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**Variation within and between MLST CC of *S. aureus* based on panGenome analysis**

Dmitriy Babenko\*<sup>1</sup>, Antonella Chesca<sup>2</sup>, Mark Alexander Toleman<sup>3</sup>

<sup>1</sup>*Karaganda State Medical University; Scientific Centre*

<sup>2</sup>*Transilvania University of Braşov*

<sup>3</sup>*Cardiff University*

**Background:** Multilocus sequence typing (MLST) as a genotyping method based on sequencing of internal fragments of some housekeeping genes is extensively used for study pathogens. This molecular tool is useful in understanding both evolution and population dynamics of microorganisms. We explored the variation within and between MLST Clonal Complexes (CC) of global collection of *S. aureus* based on panGenome data to understand how they differ from each other.

**Material/methods:** 5225 *S. aureus* genomes from GenBank were analyzed with *Microbial in silico typer* (MIST) software and *FindMyFriend* R packages to determine MLST type and panGenome data table. MLST CC were defined by eBURST algorithm. Genetic distance was calculated with Nei formula (Nei M., 1972) using panGenome data including 48576 ortholog groups in total.

**Results:** There were 232 STs that were grouped into 53 MLST CC. Six of them were dominant and included 4895 isolates in total (figure 1). There were 50 different MLST types in CC8. MLST CC5, CC22, CC398, CC30 and CC45 included 53, 17, 13, 17 and 9 different sequence types, respectively.

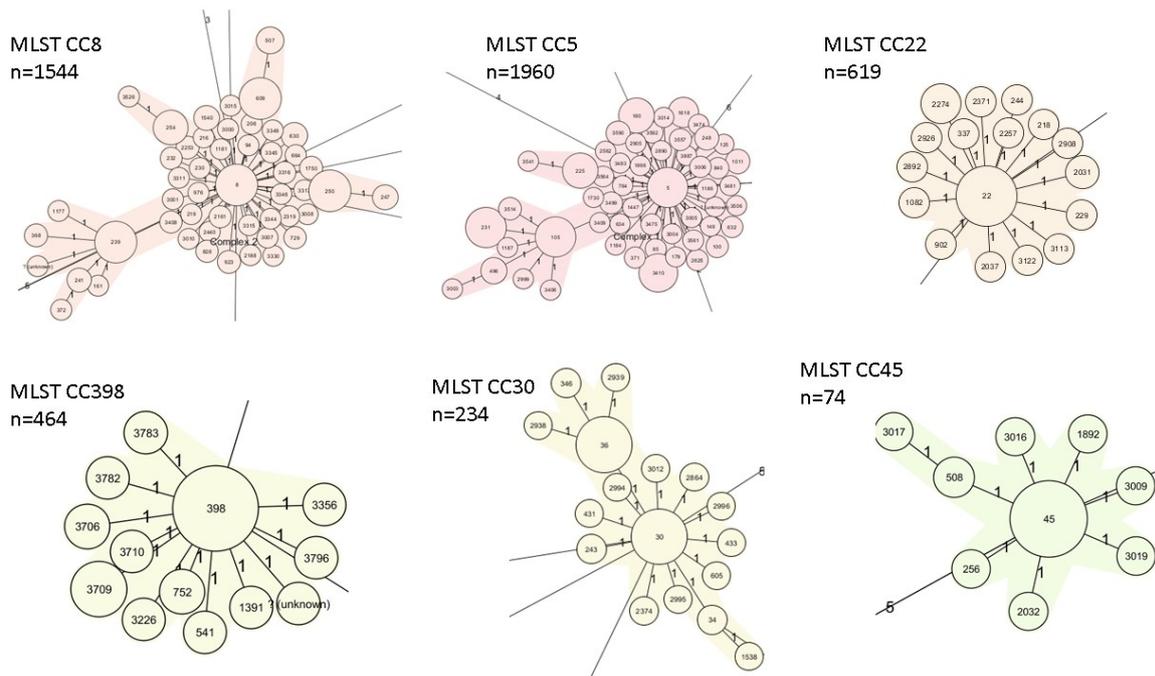


Figure 1. Six Major MLST CC which have been analysed in our study

Genetic variation between *S.aureus* isolates belonging the same MLST Clonal complex and different CC estimated on panGenome data and presented in table 1.

Table 1 PanGenome variation of *S.aureus* strains within and between MLST CC

Clonal Complex	Difference within CC (%)			Difference between CC in % (mean_median_max)				
	Mean	Median	Min-Max	CC5	CC22	CC398	CC30	CC45
CC8	0.75	0.75	0-14.7	1.3_1.3_14.7	1.2_1.1_14.7	1,3_1,2_14,7	1,5_1,3_14,7	1,77_1,31_14,7
CC5	0.51	0.5	0.01-1.8	-	-	-	-	-
CC22	0.32	0.27	0.02-3.9	0.84_1.03_3.9	-	-	-	-
CC398	0.47	0.47	0.02-1.5	0.95_1.12_2.2	0.81_0.98_3.9	-	-	-
CC30	0.55	0.51	0.01-1.6	0.95_1.16_2.2	0.89_1.07_3.9	0.98_1.13_2.21	-	-
CC45	0.68	0.62	0.01-1.9	0.97_1.08_1.9	1_1.11_3.9	0.99_1.14_2.0	1.04_1.16_1.88	-

**Conclusions:** PanGenome analysis of global collection of *S.aureus* isolated from different sources and places showed that despite a statistically significant greater interclonal in comparison with intraclonal variation ( $p < 0.05$ ), in general, there were low genetic variations between isolates both from the same clonal complex (not more than 0.75%, on average) and from different clonal complexes (2.15% on average). MLST CC8 was as an exception where panGenome difference reached 14.7%. This might be possible due to the including strains with strong genetic differences in the complex.