

Investigating the novel ISS *Methylobacterium* species for PHA biosynthesis

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Polyhydroxyalkanoates (PHAs) are gaining attention in the family of polyesters polymers due to its biodegradability and biocompatibility. The polymer molecular structure is decided by the biosynthetic pathways of microbes employed for PHA synthesis which is influenced by the bacterial species, substrate utilized, and the culturing conditions provided. There are more than 100 PHA polymer monomeric units and the composition of these sub-units in polymer structure determines their physical and thermo-mechanical features. This variability has produced PHAs with drastically different polymer properties. In this context, it is of interest to explore PHA producers with properties having desirable functionality. In this study, we investigate novel *Methylobacterium* species isolated from the International Space Station for the potential PHA synthesis. The research focuses on comprehensive in-silico analysis of the whole genome sequences and metabolic pathways entailed in methanol to PHA production. Cell biomass production was assessed, and the DNA extracted from these strains were used in molecular targeting of the essential genes for PHA synthesis. PHA extraction protocol is optimized and confirmation of PHA in the extract was ensured by biophysical techniques. The physical and thermal properties of the extracted PHA polymers are reported. The findings further elucidate the relationship between carbon substrate, and the biochemical pathways resulting in polymer characteristics.

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