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Paper Poster Session

Staphylococcal pathogenesis

Genetic diversity of *Staphylococcus aureus* strains isolated from patients with acute invasive and chronic infection

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Background: The aim of the study was to compare molecular features of *S. aureus* from hospitalized patients with acute and chronic infections.

Material/methods: 209 *S. aureus* strains from patients with invasive staphylococcal infections were isolated in hospitals in Moscow (4), St. Petersburg (1), and Yekaterinburg (4) in 2005-2011, from blood (105), tracheal aspirates and sputum (75), lung tissue at necropsy (29). 72 *S. aureus* strains, isolated in 2012 from patients with chronic osteomyelitis, were tested. Susceptibility to antibiotic was determined by disk diffusion method. Genotyping was performed by *spa*- and *SCCmec* typing. *Sea*, *seb*, *sec*, *seg*, *sep*, *tst*, *pvl* were tested by m-PCR according Holtfreter S. et al., 2007.

Results: 1. **Molecular features of *S. aureus* from patients with invasive infections.** 119 (56.9%) isolates were methicillin-resistant (MRSA). The most of MRSA belonged to the two previously identified epidemic MRSA: REMRSA-3 (*spa* t-030, *SCCmec* III:) – 65/119 (54.6%) of the isolates and REMRSA-2 (*spa* t-008; *SCCmec* IV with additional complex *ccr1*) - 48/119 (40.3%). This *SCCmec* type carried isolates of *spa* t-032, t-084 and t-024. 50 *spa* types were observed among the MSSA isolates, including t-002, t-015, t-284, t-127, t-095, t-008, t-030, t-267. 92.4% MRSA isolates carried *sea*, while *seg* dominated in MSSA (48.9%). *Sec* had the second highest frequency among MRSA (31.1%) and MSSA (24.5%). *Tst* was detected in 15 (7.1%) isolates: both MRSA and MSSA. *Pvl* were found in 7 MSSA isolates. **Bloodstream MSSA isolates had the greatest diversity of toxin genes: 25.5% of them carried two toxin genes, and 31.4% - 3 or more toxin genes in various combinations.** Analysis of autopsy isolates revealed that 69.2% MRSA carrying one of the following genes: *sea*, *seg*, *sec*, *tst*. 23.1% carried two genes: *sea*, combined with *sec* (15.4%) and *sea* with *seg* (7.7%). 46.7% of MSSA were positive for one of the following genes: *sea*, *seg*, *sec*. No one toxin genes tested were detected in 23(11%) isolates, including 4 MRSA and 19 MSSA. 2. **Molecular features of *S. aureus* from patients with chronic infection.** MRSA accounted for 26.3% of isolates. Two dominant epidemic MRSA were identified: REMRSA-2 (55%) and REMRSA-3. *Seg*, *sea*, *sec* and *tst*, were detected in 54.2%, 27.7%, 9.7% and 9.7% of the isolates. *Seb* was detected in 4.1% of the isolates. *lukS-PV* and *lukF-PV* was found in the one MSSA isolate. **Only 11.1% of isolates carried two or more tested toxin genes.**

Conclusions: Superantigens play a key role in the development of invasive infections. Enterotoxins SEA, SEG and less SEC are prevailing superantigens in *S. aureus*, circulating in Russia. Epidemic strain MRSA circulating in the local hospitals are able to acquire additional toxin genes. Findings should be considered in the vaccines creating.