How does the start and the end of the vegetation season affect the chemistry and the mycobiome structure of soils under monoculture maize cultivation?

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THE AIM OF THE STUDY

- to determine: changeability of chemical factors (pH, TOC, forms of N, P, selected elements – K, Mg, Ca), and
- soil mycobiome structure as influenced by time of the vegetation season on the example of maize monoculture

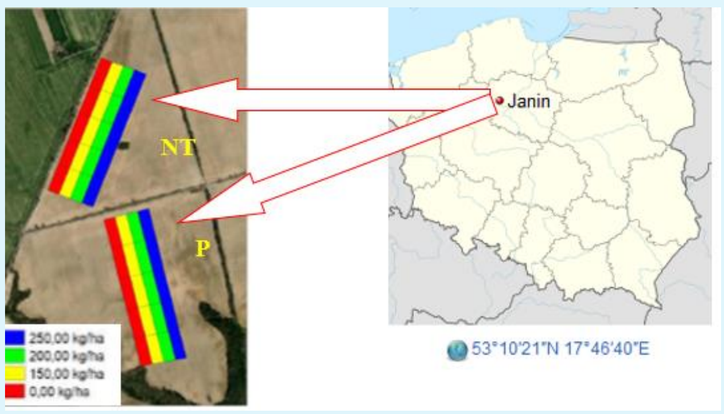

Fig. 1. Location of sampling area on Poland territory with gradient of fertilization applied on plowed (P) and no-till (NT) fields used for maize cultivation

RESULTS

RDA analysis indicates that the factor that differentiated the soils taken before sowing was the content of PO_4 (**Fig. 2**).

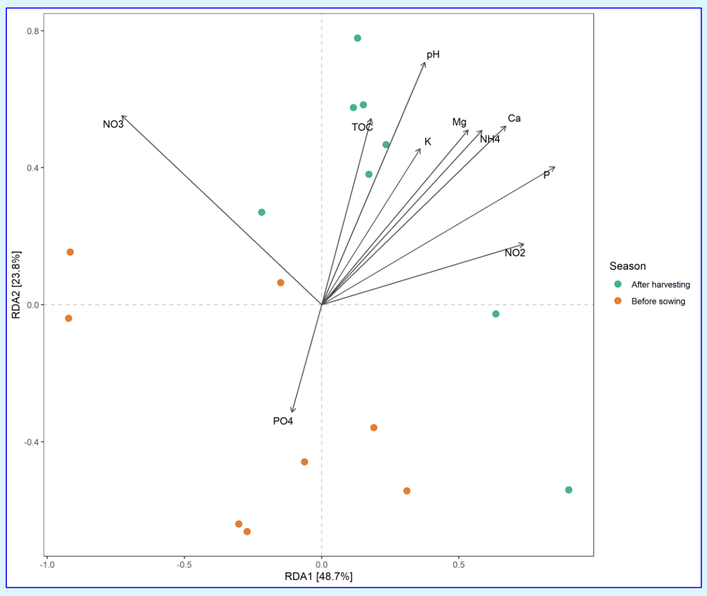

Fig. 2. RDA analysis conducted for the tested soils on two terms of the 2022 growing season

ANOVA analysis identified statistically significant differences between the analyzed samples taken at the beginning and the end of the maize vegetation season. It was shown that the term of soil sampling resulted in increase of pH, TOC, NH_4, P, Ca, Mg, and K contents, however, the content of NO_3 decreases (**Fig. 3**).

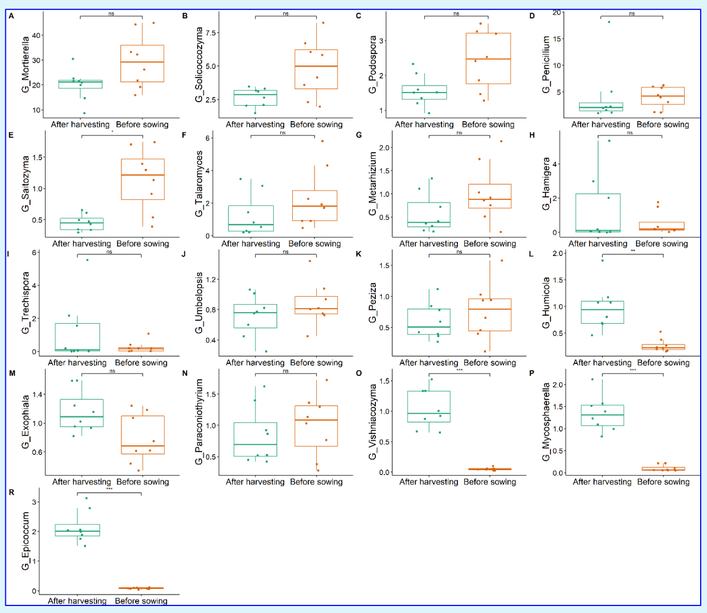

Fig. 3. ANOVA analysis conducted for selected physical and chemical properties of the soils studied

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MATERIAL AND METHODS

The study site was located in **Janin** on the agricultural area belonging to Potulicka Foundation Economic Center (**Fig. 1**). Representative soil material were taken form **10-ha field** (according to PN-ISO 10381–6,1998) **two times a year**: **in spring** (March 2022 – before maize sowing – start of vegetation season), and **autumn** (November 2022 – after maize harvesting – end of vegetation season). Soils (0-20 cm layer) were taken using an automatic sampler Wintex 1000 equipped with an Egner stick.

