

# High-throughput genetics and phenotyping, or how to unravel plant quantitative resistance to a root pathogen

The root parasite *Aphanomyces euteiches* (*Ae*) is the main pathogen of pea in Europe and is also an important limiting factor of alfalfa production in USA. Since no chemical control is available against it, genetic programs to improve crop resistance is the best hope to prevent the spread of this disease.

To accelerate genetic improvement of crop legume resistance against this parasite, we took advantage of the increasing genetic and genomic resources developed for the model legume *Medicago truncatula*, a close relative of alfalfa and pea and a natural host for *Ae*. While many lines are susceptible, the parasite development can be delayed or halted at various stages of the infection, allowing some plants to grow despite the presence of external root symptoms. These results indicate that, like pea or alfalfa, *M. truncatula* displays partial resistance to *Ae*. Unlike monogenic qualitative resistance which is usually rapidly circumvented in field by pathogens, such quantitative resistance is potentially more durable by reducing selective pressure on the pathogen. However, the genetic bases of quantitative resistance are poorly documented.

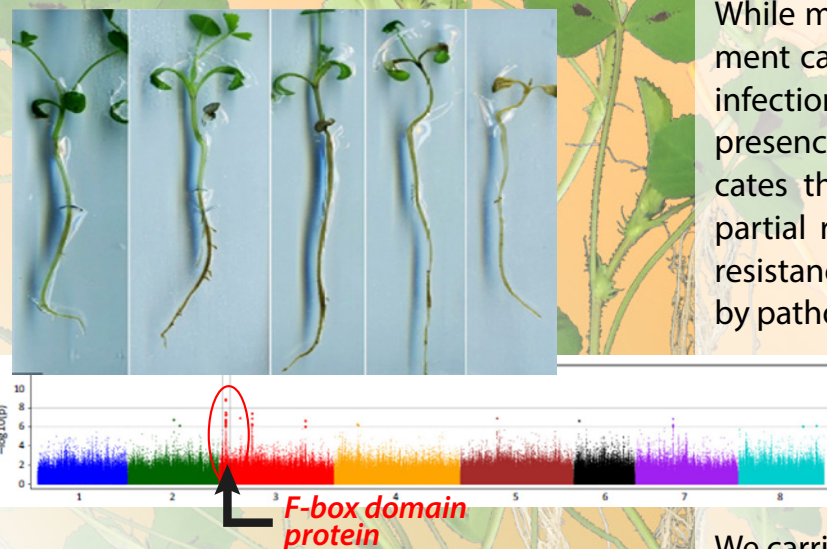


Illustration of symptom variation observed *in vitro* upon *M. truncatula* infection with *Ae* (up), and results of genome-wide association study (down), highlighting the F-box protein coding locus, on chromosome 3

We carried out a high-density genome-wide association mapping approach following *in vitro* and greenhouse phenotyping evaluation performed on a representative sample of 179 *M. truncatula* accessions ( $\approx 10,000$  plants), and exploitation of sequence data generated by the Medicago HapMap Project that produced 5,1 millions of SNPs markers. Among several candidate genes associated with resistance, the most significant encoded an F-box protein. Transcriptional and sequence analyses suggest that quantitative resistance is linked to mutations directly affecting the interaction domain of the protein, implying that the complete and functional protein is a negative regulator of resistance. Future prospects aim at identifying the molecule interacting with this F-box protein and investigating whether a pea line that displays mutations in the orthologous F-box gene can be used as a new source of resistance in a genetic program to increase pea resistance to *Ae*.