



Degradation of polyhydroxyalkanoates in eutrophic reservoir

T.G. Volova^{a,b,*}, M.I. Gladyshev^{a,b}, M.Y. Trusova^b, N.O. Zhila^b

^a Siberian Federal University, Svobodny av. 79, Krasnoyarsk 660041, Russia

^b Institute of Biophysics of Siberian Branch of Russian Academy of Sciences, Akademgorodok, Krasnoyarsk 660036, Russia

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Abstract

During the summers of 1999–2001 the dynamics of polyhydroxyalkanoate degradation in a small recreational eutrophic reservoir was studied experimentally. It has been shown that biodegradation of polyhydroxyalkanoates in the environment is determined by the structure and physicochemical properties of the polymer and by local weather conditions, which influence the state of the aquatic ecosystem. Species (clones) of bacteria able to utilize polyhydroxyalkanoates in the reservoir were identified using molecular phylogenetic analysis of 16S rRNA genes.

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1. Introduction

Annual outputs of non-degradable synthetic plastics have reached 140 million tons, and their accumulation presents a global ecological problem [1]. So, development of new, environmentally friendly materials, which can be involved in the biosphere cycling, is in line with the concept of ecologically safe sustainable industrial development. For the past 25–30 years, much consideration has been given to the production of biodegradable plastics. The best known of the currently available types of biodegradable aliphatic polyesters are poly(ϵ -caprolactone), polymers of lactic and glycolic acids (polylactides and polyglycols, respectively), and polyesters of microbiological origin (polyhydroxyalkanoates, PHAs) [2,3]. PHAs – biodegradable and thermoplastic polymers, whose physicochemical properties are similar to those of polypropylene and polyethylene – have recently attracted much academic and commercial interest [4,5]. Among the most important issues are mechanisms of degradation of these polymers, which can be degraded intracellularly and extracellularly, by microbial depolymerases.

Degradation can occur in fresh and marine water, soil, sludge, and compost. Under aerobic conditions PHAs are degraded to end products – carbon dioxide and water; under anaerobic conditions – to water and methane [6]. PHAs are efficiently degraded by various frequently occurring soil and water bacteria (*Pseudomonas*, *Alcaligenes*, *Comamonas*, *Streptomyces*, *Ilyobacter*) [7–10] and by fungi (*Ascomycetes*, *Basidiomycetes*, *Deuteromycetes*, *Mastigiomycetes*, *Myxomycetes*) [6,11].

Potential PHA-degraders are usually isolated by plating microbiological samples on solid agar media or latex media containing PHA particles or granules as a sole source of carbon and energy. Exodepolymerases hydrolyze the polymer to water-soluble products and lysis zones are formed on the plates; colonies for further investigations are selected in these zones. One of the most recent approaches to identification of PHA degraders is application of molecular genetic methods. The analysis of the 16S rRNA gene sequence made it possible to identify a new tropical marine bacterium, *Pseudoalteromonas* sp. NRRL B-300083, which degrades the hydroxybutyrate–hydroxyvalerate (PHB/PHV) copolymer in marine water [12], and to isolate several strains of *Comamonas testosteroni*, a denitrifying bacterium, which hydrolyzes polyhydroxybutyrate (PHB) and PHB/PHV, from activated sludge [13].

As the field of PHA application expands, the importance of knowing mechanisms of degradation of these polymers in

* Corresponding author. Siberian Federal University, Svobodny av. 79, Krasnoyarsk 660041, Russia. Fax: +7 3912 433400.

E-mail address: lhab@ibp.ru (T.G. Volova).