Canine saliva: a possible interspecies medium for mobile antimicrobial resistance genes

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Introduction

Standards and behaviors associated with keeping companion animals has undergone an evolution in the past decades. The process has even been accelerated by the COVID-19 pandemic. Visits at small animal veterinarians and clinical intervention, including the administration of antibiotics, turned relatively regular. In the meantime, the coexistence of pets and their owners has become physically proximate. Companion animals often sleep with their owners, lick them, and unfortunately, sometimes also bite them.

Objectives

Our aim was to determine the following metagenomic subsets of the canine salivary datasets:

- **Bacteriome:** bacterial composition accounting the relative bacterial abundances
- **Resistome:** antimicrobial resistance gene (ARG) content associated with antibiotics affected
- **Mobilome:** plasmid, bacteriophage, integrative mobile genetic element content related to ARGs

Methods

Bioinformatic metagenome analysis was performed on 26 next generation sequencing canine saliva datasets from 2020 and 2021. The datasets were reposited in NCBI SRA (Short Read Archive) by the 10,000 Dog Genome Consortium (PRJNA648123) and the Broad Institute within Darwin's Ark project (PRJNA683923).

Results

Bacteriome

The relative abundances of genera that achieved more than 1% of the bacterial hits in any of the samples were visualized. The dominant genera (with mean prevalence) in descending order were *Porphyromonas* (49%), *Prevotella* (15%), *Pasteurella* (12%), *Neisseria* (10%), *Capnocytophaga* (9%), *Conchiformibius* (7%), *Frederiksenia* (7%), *Cutibacterium* (6%), *Actinomyces* (5%), *Campylobacter* (4%), *Desulfomicrobium* (4%), *Bacteroides* (3%), *Fusobacterium* (3%), *Mycoplasmopsis* (3%), *Treponema* (3%), *Streptococcus* (2%).

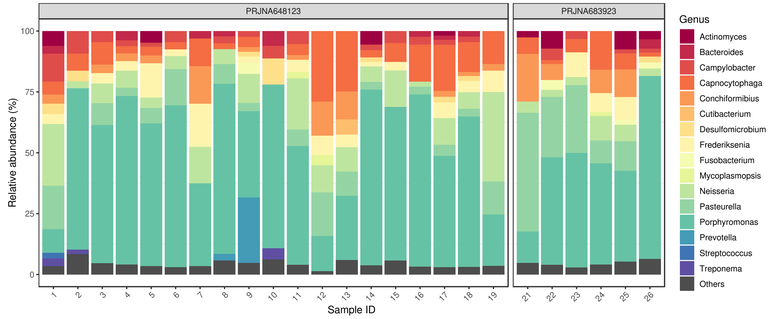

Figure 1. Core bacteriome of the canine saliva samples.

Resistome

For each sample-ARG combination, the best finding was plotted. On Figure 2 the size and the colour of the dots correspond to the coverage and the sequence identity of hits on reference genes, respectively. The gene names that are too long have been abbreviated (*acrA*: *Escherichia coli acrA*; *emrE*: *E. coli emrE*).

