



From tidal wetland to paddy rice fields – Changes in soil microbial communities during 2000 years of rice cultivation

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In many areas of China tidal wetlands have been converted into agricultural land for lowland rice cultivation. However, the consequences and effects on soil microbial communities are poorly understood. Therefore, we investigated bacterial and archaeal communities involved in nitrification and denitrification based on diversity and abundance pattern of the corresponding functional genes in a tidal wetland and two paddy soils cultivated for 50 years respectively 2000 years with rice. The abundances of all measured genes increased from the tidal wetland to the 2000 years paddy soil in reference to one gram of soil due to a significant increase of the microbial biomass. When relating the functional gene copies to the extracted microbial biomass highest copy numbers were observed in the paddy soil with 50 years of rice cultivation history with exception of the archaeal nitrification gene *amoA*. T-RFLP data of the archaeal *amoA* gene and the bacterial denitrification gene *nosZ* revealed significant differences in community composition in the three investigated soils. Overall, our results indicate clear changes in abundance and diversity pattern of microbial communities participating in nitrogen cycling during rice paddy evolution.