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Dynamics of the taxonomic structure microbiome of the arable land

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Microbial diversity reflects the diversity of soil conditions. To study the soil microbiome, it is necessary to use not only the methods of classical microbiology, but also the methods of metagenomics to assess the phylogenetic diversity of microbial communities. The purpose of the work is to study the dynamics of changes in microbial communities during the year on the arable soil of the Belgorod region (Russia). The study area is an arable land formed by typical chernozem soil, on which Hordeum vulgare L. v. medicum grows. At the place of sowing, standard agrotechnical methods of tillage were used. The study area is characterized by a temperate continental climate with an average July temperature of 19.3ºC, an average January temperature of -10.4ºC, and there are also 145 frosty days a year and 480 mm of precipitation per year. One monitoring site was investigated and sampled during 2021 (February, April, July and October). Sampling was carried out at a depth of 0 to 20 cm in accordance with ISO 10381-1 (2002). DNA was isolated from the samples using the FastDNA SPIN Kit for Soil protocol (MP Biomedicals, UK). Libraries were prepared according to the protocol "Preparing 16S Ribosomal RNA Gene Amplicons for the Illumina MiSeq System" using a universal primer pair on the V3-V4 variable region of the 16S rRNA gene. Sequencing was performed on the MiSeq platform (Illumina) with v3 reagents (600 cycles) at the BioSpark (https://biospark.pro/). A detailed physical and chemical agronomic analysis of the soil was carried out at the monitoring site. It has been established that soil acidity ranges from slightly alkaline in spring to slightly acidic in summer. Soil carbon content is high (from 7,4±0,7 % to 8,6±0,9 %) and only decreases in spring (5,0±0,5 %) due to the depletion of plant residues by this time of year. The amount of available nitrogen (from 35,0±2,2 mg/kg to 45,5±1,9 mg/kg), phosphorus (from 190±16 mg/kg to 354±45 mg/kg) and potassium (from 590±71 mg/kg to 1260±180 mg/kg) is large. All considered soil characteristics indicate that the soil is fertile and not depleted. The sequences were analyzed using the QIIME2 v.2022.2 program (Bolyen et al., 2019). Sequence quality control was performed using the Deblur plugin (Amir et al., 2017) with Positive mode (chimeric sequences are removed by consensus; then SortMeRNA is used, which compares all raw reads to the GreenGenes reference database (Bokulich et al., 2018); sequences with e-value ≤ 10 are retained after this read step has been shortened in length), so amplicon sequence error correction and denoising with sOTU generation is performed.