

**EP0310**  
**ePoster Session**  
**Novel techniques in diagnostic microbiology**

**Practicability of molecular typing scheme for *Staphylococcus aureus* in the genomic era**

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**Background:** There are several accepted typing schemes for *S. aureus* which may be used for outbreak investigation and microbial population analysis such as *spa* typing and multi-locus sequence typing (MLST). The introduction of whole genome sequencing (WGS) mandates the development of new typing schemes whilst maintaining reverse compatibility with traditional ones. Indeed, a core genome (cg) based MLST has recently been proposed as a highly discriminatory yet standardised approach. We sought to evaluate the practicability of applying these typing schemes on a large convenience sample of publicly available *S. aureus* genomes.

**Material/methods:** Available *S. aureus* genome assemblies were downloaded from NCBI and checked for quality using several tools. The genomes were analysed using an in house *S. aureus* pipeline at the Surveillance and Pathogenomics Israeli Centre of Excellence (SPICE) as well as the SeqSphere+ (Ridom GmbH). The *spa* and MLST types were determined by extraction and analysis of sequences of the respective genes. cgMLST determination was performed according to the gene-based scheme proposed by Leopold et al. (JCM 2014) containing >1,800 gene loci. The Simpson's diversity index (DI) was calculated for each method to compare performance.

**Results:** Overall, 4,262 genomes were analysed, of which 4,047 were typeable by MLST (215 were untypeable mostly due to sample quality). There were 98 identified STs of which ST5 accounted for 43%, ST8 19%, ST398 17% and ST105 14% of samples. Additional 41 STs included 2 or more samples (range 2 to 84) and 53 STs were singletons. *spa* typing was unsuccessful for 850 samples, including 286 presumably new types and 564 failures. For cgMLST, a 'cluster type' was assigned for 2,412 samples (57%) and included 121 different types according to the current scheme but the vast majority of samples were typeable when 'unknown targets' were not excluded. The three schemes are summarised in the:

Method	No. of loci in scheme	No (%) untypeable	No. of different types assigned	Simpson's DI	Confidence interval for DI
MLST	7	5%	98	0.767	0.852-0.871
<i>spa</i> typing	1	20%	296	0.861	0.758-0.776
cgMLST	>1,800	0.1%	3,979	1.0	1.0-1.0

**Conclusions:** Based on analysis of a large sample of genomes, MLST was successfully determined for the vast majority of good quality samples thus corroborating the reverse compatibility of WGS with MLST. *spa* typing showed a higher DI compared to MLST but also a higher failure rate that should be further investigated and rectified. cgMLST exhibited a maximal DI that emphasises its potential to become a standard typing tool for WGS typing of *S. aureus* and the need to further develop the nomenclature related to this scheme. Application of the schemes on a large collection of publicly available genomes adds to the understanding of the global diversity of *S. aureus*.