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Whole-Genome Sequence of the Ancestral Animal-Borne ST398 Staphylococcus aureus Strain S123

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Sequence type 398 (ST398) Staphylococcus aureus was originally reported in livestock. We announce the complete genome sequence of an ST398 methicillin-susceptible S. aureus strain of animal origin, S123. The genome sequence reveals a wild-type genome that probably corresponds to an ancestral clone.

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Sequence type 398 (ST398) Staphylococcus aureus was originally described in livestock (1) but was recently reported as the causative agent of severe infections in humans (2). An evolutionary hypothesis suggests that an ancestral wild-type S. aureus strain acquired mobile genetic elements triggering host adaptation and evolution to the methicillin-resistant genotype after insertion of a functional type I restriction system.

The genome of strain S123 encodes known virulence factors, such as pore-forming toxins (only hemolysins) and bacterial adhesins. Annotation confirmed the absence of important resistance determinants, except those for tetracycline and erythromycin. Interestingly, strain S123 is missing a type IV restriction system. Similar to many other sequenced ST398 strains, S123 is devoid of DNA from phagic elements despite the presence of a functional type I restriction system.

We conclude that S123 is potentially an ancestral clone still missing a phagic element that contributes to host adaptation.

Nucleotide sequence accession number. The whole-genome sequence of S. aureus S123 was deposited in the DDBJ/EMBL/GenBank databases under the accession number AUPU00000000.

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