

Session: EP034 Molecular typing

Category: 4c. Molecular bacterial typing methods22 April 2017, 16:00 - 16:05
EP0201**Analysis of spa types with small repeats with wgMLST data**Dmitriy Babenko¹, Antonella Chesca², Mark Alexander Toleman³¹*Karaganda State Medical University; Scientific Centre*²*Transilvania University of Braşov*³*Cardiff University*

Background: *Staphylococcus aureus* is responsible for a variety of diseases and now is considered as the leading cause of nosocomial infections. Typing is an important prerequisite for targeted control measures. One of different typing methods is spa typing that is based on the length polymorphism in spa amplicons. Usually, clustering of Spa types is based on BURP algorithm implemented in the StaphType software (Ridom). One of the disadvantages of this clustering method is the exclusion of spa types with small number repeats. We explored *S.aureus* isolates with small spa repeats using wgMLST data.

Material/methods: 4976 whole *S.aureus* genomes from NCBI GenBank have been analyzed to determine Spa type and wgMLST data using SeqSphere (Ridom). Spa types with two spa repeats were clustered with other spa types based on EDSI algorithm to infer the spa CC relatedness. Genetic distance of spa types with small repeats were calculated on wgMLST data with 1714 loci using Nei formula (Nei M., 1972). Clustering of *S.aureus* into groups was performed by creating dendrogram with single linkage algorithm and 5% cut-off.

Results: As a result, 507 different spa types were determined on 4976 *S.aureus* genome where 8 of them were with 2 spa repeats. Short spa types, their belonging to spa CC and possible grouping with other short spa types are presented in table.

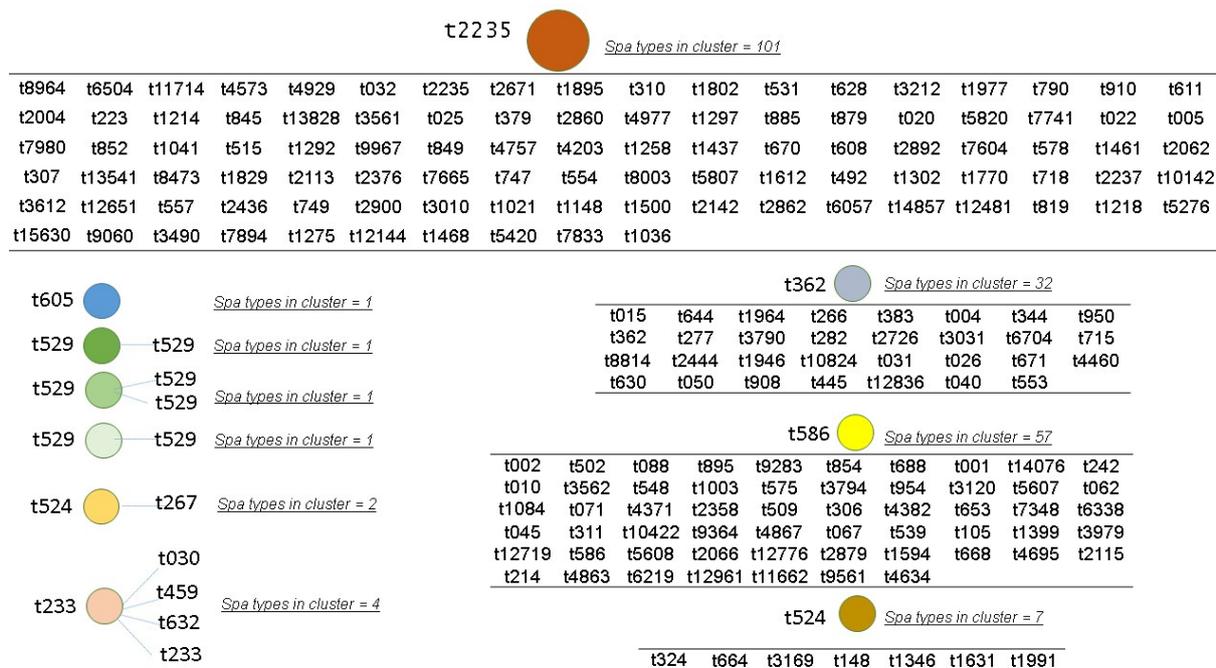
Spa type	Spa repeat	representative of spa CC (spa type*spa repeat)	# spa types in spa CC	Possible relatedness with other short spa types.
t605	07-23	t044*07-23-12-34-34-33-34	27	t2235*26-23
t529	04-34	t437*04-20-17-20-17-25-34	10	t524*04-17

				t362*09-34
t2235	26-23	t002*26-23-17-34-17-20-17-12-17-16	95	t605*07-23 t586*26-16
t524	04-17	t078*04-21-12-41-20-17-12-12-17	11	t529*04-34 t1991*08-17
t362	09-34	t004**09-02-16-13-13-17-34-16-34	16	t529*04-34
t233	15-12	t030*15-12-16-02-24-24	28	-
t586	26-16	t003*26-17-20-17-12-17-17-16	95	t2235*26-23
t1991	08-17	t1149*08-16-34-24-34-17-17	5	t524*04-17

Some spa types, such as spa t529, t523 and t586, were determined in several *S.aureus* genomes. The level of genetic variation in the short spa types were estimated on wgMLST typing and presented in the table.

spa	#	%Difference (min-max)
t605	1	-
t529	8	0-34%
t2235	1	-
t524	2	93%
t362	1	-
t233	1	-
t586	2	16%
t1991	1	-

Results of clustering of spa types with 2 repeats with other spa types using wgMLST typing and their interrelationship based on genetic similarities are shown in figure.



Conclusions: Analysis of spa types with 2 repeats revealed a number of interesting facts:

1. BURP clustering based EDSI algorithm can establish the similarities with other short spa types belonging to different Spa CC;
2. High genetic diversity within the spa types with a small number of repeats.
3. Comparison of short spa types with other spa types on genome wide MLST data can establish genetic linkage with spa types belonging to different spa CC.