## P-139

## Soil microbial community structures and activities in relation to nitrogen cycling in two contrasting soils in Malawi - community responses to added carbon

⊖ Akane Chiba¹, Yoshitaka Uchida¹, Satoshi Ishii², Patson Nalivata³, Keston Njira³

<sup>1</sup>Grad. Sch. of Agri., Hokkaido Univ., <sup>2</sup>University of Minnesota, USA, <sup>3</sup>Lilongwe University of Agriculture and Natural Resources, Malawi

E-mail: akane.101@hotmail.com

Fallowing is known as one of the conservative farm management techniques, which results in high crop yields and quality, potentially due to some changes in soil microbial structures and activities. However, few studies have investigated these changes in sub-Saharan Africa, where decreasing soil fertility is a serious issue. In this study, we examined the effects of different farm managements on the soil microbial community structures using soils sampled in Malawi, sub-Saharan Africa. Two sites located next to each other were selected. One was the conservatively managed soil (maize after bean, followed by 1 year fallow) and another was the intensively farmed soil (maize after maize, continuous). Meanwhile, the addition of crop residues, including rice straw, is known as a technique to prevent the decrease of soil fertility. Thus, we performed short-incubation studies to investigate soil microbial responses of these soils to rice straw application. Changes in the bacterial diversities in these soils following the addition of rice straw were investigated with 16S rRNA gene approach on Miseq. As an index of nitrogen activity,  $N_2$  O emission, nitrate-N (NO<sub>3</sub><sup>-</sup>-N) and ammonium-N (NH<sub>4</sub><sup>+</sup>-N) were measured at day 3, 12, 25 and 33. The similar trend of nitrogen activities, such as the rapid decrease in soil  $NO_3^-$ -N after rice straw application, were observed in the two soils. However, changes in bacterial community suggested that the responses of dominant groups, such as Firmicutes and Betaproteobacteria, to added carbon were different between the soil managements. At day 33, Firmicutes markedly decreased in continuous soil while it was still abundant in fallow soil. Future studies should focus more on functional genes to understand the gap between soil microbial activities and community.