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Responses to *Neonectria ditissima* infection in apple: what do expression studies on partially resistant and susceptible cultivars tell us?

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European canker, caused by the fungus, *Neonectria ditissima*, is the most detrimental disease in Swedish apple production. Resistance to canker is quantitatively inherited and so far poorly understood. Also, basically nothing is known about the genes involved in susceptible and resistant responses in apple to *N. ditissima* attack at the gene expression level.

In this study we conducted RNAseq analyses to identify differentially expressed genes (DEGs) in response to *N. ditissima* infection between the partially resistant cultivar 'Jonathan' and the highly susceptible cultivar 'Prima'. Samples of *N. ditissima*-inoculated and water-inoculated (control) wood were taken from three biological replicates at three different time points, i.e., 5 (T1), 15 (T2), and 30 (T3) days after inoculation (dai) when measurable lesions had not developed yet.

The fraction of reads mapped to the *N. ditissima* genome sequence increased from T1 to T3, being more pronounced in 'Prima' which confirmed an adequate choice of sampling occasions.

The number of DEGs when comparing infection to control at each time point, increased from 11 in T1 ('Prima': 2, 'Jonathan': 9) to 10,635 in T2 ('Prima': 5,077, 'Jonathan': 5,558) to 17,467 in T3 ('Prima': 10,838, 'Jonathan': 6,629), some of which co-localized with previously established QTL intervals. Verification of a number of DEGs is in progress.

To examine reproducibility and generalization of results, this experiment was repeated with 'Jonathan' and 'Prima', and extended with: two partially resistant ('Aroma' and 'Golden Delicious') and two highly susceptible cultivars ('Discovery' and 'Katja').