The changes in maize rhizobiom composition occurring in the vegetation cycle

Burkowska-But, A.[1,2], Wiśniewski O.[2], Osińska, A.[2], Walczak, M.[1,2]

[1] *Nicolaus Copernicus University, Department of Environmental Microbiology and Biotechnology, Polna 148, 87-100 Toruń*

UNIWERSYTET
MIKOŁAJA KOPERNIKA
W TORUNIU

[2] *Bacto-Tech sp. z o.o., Gagarina 5/102, 87-100 Toruń*

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Introduction

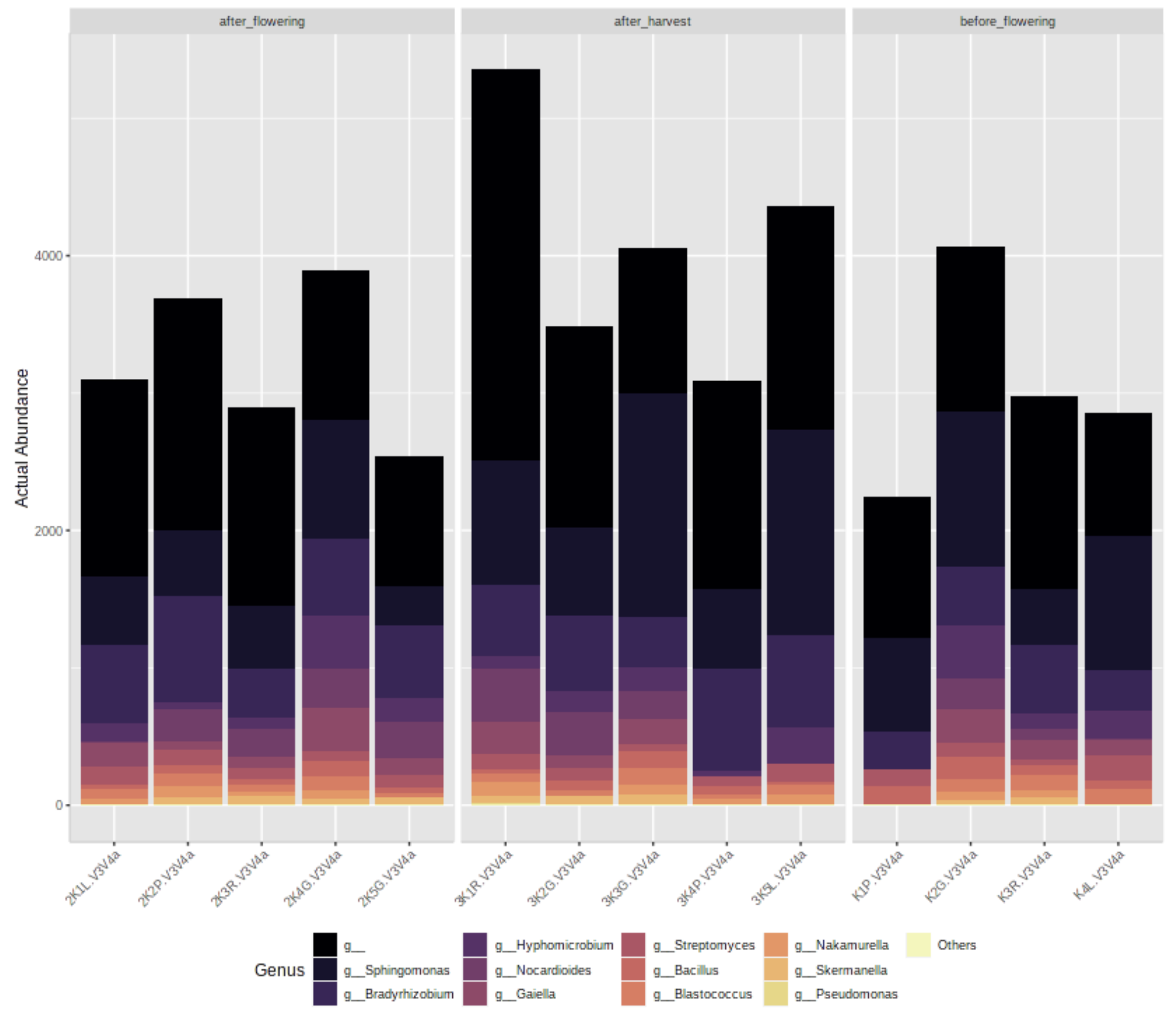
Plant–microbiome interactions are significant determinants for plant growth, fitness, and productivity. The knowledge of structural and functional diversity within the plant microbiome could provide an opportunity to develop new, sustainable agricultural practices (Gupta et al. 2021). Due to the selection of strains and their intended use, they can be used continuously or ad hoc, as a biofertilizer or biological control agent (Compant et al. 2019).

