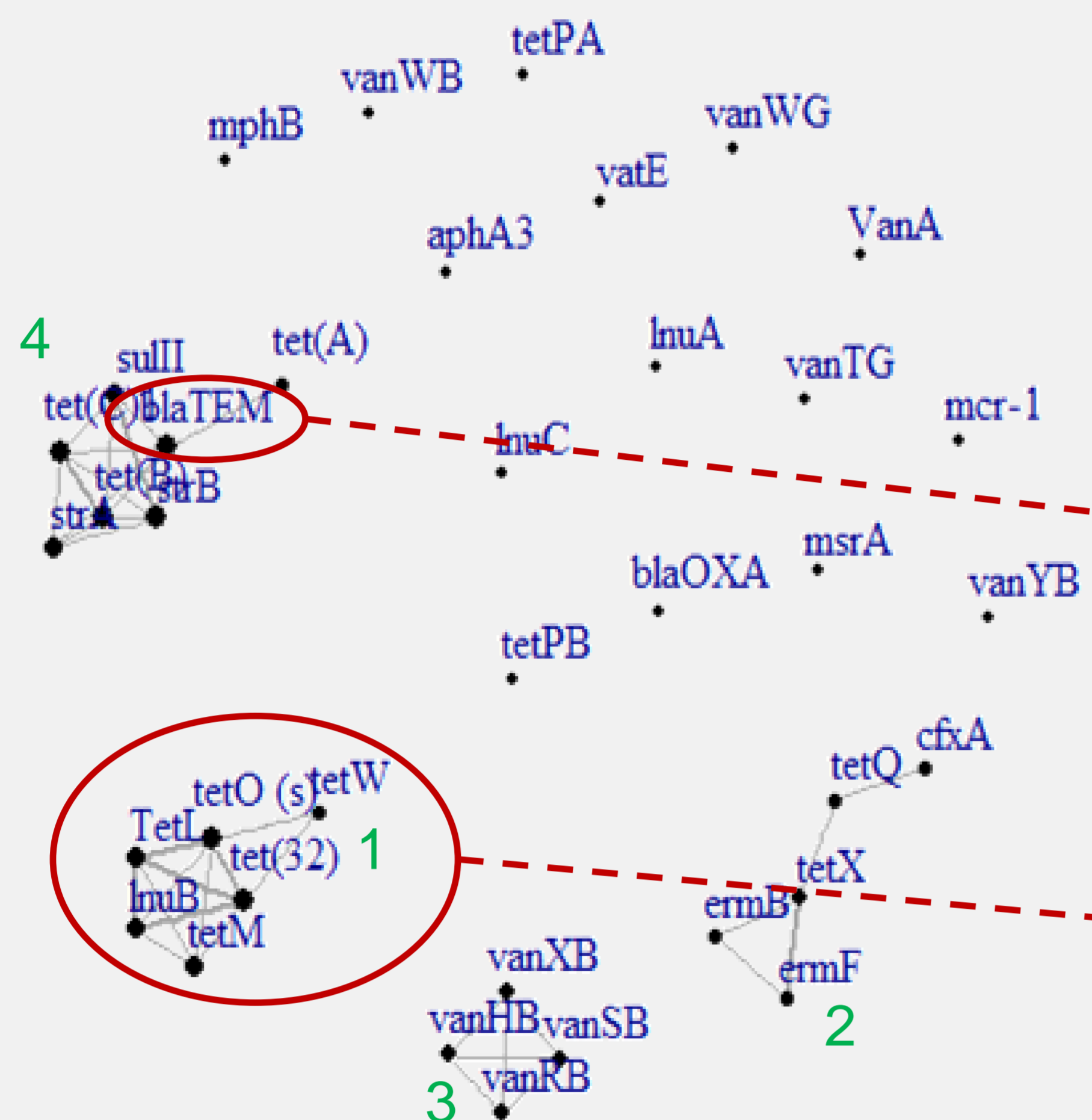


Clusters of genes associated with antimicrobial resistance in Danish pig farms

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Cluster plot: Significant correlations between RQ values of genes with Spearman $\rho > 0.5$ are indicated by grey links. Four distinct and independent clusters can be identified.

Three clusters predominantly contain genes associated with Tetracycline¹, Macrolides², or Vancomycin³ resistance, while one cluster contains genes not associated with one particular group of antimicrobials⁴.

Motivation, Conclusion and Perspectives

Clusters of genes associated with antimicrobial resistance may ease surveillance and simulation modelling of antimicrobial resistance in the Danish pig population, as it may be possible to survey/model only on cluster level, as opposed to on individual genes.

i.e. blaTEM detects a group of beta-lactamase genes that include several extended spectrum beta-lactamases (ESBLs). The presence of blaTEM may indicate an increased risk of ESBL presence.

Tetracycline resistance is driven by many genes, but if these genes cluster, resistance towards tetracycline may be easier modelled on the cluster level.

Method

A cross-sectional study: 5 pigs from 681 Danish pig farms had fecal samples taken at the slaughterhouse.

The 5 samples from each farm were pooled to one sample.

The pooled samples were quantified using qPCR for 37 genes coding for antimicrobial resistance.

The values reported are relative quantities (RQ) of genes compared to 16S.

The correlation of RQ values between farms were tested using Spearman rank correlation.

