Spatial patterns of antimicrobial resistance genes in a cross-sectional sample of pig farms with indoor non-organic production of finishers

Antimicrobial resistance (AMR) in pig populations is a public health concern. There is a lack of information of spatial distributions of AMR genes in pig populations at large scales. The objective of the study was to describe the spatial pattern of AMR genes in faecal samples from pig farms and to test if the AMR genes were spatially randomly distributed with respect to the geographic distribution of the pig farm population at risk. Faecal samples from 687 Danish pig farms were collected in February and March 2015. DNA was extracted and the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)) were quantified on a high-throughput real-time PCR array. Spatial differences for the levels of the AMR genes measured as relative quantities were evaluated by spatial cluster analysis and creating of risk maps using kriging analysis and kernel density estimation. Significant spatial clusters were identified for ermB, ermF, sulII and tet(W). The broad spatial trends in AMR resistance evident in the risk maps were in agreement with the results of the cluster analysis. However, they also showed that there were only small scale spatial differences in the gene levels. We conclude that the geographical location of a pig farm is not a major determinant of the presence or high levels of AMR genes assessed in this study.

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