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UNRAVELING POLYOLS METABOLISM IN *Rhodococcus*

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Rhodococcus is a versatile genus recognized by its great potential for biotechnological applications based on its wide capacity to synthesize compounds with industrial value such as triacylglycerols (TAG). Nevertheless, studies of its metabolism have been mainly focused on carbon sources such as organic acids and mono or disaccharides. Polyols are defined as organic compound containing multiple hydroxyl groups, among them we find mannitol and sorbitol. Although metabolism for polyols has been studied in Actinobacteria such as *Mycobacterium smegmatis* and *Streptomyces coelicolor*, how *Rhodococcus* representatives behave when grown on polyols have never been considered. In this work we explored the ability of four *Rhodococcus* species belonging to different taxonomic clades to metabolize and accumulate TAG from two polyols, mannitol and sorbitol. *R. erythropolis* DSM 43060, *R. opacus* PD630, *R. fascians* F7 and *Rhodococcus* sp. 24CO were selected based on their different metabolic capacities and genome sizes that could result in different biomass and TAG yields. Growth was tested on rich and poor nitrogen media (MSM1 and MSM0.1, respectively) with mannitol or sorbitol as carbon sources. Optical density at 600nm was registered at different times until reaching stationary phase. Considering that TAG accumulation requires an unbalanced (>1) carbon/nitrogen relation, dry cell pellets from MSM0.1 plus mannitol or sorbitol cultures were collected. Semi-quantitative analysis of TAG was performed through thin layer chromatography. Based on available genomic data, each studied species was placed in a *Rhodococcus* phylogenetic tree. Focusing on polyols metabolism, we reconstructed the possible catabolic routes followed by each strain. Our results demonstrated that *Rhodococcus* genus has the potential to grow and accumulate TAG from polyols such as mannitol and sorbitol. Moreover, some strains showed a better performance on TAG accumulation. Furthermore, we found a conserved transporter in all the strains, which has been also reported for *M. smegmatis* and *S. coelicolor*. Interestingly, next to the putative transporter, key enzymes for the metabolism of the polyols were found. Only *Rhodococcus* sp. 24CO presented a second cluster for a putative transporter for sorbitol. Finally, polyols metabolism was similar among

Rhodococcus species and included the internalization of the respective polyol through an ABC transporter, the passage to fructose by a polyol-specific dehydrogenase and the further phosphorylation by a fructokinase, then following the reported metabolism for fructose. Based on our results, polyols which are usually found in high amounts in lucrative crops and wastes derived from them, are suitable to support growth and TAG accumulation on *Rhodococcus* genus.

Palabras clave: *Rhodococcus* - Polyols metabolism – Triacylglycerol