ABSTRACT

THE BACTERIOCENOSES OF MICROBIAL MATS OF THE PROGLACIAL ZONE OF THE ECOLOGY GLACIER (KING GEORGE ISLAND, ANTARCTICA) - TAXONOMIC STRUCTURE AND PHYSIOLOGICAL POTENTIAL

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The goal of the conducted research was to understand the taxonomic structure and physiological potential of bacteriocenoses of microbial mats occurring in ephemeral aerial and lenitic reservoirs in the proglacial zone of the Ecology Glacier (King George Island). To achieve the main objective, specific objectives were set, as stated below: a) metagenomic taxonomic analysis of the bacteriocenosis of the tested microbial mats in relation to the structure of the soil microbiota, b) isolation and molecular identification of heterotrophic strains of bacteria derived from microbial mats; creating a strain bank, c) phenotypic "fingerprinting"; analysis of the metabolic potential of bacterial strains, d) determination of the environmental potential of isolates: growth conditions, resistance to freezing and UV radiation, antagonistic effects and bactericidal properties, ability to adhere and form a biofilm, and antibiotic resistance. Metagenomic data of the tested microbial mats made it possible to identify bacteria belonging to 12 phyla. A characteristic feature of the bacteriocenoses of the studied mats was the high abundance of blue-green algae belonging to the genus Phormidium, which accounted for over 60% of the identified sequences. The second group in terms of frequency were bacteria belonging to the Proteobacteria phylum, which accounted for over 20% of the identified sequences. Among the remaining taxa, bacteria belonging to the phyla: Verrucomicrobia, Actinobacteria and Bacteroidetes prevailed. Compared to the stream mats, the number of Actinobacteria, Planctomycetes, Verrucomicrobia and TM7 sequences was several times higher in the astatic reservoirs. The main environmental factors correlated with the taxonomic structure of the bacteriocenoses of mats were the physicochemical and hydrological properties of water. In the flowing, oligotrophic waters of the streams, a structurally limited bacteriocenosis of mats developed. A more complex taxonomic composition occurred in mats developing in astatic reservoirs, characterized by a higher concentration of organic and mineral matter. Taxonomically, rich assemblages of bacteria belonging to 22 phyla were found in the soils. A structural interdependence was found between mats and soil bacteriocenoses. At the phylum level, all the bacterial communities which make up the mat microbiomes were also found in soils. The obtained results confirmed the formulated research hypothesis assuming the important role of soil bacteriocenosis, which affects the structure and development of microbial mats in the process of migration and colonisation of aquatic environments.

The bacterial strains derived from the microbial mats were characterized by significant physiological activity and a wide metabolic potential, enabling the use of various substrates. Numerous strains showed the ability to utilize mono- and disaccharides, sugar alcohols, sugar acids, as well as amino acids and proteins. Statistically, higher activity was found in strains isolated from stream mats. This is important in the development of these microbiocenosis in low-trophic environments. *Arthrobacter psychrochitiniphilus, Rodoferax ferrireducens, Pseudomonas azotoformans* and *Pseudomonas poae* had a particularly high biochemical potential. The tests of microbial mats showed the presence of numerous bacteria resistant to toxic compounds and antibiotics, among which multi-antibiotic-resistant strains constituted a significant group. This phenomenon may be conditioned by the existence in mat bacteriocenoses of effective processes related to the development of natural resistance and resistance acquired as a result of horizontal gene transfer. A specific feature of mat bacteriocenoses was the resistance of bacteria to UVB radiation, which was found in over 80% of the strains. This indicates the presence of protective and repair mechanisms which determine the survival of bacteria during the period of intensive insolation. The highest resistance was found in: *Salinibacterium xinjiangense, Arthrobacter scleromae, Pedobacter sp.* and *Bosea lathyri*. An important adaptation to polar conditions of bacterial strains isolated from mats was their resistance to freezing. Intensive production of anti-ice proteins was demonstrated in the following strains: *Rhodococcus erythropolis, Flavobacterium tiangeerense, Pedobacter terrae* and *Bosea lathyri*. The majority of strains isolated from mats showed antagonistic abilities. Also, most of the tested strains showed the ability to adhere. Both types of interactions are of decisive importance in shaping the structure of microbial mats, characterised by a high density of bacteria and strong intercellular interactions. The demonstrated correlation between the antagonistic activity and resistance to antibiotics confirmed the existence of intensive interactions in the bacteriocenosis of mats. A group of bacterial strains from the genera *Agreia, Pseudomonas* and *Flavobacterium* was isolated, which inhibited the growth of phytopathogens and potential pathogens of animals and humans, including *Agrobacterium tumefaciens, Erwinia carotovora, Escherichia coli, Pseudomonas fluorescens* and *Staphylococcus aureus.* Strains of bacteria with unique features, the ability to produce anti-ice proteins, protective dyes and antibacterial compounds are valuable material in biotechnological and medical application research.

The obtained results confirmed the adopted research hypothesis: bacteriocenoses of microbial mats develop as structurally and functionally specialised ecosystems, characterised by a high metabolic and environmental potential. The Baas-Becking hypothesis indicating the role of environmental factors in the selection of biotic components of microbial mats was confirmed. Polar microbial mats are dynamic, self-regulating microbiocenotic systems in which the dynamics of primary and secondary production as well as bioconversion and regeneration of nutrients are balanced.