Abstract

N_2O emission in dent corn has been an urgent issue involved in rising earth temperature. This N_2O emission mainly occurs due to the nitrification and denitrification by the microbial activity in the cultivation soil. This study used the nitrification functional gene (*amoA*(AOB) and *amoA*(AOA)), denitrification functional gene (*nirS, nirK, norB,* and *nosZ*), and 16S *rRNA*-based community identification to investigate the nitrification and denitrification activity in dent corn fields treated with 6 fertilization treatments. The fertilization treatments including no fertilization (CT), chemical fertilizer (CF), pig manure (PM), pig manure with bone meal addition (PM+B), composted sewage sludge (CS), and composted sewage sludge with bone meal addition (CS+B). This study discovered that the fertilization treatments only affect *nirK* significantly ($p<0.05$), however, there is a tendency of increasing *nirS+nirK/nosZ* ratio on the CF indicating there is a higher N_2O production activity due to the higher nitrogen release by the CF. In opposite, organic fertilizer tends to lower the N_2O production activity. Denitrification seems to be the main source of the N_2O emission in dent corn fields due to the significant correlation ($p<0.05$) between *nirS* (0.50*), *nirK*(0.67**), and *nosZ* (0.63**) with N_2O emission. Higher activity on CF was also projected on the higher nitrifying bacteria (1.94×10^8 copies 16S rRNA.g dry soil^{-1}) and denitrifying bacteria (3.11×10^8 copies 16S rRNA.g dry soil^{-1}) abundance found in the community. This study found some important nitrifying-denitrifying and denitrifying bacteria that play an important role in N_2O production, such as *Pseudomonas, Bacillus, Rhodococcus, Agrobacter, Rhizobium, Balneimonas*, and also *Dechloromonas* as an important bacteria in N_2O reduction in dent corn fields.

Keywords: N_2O emission, dent corn, fertilization, functional gene, microbial community