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Title: Etiological diagnostics of tuberculous pleurisy (PTB) in HIV-positive and HIV-negative patients

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Body: Purpose: verification of PTB by molecular-genetic methods (MG) in patients with and without HIV co-infection. Methods: pleural fluid (PF) of the patients was analyzed using MG. Isolation of DNA and amplification of nucleotide sequence IS6110 which is a marker of Mycobacterium TB (MTB) was carried out using real time PCR method (RT-PCR). Express evaluation of MBT drug resistance (DR) was performed using "TB-BIOCHIP" (TBCh) system. This method helps to identify IS6110 sequence in the sample and simultaneously identify mutations in rpoB gene associated with DR in rifampicin (R)-resistant strains, and in genes katG, inhA and ahpC-oxyR in isoniazid (H)-resistant strains. Results: group 1 included 72 HIV-infected patients with PTB. DNA of MBT was isolated in PF of 63.8%(n=46) cases. TBCh was made in 40 specimens. Mutations in rpoB gene were found in 29(72.5%) samples, among them 20(68.9%) were due to codon 531(Ser-Leu) replacement. Other common replacements were in codons 511(n=4), 512(n=4). DR to H was found in 30(75.0%) samples. KatG mutations were found in 26(86.6%) samples, mostly in the katG315–80.7%(n=21) and inhA mutations - in 26.9%(n=7) cases. Mutations confirming HR resistance were present in 24(60.0%) samples. 95 HIV-negative patients with PTB were group 2 among them DNA MBT was found in 21 tests (22.1%). DR to H was presented by gene katG mutations in codon 315(66.7%). DR to R was determined by gene rpoB mutations in codons 531(57.1%), 526(n=4), 516(n=2). Conclusion: Sensitivity of MG methods in detection of PTB was more promising in HIV(+) than in HIV(-) patients (p=0.001). Though total DR prevalence was high, the DR rates were similar in both groups.