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Fund “Nauka” Project № 24019 Resume – Autumn Competition-based Session 2024:

“Antimicrobial resistance and invasive infections in patients after hematopoietic stem cell transplantation”

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Objective: Investigation of antimicrobial drug resistance in clinically significant microorganisms (bacteria, viruses, fungi), isolated from clinical samples of patients after hematopoietic stem cell transplantation (HSCT) and with evidence of invasive infection, and comparison of the microbial isolates with high-risk hypervirulent strains with global distribution.

Tasks:

1. Selection of patients who have undergone hematopoietic stem cell transplantation with evidence of invasive infection (bloodstream, central nervous system or lung infection) according to defined criteria;
2. Collection of the necessary biological samples from patients according to the localization of the infectious process (blood, cerebrospinal fluid, sputum, bronchoalveolar lavage, puncta, etc.) for further investigation;
3. Identification of the etiological agent of the invasive infection;
4. Determination of the susceptibility to antimicrobial drugs in cases of bacterial and fungal causative agents;
5. Selection of patients on antiviral therapy with persistence or increase in viral load (lack of response to therapy);
6. Identification of molecular-genetic mechanisms of resistance to major groups of antimicrobial drugs (beta-lactams, glycopeptides, quinolones, aminoglycosides, sulfonamides, triazoles, echinocandins, antiviral agents);
7. Investigation of the genetic relationship between invasive microbial isolates and high-risk multidrug-resistant strains with confirmed global distribution.

Materials: clinical materials (blood, cerebrospinal fluid, sputum, bronchoalveolar lavage, punctates) of patients after HSCT with evidence of invasive infection will be examined.

Methods:

1. Determination of pathogens’ species identification by MALDI BIOTYPER SIRIUS (Bruker, Germany) and by molecular-genetic methods (PCR, DNA sequencing);

2. Determination of susceptibility/ resistance to antimicrobial agents by classical (disk diffusion method, epsilometry) and automated (Vitek 2, bioMérieux, France) methods and confirmed by DNA sequencing;
3. Investigation of genetic relatedness between isolates by next generation DNA sequencing.

Expected results:

1. Predominance (more than 50%) of multidrug-resistant Gram-negative bacteria in the etiological spectrum of invasive infectious complications in patients after HSCT;
2. Reactivation of latent viral infections (mainly Cytomegalovirus) in about 70% of the patients;
3. Lower relative proportion of invasive fungal infections (about 15%) and mainly associated with Aspergillus sp.;
4. A large proportion of resistant microbial isolates will be genetically related to globally distributed, high-risk and highly epidemic strains.