

Comparative Genomic Insights into *Staphylococcus pseudintermedius* from Healthy Dogs and Those with Pyoderma

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Introduction

- Staphylococcus pseudintermedius* (*S. pseudintermedius*) is a commensal bacterium of canine skin and mucosal membranes.¹
- S. pseudintermedius* is also an opportunistic pathogen, causing disease when the host has underlying health issues¹. It is the predominant pathogen responsible for canine pyoderma.²
- Canine pyoderma is becoming increasingly challenging to treat due to the increase of antimicrobial resistance in *S. pseudintermedius*¹. Specifically, MDR (multi-drug resistance) and MRSP (methicillin resistant *S. pseudintermedius*) pose great concerns to the veterinary community.¹
- Understanding genomic differences between commensal and pathogenic *S. pseudintermedius* isolates could lead to advancements in prevention and treatment options.

Objectives and Hypothesis

- The objectives of the study were to characterize phenotypic and genotypic differences of *S. pseudintermedius* isolates from dogs with pyoderma and those with apparently healthy skin.
- It was hypothesized that compared to isolates from healthy dogs, *S. pseudintermedius* isolates from dogs with pyoderma will differ in their genotypic and phenotypic profiles.

Methodology

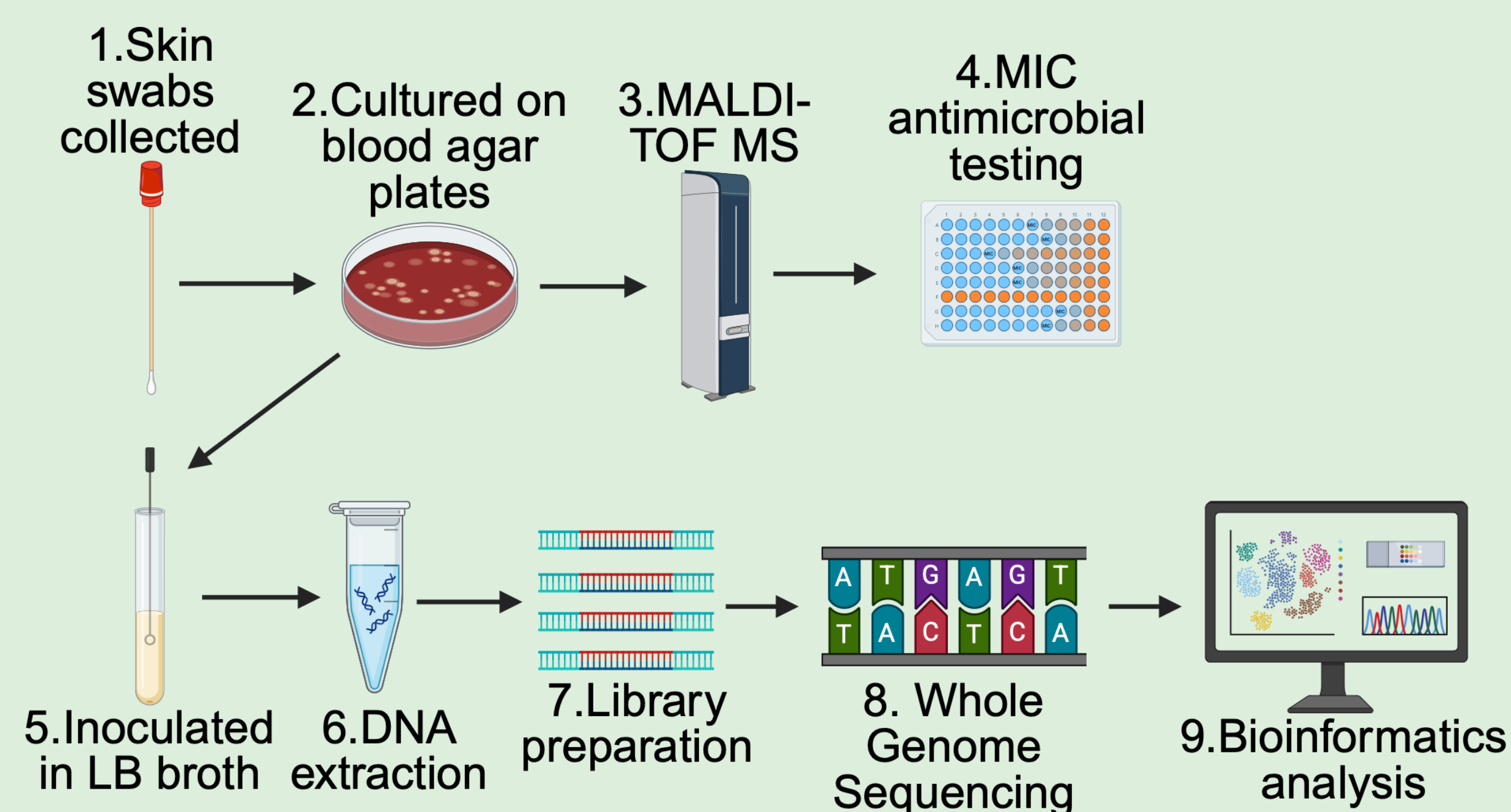


Figure 1: Depiction of methodology used to collect phenotypic and genotypic data. 48 dogs participated in the study including dogs with apparently healthy skin (n=22) and dogs diagnosed with pyoderma (n=26)

