



A highly syntenic *nic*-genes cluster is present in several related bacterial strains

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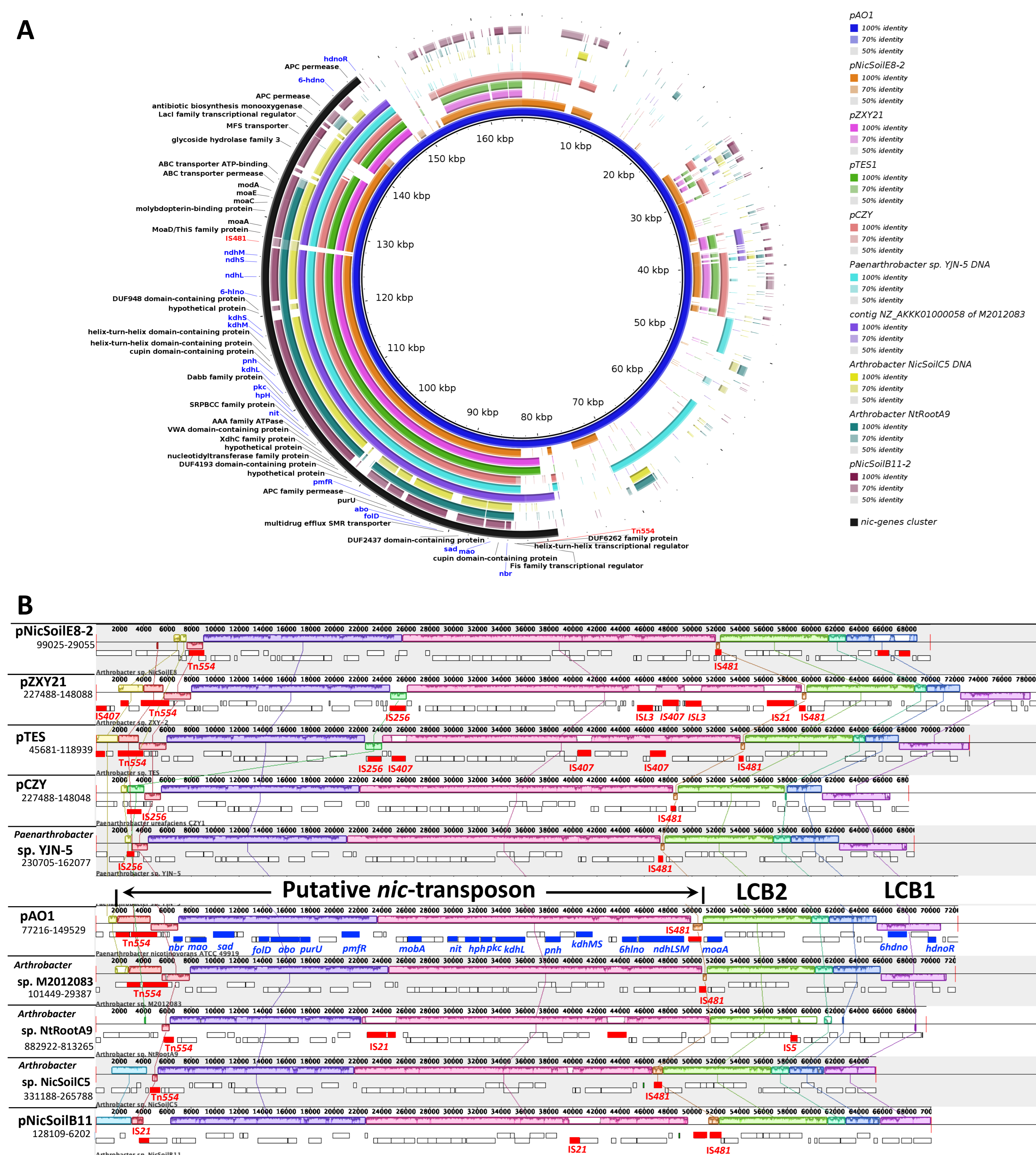
1. Introduction

The genes encoding pyridine-pathway for nicotine degradation (*nic*-genes) present in *Paenarthrobacter nicotinovorans* ATCC 49919 can serve as a model for studying the molecular evolution of catabolic pathways.

