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ACCUMULATION OF ANTIBIOTICS AND TET RESISTANCE GENES FROM SWINE WASTEWATER IN WETLAND SOILS

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Abstract

The accumulated characteristics of typical veterinary antibiotics (tetracyclines, sulfonamides, quinolones and macrolides) and tetracycline resistance (*tet*) genes in the different wetland soils (Krasnozem and Chernozem), and the effects from *Phragmites australis* were evaluated in this study. Results indicated that the concentrations of targeted antibiotics and *tet* genes in soils with swine treatment would increase as time progressed. The *tet* genes and targeted antibiotics (except sulphonamides) at different depth profiles showed a similar change tendency, namely the concentrations of those remained at a consistently higher level in the surface layer of the soils system (P < 0.05). The targeted tetracyclines showed the highest concentration in the soils (61.73-998.9 µg/kg) compared with the others antibiotics, and *tet* M (5.8×10^{-1} - 9.31×10^{-2} for the relative abundance range) was the predominant *tet* gene in the all soil samples. However, due to the different physicochemical properties of the two kinds of soils, the behaviours of antibiotics and *tet* genes in the different soils also exhibited obvious difference. The presence of *P. australis* could play a role in reduction of sulfonamides in the soils (P < 0.05), while the accumulated concentrations of tetracyclines, quinolones and macrolides in the soil systems with plant were similar to those in their unplanted equivalent (P > 0.05). Furthermore, there was not a significant influence of plant growth on the relative abundance of *tet* M, *tet* W and *tet* O in the soils (P > 0.05).

Key words: antibiotics, antibiotic resistance genes, constructed wetland, livestock wastewater, plant

Received: March, 2016; Revised final: September, 2016; Accepted: October, 2016

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