A multi-omic study of nicotine catabolism in Paenarthrobacter nicotinovorans

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Paenarthrobacter nicotinovorans is a soil actinobacterium that degrades nicotine using the pyridine pathway encoded by the pAO1 catabolic megaplasmid. Only half of the 40 putative *nic*-genes have experimentally proven functions. The strain is a potential key biological agent for the degradation of nicotine from tobacco waste and contaminated natural resources. Since the bacterium can convert toxic nicotine into non-toxic derivatives, it could be used as a green chemicals factory to produce valuable compounds such as 6-hydroxy-L-nicotine, γ-aminobutyric acid, methylamine, succinic acid, and α-ketoglutaric acid. The interplay between the general metabolism of the bacterial cell and the nicotine degradation pathway encoded by pAO1 is still unexplored. Further knowledge of the mechanisms which regulate nicotine catabolism would facilitate the biotechnological applications of *P. nicotinovorans*. This study aims to perform the first transcriptomic analysis of nicotine catabolism in this strain and to integrate it with the already available proteomic data (ProteomeXchange: PXD008756). The bacterium was grown in the absence and presence of nicotine. Cultures were sampled at three key time points of nicotine catabolism: start of exponential phase, late exponential phase, and late stationary phase. Direct-RNA long-read sequencing was performed using the MinION Mk1B device coupled to a Flongle adapter. Raw data was basecalled using Guppy_6.3.2 with high accuracy. The generated transcriptomic data (NCBI GEO: GSE240220) was analysed using nf-core/nanoseq v3.1.0, and DE genes at the three key time points were evaluated. We identified 8 pAO1 genes and 10 chromosomal genes (padj< 0.1) that were previously unknown as having nicotine-related expression. The transcriptomic data is currently being integrated with the proteomic dataset using Pathview and SBGNview for pathway enrichment analysis. Finally, this study will provide the first multi-omic study of nicotine catabolism in bacteria.

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