Genome Mining of Psychrophilic Deep-Sea Bacterium from the OceanX Expedition for Sustainable Production of Secondary Metabolite

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Abstract

The genus Rhodococcus is renowned for its metabolic versatility and capacity to produce diverse secondary metabolites. This study presents a comprehensive genomic analysis of *Rhodococcus* sp. 4 mz, integrating circular genome visualization, phylogenetic placement, and biosynthetic gene cluster (BGC) identification. The genome map reveals a single circular chromosome of approximately 4.6 Mb with a G+C content of 62.4%, harboring key genes for natural product biosynthesis (e.g., mbtH, pks13). Phylogenetic analysis based on 16S rRNA or core genome sequences firmly places strain 4 mz within the *Rhodococcus* genus, showing a close evolutionary relationship to *R. fascians* and *R. luteus*. Most notably, antiSMASH analysis identified 16 distinct secondary metabolite regions, including high-confidence clusters for ectoine, terpenes, and a non-ribosomal peptide synthetase (NRPS) region with 100% similarity to ε-Poly-L-lysine. These findings underscore the strain's genetic potential for producing valuable bioactive compounds, particularly osmoprotectants and antimicrobial peptides, warranting further experimental validation.

Keyword: Genome Bioprospecting, Deep Sea Bacteria, NRPS.

Introduction

The Actinobacteria, particularly the genus *Rhodococcus*, are widely distributed in diverse environments, including soil, water, and contaminated sites. They are well-known for their robust catabolic capabilities and their ability to synthesize a wide array of secondary metabolites with pharmaceutical, agricultural, and industrial relevance (Ceniceros et al., 2017). Despite this potential, the biosynthetic repertoire of many *Rhodococcus* species remains underexplored. *Rhodococcus* sp. 4 mz represents a promising candidate for genome mining. This study aims to elucidate the genomic architecture, taxonomic identity, and biosynthetic potential of this strain through a combination of genome visualization, phylogenomics, and bioinformatic prediction of BGCs.

