

Genomsequenzierung von *Staphylococcus aureus*

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Key words

Staphylococcus aureus, cattle, mastitis, whole-genome sequencing, zoonosis

Aim of the study

Staphylococcus aureus (*S. aureus*) is a very well-known mastitis pathogen in cattle causing high financial losses. According to our previous study, there are various bovine subtypes of *S. aureus*. One of them, genotype B (GTB), is highly contagious and pathogenic causing serious problems in dairy farming. Together with Prof. J. Schrenzel, University of Geneva, we could demonstrate that, based on „multilocus sequence typing“, GTB is identical to *S. aureus* CC8. The latter one is known as a pathogen which may cause severe cases of secondary, purulent infection and bacteraemia in humans. In addition, a considerable number of these isolates are resistant to methicillin (MRSA). The aim of the present project was, therefore, to sequence the whole genome of a GTB strain and to compare it to publically available sequences of CC8 strains. In the case of identity, the disease needs to be considered as a novel zoonosis requiring epidemiological control to keep the risk of transmittance minimal between cattle and humans.

Material and methods

A typical GTB strain isolated from a cow with subclinical mastitis and housed on farm with a GTB herd problem was fully sequenced in Prof. J. Schrenzel's laboratory using the Illumina technology. The resulting contigs were concatenated and a closed genome was prepared. The genes were annotated with the help of the online BASys software. Phylogenetic analyses were performed using 6 concatenated core adhesion genes of all *S. aureus* strains whose whole genomes were available at that time ($n = 21$).

Results and significance

The size of the GTB genome is composed of 2.769067×10^6 bp. The whole genome contains 2761 genes whereby 879 of them (31.8%) code for hypothetical proteins. The core genome (>2.5 Mb) shows a similarity of 99.95% with the human-pathogenic strain USA300 (CC8; community-acquired, invasive, massively spreading in USA) and of 97.70% with the bovine, mastitis-pathogenic strain RF122 (CC705). The GTB strain is CC8-positive. The only major chromosomal difference compared to USA300 is the presence of a newly detected staphylococcal chromosomal cassette which is a chimera of cassettes found in *Staphylococcus epidermidis*, *S. aureus* MW2 and *S. aureus* COL; the *mecA* gene (methicillin resistance) is absent. Interestingly, all the remaining mobile elements of GTB which generally harbor the staphylococcal virulence genes were fully identical at the gene level with those of the USA300 strain and clearly differed from those of the RF122 strain. Furthermore, the core adhesion genes of GTB are almost fully identical with those of USA300. Phylogenetic analyses revealed that *S. aureus* GTB was a descendant of a primarily human-pathogenic strain which established in cattle and which showed no phylogenetic differences towards the USA300 and other CC8 strains. A homoplasy (convergent evolution) can be ruled out by the very high similarity present between both core genomes. As a consequence, adhesion, pathogenicity, and transmission of *S. aureus* GTB/CC8 between cattle and human is very probable and a zoonosis cannot be excluded.

Publications, posters and presentations

Graber, H.U.; Boss, R. (2011) "*Staphylococcus aureus* GTB: whole-genome sequencing." Professional presentation, Geneva.

Graber, H.U.; Boss R.; Syring, C. (2011) "*Staphylococcus aureus*: detection of the contagious subtype in bulk tank milk." Professional presentation, Berne.

Project 1.09.08

Project duration August 2009 – August 2011