Phenotypic Results

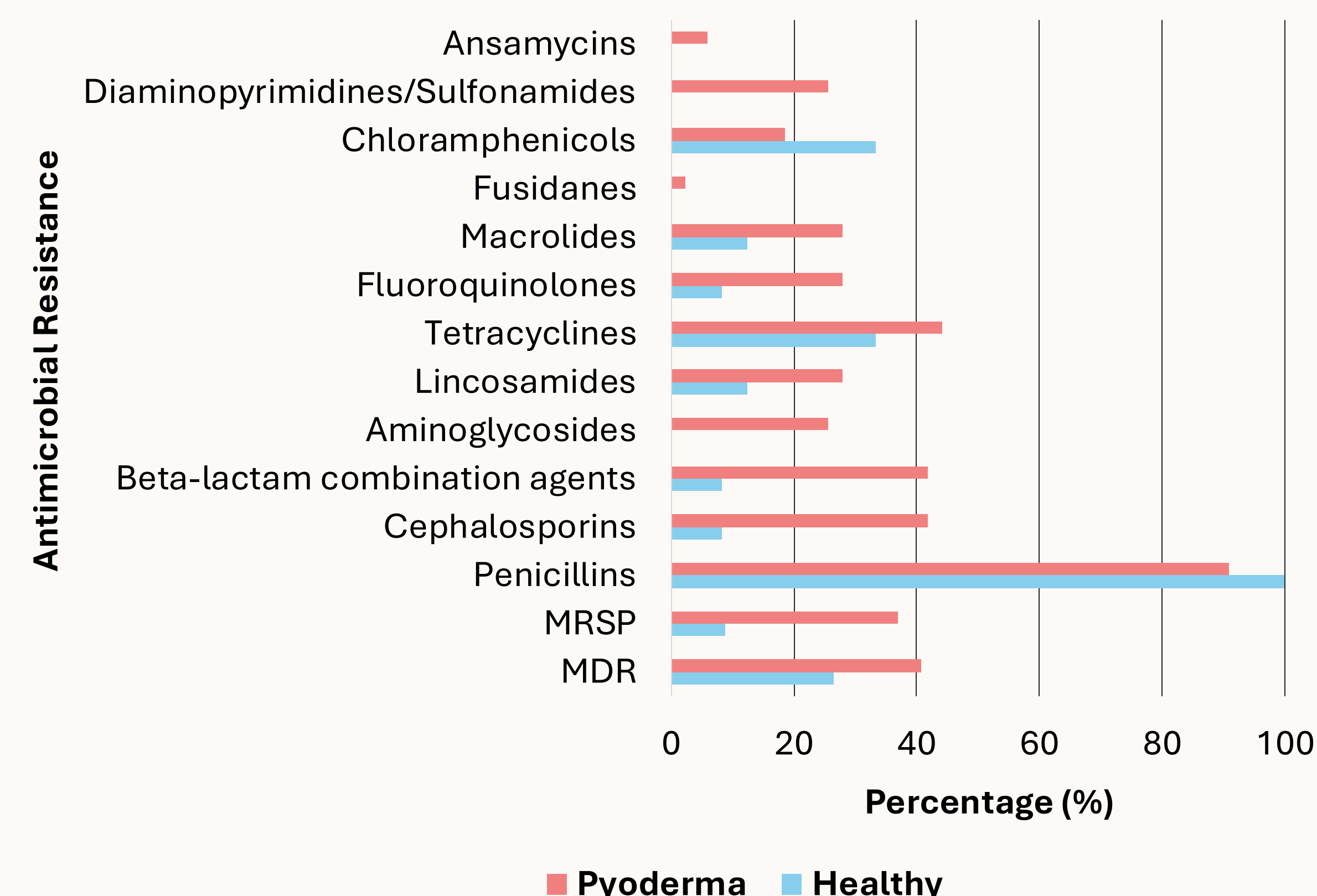


Figure 2: Percentage of dogs with pyoderma and apparently healthy skin harboring *Staphylococcus pseudintermedius* isolates with resistance to selected antimicrobial classes, methicillin resistance (MRSP), and multidrug resistance (MDR)

