

O0986 Epidemiological typing of methicillin-resistant *Staphylococcus argenteus* in Stockholm, Sweden

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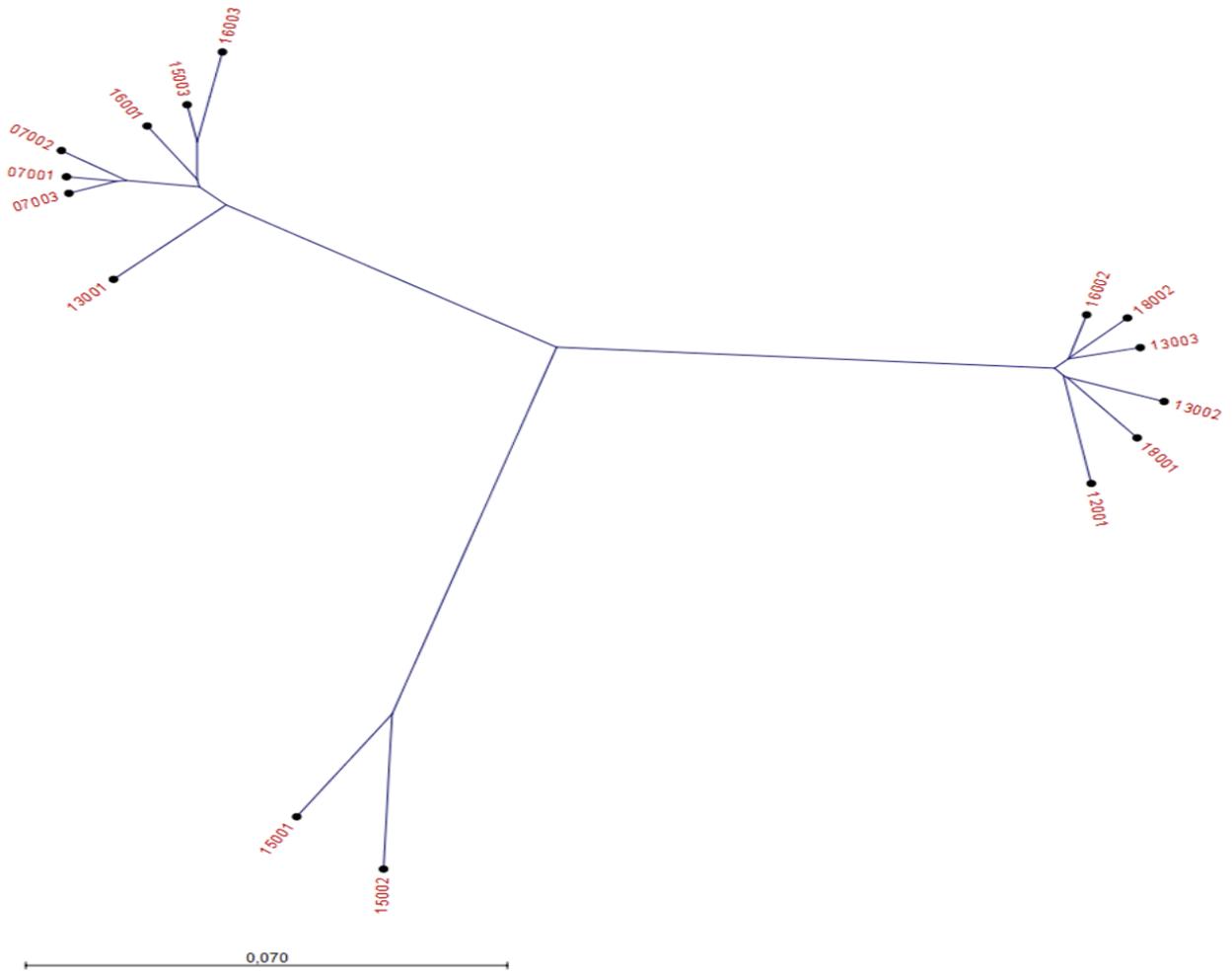
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Background: *Staphylococcus argenteus* was defined as a novel staphylococcal species in 2015. We describe here the genomic epidemiology of methicillin-resistant *S. argenteus* in Stockholm, Sweden over the last decade.

Materials/methods: Fifteen methicillin-resistant *S. argenteus* isolates were identified from 2007 to October 2018. Fourteen of them were initially identified as *Staphylococcus aureus*. All isolates were positive for the *mecA*-gene and resistant to ceftazidime. Isolates except for the two detected in 2018 were genotyped by pulsed-field gel electrophoresis (PFGE), and all isolates by whole-genome sequencing (WGS). A *S. argenteus* core-genome multi-locus sequence (cgMLST) scheme, based on 1997 core genes, was used (1928 Diagnostics, Gothenburg, Sweden). The genetic relationship of the isolates was investigated by cgMLST, single nucleotide polymorphisms (SNPs) and *k*-mer.

Results: All isolates were best matched to the *S. argenteus* type strain MSHR1132 in the NCBI database. Seven, six and two isolates were assigned to ST1223, ST2250 and ST2793, respectively, with the *S. aureus* MLST-scheme. The isolates were grouped as ST1223-cluster and ST2250-cluster by *k*-mer and PFGE. In the cgMLST, >99%, >96% and >95% of the core genes were identified in ST2250, ST1223 and ST2793 isolates, respectively. SNPs and cgMLST revealed that three ST1223 cases in 2007 were strongly genetically related, having 2-4 SNPs and 0-1 differed alleles in cgMLST, indicative of clonal spread. Patient 07001 was the index case and his parents were found to be colonized by the same strain after 23 days. The clonal relatedness of four ST1223 isolates during 2013-2016, two ST2250 isolates in 2018, and two ST2793 isolates in 2015 could be excluded by >100 SNPs and >50 differed cgMLST alleles. However, the genetic relationship among four ST2250 isolates from 2012 to 2016 could not easily be determined without well-established cut-off for this species, meanwhile genomic variability should be considered in these cases where a four-year period was spanned.

Conclusions: Methicillin-resistant *S. argenteus* emerged in Stockholm as early as in 2007, and the prevalence of this pathogen can be better assessed with the advances in species determination. To our knowledge, this is the first report of WGS-based epidemiological typing by using a *S. argenteus*-specific cgMLST scheme.



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