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Abstract

Study Of PHA Synthase Phylogenetic Trees And Operon Structures For The Optimal Production Of Industrially Relevant Polyhydroxyalkanoates

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Abstract: Plastics are produced worldwide as high-value products. However, they have become a very important ecological problem. The biosynthesis of eco-friendly materials as an alternative to traditional plastics has become a significant topic of research. One of these alternative materials are polyhydroxyalkanoates (PHAs), which are bacterial biopolymers of high rate biodegradability. Their main drawback is the relatively high cost of production. Metabolically, a classification exists based on types of PHA synthases (enzymes responsible for the biosynthesis of PHA), substrate specificity and monomer sizes, where class II synthases produce PHAs with latex-like properties of commercial interest, unlike classes I, III and IV which produce stiff and brittle PHAs. Thus, in this work we report the categorizing of PHAs gene clusters by phylogenetic analysis as a theoretical predictive method, helpful to improve the discovery of new strains of industrial relevancy for PHAs biosynthesis. From all synthases, class IV was more predominant with 33%, followed by class III and II (28 and 25%). For classes III and IV, the most predominant transcriptional regulator was *GntR* with 19.6% and 24.9%, in contrast with the predominant transcriptional regulators *OmpR* for class I and *AcrR* and *TetR* for class II.

Keywords: Native bacteria, Polyhydroxyalkanoates biosynthesis, Phylogenetic analyses, Bioplastics

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