

Le Corps professoral de  
Gembloux Agro-Bio Tech - Université de Liège vous prie  
de lui faire l'honneur d'assister à la défense publique de la dissertation originale que

**Monsieur MA Mingchao,**

**Titulaire d'un diplôme de *master of engineering specialised in environmental sciences,***

présentera en vue de l'obtention du grade et du diplôme de

**DOCTEUR EN SCIENCES AGRONOMIQUES ET INGENIERIE BIOLOGIQUE,**  
le 6 juillet 2018, à 9 heures précises (personne ne sera admis après cette heure),  
en l'auditorium CA (Chimie Analytique, bât. 8),  
Passage des Déportés, 2, à 5030 GEMBLoux.

Cette dissertation originale a pour titre :

« Effect of long-term fertilization strategies on microbial community composition in a  
35-year field experiment of Chinese Mollisols ».

**Le jury est composé comme suit :**

Président : Prof. P. JACQUES, Professeur ordinaire,

Membres : Prof. M. ONGENA (Promoteur), Prof. J. LI (Promoteur - CAAS, Chine), Prof.  
S. MASSART, Prof. F. FRANCIS, Prof. P. FICKERS, Prof. B. BODSON, Prof. R. LI (Nanjing  
Agricultural University, Chine).

## Summary

Long-term intensive fertilizations are often accompanied by inefficiencies that result in pollution and soil degradation of Mollisols in northeast China, especially the overuse of inorganic nitrogen input. Organic manure can improve soil quality and may be potential as substitution of N fertilizer. However, we know limited about the impacts of inorganic fertilizer and organic manure applications on microbial community composition, which functions as sensitive indicator for soil biological fertility. To broaden our knowledge, high throughput pyrosequencing and quantitative PCR (qPCR) were used to explore the responses of soil property and bacterial and fungal community composition to long-term fertilization strategies. Soils were collected from a 35-year experimental field of Chinese Mollisols with six treatments: 1) no fertilizer (CK), 2) inorganic phosphorus and potassium fertilizer (PK), 3) inorganic P, K and nitrogen fertilizer (NPK), 4) manure (M), 5) inorganic P, K fertilizer plus manure (MPK), and 6) inorganic P, K, N fertilizer plus manure (MNPK). Treatments 1), 2) 3) and 5) were analyzed for bacterial and fungal community, and treatments 1), 3), 4) and 6) were used for arbuscular mycorrhizal fungi (AMF). All fertilization strategies significantly changed soil properties and increased the soybean yields, with the highest increase observed in MPK regime. The application of manure also had beneficial effects on soil acidification alleviation and soil organic matter (OM) accumulation, while long-term chemical fertilizer application (NPK and PK) significantly decreased soil pH. With regards to microbial abundance, 16S rRNA gene copy number was significantly increased in MPK regime. Compared with CK, long-term MPK application indicated a good effect on the soil shift from “fungal-based” to healthier one, namely “bacterial-based” soil, by decreasing ITS gene copy numbers and increasing the Bacteria-to-Fungi ratio, while chemical fertilization application (PK and NPK) exhibited the opposite pattern. Furthermore, the community richness indices (Chao1 and ACE) in MPK regime were also higher than other regimes, which implied resilience of microbial diversity and stable agroecosystem. The diversity and richness of AMF were negatively affected by chemical fertilizer, implying a reduction of mutualism in plant–AMF symbiosis; however, a reverse trend was observed for the application of manure. Regarding bacterial community composition, Proteobacteria, Acidobacteria, Actinobacteria and Verrucomicrobia were dominated phyla, and phylum Ascomycota was absolutely dominated in fungi in all samples, followed by Zygomycota, Basidiomycota, Chytridiomycota and Glomeromycota. The community composition considerably varied by different fertilization strategies at each taxonomic level. NPK application might induce the incidence rate of soil-borne disease, because more harmful fungal taxa were overrepresented in this regime, such as order Chaetothyriales, family *Chaetothyriaceae*, Genuses *Corynespora*, *Bipolaris*, *Pleosporaceae*, *Cyphellophora*, *Sphingomonas* and *Xanthomonas*. NPK application might cause a loss of plant-fungal symbioses, N loss in soil and greenhouse gas emission, due to the shift of classes Leotiomycetes and Eurotiomycetes. In contrast, more taxa with positive impact on soil quality were overrepresented in MPK regime, including phyla Proteobacteria, Bacteroidetes, class Alphaproteobacteria, family *Claroideoglomeraceae*, and genera *Variovorax*, *Chthoniobacter*, *Massilia*, *Lysobacter*, *Claroideoglossum*, *Catelliglobospora* and *Steroidobacter*. These beneficial bacteria were in association with plant growth promotion, OM accumulation, P acquisition, pathogen suppression, and soil enzyme activity arising. In conclusion, different fertilization strategies led to distinct variances in microbial community composition. Such shifts primarily derived from the changes of soil pH and OM. Our findings determined the response of microbial community composition to long-term application of inorganic fertilizer and organic amendment, and highlighted the benefits of substitution of inorganic N fertilizer by organic manure for sustainable development of agriculture in Chinese Mollisols.