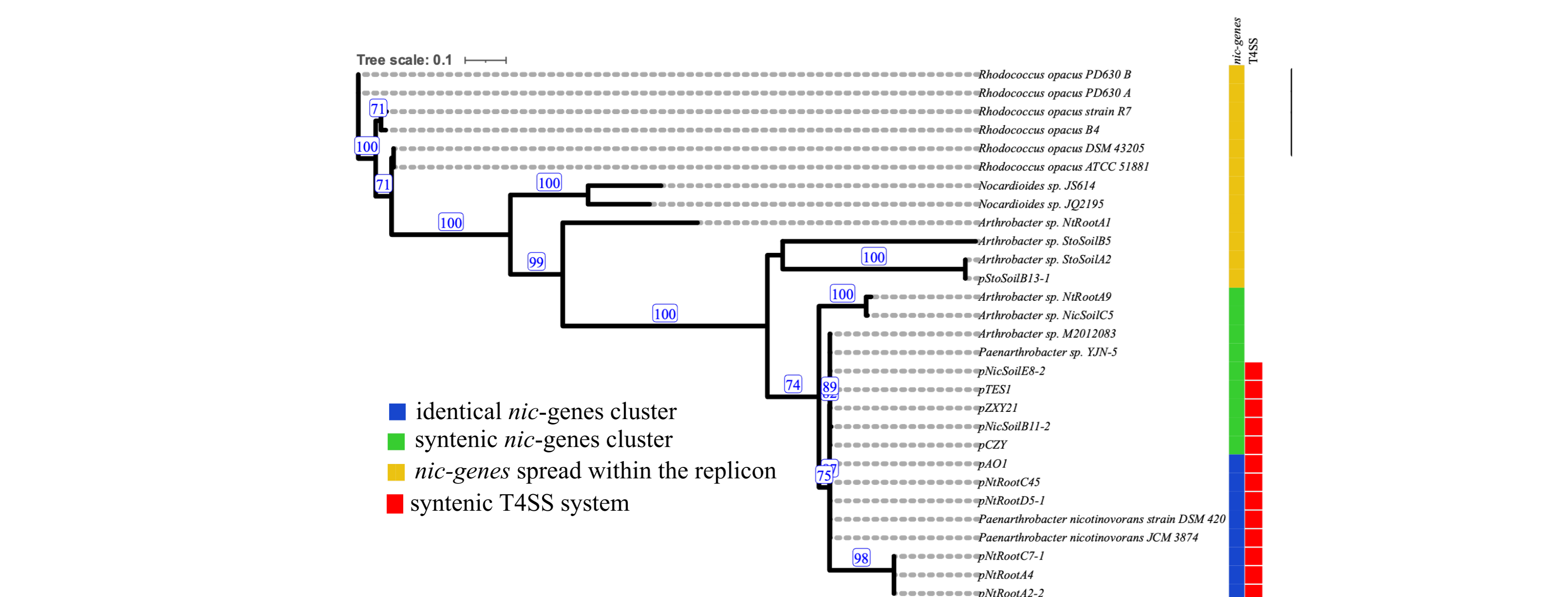
2. Methods

The newly released genome of the strain (GenBank CP089293, CP089294) was used as a reference and an extensive comparative genomics study was performed on a total of 65 related genomes. All pairwise comparisons among the set of genomes were conducted using GBDP available in TYGS, digital DNA-DNA hybridization (dDDH) values and confidence intervals were calculated using GGDC 3.0 and average nucleotide identity (ANI) values were calculated using the OrthoANI algorithm. Species clustering was done using a 70% dDDH cutoff. Comparative analysis of *nic*-genes cluster was performed with progressive Mauve using the HOXD scoring matrix.

Highly syntenic *nic*-genes clusters



Nine highly syntenic *nic*-genes clusters identified in various *Arthrobacter* and *Paenarthrobacter* genomes. (A) BRIG comparative genomic analysis of the pAO1 megaplasmid against the strains harboring the *nic*-genes listed in the legend. External black circle – the localisation of the *nic*-genes cluster on pAO1; blue labels – pAO1 genes experimentally related to nicotine metabolism; red labels – genes related to recombination events. (B) Mauve alignments of the *nic*-genes clusters.



