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# Molecular typing of *Staphylococcus pseudintermedius* canine strains by three commonly used techniques

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## Abstract

*Staphylococcus pseudintermedius* is a newly described species of *Staphylococcus* regarded as the main causative agent of canine pyoderma (Devriese *et al.*, 2005). *S. pseudintermedius* infection was recently described in humans. An important feature of this pathogen is the high genetic identity with two other species of staphylococci, namely *S. intermedius* and *S. delphini,* which are included all together in the *Staphylococcus Intermedius* Group (SIG) (Fitzgerald, 2009). This scenario seriously hampers phenotypic differentiation of these three pathogens. Despite this, only in 2008 was described the first molecular protocol for diagnostic identification of *S. pseudintermedius* (Bannoehr *et al.*, 2009). The aim of this work was to investigate the presence of different biotypes of *S. pseudintermedius* obtained from clinically relevant cases of pyoderma in dogs using three molecular methods commonly used to type bacteria: the Ribosomal Spacers Amplification (RSA), the Random Amplification of Polymorphic DNA (RAPD) and the Restriction Fragment Length Polymorphism (RFLP). A total of 46 different strains were included in this work. The application of the RSA technique, which was applied here for the first time, identified the presence of *S. pseudintermedius,* although it did not allow any differentiation between biotypes. The RAPD assay showed a single cluster that assembles all the interested strains that are grouped in three different sub-clusters (Fig. 1). The RFLP technique showed the most discriminative power, providing the opportunity to clearly identify this bacterium. In conclusion, the use of these three different techniques allows to clearly identify *S. pseudintermedius* and to observe the presence of different biotypes. In future it could be interesting to couple these results with the determination of the antibiotic resistance in order to verify if certain Multi Drug Resistant strains have particular RSA and RAPD profiles.
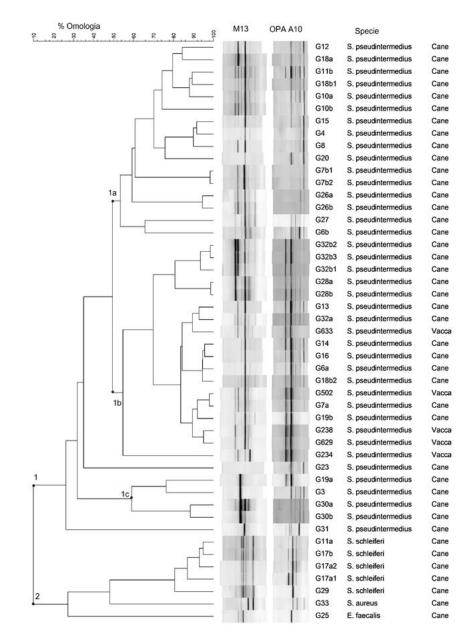
*Fig. 1: Dendrogram derived from the Random Amplification of Polymorphic DNA (RAPD-PCR) profiles generated with primers M13 and OPA A10. The RAPD-PCR profile grouping was done with the Gel Compar 4.1 software package using the Pearson product-moment correlation coefficient and unweighted pair group method with arithmetic mean (UPGMA) cluster analysis.*

# References

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