

N.U. CHERNYSHEVA, G.N. LIKHATSKAYA,
O.I. NEDASHKOVSKAYA, M.P. ISAEVA

Comparative genomics of *Zobellia*: analysis of polysaccharide lyases genes and operons

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Marine flavobacteria are well-known microorganisms applied in bioconversion of complex organic materials into bioactive substances. These bacteria are a valuable source of hydrolytic enzymes, such as polysaccharide lyases that are promising for effective algal biomass utilization [2]. *Zobellia galactanivorans* is one of the most prominent and well-studied species in terms of algal carbohydrates degradation [1]. Therefore, genome investigation of the other representatives of the genus *Zobellia* has good prospects for the discovery of new commercially relevant enzymes.

We sequenced genomes of two flavobacteria *Zobellia amurskyensis* KMM 3526^T and *Zobellia laminariae* KMM 3676^T, which were isolated from seawater and brown algae samples [3]. The genomic evaluation of the genus *Zobellia* for hydrolytic potential reveals that the genomes contain numerous genes of carbohydrate active enzymes. Half of them occur separately in the genomes, and others are localized within clusters comprising additional transporter genes. Both flavobacteria contain up to 19 putative alginate lyases. Genomes encode a complex alginolytic system that provides a stepwise depolymerization of alginates and assimilation of products into the central metabolism. Detailed phylogenetic and comparative analysis of alginate lyases was performed. It was found that PL7 alginate lyases are duplicated and refer to two subfamilies, one of them is novel. The results of computer modelling suggested that the alginate lyases have different modes of action.

Sequencing and analysis of the genomes revealed a huge potential for polysaccharide bioconversion, including alginate catabolism. Specific alginate lyases of PL7 family can be used for potential application in biotechnology and industry.

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* CHERNYSHEVA Nadezhda Uryevna - Junior Researcher, LIKHATSKAYA Galina Nikolaevna – PhD, Senior Researcher, NEDASHKOVSKAYA Olga Ilinichna – DSc, Leading Researcher (G.B. Elyakov Pacific Institute of Bioorganic Chemistry, FEB RAS, Vladivostok, Russia), ISAEVA Marina Petrovna – PhD, The Head of The Laboratory (G.B. Elyakov Pacific Institute of Bioorganic Chemistry, FEB RAS, Vladivostok, Russia; Far Eastern Federal University, Vladivostok, Russia). *E-mail: Chernysheva.nadezhda@gmail.com