

## Integrative genomics and metabolomics approaches to decipher mechanisms underlying quantitative resistance to blackleg in oilseed rape

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Quantitative resistance controlled by multiple genetic factors with low or moderate effect appears to be significantly more durable than major resistance genes or has been shown to increase the potential for durability of major resistance genes [1]. Molecular mechanisms underlying quantitative resistance are not widely known but appear to be quite diverse [2]. The interest of oilseed rape quantitative resistance to control *Leptosphaeria maculans*, the blackleg (stem canker) agent, epidemics and population adaptation has been shown [3; 4]. Wide genetic analyses [5] showed that this resistance is controlled by a high number of quantitative trait loci (QTL). As a complement to these genetic analyses, we combined different approaches to investigate the mechanisms underlying quantitative resistance to blackleg in oilseed rape. A transcriptomic approach was applied for the comparison of susceptible and resistant genotypes that were mock-inoculated or inoculated at different stages with two isolates of *L. maculans* in controlled conditions, or that were harvested from blackleg field experiments. We aimed at studying the differential response of the two plant genotypes to *L. maculans* infection and the constitutive differences between the two genotypes that could be associated with the quantitative resistance. The potential role of some defense and secondary metabolite pathways were more specifically investigated. This allowed the identification of candidate genes, of which some are located in previously identified QTL. Quantification of some metabolites and in situ spatial metabolomics performed on histological sections are being used as complementary approaches to validate RNAseq results and identify metabolites differentially accumulated between the two plant genotypes.

### References

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