Published: April 30, 2025 | Pages: 99-100

MICROBIAL COMPOSITION OF THE RHIZOSPHERE OF FERULA KUHISTANICA GROWING IN UZBEKISTAN

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ABSTRACT:

This study investigates the rhizosphere microbiota of Ferula kuhistanica, a species belonging to the Ferula genus. The results were compared with those of Ferula sinkiangensis. In the rhizosphere of F. kuhistanica, Firmicutes (50%) and Proteobacteria (42.5%) were found to be dominant. The observed differences in microbial composition between the two species are likely due to variations in environmental conditions and geographical distribution. The bacterial communities identified in the rhizosphere are considered to possess plant growth-promoting traits and potential biotechnological significance.

Keywords: Ferula kuhistanica, rhizosphere, bacteria, microbiota, microorganism, Firmicutes, Proteobacteria.

INTRODUCTION

Plant species belonging to the genus Ferula are well known for their medicinal properties; however, their rhizosphere microbiota remains largely unexplored [5]. Previous studies conducted by Chinese researchers have examined the rhizosphere microflora of local Ferula species. In particular, in the rhizosphere of Ferula sinkiangensis, bacterial isolates belonging to the phyla Proteobacteria, Gemmatimonadetes, Bacteroidetes, Actinobacteria, and Acidobacteria were identified, with Actinobacteria and Acidobacteria being the dominant groups [1;3].

In comparison, our findings revealed that in the rhizosphere of Ferula kuhistanica, Firmicutes (50%), Proteobacteria (42.5%), and Actinobacteria (7.5%) were present, with Firmicutes and Proteobacteria being predominant. Despite both species belonging to the same genus, differences in their rhizosphere microbial communities may be attributed to environmental factors such as soil characteristics, pH, moisture content, organic matter availability, and geographical distribution. Many members of the Firmicutes and Proteobacteria phyla are known as plant growth-promoting rhizobacteria (PGPR). Therefore, the bacterial communities found in

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the rhizosphere of Ferula kuhistanica may represent microorganisms with significant biotechnological potential.

Additionally, the rhizosphere microbiota of other Ferula species such as F. gracilis, F. syreitschikowii, F. lehmannii, F. ferulaeoides, and F. songorica has also been studied, and the biotechnological potential of these microbial communities has been highlighted [2;4].

In conclusion, the rhizosphere of Ferula kuhistanica was found to be dominated by bacterial groups belonging to the Firmicutes and Proteobacteria phyla. The differences observed in comparison to Ferula sinkiangensis are likely due to ecological and geographical factors. The identified bacterial communities exhibit characteristics of plant growth-promoting rhizobacteria and demonstrate promising potential for biotechnological applications. Further investigation into the rhizosphere microbiota of other Ferula species is warranted to explore their ecological roles and applied prospects.

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