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Biomolecular methods in comparison to bacteriological method using to establish the aetiology of infective endocarditis via investigating affected valve tissues

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Background: Infective endocarditis (IE) is difficult to diagnose and associated with high mortality. In the majority of cases, the effectiveness of the therapy is based on the verification of etiological agent in blood. It is reported that infectious agents, which are found in the valve tissue and those found in the bloodstream are not always identical. To make etiologic diagnostics more precise we suggest using biomolecular methods, such as polymerase chain reaction (PCR). Studies dedicated to the comparison of traditional and biomolecular methods in blood and affected valve tissues are very few and limited in patients. Therefore, a number of questions about false-negative and false-positive results of both methods still remain unsolved. The objective of the study is to investigate peculiarities of bacteriological and biomolecular methods used to establish the etiology of IE.

Material/methods: 53 patients with verified IE (DUKE 2015), hospitalized and treated in city clinical hospital №64 in Moscow from September 2012 to January 2015, were included in the study. All patients were performed parallel one-moment bacteriological and biomolecular (PCR or PCR with follow-up sequenition) tests. In case of death, affected valves (n=8) were tested with the same technique. Bacteriological diagnostic tests were done according to the standard protocol. The PCR method with hybridization and fluorescence detection of results was used to detect DNA of MSSA and

MRSA species of *S. aureus,* MRSA species of coagulase-negative *Staphylococcus spp.*, DNA of *Enterobacteriaceae*, *Candida*, enterococci's, *Streptococcus spp., A.baumanii, K.pneumoniae, P.aeruginosa, E.coli, S.agalactiae, S.pyogenes.* The average duration of bacteriological test was 5-7 days, PCR – 4-6 hours, PCR with follow-up sequenition – 1-2 days.

Results: We studied 53 patients with IE (DUKE 2015), age median 62 [34-73], 31 (58,5%) male and 22 (41,5%) female. Affected valve tissue samples were analyzed in 8 patients. There was full coincidence of results of both methods in three cases (37,5%) in both blood and autopsy material. In two cases there was a wider specter of agents found by PCR method than in blood and valve tissues. In one case it was not possible to detect DNA of *C.albicans* using biomolecular method, and one patient the results were completely different. There was one case of contaminated venous blood confirmed by traditional method: live-time growth of *Gemella haemolysans* was detected by using bacteriological method, DNA of *S.constellatus* was identified by biomolecular method, later confirmed in affected valve tissues. Moreover, growth and DNA of other bacteria were confirmed by both methods.

Conclusions: Investigation of affected valve tissues, resected for etiological agent identification in 8 IE patients, demonstrated a wider specter of bacteria than in blood culture. This is probably caused by the presence of bacterial biofilms on affected valves. Biomolecular methods demonstrated wider possibilities in comparison with traditional bacteriological techniques.