Genotypic Results

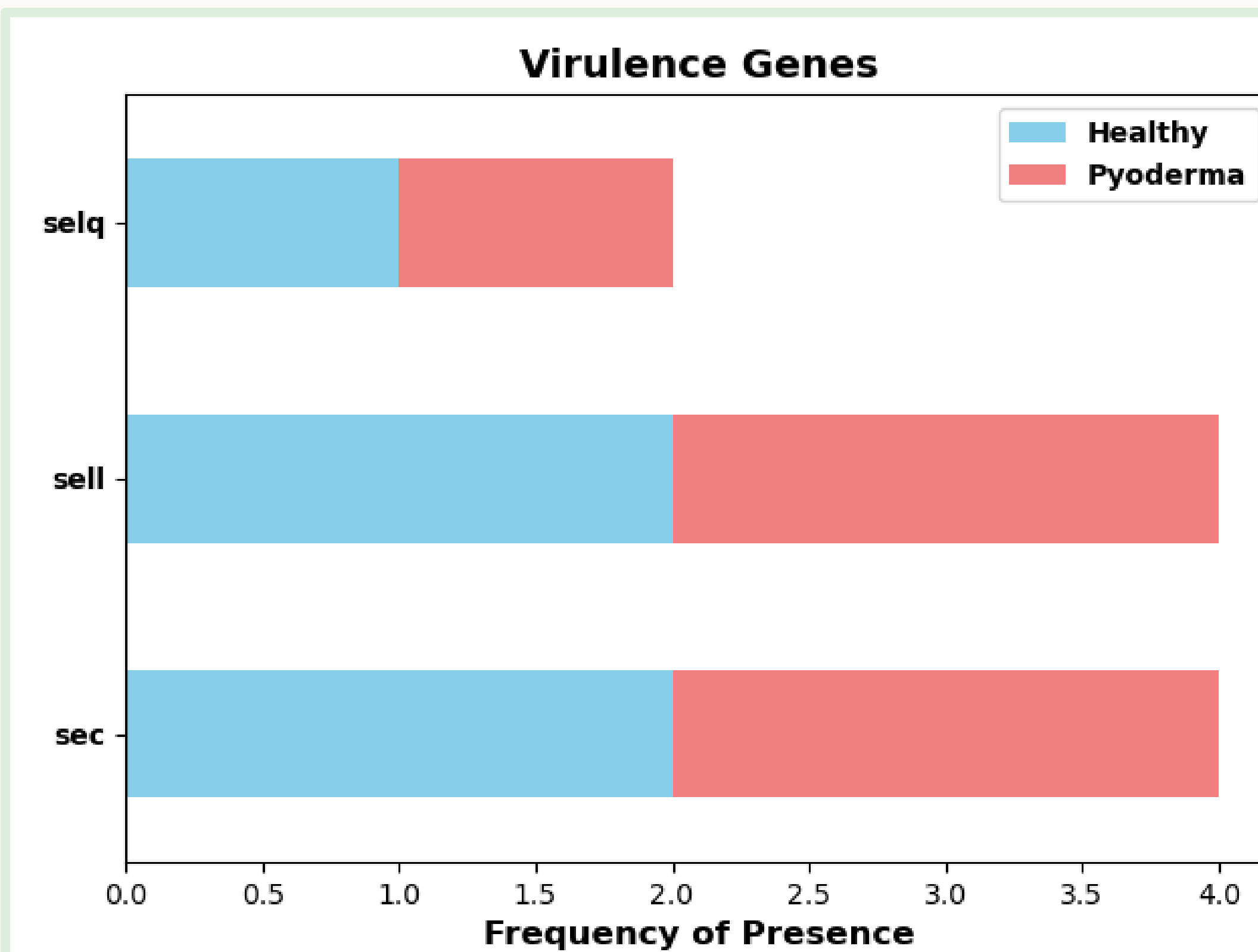


Figure 3: Virulence genes detected in *S. pseudintermedius* isolates from healthy dogs and those with pyoderma using virulence factor database (VFDB)

