



BACTERIAL DISEASES

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ASSOCIATION OF SEQUENCE WITH SEROTYPE, VIRULENCE, AND ANTIMICROBIAL RESISTANCE IN *ACTINOBACILLUS PLEUROPNEUMONIAE*

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Introduction

Actinobacillus pleuropneumoniae (App) is responsible for significant economic losses in worldwide pig production. Peracute cases of sudden deaths, severe hemorrhagic and necrotizing or fibrinous pleuropneumonia and decreased performance during subclinical infections are typical manifestations. Strains are highly variable regarding serotype, virulence and antibiotic resistance, leading to massive problems in diagnostics, therapy and vaccination. The aim of the present, ongoing study is to identify molecular markers of App in association with well characterized strains from the field.

Material & Methods

21 genome sequences, publicly accessible on the NCBI genome database, were compared using ANI (average nucleotide index) software. A 1000 nucleotides frame of the core region was compared among the strains on the nucleotide and amino acid level. About 100 strains resembling different features of App were sampled on commercial herds, phenotypic characterized and sequenced on a genome-wide level.

Results

As a result of the ANI analysis, the compared strains, although mostly representing individual serotypes, showed only low genetic difference (max 2.09%). Genetic variability between strains of the same serotype only differed by 0.02 to 0.09%. Strains of the same serotype and the same serotype group (e.g. 1/9/11) were clustered within the same branch of a phylogenetic tree, underlining their high degree of genetic homology.

Discussion & Conclusion

The in silico analysis of App genome sequences proved a high degree of homology, although the strains differed obviously in their phenotypes. Based on the results of the first part of the study, the second and ongoing part aims to identify specific sequence motives and SNPs, associated with virulence, serotype and antibiotic resistance. The results will help to improve diagnostic, therapeutic and prophylactic measures in the future.