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Rémi Ollivier, Marie-Laure Pilet-Nayel, Jean-Christophe Simon, Akiko Sugio. A major-effect genetic locus, ApRVII, controls resistance against adapted and non-adapted aphid biotypes in pea. Biennial meeting of the North American Pulse Improvement Association (NAPIA), Nov 2021, Virtual Meeting hosted by the U. of Saskatchewan, Canada. hal-03594698

HAL Id: hal-03594698

<https://hal.science/hal-03594698>

Submitted on 9 Mar 2022

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A major-effect genetic locus, *ApRVII*, controls resistance against adapted and non-adapted aphid biotypes in pea.

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Context

- Pea (*Pisum sativum*) is a legume crop of major interest in the world for their high protein content and environmental benefits in low-input cropping systems.
- Yields of pea crops have become unstable due to rising insect damages with reduced use of pesticides.
- The development of cultivars resistant to insect pests is crucial for an integrated pest management.
- The pea aphid (*Acyrtosiphon pisum*) forms a complex of various biotypes, each one adapted to one or a few legume species¹.
- Some loci have been identified for *Pisum fulvum* (8 QTLs) and *Medicago truncatula* (1 QTL) resistance against *A. pisum* but not in *P. sativum*²³.

Objectives

- Investigate the natural variability of pea response to *A. pisum*.
- Identify the loci and candidate genes involved in pea resistance against *pea-adapted* and *non-adapted* *A. pisum* biotypes.



Materials and methods

- A pea collection of 240 genotypes: cultivated varieties either spring or winter peas, landraces and wild relatives.
- Phenotyping assessment of *pea-adapted* (ArPo28) and *non-adapted* (LSR1) *A. pisum* biotypes on the 240 genotypes (controlled environment).
- Genome-wide association study by mixed linear model (including structuration and kinship) on 220 genotypes using 487,686 SNPs from exome-capture sequencing data⁴.
- Identification of putative causal variants by analysis of SNP effect.

Results

- Partial resistance of some genotypes against the *pea-adapted* biotype. Many highly resistant genotypes against the *non-adapted* biotype, but some exhibiting partial susceptibility. A significant correlation was obtained between both resistance scores.
- Identification of the quantitative trait locus, *ApRVII*, on chromosome 7. *ApRVII* covers linkage disequilibrium blocks significantly associated with resistance to one or both of the two aphid biotypes studied.

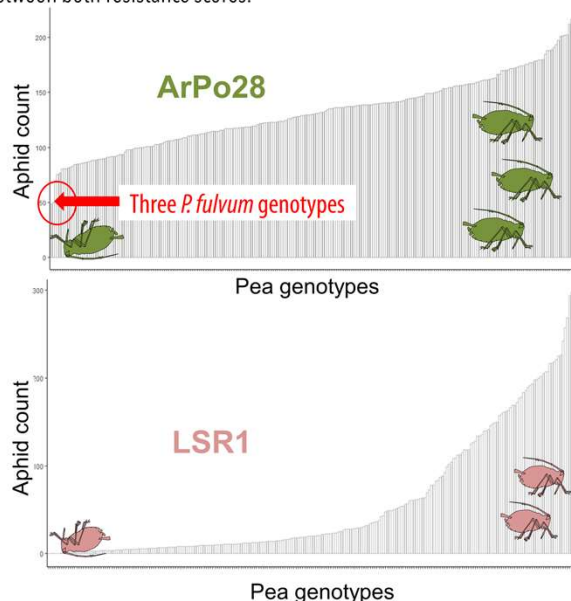


Fig.1 Fecundity assay of the *pea-adapted* (N=13) and the *non-adapted* (N=12) biotypes on the 240 pea genotypes. This assay informs plant resistance through aphid performance.

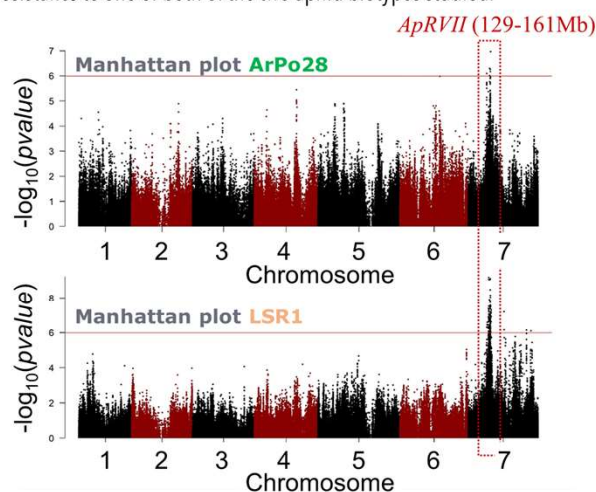


Fig.2 Association studies of resistance to ArPo28 and LSR1 aphids by mixed linear model.

- 122 genes, including 55 candidate genes with significant SNPs (4 common to both resistances). Three candidate genes shared for both resistances encode for FAD binding domains (probably involved in the biosynthesis of isoquinoline). Some of the other candidate genes comprise putative functions involved in the biosynthesis or the transport of secondary metabolites and the transcriptional and post-transcriptional regulation.

Conclusion/ Perspectives

- Screening of the pea collection revealed a continuum of resistance suggesting common genetic factors controlling the resistance against *pea-adapted* and *non-adapted* *A. pisum* biotypes and providing usefull germplasm for breeding programs.
- ApRVII*, is the first resistance-associated locus identified for *P. sativum* resistance against *A. pisum*. Importantly, this QTL is involved in the resistance against both biotypes of *A. pisum*.
- This study set the ground for molecular characterization by transcriptomic and metabolomic approaches and thus the selection of candidate genes for functional analyses.

References:

- ¹ J. Peccoud et al., (2009) A continuum of genetic divergence from sympatric biotypes to species in the pea aphid complex.
- ² E. Barilli et al., (2020) Identification of potential candidate genes controlling pea aphid tolerance in a *Pisum fulvum* high-density integrated DArTseq SNP-based genetic map.
- ³ S. Stewart et al., (2009) The RAP1 Gene Confers Effective, Race-Specific Resistance to the Pea Aphid in *Medicago truncatula* Independent of the Hypersensitive Reaction.
- ⁴ J. Kreplak et al., (2021) Exome capture genotyping data on the pea Architecture Multi-Stress collection (Peamust project).

Partners:

