Comparative genomics and molecular mechanisms of quantitative resistance to *Aphanomyces euteiches* in main pulses

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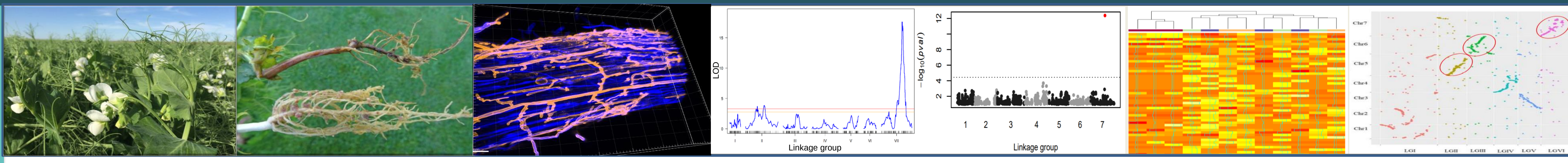

Social-economic context

Quantitative genetic resistance is a promising and durable method to control crop pathogens. *Aphanomyces euteiches* is a soilborne oomycete and a causal agent of the root rot disease. *A. euteiches* shows a broad host range in legumes and can cause the total loss of pea crop in France in highly infested fields.

Scientific context

Studies carried out at INRAE in the last 20 years identified QTL (Quantitative Trait Locus) controlling partial resistance to *A. euteiches* in pea (Hamon et al., 2011, 2013 ; Desgroux et al., 2016). However, the mechanisms associated with the QTL and their conservation in other pulses than pea, including faba bean and lentil, remain unknown.

Objectives

My PhD research activities focus on the following three points:

(a) diversity of QTL involved in partial resistance to *A. euteiches* in pea,
(b) genetic conservation of QTL between pea, lentil, and faba bean,
(c) identification of the molecular pathways associated with partial resistance to the disease in pea and faba bean.

Linkage analysis was performed in two advanced backcross (AB) populations, and a genome-wide association study (GWAS) was conducted with the pea-Aphanomyces collection (Desgroux et al., 2016) and will be carried out with a collection of 240 Pisum genotypes to investigate the diversity of QTL for partial resistance to *A. euteiches*.

QTL will be identified in a RIL population of faba bean and GWAS will be performed in a lentil collection in order to study the genomic conservation of QTL between pea, faba bean, and lentil.

Candidate genes contained in the genomic sequence of a fine-mapped major QTL for partial resistance to *A. euteiches* in pea, as well as gene expression networks regulated by this QTL in NILs, will be identified using RNA-seq and targeted metabolite analysis. Differentially expressed genes detected in pea will be compared to the ones previously identified by transcriptomic analysis in faba bean.

Results

A total of 53 resistance QTL to *A. euteiches* were identified, by integrating QTL mapping in the AB populations to previous QTL and GWAS results, validating most of the previously reported QTL (Figure 1). No new consistent resistance QTL was detected in the AB populations. However, a high diversity of haplotypes was identified in a GWAS collection at 11 consistent haplotype blocks. An accumulation of favorable haplotypes at these 11 regions was confirmed in the most resistant lines of the collection.

