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Genome Sequence of *Staphylococcus aureus* Newbould 305, a Strain Associated with Mild Bovine Mastitis

Damien Bouchard,a,b Vincent Peton,a,b Sintia Almeida,a,b,c Caroline Le Maréchal,a,b,c Anderson Miyoshi,c Vasco Azevedo,c Nadia Berkova,a,b Lucie Rault,a,b Patrice François,d Jacques Schrenzel,a Sergine Even,a,b David Hernandez,d and Yves Le Loir,a,b

INRA, UR1253 Science et Technologie du Lait et de l’Œuf, Rennes, France; AGROCAMPUS OUEST, UR1253 Science et Technologie du Lait et de l’Œuf, Rennes, France; UFMG, ICB, Departamento de Biologia Geral, Belo Horizonte, MG, Brazil; and Genomic Research Laboratory, University Hospitals of Geneva (HUG), Geneva, Switzerland

*Staphylococcus aureus* is one of the main pathogens responsible for ruminant mastitis. Staphylococcal mastitis severity is highly variable, ranging from subclinical to gangrenous infection. *S. aureus* strains isolated from bovine or ovine/caprine hosts differ from human isolates, as documented previously (4). However, detailed genomic data regarding ruminant isolates are still scarce (4, 5, 8, 10, 11). There is thus a need for genomic data to better understand mastitis and identify bacterial factors responsible for the severity of the disease.

We previously characterized *S. aureus* bovine strain Newbould 305 (ATCC 29740) (12), which was isolated in 1958 from a cow in Orangeville, Ontario, Canada, with a clinical case of mastitis (4, 12). Newbould 305 reproducibly induces chronic mastitis with mild symptoms in cases of experimental cow mastitis (2, 6). It was previously shown to be clonally related to other bovine strains in ST115, whereas *S. aureus* RF122, another well-documented bovine strain (8) associated with severe mastitis symptoms, clustered in ST151 and was more closely related to ovine and caprine strains RF122. The majority of the genes (contig 5) were found in Newbould 305 compared to RF122. Among the SNPs had homology to SaPI genes in *S. aureus* strains of bovine (RF122), ovine (O46), or human (MW2) origin. The contig that was reported as a potential plasmid was further confirmed by homology and was designated pNewbould305.

Further analysis of the Newbould 305 genome is now under way. It will be further compared to the RF122 genome to identify specific factors that might explain the different phenotypes observed in infection acuteness.

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AKYW00000000. The version described in this paper is the first version, AKYW01000000.

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Address correspondence to Yves Le Loir, Yves.LeLoir@rennes.inra.fr.

* Present address: Caroline Le Maréchal, ANSES, Plouffragan, France.

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