The Biology of Antibiotic Resistance in Oral Streptococci

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Introduction
Antibiotic resistant-oral streptococcal species have become increasingly common to isolate in the recent years. Conjugative transposons (cTns) are mobile genetic elements which could have a panel of antibiotic resistance genes. These mobile genetic elements can move between different bacterial populations along with the antibiotic resistance genes they encoded for. The cTns, like Tn916 (1), are so widespread, in terms of both host range and geography. The aims of this project are to determine the frequency and diversity of Tn916-like elements found in oral streptococci and study the persistence of these elements in oral streptococci and how their biology contribute to the escalating problem of antibiotic resistance in the clinic.

Figure 1: Schematic representation of Tn5397, Tn916, and Tn6000. Coloured arrows depict ORFs pointing in the probable direction of transcription with the designated names above. Colours indicate genes involved in excision / insertion (red), conjugation (light blue), and regulation (light green). Accessory genes are grey (tetracycline resistance) or dark blue; (M; Methylase, Mt; methyltransferase, vap’ virulence associated protein, hel; helicase). Group II introns are dark green. Note, there are differences in the attenuator region (orf12 in Tn916) upstream of the tetracycline resistance gene

Research questions
The principle questions to be addressed are organized in two packages. Question I and II are belonging to package one while questions III and IV are in package two: (i) Are Tn916-like elements present in oral streptococcus species stable under non-selective and selective conditions within the bacterial population? (ii) What is the biological cost and how quick oral streptococcus species with Tn916-like elements evolve to restore fitness? (iii) What is/are the adaptation mechanism(s) in order to minimise any fitness loss? (iv) Can two different Tn916-like mobile elements recombining in host cell?

Molecular biology methods
- Bacterial DNA extraction from saliva
- Digital PCR to check presence and levels of antibiotic resistance genes (Figure 2)
- Conjugation assay to study transfer frequency of mobile genetic elements carrying antibiotic resistance genes
- Next Generation Sequencing to analyze bacterial adaptation mechanisms to the acquisition of mobile genetic elements

References

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