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Effects of dairy manure management in annual and perennial cropping systems on soil microbial communities associated with in situ N2O fluxes

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Liquid dairy manure (LDM) application and ploughing events may affect soil microbial community functioning differently between perennial and annual cropping systems due to plant-specific characteristics stimulating changes in microbial community structure. Understanding how these microbial communities change in response to varied management, and how these changes relate to in situ N2O fluxes may allow the creation of predictive models for use in the development of best management practices (BMPs) to decrease nitrogen (N) losses through choice of crop, plough, and LDM practices. Our objectives were to contrast changes in the population sizes and community structures of genes associated with nitrifier (amoA, crenamoA) and denitrifier (nirK, nirS, nosZ) communities in differently managed annual and perennial fields demonstrating variation in N2O flux, and to determine if differences in these microbial communities were linked to the observed variation in N2O fluxes. Soil was sampled in 2012 and in 2014 in a 4-ha spring-applied LDM grass-legume (perennial) plot and two 4-ha corn (annual) treatments under fall or spring LDM application. Soil DNA was extracted and used to target N-cycling genes via qPCR (n=6) and for next-generation sequencing (Illumina Miseq) (n=3). Significantly higher field-scale N2O fluxes were observed in the annual plots compared to the perennial system; however N2O fluxes increased after plough down of the perennial plot. Nonmetric multidimensional scaling (NMS) indicated differences in N-cycling communities between annual and perennial cropping systems, and some communities became similar between annual and perennial plots after ploughing. Shifts in these communities demonstrated relationships with agricultural management, which were associated with differences in N2O flux. Indicator species analysis was used to identify operational taxonomic units (OTUs) most responsible for community shifts related to management. Nitrifying and denitrifying soil bacterial communities are sensitive to agricultural management (annual or perennial crop type, LDM management, and ploughing) and communities will respond to variations in management, affecting field N2O fluxes.