

Detection of antibiotics and antibiotic resistance genes in manures from different pig producing systems and in biogas plants

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Antibiotics are extensively used in animal livestock and are often excreted unchanged or as active metabolites by treated animals. These antibiotics lead to a fitness advantage of resistant bacteria present not only in the intestine of the animals, but also in soil to which the manure is applied as fertilizer. In turn the abundance of resistant bacteria and of corresponding antibiotic resistance genes (ARGs) in the microbial community is assumed to increase. Via mobile genetic elements these genes can spread even among phylogenetically distant bacteria and new resistant genotypes of pathogens may emerge.

The aim of our project is to monitor antibiotics and ARGs in manures in order to develop mitigation strategies and to minimize the risk of resistance transfer to pathogens.

To identify parameters influencing the degradation of antibiotics and the reduction of ARGs during storage of manure or its treatment in biogas-plants we sampled 16 different pig

producing facilities and 9 biogas plants (fermenters are fed with pig manure) at different process steps. The samples were analyzed for the presence and content of antibiotics (via LC/MS/MS), ARGs and mobile genetic elements (via PCR, Southern blot and quantitative real time PCR).

Changes in the composition of the microbial communities in manure from different farms and during the fermentation process of biogas-plants were analyzed by using DGGE of 16S rRNA gene fragments amplified from total community DNA.

We were able to detect plasmids of different incompatibility groups (IncN, IncQ, IncP-1, IncW, IncU, Low GC), integrons containing gene cassettes of different sizes and several ARGs (*sul1*, *sul2*, *sul3*, *tetA*, *aadA1*) in many of the samples. Our data indicate that not only piggery manure but also the fermentation residues from biogas plants used for fertilization of field soils might contribute to spreading antibiotic resistance genes and mobile genetic elements.