

Multiplex analysis of serum cytokine profiles in patients with multiple sclerosis and systemic lupus erythematosus

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Motivation and Aim: Dysregulation of cytokine networks is known to be associated with various autoimmune diseases including multiple sclerosis (MS) and systemic lupus erythematosus (SLE) [1]. Many studies have shown changes in serum cytokine levels in MS and SLE [2, 3]. However, the detailed changes in serum cytokine profiles in MS and SLE are poorly understood. Besides, comparisons of cytokine profiles in these diseases have not been performed. The aim of this work was to investigate changes in the serum cytokine profiles in MS and SLE in comparison with healthy donors in one series of experiments.

Methods and Algorithms: The analysis was carried out in the following groups: a group of SLE patients – 60 people, a group of MS patients – 55 people, a group of healthy donors – 36 people. The concentration of 41 cytokines was determined using a MAGPIX multiplex analyzer (Luminex, USA) using the MILLIPLEX MAP Human Cytokine/Chemokine Magnetic Bead Panel – Premixed 41 Plex – Immunology Multiplex Assay (Merck Millipore, USA). Statistical analysis (Kruskal-Wallis ANOVA, Dunn's test, Spearman correlation analysis, Bonferroni correction for multiple hypothesis testing) was carried out in STATISTICA 10 and ORIGIN 2021 programs. Volcano plots that reflect the dependence of the Log2 fold changes of the median values on the -Log10 p-value were plotted. Analysis of changes in cytokine profiles was performed by principal component analysis and partial discriminant least squares analysis using the CytokineExplore online resource (<http://al-saleh.cc/exabx.com/apps/cytokineexplore/>).

Results: Principal component analysis and discriminant least squares analysis showed that the combined multicytokine profiles of the studied groups differed. The following cytokines changed significantly in the group of healthy individuals compared with the group of SLE patients (in decreasing order of significance): IL-15, IL-1RA, IL-6, TNF α , Fractalkine, IL-9, MDC, sCD40L, IL-10, IL-1b, PDGF-AA, MCP-1, MIP-1a, MIP-1b, G-CSF, GM-CSF, IL-1a. Most of these cytokines were higher in SLE patients. The concentrations of the following cytokines changed significantly in healthy donors compared with MS patients (in decreasing order of significance): sCD40L, EGF, PDGF-AA, TGF- α , PDGF-AB/BB, IL-8, VEGF, MIP-1b, MCP-1, MDC, Eotaxin, GRO, TNF β , IL-7, IP-10. Most of these cytokines were lower in MS patients. Interestingly, IFN α 2 and PDGF-AB/BB levels were significantly different in patients with primary progressive MS compared with patients with relapsing-remitting MS ($p < 0.03$). The following cytokines changed significantly in the group of MS patients compared with the group of

SLE patients (in decreasing order of significance): IL-8, EGF, TGF- α , MIP-1b, sCD40L, MCP-1, VEGF, PDGF-AB/BB, PDGF-AA, IL-1RA, TNF α , MIP-1a, IL-15, IL-7, Eotaxin, IFN γ , GRO, IL-6, IL-1b, IL-17A, G-CSF, IL-10, GM-CSF, Fractalkine, IL-12P70, IL-3, IL-2, RANTES, IL-9, IL-4, IFN α 2. Thus, the levels of the 31st cytokine (out of 41 analyzed) differed in SLE and MS. Most of these cytokines were higher in SLE patients.

Conclusion: Thus, cytokine profiles in SLE and MS differ significantly both in comparison with healthy individuals and between these diseases. These data will help to better understand the differences in cytokine network dysregulation in MS and SLE.

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