Fate and effect of sulfadiazine in bulk soil and in the rhizosphere of maize: a mesocosm study

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Spread and evolution of antibiotic resistance genes through agriculture pose a possible risk for human health, e.g. by increasing resistance problems in human antibiotic therapy. The "DFG Forschergruppe FOR566" aims at identifying key processes that control the fate and effects of veterinary medicines in soil. Sulfadiazine (SDZ), used as a model compound in this project and belonging to the class of sulfonamides, is among the most widely used veterinary antibiotics in the EU (KOOLS *et al.*, 2008). It is excreted largely unchanged by the animals and enters agricultural soils through the use of manure and slurry as fertilizer. Thereby, it can have effects on the functional and structural composition of the soil microbial community and its activity and may promote the formation and spreading of resistance genes by mobile genetic elements such as plasmids (HEUER *et al.*, 2011). Recently it was shown by BRANDT *et al*. that the addition of artificial root exudates increased the bacterial community tolerance towards SDZ, indicating that the rhizosphere might be a hotspot of resistant bacteria (BRANDT *et al.*, 2009). On the other hand, the dissipation of bioaccessible SDZ-concentrations was accelerated in rhizosphere soil (ROSENDAHL *et al.*, 2011). However, knowledge of the abundance and dynamics of sulfonamide resistance genes in the rhizosphere is scarce. We therefore will present results on the fate and effect of SDZ in bulk soil and rhizosphere of maize plants which were studied in a mesocosm experiment. The abundance and dynamics of sulfonamide resistance genes (*sul1*, *sul2*) and major plasmid vectors were assessed by cultivation-independent approaches (qPCR; exogenous plasmid isolation). The main findings were (I) the significantly increased abundance of *sul* genes when the soil was treated with manure containing SDZ, (II) the majority of the plasmids captured belonged to the novel LowGC-type family, and (III) unexpectedly the relative abundance of *sul* genes was lower in the rhizosphere compared to bulk soil.

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