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RNAseq expression analysis of potato tubers differing in resistance to soft rot caused by bacteria *Dickeya solani*

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Soft rot of potato tubers caused by several species of pectinolytic bacteria is an important constraint to potato growers worldwide. Resistance to these bacteria is a complex polygenetic trait. A higher level of resistance than in tetraploid potato cultivars was found in diploid interspecific hybrids of *Solanum tuberosum* and wild *Solanum* species. The most resistant individuals and the most susceptible ones were selected within the mapping population DS-13 evaluated in previous studies [1]. For RNAseq expression analysis fragments of tuber tissue were collected 8 and 24 hours post inoculation with bacteria *D. solani* from tubers inoculated in wounds (B), not inoculated (NT) and wound-water-treated tubers. (W) . Bulks were prepared from resistant (NTR, BR, WR) and susceptible (NTS, BS, BR) individuals. Sequencing was performed using the NovaSeq6000 (Illumina). Genes of high ($\log_2FC \geq 2$) different expression within the bulks, were then selected and verified in single potato individuals. These genes are related to stress response, resistance to bacteria, pathogenesis, resistance genes, defence mechanisms, pathogen recognition, wound healing, and suberization. Most of

them were also found to be differentially expressed in bulk analysis of RNA collected 24 hours post-inoculation of potato tubers. Functional enrichment analysis of obtained data was performed using Gene Ontology and Kyoto Encyclopedia of Genes and Genomes (KEGGs). According to KEGGs the pathways involved in “Protein processing in endoplasmic reticulum”, “2-oxocarboxylic acid metabolism”, “Biosynthesis of amino acids”, “Citrate cycle”, “Carbon metabolism”, “Spliceosome”, “Ribosome” were commonly significantly enriched in BS vs BR, WS vs WR, NTS vs NTR. Additionally, “Valine, leucine, isoleucine degradation”, “Protein export” and “Glutathione metabolism” were enriched in BS vs BR up-regulated genes.

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