

DIVERSITY AND BIOTECHNOLOGICAL POTENTIAL OF THE MICROBIOME OF SALSOLA PLANTS DISTRIBUTED IN THE DESERT REGIONS OF UZBEKISTAN

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Annotation: The thesis examines the composition of the microbiome associated with Salsola plants growing in the desert regions of Uzbekistan (Kyzylkum, Ustyurt) and its biotechnological potential. Rhizosphere soil, root, stem and leaf samples were analyzed using classical culture-based methods combined with 16S rRNA and ITS gene sequencing. Strains belonging to the genera Bacillus, Pseudomonas, Streptomyces, Halomonas and Micrococcus were shown to synthesize phytohormones, fix nitrogen, solubilize phosphates and display antimicrobial activity. The findings indicate that the halophyte microbiome is a promising source for developing agricultural biopreparations.

Keywords: Salsola, microbiome, halophytes, desert ecosystems, plant growth-promoting rhizobacteria, biotechnological potential, Uzbekistan.

Annotatsiya: Tezisdagi O'zbekiston cho'l hududlarida (Qizilqum, Ustyurt) tarqalgan Salsola turkumi o'simliklari bilan assotsiatsiyalangan mikrobiom tarkibi va uning biotexnologik salohiyati o'rganilgan. Ildiz atrofi tuprog'i, ildiz, poya va bargdan olingan namunalar klassik kultural usullar hamda 16S rRNK va ITS-genlarini sekvenlash orqali tahlil qilingan. Bacillus, Pseudomonas, Streptomyces, Halomonas va Micrococcus avlodlariga mansub shtammlarning fitogormon sintezi, azot fiksatsiyasi, fosfat solyubilizatsiyasi va antimikrob faollikka ega ekanligi aniqlangan. Natijalar galofit mikrobiomining qishloq xo'jaligida biopreparatlar yaratish uchun istiqbolli manba ekanligini ko'rsatadi.

Kalit so'zlar: Salsola, mikrobiom, galofitlar, cho'l ekotizimlari, o'simliklarni o'stiruvchi rizobakteriyalar, biotexnologik salohiyat, O'zbekiston.

Аннотация: В тезисе рассмотрен состав микробиома, ассоциированного с растениями рода Salsola, произрастающими в пустынных регионах Узбекистана (Кызылқум, Устюрт), и его биотехнологический потенциал. Образцы ризосферной почвы, корней, стеблей и листьев проанализированы классическими культуральными методами в сочетании с секвенированием генов 16S рРНК и ITS. Показано, что штаммы родов Bacillus, Pseudomonas, Streptomyces, Halomonas и Micrococcus способны синтезировать фитогормоны, фиксировать азот, солюбилизировать фосфаты и проявлять антимикробную активность. Результаты свидетельствуют о перспективности микробиома галофитов как источника биопрепаратов для сельского хозяйства.

Ключевые слова: Salsola, микrobiom, галофиты, пустынные экосистемы, ПРОР-бактерии, биотехнологический потенциал, Узбекистан.

INTRODUCTION

Plants of the genus Salsola (saltwort) are typical representatives of the halophytic flora of the arid and semi-arid territories of Central Asia, widely distributed across the desert zones of Uzbekistan — Kyzylkum, Ustyurt, and the adjoining foothill plains. Growing under conditions of high soil salinity, acute moisture deficit, intense insolation and sharp daily temperature

fluctuations, these plants have developed a set of physiological and ecological adaptations, among which the symbiotic interaction with the associated microbiota plays a crucial role.

Rhizospheric and endophytic microorganisms colonizing the root system, stems and leaves of halophytes participate in maintaining the water and ionic homeostasis of the host plant, increase its resistance to abiotic stresses, and are themselves adapted to extreme environmental conditions. Such microorganisms are of independent interest as a source of new strains resistant to salinity, drought and high temperatures, and capable of synthesizing biologically active compounds, enzymes and metabolites with potential for practical application in agriculture, medicine and industry.

Several foreign studies confirm the high taxonomic and functional variability of the *Salsola* microbiome: Proteobacteria and Actinobacteria were shown to dominate the microbiome of *Salsola stocksii* [1]; halotolerant bacteria of the genera *Bacillus*, *Halobacillus* and *Kocuria* were isolated from the rhizosphere of *Salsola stocksii* and *Atriplex amnicola* [2]; and Actinobacteria were found to occur at a higher proportion in the root endosphere than in the rhizosphere of desert halophytes [3]. Bacterial strains isolated from *Salsola imbricata* have also been shown to display antagonistic activity against phytopathogenic oomycetes [4]. Nevertheless, the microbiome of *Salsola* plants growing directly within the territory of Uzbekistan remains insufficiently studied, which determines the relevance of the present research.

