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TITLE

PREVALENCE AND GENOMIC CHARACTERISTICS OF ERYSIPELOTHRIX RHUSIOPATHIAE IN HEALTHY SWEDISH PIGS

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CONTENT

Introduction

The gram-positive bacterium *Erysipelothrix rhusiopathiae* (ER) may cause erysipelas in a wide range of animals. ER can persist for long periods in the environment and be carried asymptotically by animals. The aim of this study was to investigate the prevalence of ER among healthy Swedish pigs and characterize recovered isolates by whole-genome sequencing.

Material & Methods

Tonsils were collected from 200 apparently healthy pigs at slaughter, from 10 abattoirs in Sweden. Only one pig per herd was sampled. Samples were cultured using selective media. Growth of ER was confirmed by MALDI-TOF MS.

All recovered isolates were whole-genome sequenced on an Illumina MiSeq instrument. The isolate sequence data were compared to each other and 100 previously sequenced isolates from various sources using an in-house whole-genome SNP analysis pipeline.

Results

ER was isolated from six samples, corresponding to a prevalence of 3.0% (95% CI 1.2-6.5%). None of the six recovered isolates were identical by whole-genome SNP analysis and there was no clear link between genotype and geography. Of the investigated isolates, four belonged to clade 1, a subgroup that has been recovered from multiple sources and particularly from marine animals. The remaining two isolates belonged to clade 2.

Discussion & Conclusion

The lower prevalence of ER than earlier reported was assumed to mirror rearing of pigs indoors and improved biosecurity (age segregated rearing). To our knowledge, ER clade 1 has never been recovered from pigs. Clade 1 isolates are distinct from the other clades in terms of carriage of virulence genes and carry distinct variants of the Spa gene which is known to be involved in *Erysipelothrix* pathogenesis. Thus, it is an intriguing possibility that clade 1 is widespread among wild and domestic animals but has been overlooked due to limited sampling of asymptomatic animals.