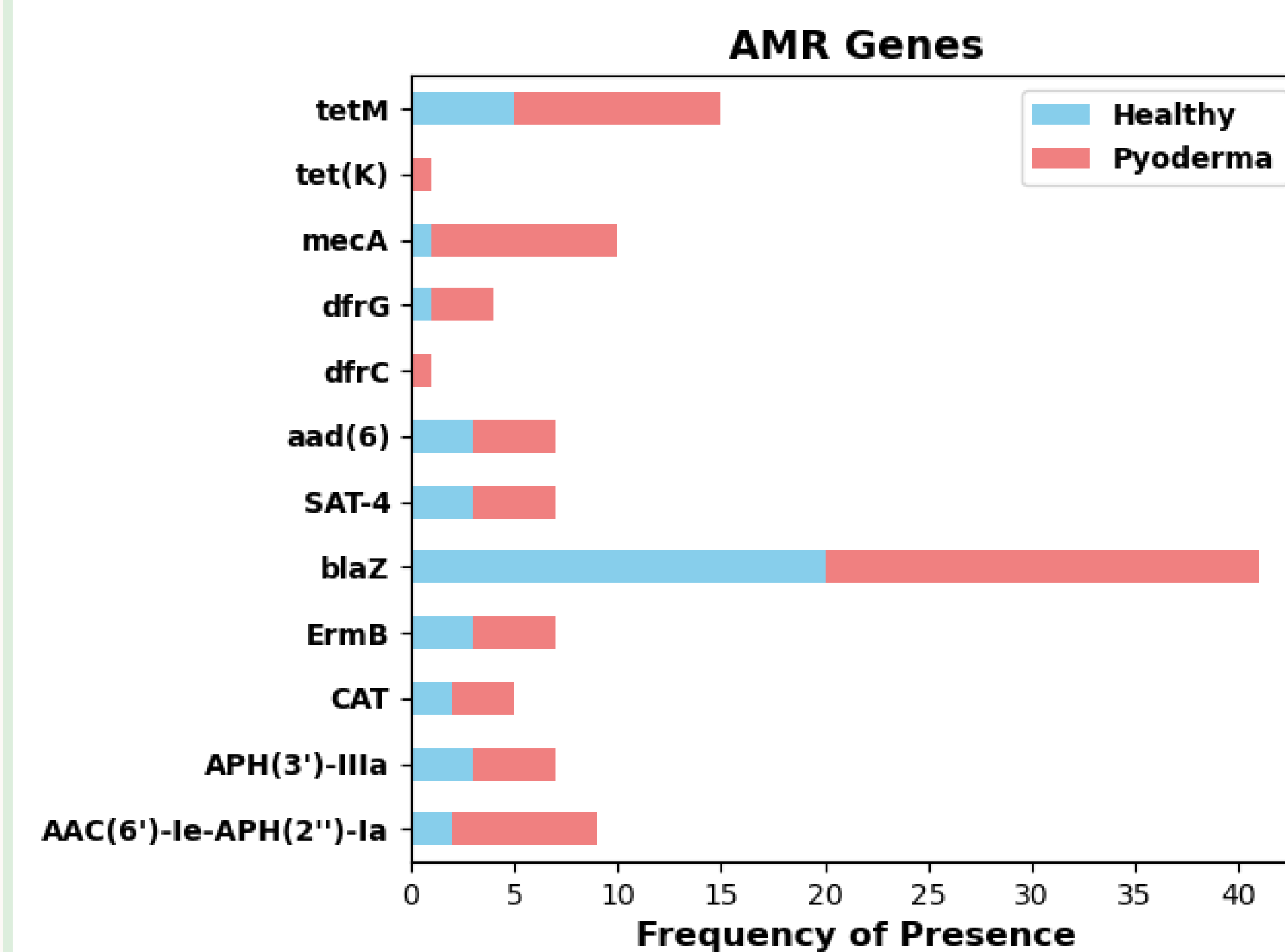


Figure 4: Antimicrobial resistance (AMR) genes in *S. pseudintermedius* isolates from healthy dogs and those with pyoderma detected using Comprehensive antibiotic resistance database (CARD)

Acknowledgements

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- Figure 1 was created using Biorender.com

References

- Bannoehr, J., & Guardabassi, L. (2012). *Staphylococcus pseudintermedius* in the dog: taxonomy, diagnostics, ecology, epidemiology and pathogenicity. *Veterinary dermatology*, 23(4), 253–e52. <https://doi.org/10.1111/j.1365-3164.2012.01046.x>
- Weese, J. S., & van Duikeren, E. (2010). Methicillin-resistant *Staphylococcus aureus* and *Staphylococcus pseudintermedius* in veterinary medicine. *Veterinary microbiology*, 140(3–4), 418–429. <https://doi.org/10.1016/j.vetmic.2009.01.039>

