranger, et al.

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Common root rot of pea, due to Aphanomyces euteiches, is one of the most damaging diseases in many pea growing countries. The development of resistant varieties is a major objective to manage the disease. Several consistent Quantitative Trait Loci (QTL) controlling partial resistance were discovered from different Recombinant Inbred Line (RIL) populations (Hamon et al., 2013).

This study aimed to validate the resistance QTL effects, individually or in combination, in different agronomic backgrounds, by creating and evaluating Near-Isogenic Lines (NILs) at 0, 1, 2 or 3 of the main resistance QTL.

**Fig. 1:** Principle of Marker-Assisted Back-crossing (MAB) scheme to create NILs carrying QTL for resistance to Aphanomyces euteiches in pea

Between 2008 and 2016, two MAB schemes (MAB1, MAB2) were developed to create NILs derived from crosses between a total of seven donor lines (five lines in MAB1, two lines in MAB2) and three recipient lines. Resistance alleles brought by the donor lines RIL831.08, RIL847.50, BAP8.70/195 and BAS8.53 derived from the 90.2079, 90.2131, PI198693 and 552 resistant germplasm, respectively. After five or six back-cross (BC) generations, NILs were fixed by self-pollination. Heterozygous NILs at single QTL were also selected for future fine mapping studies. SSR, eSSR and a few SNP markers of good quality (London et al., 2005, Duarte et al., 2014) were used to control introgressions (MAB12) and return to recipient background (MAB1).

**Fig. 2:** Frequency distribution of resistance gain/loss provided by single or combined QTL on root and aerial parts of the plants in the MAB1 NILs

Resistance gain/loss = difference between lesion disease severity scores on NIL without and with QTL selected from the same cross. Lesion disease severity scores were estimated from root and aerial scoring data in 4 and 7 environments, respectively, using a linear mixed model.

Most of the NILs carrying one or several QTL showed a gain in resistance compared to NILs without a QTL.

QTL *Ae-Ps7.6*, individually or in combination with minor QTL *Ae-Ps4.1* or *Ae-Ps5.1*, increased field resistance on root parts of the plants in several recipient lines, as previously observed in controlled conditions (Lavaud et al., 2015: Fig.3).

Single or combinations of resistance alleles brought by the donor line BAP8.195 at QTL *Ae-Ps1.2*, *Ae-Ps2.2* and *Ae-Ps3.1*, increased field resistance on root and aerial parts of the plants in different genetic backgrounds. These alleles also brought undesired traits for dry pea breeding (late flowering, normal leaves, purple flowers, Hamon et al., 2013).

This study gives tools and information for the choice of resistance QTL useful in breeding to increase partial resistance to *A. euteiches* in future varieties.

It provides innovative plant material (NILs) for further studies about QTL mechanisms and action mode on pathogen populations and life cycle.