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Comparison of Individual and Pooled Samples for Quantification of Antimicrobial Resistance Genes in Swine Feces by High-throughput qPCR

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OBJECTIVE
Determine the number of samples in a pool giving a representative sample for antimicrobial resistance gene quantification in Danish pig herds.

SAMPLING
20 individual fecal samples were collected from a section in a Danish pig herd. One to five rectal fecal samples were taken from each pen with respect to the number of pigs in the pen. A total of 48 pools were made of increasing number of individual samples.

RESULTS AND CONCLUSION
There were large variations in the levels of antimicrobial resistance genes between individual samples. As the number of samples in a pool increased a decrease in sample variation was observed. A steady state in the sample variation was seen when pooling five or more samples. No significant difference was found between pools of five samples and pools of more. There were highly significant differences between pools of five or more samples and pools of less samples. Five samples in a pool is the optimal number.

MATERIALS AND METHODS
Sample pooling → DNA extraction → qPCR

Sample pooling

DNA extraction

Maxwell® 16 Instrument, Promega

qPCR

192x24 Dynamic Array, Fluidigm®

Figure 1. Relative quantification values (RQ) for \( \text{ermB} \) from individual samples and pooled samples.

Figure 2. Relative quantification values (RQ) for \( \text{tet(W)} \) from individual samples and pooled samples.