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| **Title:**  The role of multiplexed assays in characterizing samples from the clinical biobank |
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| 1) Background and aim:  Clinical biobank in the St Petersburg City Hospital №40 has gathered more than 50 thousand samples from nearly 2.5 thousand donors. The collection includes biological samples from donors diagnosed with socially significant diseases such as Parkinson’s, Alzheimer’s, cardio-vascular disease, multiple sclerosis and oncological diseases. Many samples are representative of the disease dynamics as they were collected during different stages of the disease progression.  In addition, control groups are being formed by collecting samples from healthy donors.  A wide range of biological samples is characterized by complete clinical data as well as lab test results. Additional information is acquired by genetic testing and multiplex immunoassay. At the moment there are more than 20 research studies being carried out within the framework of the biobank, that involve multiplex immunoassays of up to 122 biomarkers in 630 patients. One of the studies is presented below.  2) Methods:  The research study was conducted using samples from 63 patients diagnosed with multiple sclerosis (MS). The control group was represented by 39 healthy individuals. The patients with MS were divided in subgroups according to the disease type: relapsing-remitting MS (RRMS) (40 patients), secondary progressive MS (RRMS) (16 patients) and primary progressive MS (PPMS) (7 patients). All patients were analyzed for cytokines, chemokines, soluble cytokine receptors, neuropeptides and a wide range of biomarkers specific for neurodegenerative diseases and neurological disorders. Plasma samples were tested for 93 circular biomarkers.  3) Results:  A number of biomarkers differed significantly in levels between the patients and the control group. In addition, variations were observed across the three types of MS.  Patients with RRMS showed higher levels of eotaxin (p = 0.0172), IP-10 (p = < 0.0001), CFH (p = 0.0021), resistin (p = 0.0007), NSE (p < 0.0001), ceruloplasmin (p = 0.0006) and lower levels of PAI-1 (p = 0.0001), PDGF-AB/BB (p = 0.0013), MCP-1 (p < 0.0001).  Patients with PPMS showed higher levels of VCAM-1 (p = 0.0003), eotaxin (p = 0.003), IP-10 (p = 0.0009), CFH (p < 0.0001), resistin (p = 0.0005), NSE (p < 0.0001), ceruloplasmin (p = 0.0061) and lower levels of KLK-6 (p = 0.0004), PAI-1 (p < 0.0001), PDGF-AB/BB (p = 0.0013), contactin-1 (p = 0.0002), MCP-1 (p < 0.0001).  Patients with SPMS showed higher levels of VCAM-1 (p = 0.0008), eotaxin (p = 0.0364), CFH (p = 0.0055), resistin (p = 0.0401), NSE (p = 0.0012) and lower levels of MCP-1 (p = 0.0193).  4) Conclusion:  The use of xMAP Technology in clinical biobanking is a crucial stage in multiphenotypic analysis. This technology allows finding prognostic and predictive biomarkers for various diseases. |