

Detection of antibiotic resistance genes and mobile genetic elements in piggery manures and fermentation residues from biogas plants

Birgit Wolters¹, Susen Hartung², Arum Widyasari², Robert Kreuzig² and Kornelia Smalla¹

¹Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Department of Epidemiology and Pathogen Diagnostics, Braunschweig

²Technical University of Braunschweig, Institute of Environmental and Sustainable Chemistry, Braunschweig

Email of corresponding author: birgit.wolters@jki.bund.de

Antibiotics are used extensively in animal husbandry and treated animals often excrete them unchanged or as metabolites. These antibiotics lead to a fitness advantage of resistant bacteria present in the intestine of the animals and in agro-ecosystems to which manures and fermentation residues are applied as fertilizers. This might lead to an enrichment of resistant bacteria and corresponding antibiotic resistance genes (ARGs) in the microbial communities. If they are located on mobile genetic elements (MGEs) these genes may spread even among phylogenetically distant bacteria and new resistance phenotypes of pathogens might occur.

The aim of our project is to monitor antibiotics and ARGs in manures and fermentation residues 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 reduction of ARGs and MGEs during fermentation in biogas plants or storage of manure we sampled 8 mesophilic biogas plants (fermenters were fed with

pig manure except one which was fed with bovine manure) at different processing steps and stored manures of 16 different pig producing facilities. The samples were analyzed for the abundance of ARGs and MGEs (via PCR, Southern blot and quantitative real time PCR) as well as for the presence and content of antibiotics (via LC/MS/MS).

By using DGGE of 16S rRNA gene fragments amplified from total community DNA we analyzed differences in the composition of bacterial communities in manure from different farms and during fermentation in biogas plants.

We detected plasmids of different incompatibility groups (IncN, IncQ, IncP-1, IncW, IncU, Low GC), integrase genes of class 1 and class 2 integrons, several ARGs (*sul1*, *sul2*, *sul3*, *tetA*, *tetM*, *tetX*, *aadA1*) and the resistance gene *qacEΔ1* (against quaternary ammonium compounds) in many samples.

Our data indicate that piggery manures as well as fermentation residues from biogas plants might contribute to the spread of ARGs and MGEs in the agro-ecosystem when used as fertilizer.