Plasmid Replicon Genes

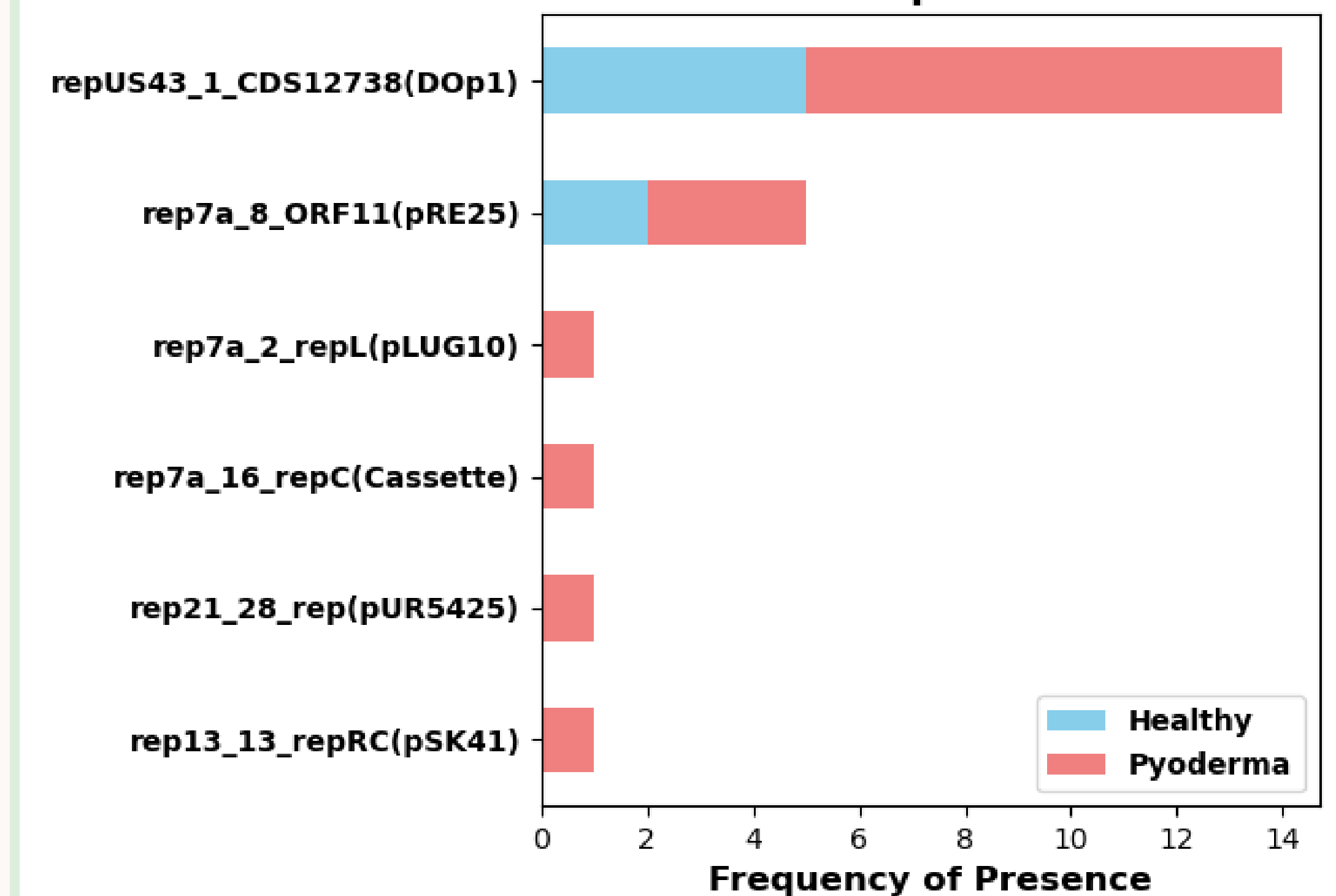


Figure 5: Plasmid replicon genes in the genome of *S. pseudintermedius* isolates from healthy dogs and those with pyoderma detected using plasmid DNA database

