Abstract

Ralstonia solanacearum, a highly destructive phytopathogen causing bacterial wilt disease, poses a substantial risk to the potato value chain, putting global food security at risk and impeding potato production. 'Cruza 148', a locally adapted potato genotype, has been reported to exhibit resistance when cultivated in areas with a background of bacterial wilt occurrences. This study aimed to acquire a deeper understanding of the factors influencing resistance and susceptibility in 'Cruza 148' and 'Shangi' potato genotypes respectively. To achieve this, RNA-seq was deployed to detect DEGs in 'Cruza 148' and 'Shangi' potato genotypes at 6 h, 24 h, 48 h, and 72 h post-inoculation with *Ralstonia solanacearum*. A total of 54.2% of the DEGs were upregulated and 45.8% were downregulated in the roots of the 'Cruza 148' potato genotype, while 45.5% and 54.5% of DEGs were upregulated and downregulated in the roots of the susceptible potato genotype 'Shangi' respectively. The gene ontology (GO) enrichment analysis indicated that the 'Cruza 148' genotype consistently displayed the 'defence response' category throughout every stage of infection. The analysis of enriched GO terms revealed 225 terms, with 132 related to biological processes, 16 linked to cellular components and 12 linked to molecular functions. The 'Cruza 148' genotype had the highest gene counts in peptide metabolic processes and cellular component assembly, while the 'Shangi' genotype had the greatest number of gene counts that responded to chemicals and cellular component assembly. Defence genes identified, included leucine-rich repeat protein, MYB transcription factor, glucan endo-1,3-beta-glucosidase, serine/threonine-protein kinase, ethylene-responsive transcriptional coactivator and disease resistance protein, which could help explain the mechanisms and pathways of resistance to *R. solanacearum*. This study presents a fundamental understanding of the transcriptional alterations that occur during pathogen interactions with potato. It will also assist in identifying potential useful genes induced during the resistance and susceptibility processes.