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Decision support system for predicting of adverse effectsin patients with HIV

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Background. Success of many diagnostic and treatment processes are inextricably linked to the use of computerized technologyon the current stage of medicine development. The aim of the present study was to createthedecision support system (DSS) to predict the risk of adverse effects in persons with HIV/AIDS.

Materials and methods. We usedimmunogenetic markers as prognostic criteria in patients with HIV infection in alternative serial Wald analysis, which allows summarize the individual prognostic indexes (PI) and when it reaches a threshold value with a certain probability argues about the character of the disease progression. Training matrix classes had between 12 and 61 realizations, which consisted of 8 recognition features: serum levels of IL-10, TNF-α (pg/ml), absolute number of CD4+ T lymphocytes (cells/μL); determination of IL-10 and TNF-αgenesgenotype. Algorithm of functioning of the proposed DSS was based on the initial immunogenetic parameters values and the intersection of recognition classes characterizing the functional state of the disease process.

Results. Inpredictingof adverseoutcomesinpersons with HIV we determinedthatreliablemodulatorsofsevere CNS lesionswereminorcarriergenotypeof IL-10 gene, heterozygousvariantof TNF-α gene,highlevels of IL-10 and TNF-α in case of severe immunodeficiency. Prognostic index of these parameters was -15.32, corresponding up to 95 % of implementation forecast of organic CNS lesions in people living with HIV. Themostunfavorableindicatorsoftheriskofpulmonarytuberculosiscanberegardedas a combinationofheterozygousvariant of IL-10 gene,homozygousmajorallelevariantof TNF-αgene, serumlevelsof IL-10 (≥10.0 pg/ml) and TNF-α (≥1.0 pg/ml), T-helpers count ≤200 cells/μL(PI=-15.12, CI >95%). Prognosticsignificanceofriskfactorsforextrapulmonarytuberculosisinpatientswith HIV infectionweregenerallysimilarto modulatorofpulmonarytuberculosis: carrierof C/A genotypeof IL-10 gene, G/GgenotypeofTNF-α gene, highlevelsofcytokinesin combination with severeimmunosuppression (PI=-11.32,CI >90%). Implementingprognosisofherpesviralinfectionsweredetermined by thecombinationof IL-10 genehomozygousmajorallelevariantandheterozygousTNF-α gene variant withhighcytokineproductionandlowvaluesof CD4+ cells (PI=-10.26, CI >90%).

Conclusions. The proposed mathematical model of the DSS may be offered for use in clinical practice to determine the risk of opportunistic infections in persons with

HIV/AIDSand can better anticipate unintended consequences taking into account the individual immunogenetic features.