

Pornpimon Buachaoko 2011: Distribution of Tetracycline Resistance Genes and Microbial Community Shift in Agricultural Soil Through Fertilization with Animal Manure. Master of Science (Soil Science), Major Field: Soil Science, Department of Soil Science. Thesis Advisor: Assistant Professor Kannikar Sajjaphan, Ph.D. 113 pages.

The study on the distribution of tetracycline resistance genes in agricultural soil through fertilization of the soil with animal manure was performed using soil microcosms. In this study, the diversity of tetracycline resistant genes (*tet* genes) in the soil microcosms was explored after fertilization of the soil with tetracycline-free swine manure which amended with tetracycline at various concentrations (0 0.2 20 2000 mg/kg soil). The certain tetracycline resistant genes *tetC tetD tetA tetG tetL tetM* and *tetO* were detected in the soil samples collected from the microcosms to which swine manure was amended with tetracycline. However, these genes were detected in almost all soil samples supplemented with tetracycline at all time intervals of soil samplings while these genes were found only in some manured amended soil samples without prior supplementation with tetracycline. In addition to those genes, other genes namely; *tetB tetO tetS tetP* and *tetX* were also detected in the soil samples collected at different time intervals from soil microcosms fertilized with manure either tetracycline-free manure or tetracycline-amended manure. The outcome of this study strongly indicated that an increase in the number of tetracycline resistant genes was detected in the soil fertilized with manure supplemented with tetracycline. The concentrations of tetracycline also affected the diversity of tetracycline resistant genes. For soil fertilized with pig manure with tetracycline supplementation even once or several times, similar diversity of tetracycline resistant genes was observed from soils fertilized with tetracycline-supplemented pig-manure, both single and repeated supplementation.

The study of the shift in the microbial community structure in the agricultural soil fertilized with animal manure was performed using DGGE and the grouping of the outcome of microbial community structure in the soil samples was performed using UPGMA programme. Analysis of the dendrogram based on the major patterns of DNA fingerprints showed 3 major groups of bacteria. Outcomes also revealed that soil samples collected from the same sampling intervals gave almost identical microbial community structure regardless of the different concentration of tetracycline supplemented in the manure.

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