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Genome Sequences of Two \textit{Staphylococcus aureus} Ovine Strains That Induce Severe (Strain O11) and Mild (Strain O46) Mastitis

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\textit{Staphylococcus aureus} is a major etiological agent of mastitis in ruminants. We report here the genome sequences of two ovine strains that were isolated from gangrenous (strain O11) and subclinical (strain O46) ewe mastitis. Both strains belong to the same clonal complex. Despite this close genotypic relationship, the two isolates were shown to reproducibly induce highly divergent types of infections, either severe (O11) or mild (O46) mastitis, in an experimental ewe model.

\textit{Staphylococcus aureus} is one of the main pathogens involved in ruminant mastitis. Staphylococcal mastitis severity is highly variable, ranging from subclinical to gangrenous mastitis. Severity partly relies on bacterial factors. \textit{S. aureus} strains isolated from bovine or ovine-caprine hosts differ from human isolates, as revealed previously (3), and genomic data regarding ruminant isolates are still scarce (4, 6). There is thus a need for more genomic data to better understand mastitis and identify bacterial factors involved in the severity of the infection.

We characterized two \textit{S. aureus} ovine strains, which were shown to be clonally related (9) and reproducibly induced severe (strain O11) and mild (strain O46) mastitis in experimental ewe mastitis (8).

We sequenced the two genomes by using an Illumina Genome Analyzer GAII (Fasteris, Geneva, Switzerland).

Base calling was performed with GAPipeline 1.4.0 software; a total of 27.6 million reads (pass filter) were obtained. After bar code selection, 13.9 and 11.8 million reads of 71 bases in a total of 27.6 million reads (pass filter) were obtained. After

Further analysis of the two genomes is now under way and will be combined to comparative transcriptome and proteome analyses to identify factors that might explain the hypervirulence of O11 in a mastitis context.

Nucleotide sequence accession numbers. The sequences determined in whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under accession no. AEUQ00000000 (O11) and AEUR00000000 (O46). The versions described in this paper are the first versions, AEUQ01000000 and AEUR0100000.

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coccus pyogenes, with a potential application to other Gram-positive bacteria. Proteomics 9:61–73.


