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Program & Abstracts



Plant-fungal interactions

*Metschnikowia fructicola*, a biocontrol yeast against postharvest diseases:  
genome sequence, assembly and characterization

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The yeast *Metschnikowia fructicola* has been reported as an efficient biocontrol agent of postharvest diseases of fruit and vegetables. Several mechanisms of action by which *M. fructicola* inhibit postharvest pathogens were suggested, including iron-binding compounds, induction of defence signalling genes, such as PRP and MAPK cascade genes, production of fungal cell wall degrading enzymes and relatively high amounts of superoxide anions. *M. fructicola* also exhibits chitinase activity and the chitinase gene, *MfChi*, was highly induced in response to fungal pathogen cell walls.. Several studies have examined differential gene expression during the interaction of the yeast, *M. fructicola*, with host fruit or with a postharvest pathogen. In the current work, we report the assembly of the whole genome sequence of two strains of *M. fructicola* using PacBio and Illumina shotgun sequencing technologies. Using the PacBio, a high-quality draft genome consisting of 93 scaffolds, with an estimated genome size of approximately 26 Mb, was obtained. Comparative analysis of *M. fructicola* proteins with three available closely-related genomes revealed a shared core of homologous proteins coded by 5,776 genes. Comparing the genomes of the two *M. fructicola* strains using a SNP calling approach resulted in the identification of 564,302 SNPs/indels with a total of 2,004 predicted high impact mutations. Based on the assembled genome, sequences were annotated with a gene description and gene ontology (GO term) and clustered in functional groups. Analysis of CAZyme family genes revealed 1,145 putative genes. Transcriptomic analysis of CAZyme expression levels in *M. fructicola* during its interaction with either grapefruit peel tissue or *Penicillium digitatum* revealed a high level of CAZyme gene expression when the yeast was placed in wounded fruit tissue. The significance of the findings in biocontrol capabilities of *M. fructicola* will be discussed.