Maize (*Zea mays* L.), as a cultivated plant, is of great importance in the world, both in terms of utility and economics. This is due to the possibility of using virtually all of the plant's biomass as feed, food or industrial raw material. In the European Union, maize is the second-most cultivated crop after wheat (EUROSTAT 2020).

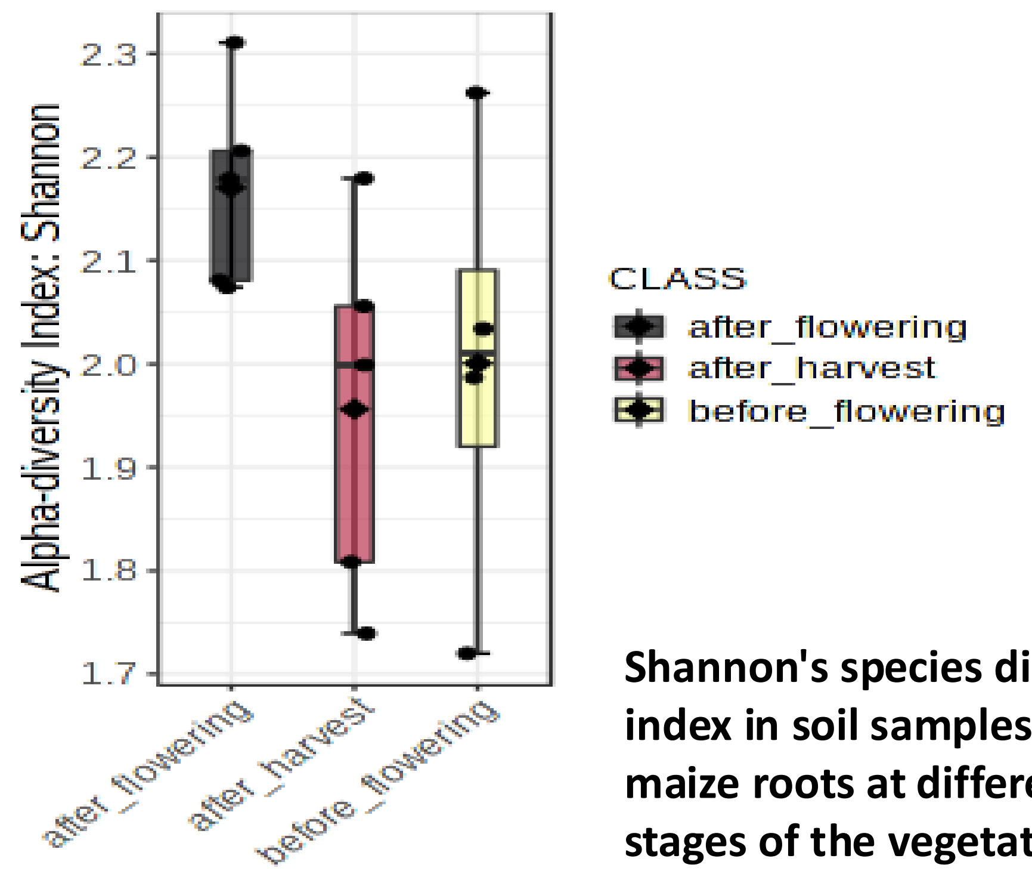
The aim of our research was to evaluate changes in the rhizobiome composition occurring in the maize vegetation cycle.

