

Ascomycota and Mortierellomycota abundance in response to different cropping systems and reduced rates of N fertilization in maize monoculture

Anna Kruczyńska¹, Agnieszka Kuźniar¹, Artur Banach¹, Sara Jurczyk², Jacek Podlewski³,
Andrzej Słomczewski³, Anna Sochaczewska¹, Agnieszka Wolińska¹

¹The John Paul II Catholic University of Lublin, Department of Biology and Biotechnology of Microorganisms, 11 Konstantynów Street, 20-708 Lublin, Poland

²The John Paul II Catholic University of Lublin, Department of Artificial Intelligence, 1H Konstantynów Street, 20-708 Lublin, Poland

³Potulicka Foundation Economic Center, 5 Wojnowo Street, 86-014 Sicienko, Poland

Introduction

Ascomycota and Mortierellomycota are widely recognized as the dominant fungal phyla in the soil environment, while nitrogen (N) is an essential element for plant productivity; hence, it is abundantly applied to the soil in the form of organic or chemical fertilizers.



Objective

Molecular recognition of the structure and richness of the soil mycobiome at the taxonomic phylum level in the face of the application of different rates of N fertilization under two cropping systems: plowing (P) and no-till (NT).

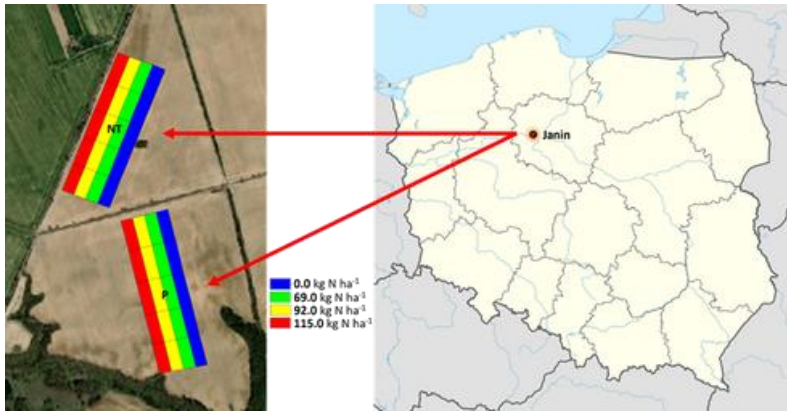


Fig. 1. Location of the studied fields and visualization of the applied fertilization gradient

Methodology

Study area: two fields (10 ha) dedicated to the cultivation of maize in the P and NT system under reduced fertilization conditions (Fig. 1, Janin, Kujawsko-Pomorskie Province);

Sampling: before sowing and after maize harvest (April and November 2022, respectively), using precision farming principles;

