

Clonal diversity and antimicrobial resistance of *Staphylococcus pseudintermedius* isolated from canine pyoderma

Vanessa Silva^{1,4*}, Ana Oliveira⁵, Manuela Caniça^{6,7}, Vera Manageiro^{6,7}, José L. Capelo^{8,9}, Gilberto Igrejas²⁻⁴, Patrícia Poeta^{1,4}

¹Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal;

²Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal;

³Functional Genomics and Proteomics Unit, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal;

⁴Associated Laboratory for Green Chemistry (LAQV-REQUIMTE), University NOVA of Lisboa, Lisboa, Caparica, Portugal;

⁵Faculty of Veterinary Medicine, University Lusófona de Humanidades e Tecnologias, 1749-024 Lisboa, Portugal;

⁶National Reference Laboratory of Antibiotic Resistances and Healthcare Associated Infections (NRL-AMR/HAI), Department of Infectious Diseases, National Institute of Health Dr Ricardo Jorge, Av. Padre Cruz, 1649-016, Lisbon, Portugal;

⁷Centre for the Studies of Animal Science, Institute of Agrarian and Agri-Food Sciences and Technologies, Oporto University, Oporto, Portugal;

⁸BIOSCOPE Group, LAQV@REQUIMTE, Chemistry Department, Faculty of Science and Technology, NOVA University of Lisbon, Almada, Portugal;

⁹Proteomass Scientific Society, Costa de Caparica, Portugal

*vanessasilva@utad.pt

Introduction

Staphylococcus pseudintermedius is a predominant cause of skin infections in dogs and the most common causative agent of pyoderma. Methicillin-resistant *S. pseudintermedius* (MRSP) have been identified in increasing frequencies in canine pyoderma. MRSP strains are usually resistant to several classes of antibiotics which leads to therapeutic failure and, potentially, zoonotic problems. This study aimed to characterize the antimicrobial resistance and genetic lineages of *S. pseudintermedius* isolated from canine pyoderma.

Methods

Sixty-one *S. pseudintermedius* were isolated from dogs with pyoderma in a veterinary hospital. The presence of *mecA* gene was detected by PCR. Antimicrobial susceptibility testing was performed by the Kirby-Bauer disk diffusion method against 17 antimicrobial agents. Multilocus-sequence-typing (MLST) was performed in all MRSP isolates as previously described (<https://pubmlst.org/>).

Results

From the 61 isolates, 31 harbored the *mecA* gene and were therefore classified as MRSP. The majority of *S. pseudintermedius* isolates showed resistance to penicillin, erythromycin, clindamycin, tetracycline and trimethoprim-sulfamethoxazole (Figure 1). Most MRSP also showed resistance to aminoglycosides. MRSP isolates were ascribed to 9 previously described sequence types (ST): ST123, ST727, ST339, ST537, ST45, ST1029, ST118, ST1468, ST71; and to 5 ST described for the first time in this study: ST2024, ST2025, ST2026, ST2027 and ST2028 (Figure 2).

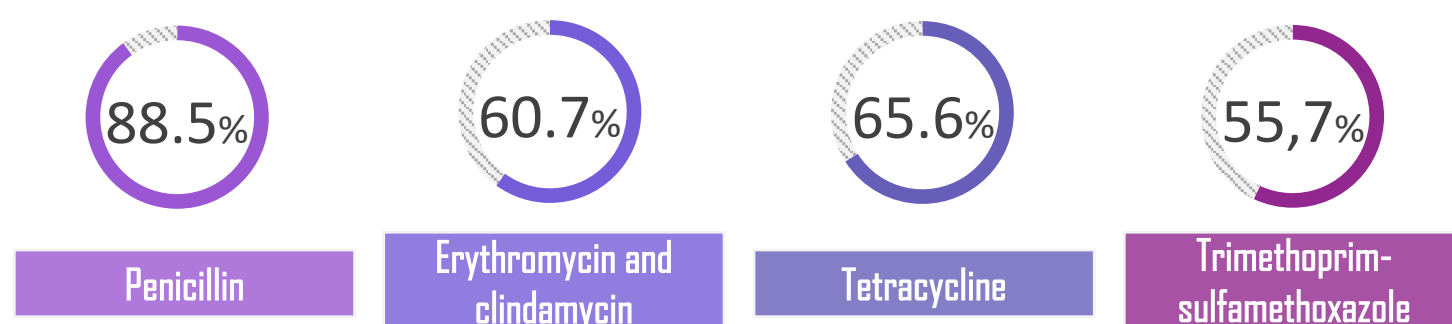


Figure 1. Percentages of the most prevalent resistances found among the *S. pseudintermedius*.

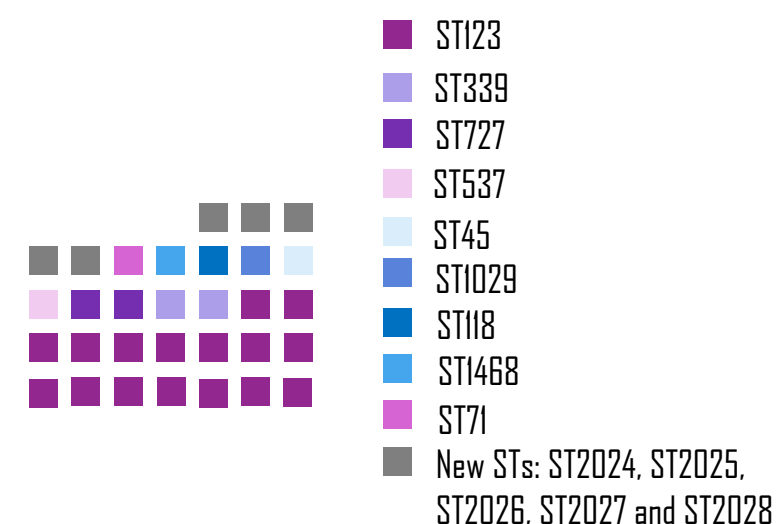


Figure 2. Distribution of 15 different STs among MRSP.

Conclusions

These results show that more than half of *S. pseudintermedius* isolated from pyoderma were resistant to methicillin. There was a difference in the antimicrobial susceptibility pattern between methicillin-resistant and -sensible *S. pseudintermedius*, in particular, for aminoglycosides. Furthermore, there was a high diversity of genetic lineages among MRSP causing pyoderma.

Acknowledgements:

This work was also supported by the Associate Laboratory for Green Chemistry-LAQV which is financed by national funds from FCT/MCTES (UID/UI/50006/2020). Vanessa Silva is grateful to FCT (Fundação para a Ciência e a Tecnologia) for financial support through PhD grant SFRH/BD/137947/2018.

