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EAPR Pathology & Pests Section Meeting

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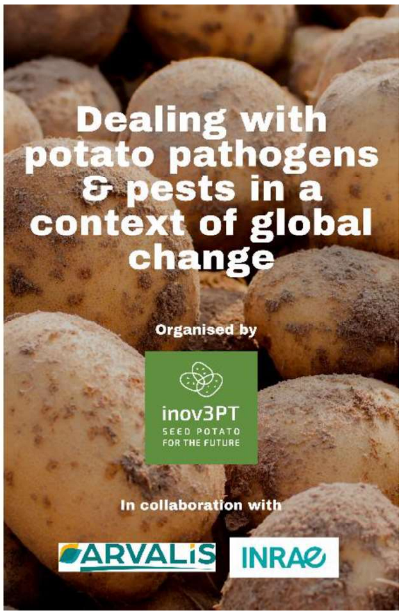
Dealing with potato pathogens & pests in a context of global change



Posters

P13

RNAseq expression analysis of resistant and susceptible potato tubers at early stage of infection with *Dickeya solani*

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QTLs for potato tuber resistance to *Dickeya solani* were identified on chromosomes II and IV in previous studies [1]. Ten diploid F1 individuals, five most resistant (R) and five most susceptible (S), were chosen for transcriptomic studies. Tubers were inoculated with bacteria *D. solani* in wounds (B), and fragments of tuber tissue were collected for RNA extraction 8 hours post inoculation. Not inoculated tubers (NT) and water-treated tubers in wounds (W) were used as control. Bulks were prepared from resistant (NTR, BR, WR) and susceptible (NTS, BS, BR) individuals. Sequencing was done on the NovaSeq6000 (Illumina). Principal Component Analysis performed of DESeq obtained from 6 different groups explained 77 % of total variation among not wounded and wounded (inoculated or water treated) potato tubers regardless of resistance level. The second component was related to resistance level and explained 15% of total variation. Significant differences in gene expressions were analysed in several comparisons: (WS vs. WR) vs. (NTS vs. NTR), (BS vs. BR), vs. (NTS vs. NTR), (BS vs. BR) vs. (WS vs. WR) as well as most frequent represented terms of gene ontology describing molecular functions and biological processes were identified.

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[1] Lebecka R. *et al.*, 2021. Plant Pathol. 70:1745-1756.