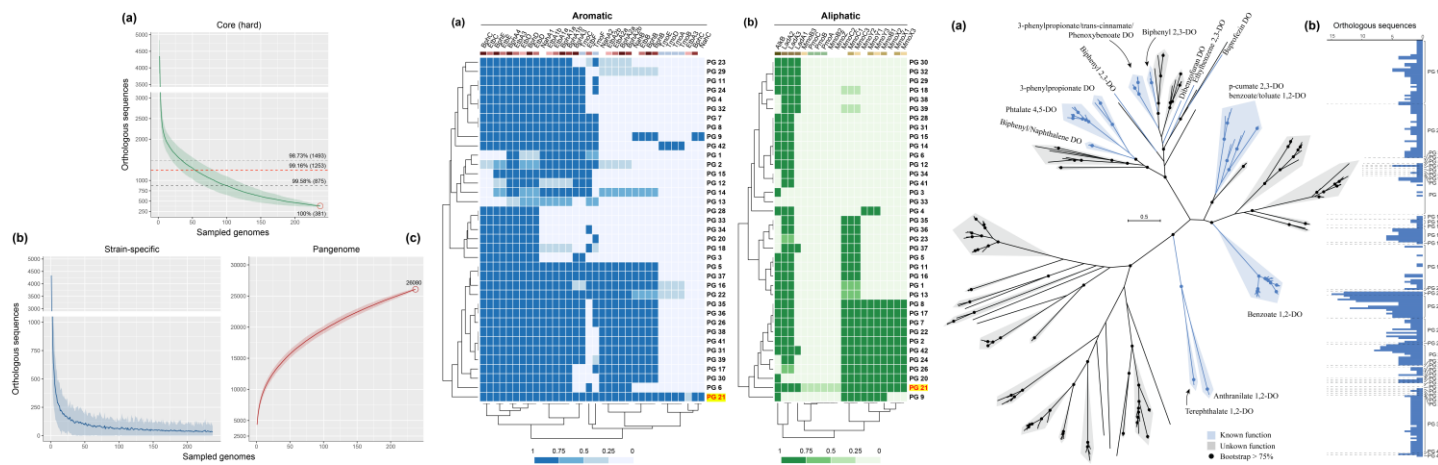
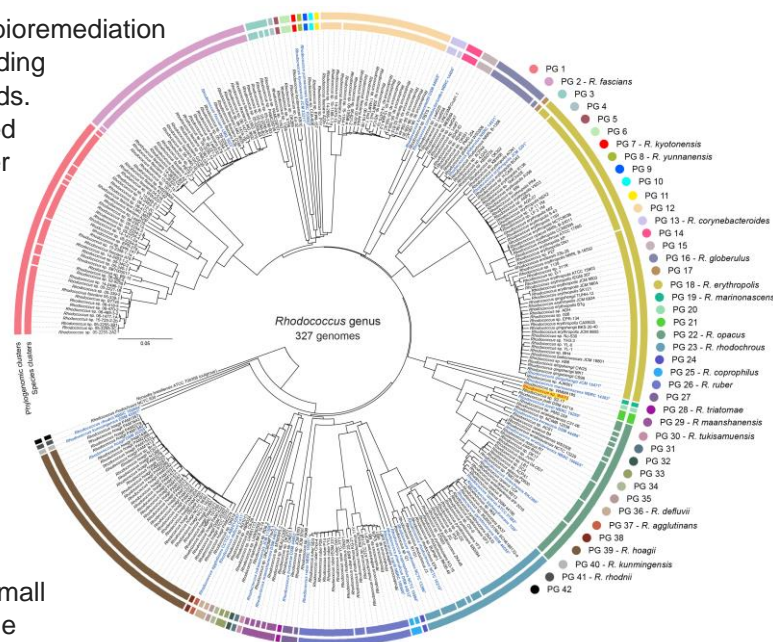


Comparative Genomics of the *Rhodococcus* Genus Shows Wide Distribution of Biodegradation Traits

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The genus *Rhodococcus* exhibits great potential for bioremediation applications due to its huge metabolic diversity, including biotransformation of aromatic and aliphatic compounds. Comparative genomic studies of this genus are limited to a small number of genomes, while the high number of sequenced strains to date could provide more information about the *Rhodococcus* diversity. Phylogenomic analysis of 327 *Rhodococcus* genomes and clustering of intergenomic distances identified 42 phylogenomic groups and 83 species-level clusters. Rarefaction models show that these numbers are likely to increase as new *Rhodococcus* strains are sequenced. The *Rhodococcus* genus possesses a small “hard” core genome consisting of 381 orthologous groups (OGs), while a “soft” core genome of 1253 OGs is reached with 99.16% of the genomes. Models of sequentially randomly added genomes show that a small number of genomes are enough to explain most of the shared diversity of the *Rhodococcus* strains, while the “open” pangenome and strain-specific genome evidence that the diversity of the genus will increase, as new genomes still add more OGs to the whole genomic set. Most rhodococci possess genes involved in the degradation of aliphatic and aromatic compounds, while short-chain alkane degradation is restricted to a certain number of groups, among which a specific particulate methane monooxygenase (pMMO) is only found in *Rhodococcus* sp. WAY2. The analysis of Rieske 2Fe-2S dioxygenases among rhodococci genomes revealed that most of these enzymes remain uncharacterized.



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