Bacteria associated with carbon cycling after application of compost and manure to three dairy pastures

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We investigated the impact of compost and manure on bacterial communities associated with soil carbon in three dairy pastures in south-western Australia. Bacterial communities involved in soil carbon and nitrogen cycling were assessed following application of compost and dairy manure under field conditions. Soil bacterial communities were characterised using community profiling (semiconductor sequencing of barcoded amplicons generated from the V3-V4 region of bacterial 16S rDNA genes). The presence of carbon degrading functional genes was predicted using the bioinformatics software: Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt). The dominant bacterial phyla in order of relative abundance were: Proteobacteria, Firmicutes, Actinobacteria, Bacteroidetes and Acidobacteria. Bacterial community structure differed among the farms but there was less effect of organic matter amendment within farms. For all three farms, soil amendment with compost or manure in combination with fertiliser increased the abundance of predicted carbon degrading functional genes associated with degradation of hemicellulose and cellulose compared with those associated with degradation of chitin, lignin and starch. Within one farm, there was an interaction between soil amendments and the abundance of predicted lignin degrading genes. The sandy soil on this farm had the lowest levels of soil carbon and soil nitrogen. For the other two farms (one with sandy soil and one with clayey soil), there was no effect of the soil amendments on the predicted gene count for carbon degrading functional genes.