Methodology

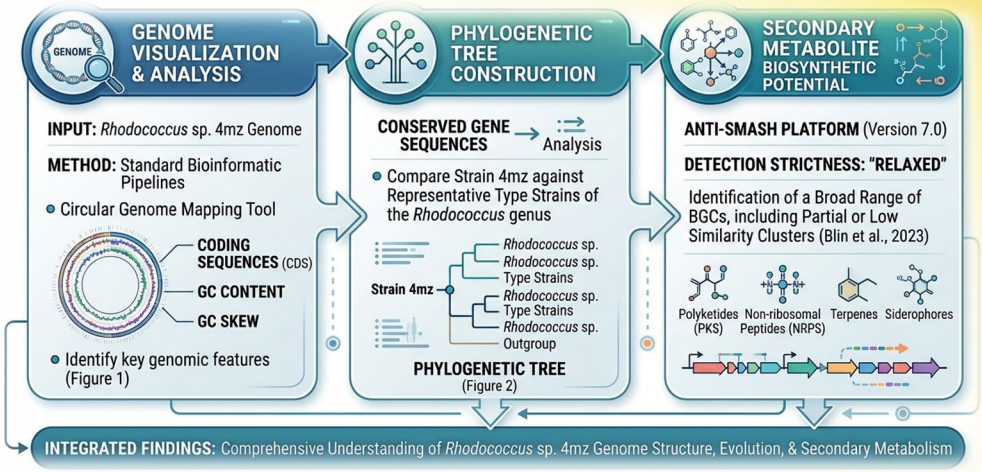


Figure 1. Genome Mining Methodology

Discussion & Result

The integrated analysis confirms *Rhodococcus* sp. 4 mz as a genetically distinct strain with biosynthetic potential. Its close phylogenetic relationship to *R. fascians* and *R. luteus* is consistent with the shared presence of core metabolic pathways (Klatte et al., 1994). The genome map highlights specific genes (e.g., mbtH, pks13) that are often associated with the regulation and production of secondary metabolites, particularly non-ribosomal peptides and polyketides (Ceniceros et al., 2017). The high-confidence ε-Poly-L-lysine (ε-PL) BGC (Region 1.16) is a homopolymer of L-lysine, widely used as a natural food preservative due to its antimicrobial activity. The presence of a complete NRPS cluster with 100% similarity to known ε-PL synthases suggests that strain 4 mz is a strong candidate for ε-PL production, a feature also observed in other *Rhodococcus* species such as *R. erythropolis* (Nazari et al., 2023). Furthermore, the identification of multiple low-confidence clusters, such as terpenes, butyrolactones, and other NRPS, suggests the strain may also produce novel, uncharacterized compounds (Czech et al., 2021). The presence of BGCs in this *Rhodococcus* genome underscores the strain's rich secondary metabolism (Ceniceros et al., 2017). Future work should focus on experimental validation through metabolic profiling and gene knockout studies to confirm the products of these clusters, particularly the ε-PL and ectoine pathways.

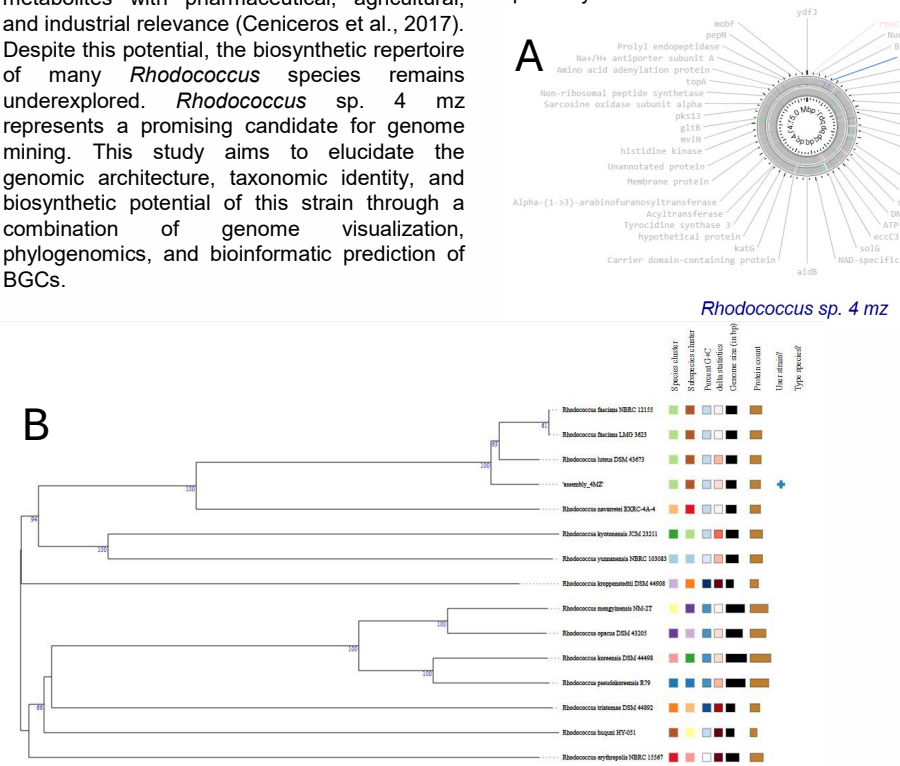


Figure 2. Genome Mining of 4mz Strain. A: Genome Assemby Characterization. B: Pyhlogenomic Analysis. C: Biosynthetic Gene Cluster Analysis

Conclusion

Rhodococcus sp. 4 mz represents a valuable genomic resource. Its phylogenetic position and diverse BGC repertoire, notably the high-confidence ε-PL cluster, make it a promising candidate for biotechnological applications. This study provides a foundation for targeted natural product discovery and metabolic engineering in this strain.