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Complete Genome Sequence of *Staphylococcus aureus* Strain M1, a Unique t024-ST8-IVa Danish Methicillin-Resistant *S. aureus* Clone

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We report the genome sequence, in five contigs, of a methicillin-resistant *Staphylococcus aureus* (MRSA) clone in 2003. This strain is sequence type 8 (ST8), *spa* type t024, and staphylococcal cassette chromosome *mec* element (SCC*mec*) type IVa.

The incident of methicillin-resistant *Staphylococcus aureus* (MRSA) in Denmark is one of the lowest in Europe. However, in 2003 an outbreak of a *spa* type t024, sequence type 8, staphylococcal cassette chromosome *mec* element (SCC*mec*) type IVa (t024-ST8-IVa) MRSA clone started and was not fully under control until 2009. Initially this outbreak was maintained in a closed setting within one of Copenhagen’s boroughs, Amager. The clone spread through the local hospital to the surrounding nursing homes, affecting 501 patients and staff as of the end of 2012 (1–3). This outbreak is now being fully investigated through whole-genome sequencing (WGS).

In order to be able to trace transmission between patients, a complete outbreak-specific reference genome is essential. The reference isolate designated M1 is the isolate from the index patient of a methicillin-resistant *Staphylococcus aureus* (MRSA) outbreak in Copenhagen, Denmark, that started in 2003. This strain is sequence type 8 (ST8), *spa* type t024, and staphylococcal cassette chromosome *mec* element (SCC*mec*) type IVa.

The WGS of M1 confirms that t024-ST8-IVa is related to other sequenced *S. aureus* genotypes, notably USA300 TCH1415 and USA300 FPR3757. M1 shares 2.764 Mb with USA300 TCH1415, corresponding to 99.8% nucleotide identity. A total of 1,107 single nucleotide polymorphisms (SNPs) differentiate the two genomes. M1 has two copies of the prophage Sa2usa and one copy of Sa3usa and is Panton-Valentine leukocidin (PVL) negative and arginine catabolic mobile element (ACME) positive (2, 4).

Further analysis of the genome is now under way to identify factors that might explain the emergence of this MRSA strain in the health care community.

**Nucleotide sequence accession numbers.** The genome data have been deposited in GenBank with accession number HF937103 for the chromosome and HF937104 for the plasmid.

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REFERENCES


