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ANTIMICROBIAL SUSCEPTIBILITY AND GENETIC DIVERSITY OF *TRUEPERELLA PYOGENES* ISOLATED FROM PIGS IN SPAIN

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Introduction

Trueperella pyogenes infections in pigs have recently become an increasing clinical and epidemiological problem, which reflects in the rising number of condemnations by lymphadenitis in slaughterhouse. The objective of this work was to determine the Minimum Inhibitory Concentration (MIC) of different antimicrobials against this pathogen and the genetic diversity of the isolates from pigs reared in intensive and extensive systems in Spain.

Material and methods

Trueperella pyogenes isolates (n=180) obtained from slaughtered pig and belonging to animals raised in intensive systems (n=89) and free-range ones (n=91) were studied. The broth microdilution test was used, according to CLSI, to determine the susceptibility to 11 antimicrobials. Isolates were genetically characterized by Pulsed-Field Gel Electrophoresis (PFGE) method, using *Bcu I* as restriction enzyme. The PFGE patterns were visually examined and analysed by BioNumerics software (Applied Maths, Belgium).

Results

Penicillin (100%), Amoxicillin (100%), Gentamicin (99.5%) and Ceftiofur (96.7%) were the most effective antimicrobials. In general, the isolates obtained from pigs reared in extensive system showed lower resistance to different antimicrobials, with difference ($p < 0.05$) with regards to Enrofloxacin (11.2% and 2.2%), Oxytetracycline (88.8% and 63.7%) and Trimethoprim-Sulfamethoxazole (33.7% and 6.6%) between isolates.

A total of 71 pulsotypes were obtained by PFGE (GD 0.39), most of which were represented by single isolates (59.2%). Eight pulsotypes included 72 isolates (40%) and 5 pulsotypes were isolated from both pig populations. The isolates could be grouped within 4 PFGE clusters (80% similitude). Cluster C included the 94% of isolates, belonging to both pig populations, different geographical localizations and persisting in time.

Discussion and conclusion

Different profiles of resistance were detected between isolates obtained from pigs reared in intensive and extensive system, despite the high genetic similitude between of the majority of isolates, which could be explained by the differences in the use of antimicrobials.