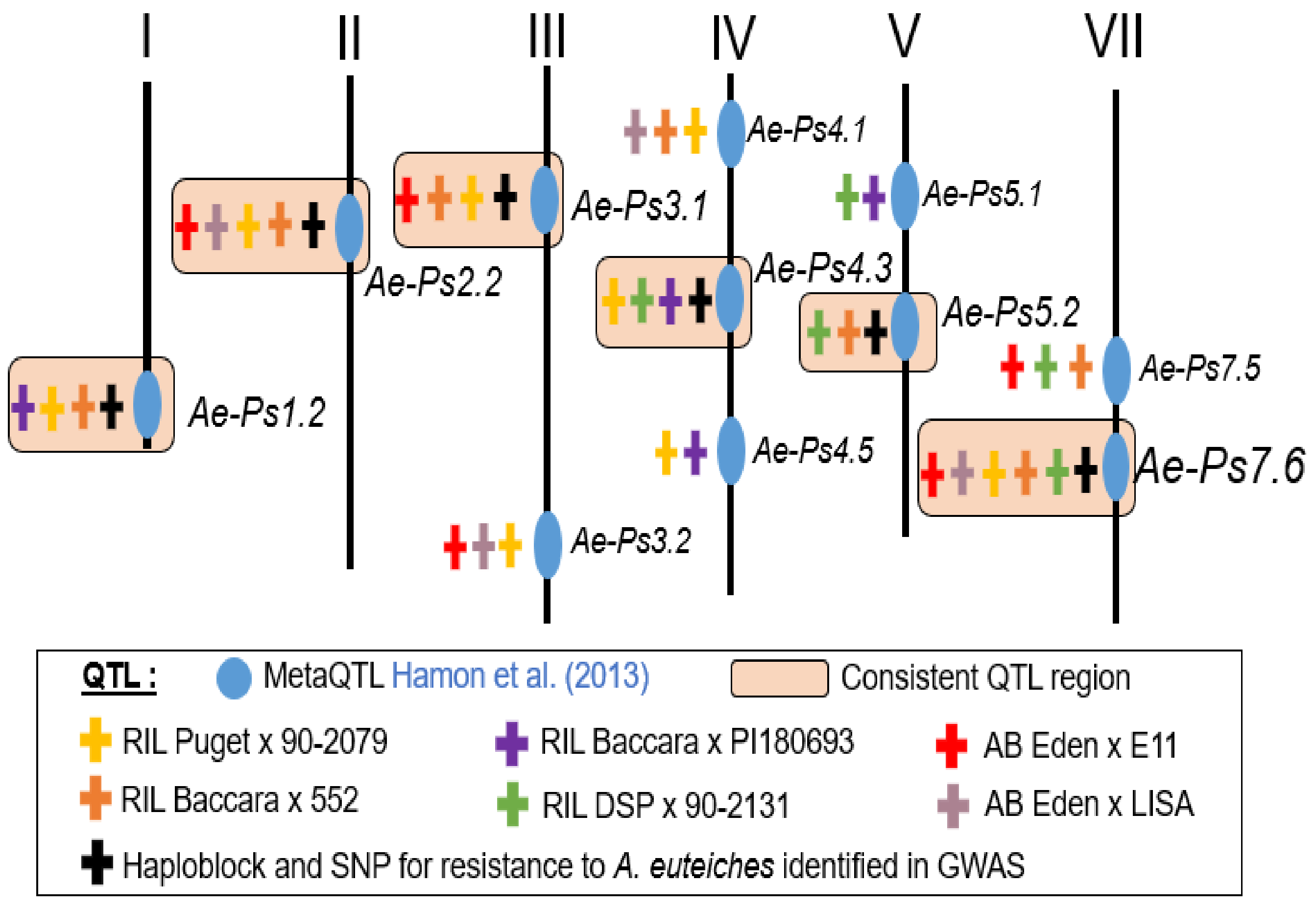

Figure 1: Genetic map showing in beige and blue, 6 consistent genomic regions and main QTL of partial resistance to *A. euteiches*, respectively identified in pea

Perspectives

Through the identification of SNP markers, molecular pathways, and candidate genes associated with QTL, this project will provide a better understanding of the mechanisms underlying the partial resistance to *A. euteiches* in main pulses and contribute to develop resistant varieties against Aphanomyces root rot disease.

Hamon, C. et al, *2011, New consistent QTL in pea associated with partial resistance to Aphanomyces euteiches in multiple French and American environments, Theoretical and Applied Genetics, vol. 123, no. 2, p. 261–281.*
Hamon, C. et al, *2013, QTL meta-analysis provides a comprehensive view of loci controlling partial resistance to Aphanomyces euteiches in four sources of resistance in pea, BMC Plant Biology, vol. 13, no. 1, p. 45.*
Desgroux, A. et al, *2016, Genome-wide association mapping of partial resistance to Aphanomyces euteiches in pea, BMC Genomics, vol. 17, no. 1.*