

# Genetic bases and comparative genomics of *Aphanomyces* root rot resistance in legumes

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Grain legumes are valuable crops that provide: (i) protein-rich seeds for human and animal consumption, (ii) nitrogen enrichment of soils through symbiotic root associations with bacteria, and (iii) crop diversification in field rotations. However, significant yield instability is commonly observed in legume-growing regions, which can discourage farmers from cultivating these crops. One of the major stresses affecting legumes is root rot disease, caused by the oomycete *Aphanomyces euteiches*. This disease has been reported worldwide, and total yield loss can occur in highly contaminated fields. Currently, no effective control method is available. The creation of resistant varieties is a major challenge in order to protect legume crops from the disease. Significant research in quantitative genetics has led to the identification of quantitative trait loci (QTL) conferring partial resistance in several legume species, especially pea (*Pisum sativum*). Notably, the first French pea varieties with tolerance to *A. euteiches*, carrying resistance QTL, have been registered in recent years. However, the resistance levels in these varieties remain insufficient to prevent pathogen multiplication in soils and to ensure long-term effectiveness of the deployed QTL. Therefore, farmers are eagerly awaiting the release of new varieties with more effective resistance obtained by combining diverse resistance alleles.

This comprehensive study aimed to explore the diversity of *A. euteiches* resistance QTL in three cool-season legumes, *i.e.* pea, faba bean (*Vicia faba*), and lentil (*Lens culinaris*), to support the development of improved future varieties. Additionally, the genomic conservation of QTL among these three species and the model legume *Medicago truncatula* was investigated to identify potentially conserved orthologous resistance genes, in order to inform QTL deployment strategies in crop rotation systems and to contribute to the long-term durability of resistance.

Using QTL mapping and Genome-Wide Association Study (GWAS) approaches applied to diverse biparental populations and diversity panels, a total of 10 consistent resistance-associated genetic regions were identified in pea, confirming two major-effect QTL (*Ae-Ps4.5* and *Ae-Ps7.6*) previously detected. A high diversity of resistance alleles at consistent QTL was identified in new pea partially resistant lines and an accumulation of resistance alleles at these QTL was confirmed in the most resistant pea lines. In addition, one major-effect QTL (*Ae-Vf3.1*) and three other low-effect loci were associated with resistance in faba bean, while only six minor-effect QTL were identified in lentil. A major-effect resistance locus, *AERI*, was confirmed and fine-mapped in *M. truncatula*, revealing three candidate genes. Comparative genomics analysis based on known QTL locations revealed no conservation of major-effect QTL conferring quantitative resistance to *A. euteiches* across pea, faba bean, lentil, and *M. truncatula*. However, conservation between major-effect QTL, *i.e.* *Ae-Vf3.1* in faba bean and *AERI* in *M. truncatula*, and minor-effect QTL in *M. truncatula* and pea, respectively, was detected in two genomic regions.

This work provided new molecular markers closely linked to *Aphanomyces* root rot resistance QTL to assist breeders in improving their germplasm and led to identify candidate genes for further functional validation. Results will support efficient and durable deployment of quantitative resistance to *A. euteiches* in legume-rich cropping systems.

**Keywords:** *Aphanomyces euteiches*, QTL mapping, GWAS, orthology, durability

## Sources :

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