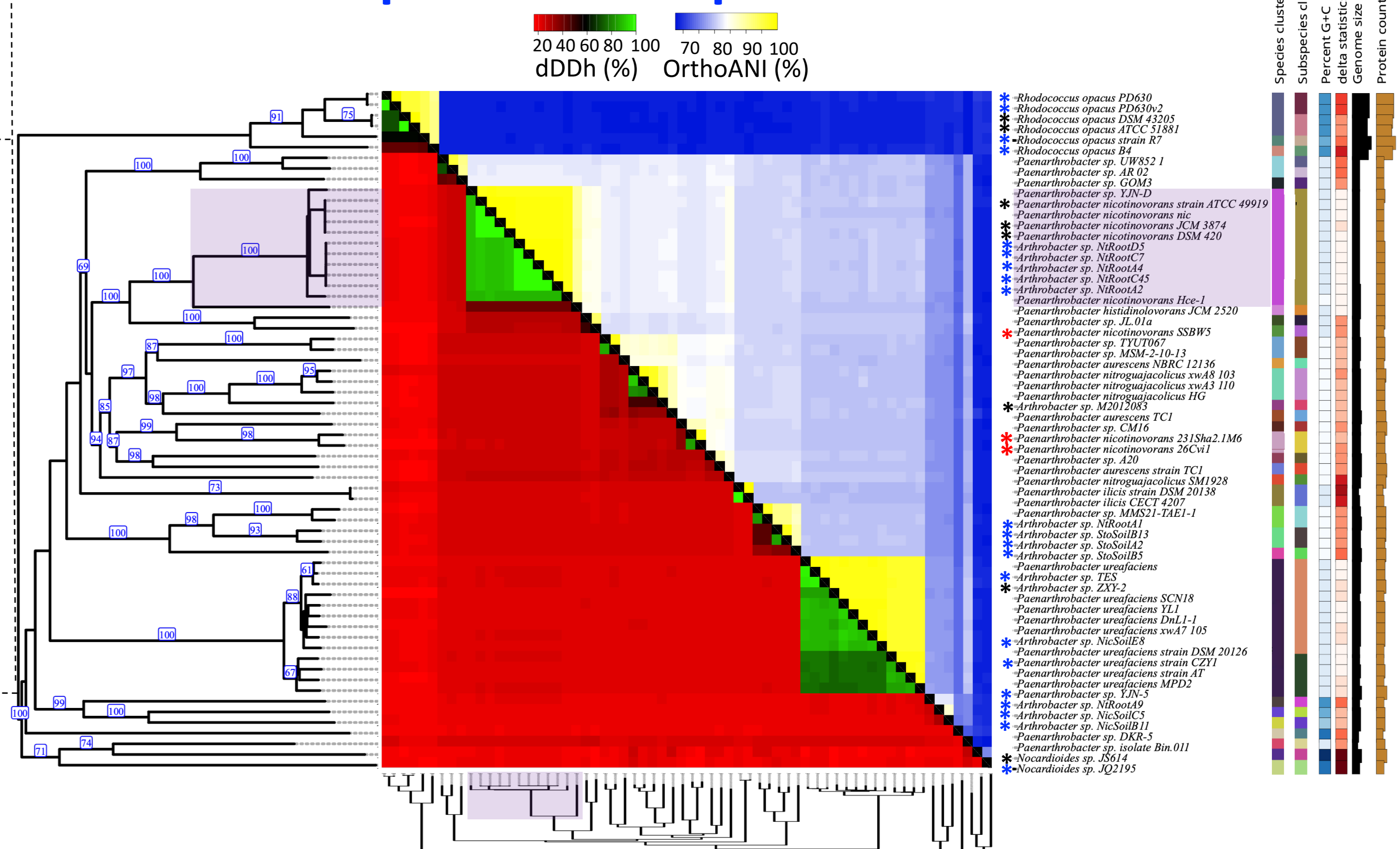
Maximum Likelihood phylogeny of the microbial pyridine pathway for nicotine degradation reconstructed from the concatenated *purU*, *pnh*, *pmfR*, *ndhL*, *kdhl* sequences.