Chemical parameters **(pH, TOC, forms of N, P, K, Mg, Ca)** were determined potentiometrically (Hach Lange); with use of an auomatic TOC (Shimadzu) and N, P analysers (Bran+Luebbe) and FAAS technique (Hitachi), respectively.

DNA extraction was performed in 0.350 g of soil within 24 h after sample collection using DNeasy PowerLyzerPowerSoilKit (Qiagen). The fungal **ITS** region was amplified from each soil sample using primers: **5.8S** and **ITS1FI2**. The diversity of soil mycobiome was analyzed through amplicon sequencing on an **Illumina MiSeq** (Genomed S.A. Poland).

Correlation analysis was performed using Spearman's correlation test and RDA analysis. Differences between results from different sampling time were presented as **ANOVA** test. All statistical analyses were prepared in R v4.1 using the microeco package.

There were **no statistically significant differences** in the content of **fungi belonging to the phyla** (**Fig. 4**). ***Saitozyma* sp.** were present in higher abundance in soil samples taken **before sowing**. In contrast, **post-harvest soil** contained a higher content of ***Humicola, Vishniacozyma, Mycosphaerella***, and ***Epicoccum*** **(Fig. 5).**

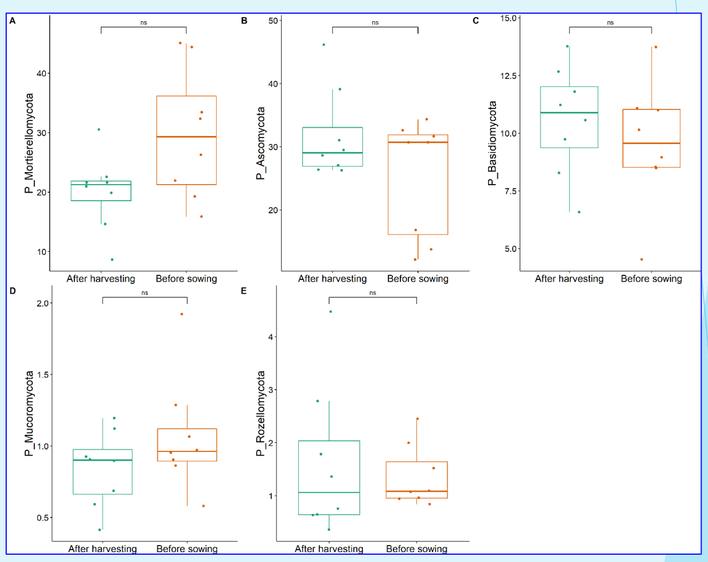

Fig. 4. ANOVA analysis conducted for the relative abundance (%) of selected fungi at the **phylum** level

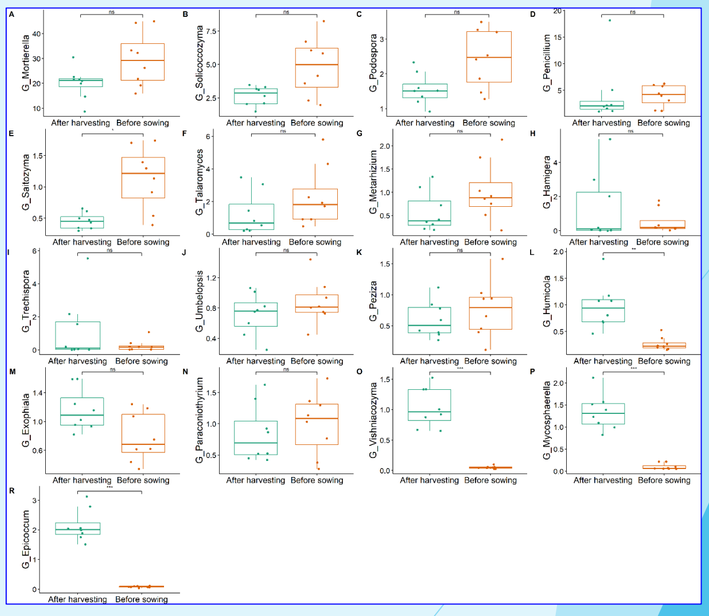

Fig. 5. ANOVA analysis conducted for the relative abundance (%) of selected fungi at the **genera** level

SUMMARY

- ✓ **The end of the vegetation season caused increase of the following chemical factors: pH, TOC, N-NH_4, P, Ca, Mg, and K**
- ✓ **Mycobiome at the phyla level was similar regardless of the date of the maize growing season, differentiation occurred at the taxonomic level of the genera**
- ✓ **Most of the identified fungal genera reached a higher relative abundance in autumn at the end of the maize growing season**