Material and methods

Rhizosphere soil samples were collected from 4 agricultural fields of maize located in Poland. All samples were collected in three periods of the vegetation cycle: before plant flowering, after flowering, and after harvest. Metagenomic DNA was isolated from the protected material using the Qiamp PowerFecal Pro Kit, Qiagen DNA isolation kit. DNA libraries were then prepared according to the 16S Metagenomic Sequencing Library Preparation Nextera XT protocol. Sequencing of the V3-V4 16S rRNA hypervariable regions was performed with the MiSeq Reagent Kit v2 with a reading length of 2x250 bp. The taxonomic classification of microorganisms was performed based on 16S rRNA amplicons using the Metagenomics program (Illumina). Statistical analysis and data visualization were performed using R Studio and MicrobiomeAnalyst software.



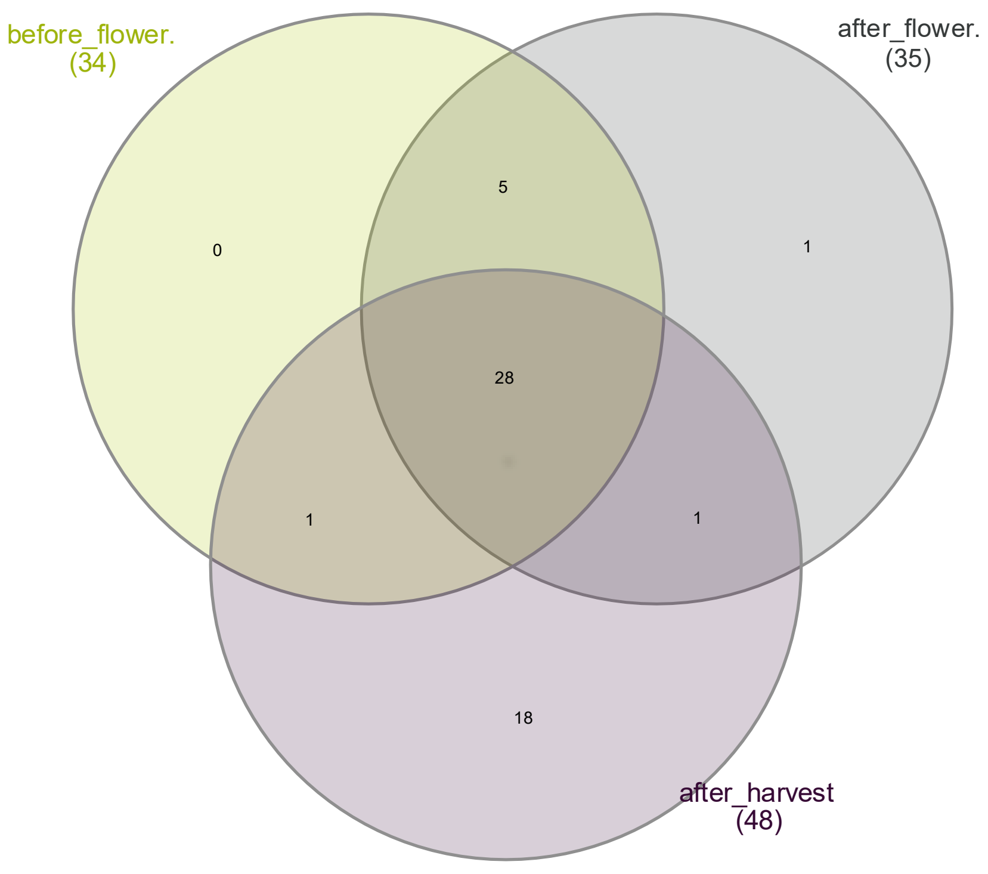
The maize rhizmicrobiome biodiversity - genus level



