Milk adaptation and pathogenic potential among members of the *Streptococcus bovis*/*Streptococcus equinus* complex

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Abstract

The *Streptococcus bovis*/*Streptococcus equinus* complex (SB/Ec) consists of species commonly found in the gastrointestinal tract (GIT) of herbivores. Certain members of the complex like *Streptococcus macdonaldii* and *Streptococcus fermentum* are frequently isolated from traditional fermented foods, mostly of dairy origin. However, some species of this complex, like *Streptococcus gallolyticus* and *Streptococcus ruminantium* are known pathogens of humans involved in a range of disease including endocarditis, meningitis, bacteremia, and cancer. The aim of this study was the identification of potential cow’s milk adaptors through the analysis of plasmid regions of *Streptococcus bovis* strain pIL5. A number of genes cluster in a plasmid and genomic expression and mapping of the plasmid pSM1A98 isolated from the *Streptococcus bovis* strain ACA-DC 198 isolated from a traditional Greek cheese revealed important traits of adaptation to the dairy environment. Subsequent alignments highlighted the presence of potential transposase genes and pseudogenes of the species. The plasmid region of the plasmid pSM1A98 suggested a diminution of potential phages for the species, suggesting a diminished pathogenic potential for the species. The presence of putative virulence factors (VF) within the SB/Ec chromosome was shown using genome alignments among members of the SB/Ec, but the evidence is not conclusive, which could be explained by the presence of recombinant plasmids or environmental factors.

Results and Discussion

Figure 1 - The circular map of the genome of *Streptococcus macdonaldii* ACA-DC 198. Genetic features appearing from the periphery to the centre of the map: 1. Forward ORFs (blue); 2. Reverse ORFs (red); 3. Putative pseudogenes (cyan); 4. tRNA genes (orange); 5. rRNA genes (green); 6. %GC plot; 7. GC skew.

Figure 2 - Genomic features of the *Streptococcus bovis*/*Streptococcus equinus* complex calculated as conserved synteny. Chromosomal alignments among *Streptococcus bovis* ACA-DC 198 and *Streptococcus macedonicus* ACA-DC 198 (B) on the chromosome of *Streptococcus bovis* ACA-DC 198 (A), *Streptococcus macedonicus* ACA-DC 198 (B) on the chromosome of *Streptococcus bovis* ACA-DC 198 (A) (C).

Figure 3 - Gene-gene analysis of members of the *Streptococcus bovis*/*Streptococcus equinus* complex. Whole-GS from diagrams of *Streptococcus bovis*, *Streptococcus macedonicus*, *Streptococcus equinus*, *Streptococcus macdonaldii*, *Streptococcus fermentum*, and *Streptococcus ruminantium*.

Figure 4 - The extra gene cluster for lactase and galactose metabolism found solely in *Streptococcus macdonaldii* among the SB/Ec members.

Figure 5 - Map of plasmid pSM1A98 isolated from *Streptococcus macdonaldii* and its annotation.

Figure 6 - Sequence alignment in a circular fashion of pSM1A98 against the tetracyclines pB116 (A), pFT22 (B) and pIL5 (C) of dairy origin. Local alignments produced by BLAST are presented using Pfam, which may correspond to four quarters of the alignment's length (not top 25%, orange under the black line). In pB116, in order to set orientation, the position of the orf on orf of pSM1A98 has been added in the figure. (D) Maximum likelihood tree of the plasmid pSM1A98 was generated using the Phylogeny phy pipeline.

Table 2 - Genes in the *Streptococcus bovis*/*Streptococcus equinus* complex identified as putative virulence factors.

Table 3 - Genes within the *Streptococcus bovis*/*Streptococcus equinus* complex potentially involved in adaptation to the rumen.

Table 4 - Genes within the *Streptococcus bovis*/*Streptococcus equinus* complex potentially involved in adaptation to the rumen.

Table 5 - Genes within the *Streptococcus bovis*/*Streptococcus equinus* complex potentially involved in adaptation to the rumen.

Table 6 - Genes within the *Streptococcus bovis*/*Streptococcus equinus* complex potentially involved in adaptation to the rumen.

References


Bibliography

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