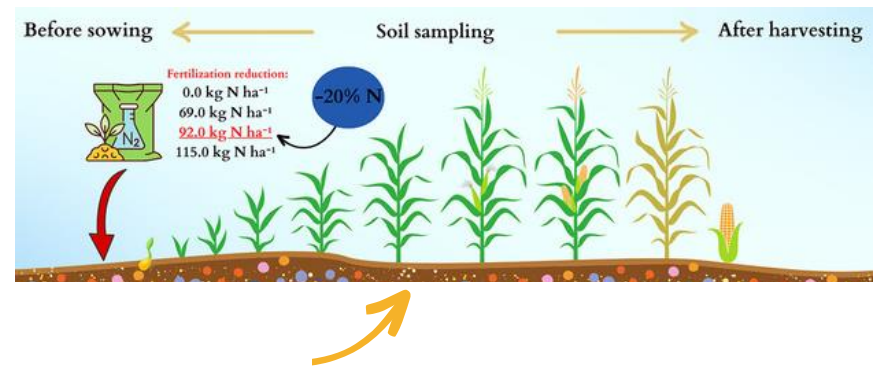
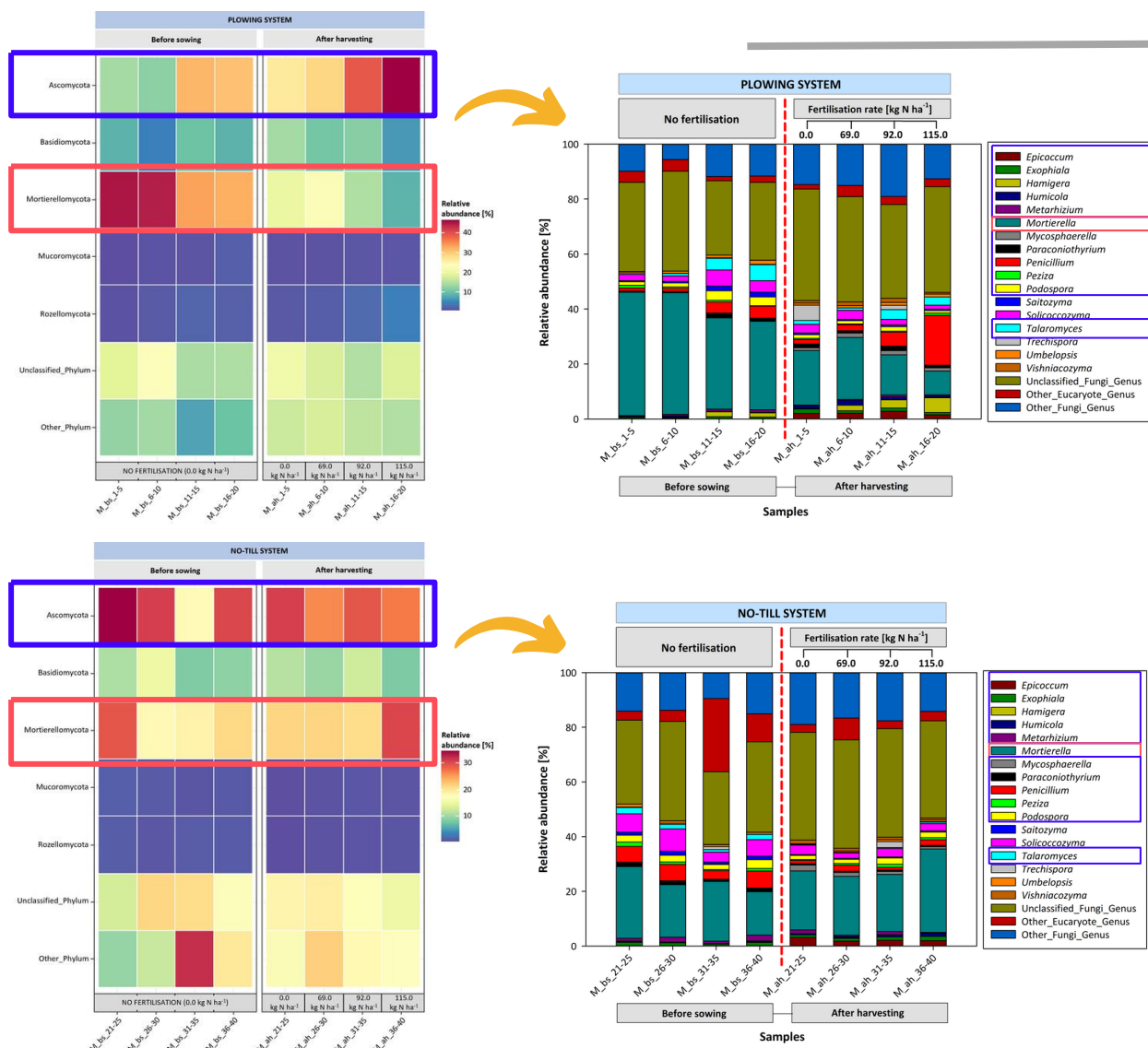
DNA isolation: DNeasyPowerLyzerPowerSoil Kit (QIAGEN);

Analysis of dsDNA quality and quantity: spectrophotometric method (BioSpectrometer, EPPENDORF) and fluorimetric method using Qubit dsDNA HS and BR Assay Kits and Qubit 4 (THERMO FISHER SCIENTIFIC);

PCR reaction: analysis for amplification with primers for fungi (ITS1/ITS4);

NGS sequencing: MiSeq Illumina technology (Genomed S.A., Warsaw, Poland). Taxonomic classification based on current reference databases RDP (v.138), SILVA and UNITE.

Results



After one growing season, the relative abundance of Ascomycota in the P system responded positively to increasing fertilization rates, and that the abundance of these fungi remained relatively comparable in the NT system (only a 20% reduction in N fertilization resulted in an increase in the relative abundance of Ascomycota). In contrast, the relative abundance of Mortierellomycota in the P system decreased significantly and declined with increasing N application rates, where, by comparison, in the NT system the richness of these fungi was highest at the maximal N application rate.

Conclusions

- The cultivation system is important in shaping the structure of the mycobiome and its relative abundance;
- Mortierellomycota may be sensitive to maize monoculture cultivation in the P system;
- N fertilization in the P system increases the relative abundance of Ascomycota.

Funding

Scientific work co-financed from the state budget within the framework of the programme of the Minister of Education and Science named "Science for Society", project number NdS/531260/2021/2021, total value of the project 625 910.50 PLN.