5. References

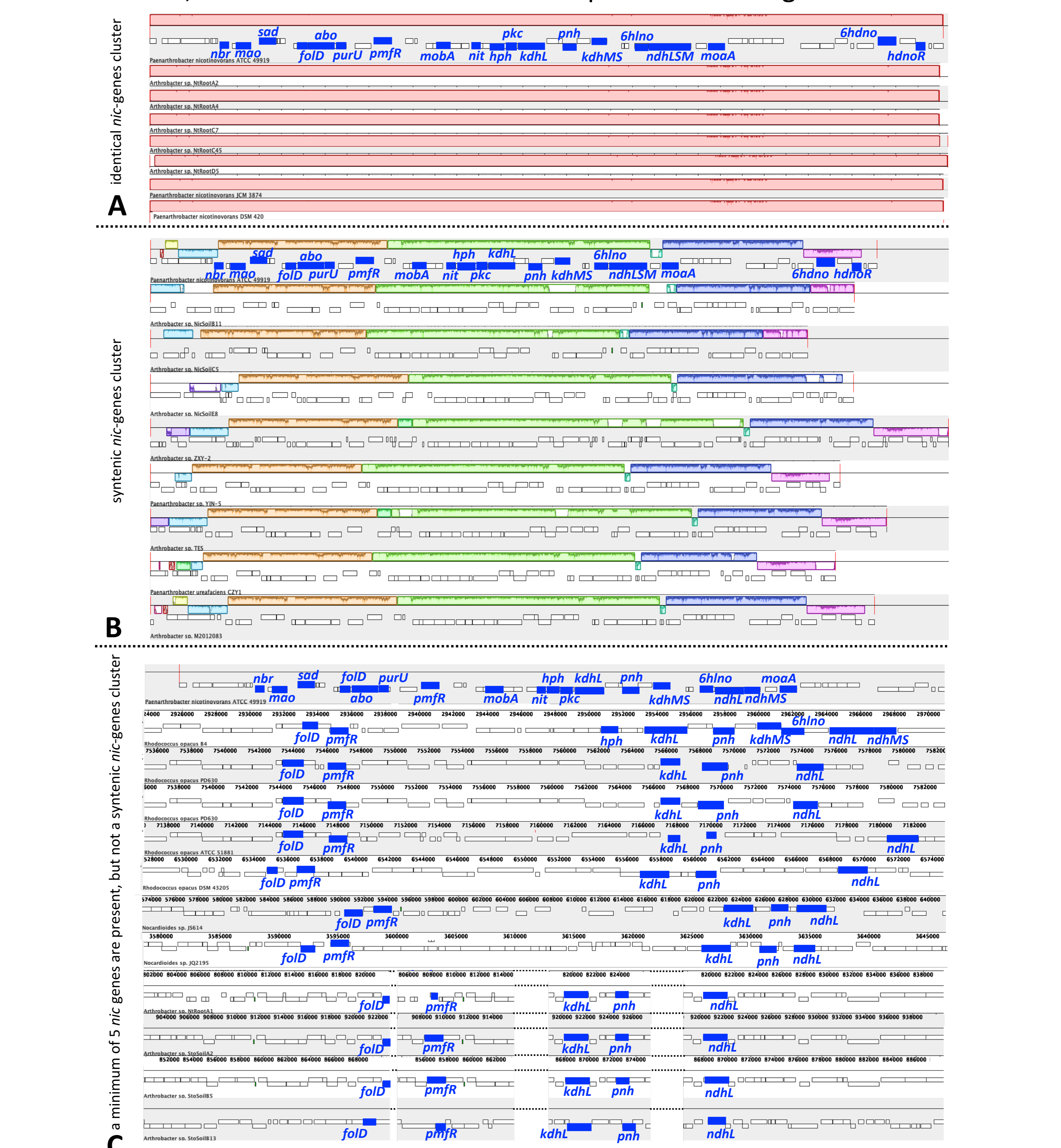
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3. Results

Genome wide pairwise comparison



Phylogenetic tree and pairwise comparisons based on both dDDH (d4) and ANI values of 64 genomes of *Paenarthrobacter* strains and of other *Arthrobacter*, *Nocardioides*, and *Rhodococcus* strains which possess the *nic*-genes.



Overview of identity and gene synteny among the *nic*-genes containing strains of *Paenarthrobacter*, *Arthrobacter*, *Nocardioides* and *Rhodococcus* evaluated in this study. **A**. The *nic*-genes form a single locally collinear block (LCB, red) in strains harboring an identical *nic*-genes cluster. **B**. Most *nic*-genes are located in three LCBs (yellow, green and magenta) in strains harboring a syntenic *nic*-genes cluster. **C**. Five key *nic*-genes (*purU*, *pnh*, *pmfR*, *ndhL*, *kdhl*) could be identified in other strains, but many genes are missing and no syntenic *nic*-genes cluster can be described.

4. Conclusions

- Five plasmids and two contigs belonging to *Arthrobacter* and *Paenarthrobacter* strains were shown here to be virtually identical with the pAO1 plasmid of *Paenarthrobacter nicotinovorans* ATCC 49919.
- a highly syntenic *nic*-genes cluster was identified on four plasmids, one contig and four chromosomes
- the *nic*-genes cluster contains two major LCBs that form a putative transposon

6. Acknowledgments

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