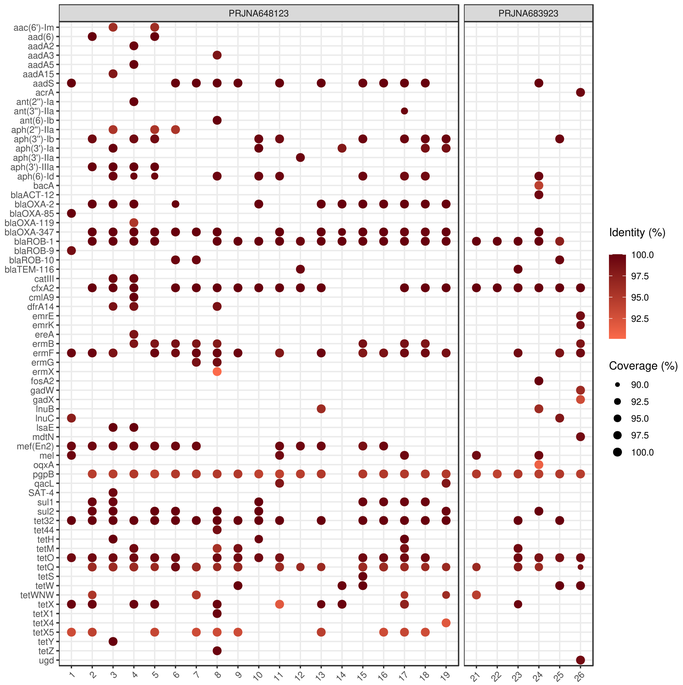

Figure 2. Identifed antimicrobial resistance genes (ARGs) by samples.

Mobilome

Many of the identified ARGs were associated with iMGEs, phages or plasmids. The frequencies of iMGEs, phages and plasmids associated with ARGs by bacteria of origin are summarized in Figure 3. Some genes could have been attached to more of the above mentioned mobility groups in the genome of one species. These findings may have an emphasized public health significance.

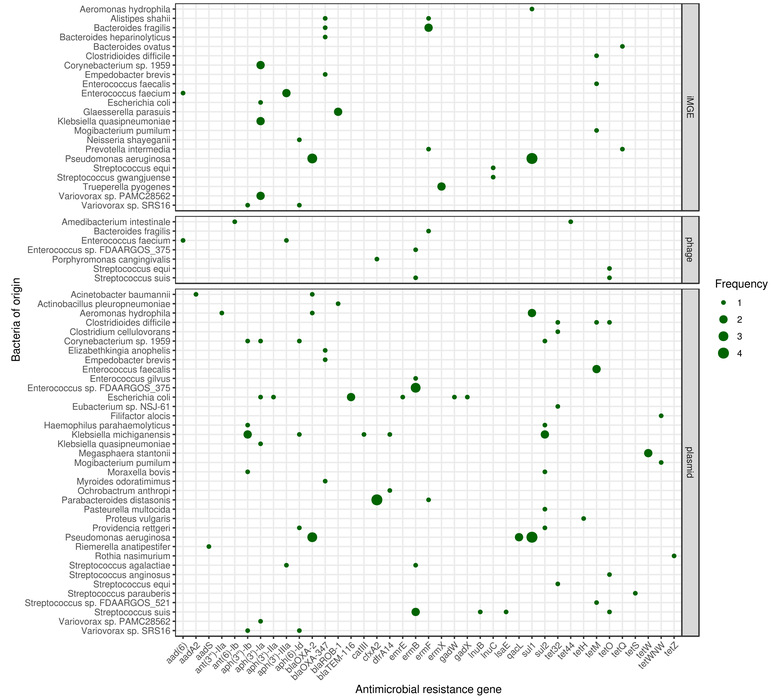

Figure 3. Mobile antimicrobial resistance gene frequency by bacteria of origin.

Conclusions

Besides the identification of possibly pathogenic bacteria that are often isolated from dog bite infections, ARGs against aminoglycosides, carbapenems, cephalosporins, glycylcyclines, lincosamides, macrolides, oxazolidinone, penams, phenicols, pleuromutilins, streptogramins, sulfonamides and tetracyclines were identified. Many of these ARGs were predicted to be mobile, including ones against amoxicillin-clavulanate, the most commonly applied antibiotic agent by dog bite infections.

According to the high number of potentially mobile ARGs, canine saliva may contribute to the interspecies spread of antimicrobial resistance.

References

[1] AG Tóth, I Tóth, B Rózsa, EG Kovács, A Dubecz, ÁV Patai, T Németh, D Kaplan, L Makrai, and N Solymosi. Canine saliva is a source of interspecies antimicrobial resistance gene transfer. *bioRxiv*, 2022.