



Antimicrobial resistance

Gaining insight into the risks and
control of antibiotic use

Top level veterinary and biomedical research for animal and public health

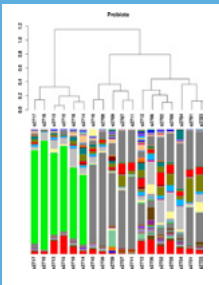


WAGENINGEN
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Probiotic
treatment/
Starter flora



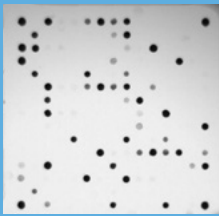
Microbiota
Composition
(16S sequencing)



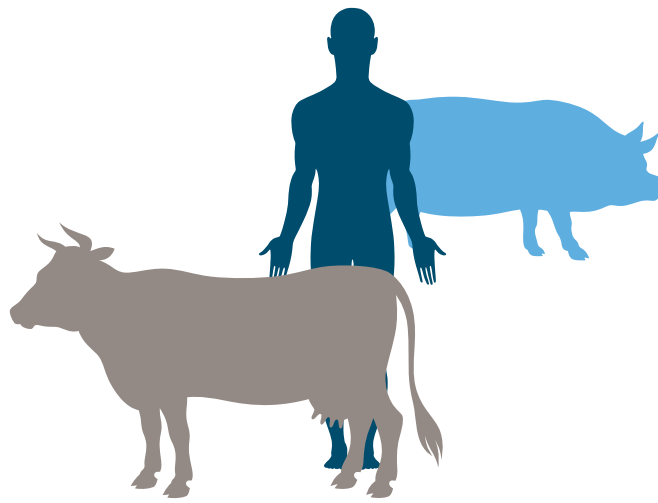
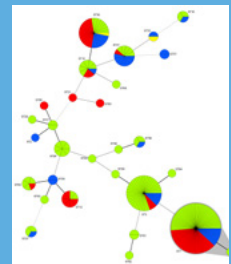
Resistome
Sequencing



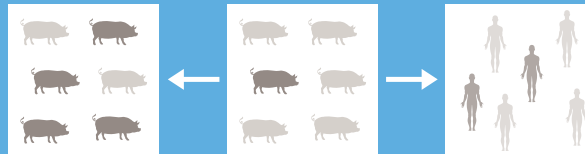
Clondiag array for
resistance genes



Plasmid Typing



Transmission of antimicrobial resistant pathogens



Antimicrobial resistance

Bacterial resistance to commonly used antimicrobials in people without a history of antibiotic treatment or hospital stay is on the increase. Bacteria with antibiotic resistant traits that are located on mobile genetic elements (plasmids) are a particular concern. These plasmids can easily be exchanged between bacteria, contributing to spread of antibiotic resistance. This could also lead to multi-drug resistant (MDR) bacteria due to the accumulation of different antibiotic resistance genes. The use of antibiotics in farm animals enhances the selection for MDR bacteria, which increases the risk of transmission to humans.

At Wageningen Bioveterinary Research the occurrence, spread and prevention of antimicrobial resistance in bacteria of animal origin is studied.

We use state-of-the-art techniques, like sequencing all antibiotic resistance genes in a population (resistome), genotyping resistant bacteria and plasmids, as well as traditional resistance tests and risk assessment studies. Dedicated microarrays to determine presence of resistance genes in a microbial population are available.

Microbiota composition

Antimicrobial resistance genes are widely spread in bacterial populations like intestinal or oropharyngeal microbiota. Resistance genes can therefore be exchanged between commensals and pathogens within these communities. At Wageningen Bioveterinary Research we determine the microbiota composition and resistome of several bacterial communities. The effect of interventions that influence microbiota composition (such as feed and probiotics) on antimicrobial resistant organisms and the number of resistance genes is also included in our studies.

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