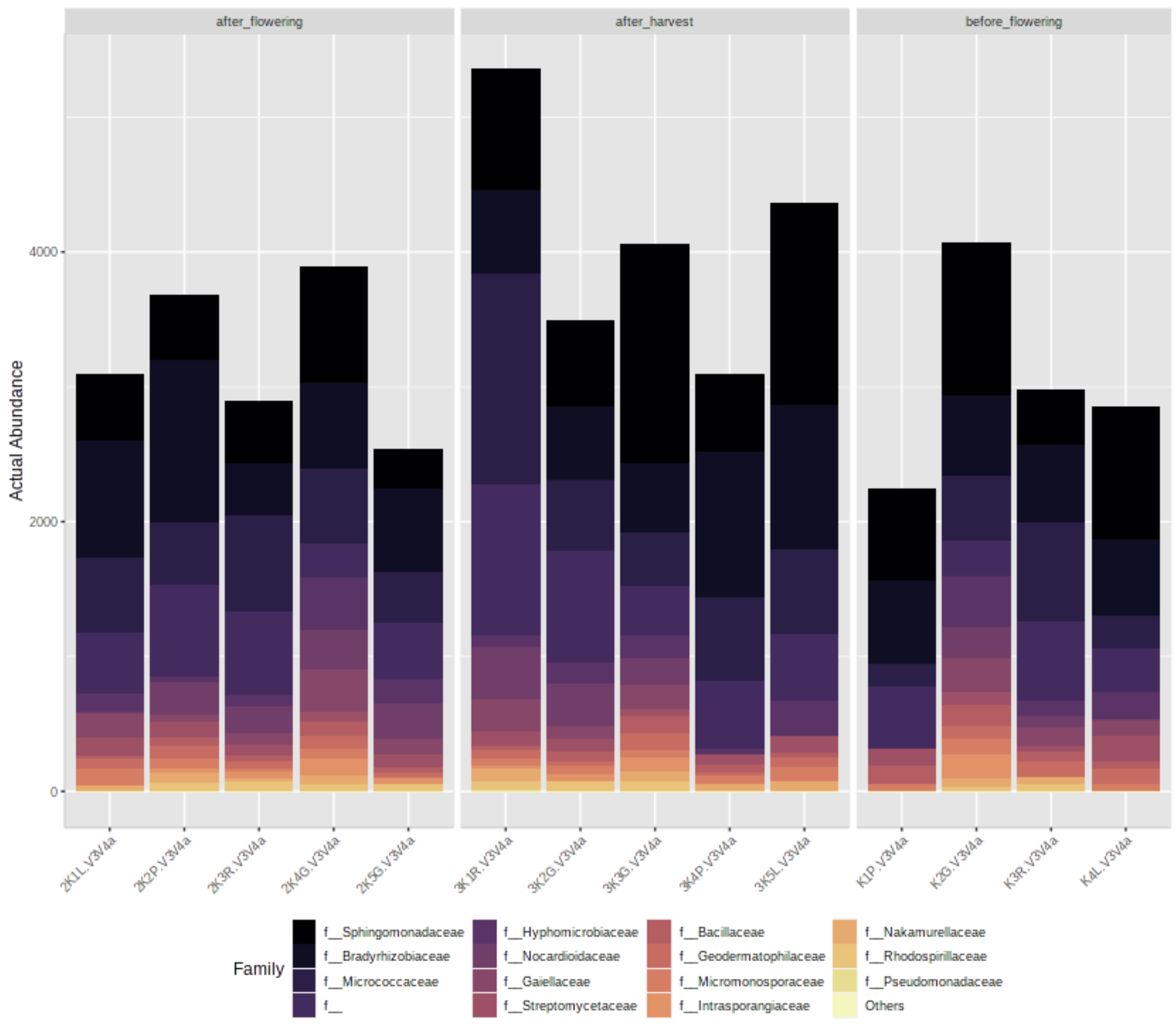
Shannon's species diversity index in soil samples from maize roots at different stages of the vegetation cycle

Results

Comparative analysis of the taxonomic composition showed 4 species of bacteria common to all soil samples taken from the roots, ie *Gaiella occulta, Gemmatimonas aurantiaca, Nitrosomonas* sp. and *Sphingomonas* sp. In addition, 28 species of bacteria characteristic of maize roots were found, which are constantly present regardless of the vegetation stage of the plant. The highest values of the Shannon biodiversity index were observed among soil samples from maize roots after flowering (index value 2.2), while the lowest for soil samples from maize roots after harvest (index value 1.95). In all the tested soil samples, the percentage advantage of bacteria of the genus *Sphingomonas* and *Bradyrhizobium* was observed, which constituted 17-29% and 13-18% of all types in the sample, respectively.



Venn diagram showing the number of shared and specific bacterial species depending on the vegetation stage of maize



The maize rhizmicrobiome biodiversity - family level

Referenses

Gupta, R., Anand, G., Gaur, R., & Yadav, D. (2021). Plant–microbiome interactions for sustainable agriculture: A review. *Physiology and Molecular Biology of Plants*, 1-15.

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Acknowledgments

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