

Antagonistic properties of actinomycetes in bottom sediments of a Mongolian river



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ABSTRACT. The first actinomycetes of the genus *Streptomyces* are found in the bottom sediments of the Chono Kharaikh River in Mongolia. The isolated strains of streptomycetes are representatives of the *Cinereus* section of the *Achromogenes* series and the *Imperfectus* section. The isolated actinomycetes showed antibacterial and antifungal activity against *Bacillus subtilis*, *Staphylococcus aureus*, *Aspergillus niger* and phytopathogenic fungi *Cladosporium* sp.

Keywords: actinomycetes, bottom sediments, Chono Kharaikh River

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1. Introduction

The abundance of terrestrial actinomycetes and their role in many biological processes is well known from various reviews. However, there are few studies on the diversity of actinomycetes in freshwater bodies, especially in rivers. Lake and river environments represent a largely untapped source of new microorganism isolation. According to the work of Terkina I.A., actinomycetes of the genera *Streptomyces* and *Micromonospora* were isolated for the first time from the water, bottom sediments and sponges of Lake Baikal - oligocarbo-philic, constant components with enzymatic and antibiotic activity (Terkina, 2004). The diversity of freshwater actinomycetes and how adaptation to lake and river environments affects the production of secondary metabolites will allow a better understanding of the potential usefulness of these bacteria as a source of useful products for biotechnology. Actinomycetes have been the most studied, where they make a significant contribution to the turnover of complex biopolymers such as lignocellulose, hemicellulose, pectin, keratin and chitin (Veiga et al., 1983; Williams et al., 1984).

Actinomycetes are widespread in various habitats in Mongolia, not only in the soil, but in the rhizo-

sphere of plants, in herbaceous plants, and there are also endophytic actinomycetes (Norovsuren, 2009; Norovsuren, 2018; Norovsuren, 2020; Liu et al., 2022). The first microbiological study of the Khuvs gul area soils was carried out in 1975. The distribution of actinomycetes was found in all soils from 22 to 235 m, their numbers ranged from 50 to 350 cells/g of raw silt (Putyanina, 1977). Actinomycetes from the bottom sediments of Lake Sangiin Dalai Nuur and Khara-Uu Nuur have been studied since 2018 in Mongolia (Norovsuren, 2020; Oyunsuren et al., 2020). In this regard, the aim of the work was to isolate actinomycetes from the bottom sediments of the Chono Kharaikh river (Mongolia) and to search for highly active and promising strains for biotechnology.

2. Materials and methods

The studies used soil samples from the bottom sediments of the Chono Kharaikh River (Khovd aimag, Mongolia). The samples were dried at room temperature for 7 days. For the isolation and differential counting of actinomycetes, the traditional method of surface seeding was used on the following media: casein-glyc-

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erol agar, medium with sodium propionate, and HVA (humus-vitamin agar) (Zenova, 2000; Hayakawa and Nonomura, 1984). To limit the growth of gram-negative bacteria and fungi, nystatin (50 µg/ml), nalidixic acid (1.5 µg/ml), and vitamin B complex were added to the selective media. Before sowing, the samples of bottom sediment soils were heated at 120°C for 1 hour. The cultures were incubated for 2-4 weeks at 28°C. For the isolation of actinomycetes in pure culture and further cultivation, Gauze 1; ISP 2 and ISP 3 media were usually used (Gauze et al., 1983; Shirling and Gottlieb, 1966). Identification of the isolated actinomycete strains was carried out according to the identification manual of Bergey (1997), using morphological indicators, as well as chemotaxonomic features: the presence of LL- or meso isomers of diaminopimelic acids and differentiating sugars in whole-cell hydrolysates (Hasegawa et al., 1983). The series of the streptomycete section were determined according to the identification manual of Gauze (Gauze et al., 1983). Antagonistic properties were determined using the agar block method (Netrusov et al., 2005). The diameter of the growth inhibition zone of test organisms was measured (mm). The following test organisms were used: *Bacillus subtilis*, *Escherichia coli*, *Staphylococcus aureus*, *Saccharomyces cerevisiae*, *Aspergillus niger* and including the phytopathogenic fungus *Cladosporium* sp. from tomato leaves.

3. Results and discussion

The river environment is a rich source of actinomycetes and can produce a wide range of biologically active secondary metabolites. In this study, we used 3 nutrient media, including 2 selective isolation media. *Streptomyces* were isolated from the first time from the bottom sediments of the Chono KharaiKh River. The number of actinomycetes growing on a selective medium with sodium propionate fluctuated within 6.6×10^3 CFU/g, on humus-vitamin agar is from 7.2×10^3 CFU/g and on casein-glycerol medium - 1.8×10^3 CFU/g (Fig.).

The search for antibiotic-producing actinomycetes from lake and river bottom sediments became the main focus of this study. Further development of drugs based on the isolated substances is expected. A total of 80 actinomycete strains were isolated from three nutrient media. They belonged to the *Streptomyces* genus includes sections *Cinereus*, *Achromogenes* series, and *Imperfectus* sections.

The isolated strains inhibited the growth of the following microorganisms: *Bacillus subtilis* (8-13 mm), *Staphylococcus aureus* (8-15mm), *Aspergillus niger* (9-15mm) and *Cladosporium* sp (13-15mm). No antagonistic effect was observed against *Saccharomyces cerevisiae* and *Escherichia coli*.

4. Conclusions

The Streptomycetes isolated from bottom sediments the Chono KharaiKh River showed antibacterial and antifungal activity against *Bacillus subtilis*,

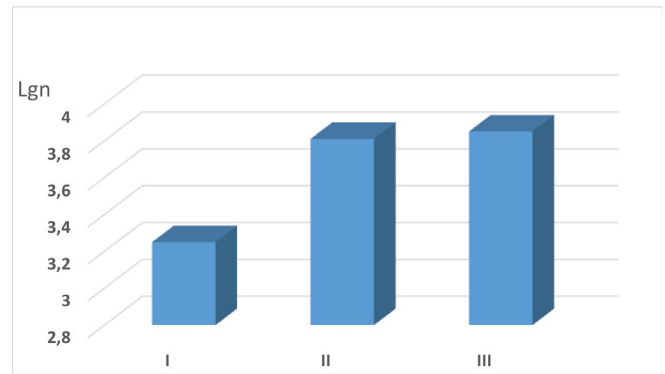


Fig. Total number of actinomycetes (Lgn). Media: I - casein glycerol medium; II - with sodium propionate medium; III - HVA - Humus-Vitamin Agar medium

Staphylococcus aureus, *Aspergillus niger* and *Cladosporium* sp. The actinomycete strains could serve as a resource for the development of new antibiotic drugs.

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Conflict of interest

The authors declare no conflict of interest.

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