

Next-generation sequencing of rhizospheric soils associated with *Cicer montbretii*

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Abstract

The soils in Strandzha were formed under the influence of the unique combination of the climate, forest tree vegetation, the enormous variety of roots and soil-forming rocks, low-mountain relief with great fragmentation, a densely located hydrographic network with short slopes and a dominant southern exposure. In Strandzha, the cinnamon forest soils predominate, followed by the mountain-specific yellow soils. They are associated with *Cicer montbretii* and greater moisture retention from atmospheric precipitation and subsoil runoff and fogs that linger in deep valleys and maintain high air humidity. In conditions of greater humidification and increased temperature, organic matter is rapidly decomposed and deep washing of bases and silicates from the soil profile, strongly acidified and enriched with aluminium and iron oxides. Wild relatives of cultivated plants are an important element of plant biodiversity. The diversity of endophytic microorganisms is essential for ecology, as it makes it possible to understand in detail the plant-microbial interactions. The objectives of this study were to isolate and identify endophytic bacteria from the roots of *C. montbretii* associated with cinnamon forest (A1) and yellow earth podzolic soils (A2). A study of endophytic bacteria in the roots of *C. montbretii* legume plant, by assessing its PCR amplicon of 16S rDNA with the Illumina metagenomics technique, was used to generate 81,782 reads from the samples. The analyses revealed that Proteobacteria were similar in cinnamon forest and yellow earth podzolic soils. Bacterioidota prevailed in yellow earth podzolic soils. Firmicutes and Actinobacteria were the common genera in cinnamon forest soil. The roots of plants grown in A1 soil have the largest composition with Proteobacteria 78%, which consisted of the genus— *Erwinia* 13%, *Pseudomonas* 11%, *Shingomonas* 11%, *Rhizobium* 5%, and *Bradirhizobium* 4%. In the A2 soil prevailed Proteobacteria 76% and Bacterioidota 15%. The most abandoned genus in A2 was *Orchobactrum* 20%, *Stenotrophomonas* 15%, *Sphingobacterium* 12%, *Serratia* 4%, and *Flavobacterium* 4%. The α -diversity analysis indicated the richness and inverse Simpson diversity index of the bacterial endophyte communities for the root tissues to be 6.551 for A1 and 4,692 for A2 soil, respectively. Endophytic bacterial communities differed among the two soil samples, indicating that the soil and the climatic conditions considerably affected the entire endophytic community.

Molecular analysis of the whole soil DNA component can effectively combine the benefits of microbiology, molecular biology, genetics, ecology and botany, and answer the question of the influence of soil microorganisms on the specific and very often restricted distribution of wild relatives.

Keywords: NGS, Endophytes, *Cicer montbretii*, Strandzha Nature Park