AIM OF THE STUDY

The aim of this work is to study the taxonomic composition, structural diversity and functional potential of the microbial community associated with *Salsola* spp. plants growing in the desert zones of Uzbekistan, as well as to evaluate the possibilities of practical application of the isolated microorganisms as a basis for biopreparations.

MATERIALS AND METHODS

The object of the study comprised samples of rhizosphere soil, as well as roots, stems and leaves of *Salsola* plants, collected from various ecotopes of the desert zone of Uzbekistan (Kyzylkum, Ustyurt) during different vegetation seasons. Sampling was carried out according to standard soil and botanical microbiology techniques, in compliance with aseptic requirements.

Culturable microorganisms were isolated by the serial dilution method with inoculation on selective and universal nutrient media (King's B medium, Czapek agar, potato-glucose agar, and a medium with elevated NaCl content for the selection of halotolerant forms). Identification of the isolates was based on morphological-cultural and physiological-biochemical characteristics, as well as molecular-genetic methods — sequencing of the 16S rRNA gene for bacteria and the ITS region for microscopic fungi, consistent with the approaches applied in comparable studies of halophyte microbiomes [1, 3, 8].

To assess the non-culturable fraction of the microbial community, metagenomic sequencing of total DNA extracted directly from rhizosphere and plant tissue samples was performed, followed by bioinformatic analysis of the resulting sequences and comparison with reference databases.

The functional potential of the isolated strains was evaluated using standard tests: the ability to fix atmospheric nitrogen, solubilize sparingly soluble phosphates, synthesize indole-3-acetic acid and other phytohormones, produce siderophores, osmoprotectants and

extracellular hydrolytic enzymes (proteases, cellulases, amylases), as well as antagonistic activity against test cultures of phytopathogenic microorganisms, following methodological approaches similar to those described in [2, 4, 6].

RESULTS AND DISCUSSION

The studies conducted revealed a high taxonomic diversity of the *Salsola* microbiome. Among the culturable bacterial isolates, representatives of the genera *Bacillus*, *Pseudomonas*, *Streptomyces*, *Halomonas* and *Micrococcus* predominated, which is consistent with data obtained for other halophyte species, in particular *Salsola stocksii* and *Messerschmidia sibirica*, where *Pseudomonas*, *Bacillus* and *Streptomyces* were likewise the dominant genera [1, 8]. Halotolerant and osmotolerant species of microscopic fungi adapted to conditions of elevated substrate mineralization were identified within the mycobiota.

Metagenomic analysis confirmed and substantially extended the picture of taxonomic diversity, revealing the presence of non-culturable and fastidious taxa not detected by classical methods, which underscores the importance of a comprehensive approach to studying the halophyte microbiome, consistent with the previously described persistent proportion of uncultured bacteria in the *Salsola* microbiome [1].

Functional testing showed that a significant proportion of the isolated strains possess pronounced plant growth-promoting (PGPR) properties: the ability to fix atmospheric nitrogen, solubilize phosphates, and synthesize auxins and other phytohormones, consistent with the role of the halophyte microbiome described in the review by Ruppel et al. [5]. A number of isolates demonstrated active production of osmoprotectants and extracellular hydrolytic enzymes (lipases, proteases, cellulases, amylases), similar in activity spectrum to strains isolated from the genus *Salsola* in Pakistan [2].

Of particular interest is the antimicrobial activity revealed in a number of strains, primarily belonging to the genus *Streptomyces*, against phytopathogenic bacteria and fungi, which is comparable to the antagonistic activity of bacteria isolated from *Salsola imbricata* against the oomycete phytopathogens *Phytophthora capsici* and *Pythium ultimum* [4, 9]. Furthermore, similar results regarding salinity tolerance and the production of biologically active metabolites were obtained in a study of the endophytic microbiome of halophytes from the Aral Sea region of Uzbekistan, where *Bacillus weizmannii* strains exhibited pronounced PGPR potential and antagonistic activity [6], while the specialized rhizosphere microbiome of *Suaeda salsa* was found to be enriched in genes responsible for adaptation to salt stress [7].

CONCLUSION

The results obtained indicate a considerable taxonomic and functional diversity of the microbiome of *Salsola* plants growing in the desert regions of Uzbekistan. The identified strains, capable of nitrogen fixation, phosphate solubilization, synthesis of phytohormones, osmoprotectants and antimicrobial compounds, represent a promising bioresource for the development of biofertilizers, biofungicides and preparations that enhance the resistance of agricultural crops to abiotic stresses, as well as for the bioremediation of saline soils. Further research should be directed toward an in-depth metagenomic and functional characterization of the non-culturable fraction of the microbiome and toward the development of specific biotechnological products based on it.

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