

***STREPTOCOCCUS SUIIS* (*S. SUIIS*) ANTIMICROBIAL RESISTANCE (AMR) GENOTYPE AND PHENOTYPE CORRELATION, AND GENOMIC SIGNATURES SUGGESTING LINKAGE OF AMR GENES**

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Introduction

S. suis is a significant zoonotic pathogen affecting pigs and humans. Quick and correct antimicrobial treatment implementation increases recovery chances. Antimicrobial resistance (AMR) can be predicted by the presence of certain genes conferring resistance.

The dynamics of horizontal gene transfer often mean that AMR genes are found within the same mobile elements such as transposons.

Materials and methods

S. suis isolates (n=628) from clinical and non-clinical pig cases were AMR tested using the minimal inhibitory concentration (MIC) method for 17 antimicrobials including lincomycin, and spectinomycin among others. Epidemiological cut-off values (ECOFF) were set by a mathematical model analysing MIC distribution patterns. Isolates with MIC > ECOFF were classified as nonwild-type (NWT). All isolates were sequenced for AMR genes reported in the literatures and spectinomycin and lincomycin phenotypes versus genotypes are reported here.

Results

The presence of AMR genes showed a close agreement with NWT phenotype. For example, 368 out of 369 isolates with lincomycin AMR genes were classed as NWT for lincomycin, and 43 out of 75 isolates with spectinomycin AMR genes were NWT for spectinomycin.

Additionally, 58 of the 628 isolates were NWT for spectinomycin, and 57 of these 58 were NWT for lincomycin also. Genes conferring resistance for lincomycin (*InuB*) and spectinomycin (*ant_6_1a*, *ant_9_1a*, *aph_3_IIIa*) were identified in conjugative transposons in at least 29 out of these 57 lincomycin + spectinomycin NWT isolates.

Discussion and conclusion

Identifying AMR genes helps to predict *S. suis* AMR phenotype and the identification of potential treatments does not require isolation and *in vitro* AMR testing.

We observed higher prevalence than expected of co-resistance to lincomycin and spectinomycin given the individual antimicrobial resistance prevalence. The presence of mobile genetic elements such as integrated conjugative transposons suggests that some AMR phenotypes will be linked in *S. suis* even in the absence of selection.