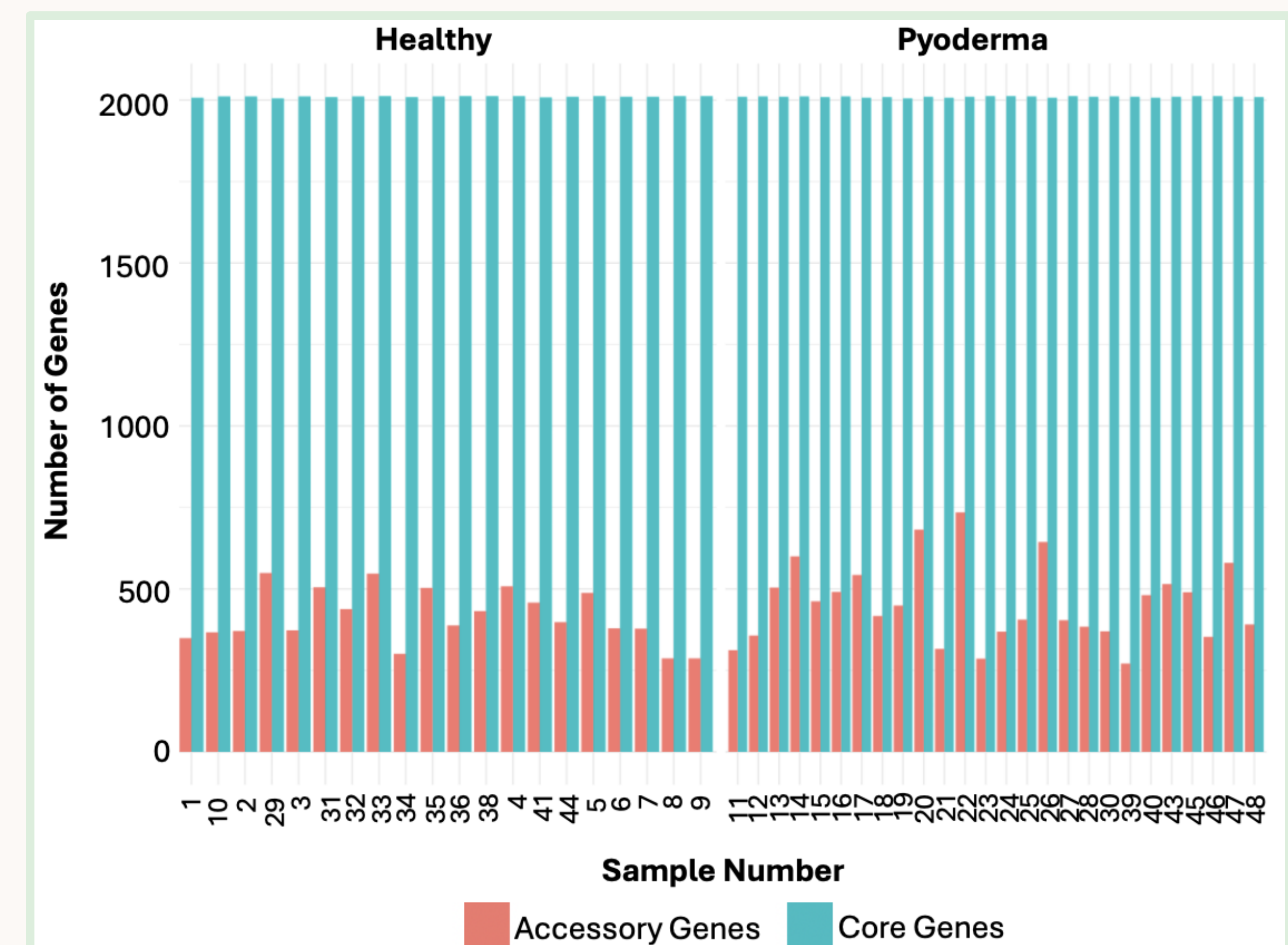


Figure 6: Core genes and accessory genes in *S. pseudintermedius* isolates from healthy dogs and those with pyoderma. Genomes were annotated using rapid prokaryotic genome annotation (PROKKA) program. Genome alignment and identification of core and accessory genes were performed using pan genome pipeline (ROARY).

Conclusions

- S. pseudintermedius* isolates from dogs with pyoderma exhibited greater phenotypic antimicrobial resistance compared to isolates from healthy dogs. Pyoderma-associated isolates also carried a higher number of antimicrobial resistance (AMR) genes and accessory genes. However, no difference was observed in the number of virulence genes between the two groups.
- Plasmid replicon genes were detected more frequently in the genomes of isolates from pyoderma cases, suggesting that horizontal gene transfer is important in the evolution of *S. pseudintermedius*.
- Based on phylogenetic analysis, no specific *S. pseudintermedius* lineages were associated with either pyoderma or healthy skin (data not shown).