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Analysis of bacterial community diversity in soils treated with ethoprophos

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Ethoprophos is an organophosphorus pesticide that is widely used in agriculture to control major insect pests, has received much concern due to its lethal neurotoxicity and accumulation in soils and groundwaters. Here changes in the bacterial community compositions with 16S rDNA analysis of meta-DNA extracted from 8 group soils with 15-days period (non-treatment, 1-day, 15-day, 30-day, 45-day, 60-day, 75-day, 90-day) during 90 days after treatment with an excessive ethoprophos, organophosphorus pesticide was examined. While ethoprophos was degraded actively in soils of from 15 days to 60 days after treatment, bacterial community of these soils has been rapidly dominated by *Proteobacteria* phylum, *Gammaproteobacteria* class, *Pseudomonadaceae* family, *Pseudomonadales* order, *Pseudomonas* genus. It was evaluated the rate of degradation by a natural microbial community in each soil after its treatment and found that more ethoprophos was degraded in 30-day soils (50% degradation) and 75-day soils (95% degradation). With the progress of degradation of ethoprophos during 90 days after treatment, total composition of the genus *Pseudomonas* was abruptly increased to 70.1% in 15-day soil from 7.6% of control soils (non-treatment), but was decreased slowly to 61.3% in 30-day soil, 38.2% in 45-day soil, resumed to 9% similar to the level of control in 75-day soil. In 60-day soil showing 70% degradation rate on total ethoprophos contents of control soil, members of genera *Collimonas*, *Sphingobium*, *Massilia* appeared suddenly in large amounts in its microbial community. These results indicate that these genera including *Pseudomonas* might majorly be responsible for the real degradation by a natural microbial community in ethoprophos over-contaminated soils.

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