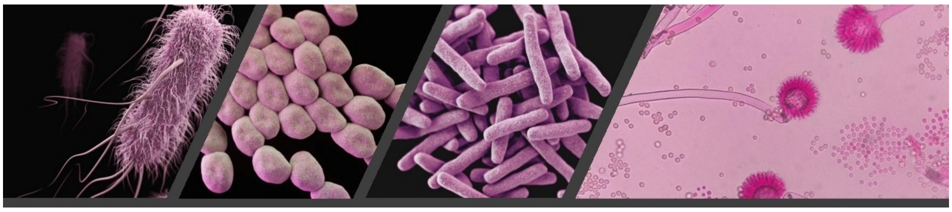

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The global epidemiology of Streptococcus canis identifies genomic features of host adaptation, virulence and antimicrobial resistance

Thursday 11 September 2025 12:00 (15 minutes)

Streptococcus canis can cause severe infections mainly in dogs, cats, and cattle with symptoms such as keratitis, dermatitis, endocarditis, sepsis, or mastitis, but also occasionally causes zoonotic disease in humans. Infections of companion animals have dramatically increased in Europe over the last decades leading to increased antibiotic usage due to the lack of alternative treatment options.

To better understand host adaptation, antimicrobial resistance, and evolutionary dynamics, we analysed the genomes of over 800 S. canis isolates from different host species and geographical locations. Lineages tended to be comprised of either one of two S. canis M (SCM) protein types, one of the pathogen's most important virulence factors. In addition, bovine S. canis isolates significantly clustered together on the phylogenetic tree suggesting a degree of host adaptation. The isolates typically had around six antimicrobial resistance genes mostly belonging to the classes tetracyclines, macrolides and aminoglycosides. We did not detect any beta-lactam resistance, but penicillin-binding-protein (pbp) genes exhibited different allele patterns.

In conclusion, this work provides fundamental knowledge on the transmission and host adaptation of S. canis for establishing a prediction pipeline to assist diagnostic labs in genomic epidemiology studies. Although no beta-lactam resistance is reported in S. canis, variation in pbp alleles might assist in selection for resistance in the future.

Keywords

Comparative genomics, host adaptation, M-protein, AMR

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