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POSTER PRESENTATIONS

P-0951

The populations of peripheral blood T-lymphocytes at different stages of differentiation in patients with Parkinson's disease

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Parkinson's disease (PD) is one of the most common neurodegenerative diseases. The mechanisms of PD development are largely associated with the processes of chronic inflammation in the brain tissue (neuroinflammation). The development of neuroinflammation involves the central nervous system's resident immune cells and the cells of the peripheral immune system migrating to the brain. We examined 31 PD patients, 33 old-aged healthy donors (OHD), 30 young healthy donors (YHD). Immunophenotyping was performed using flow cytometry. Was analyzed the populations of T-lymphocytes (CD3+) at different stages of differentiation: replicative senescence (CD56-CD57+), Naïve (CCR7+CD45RA-), Central memory (CM) (CCR7+ CD45RA-), terminally differentiated effector memory (TEMRA) (CCR7- CD45RA+), effector memory (EM) (CCR7- CD45RA-). The proportion of T-lymphocytes (CD3+CD56-) expressing the CD57 marker was lower in the PD group than in the OHD group (8.7 and 13.1, $p = 0.02$). The proportion of these cells in the group of the YHD was significantly lower than in the group of PD and OHD. There were no significant differences in the naïve, CM, EM, TEMRA populations between patients with PD and OHD in the population of T-lymphocytes (CD3+) at different stages of differentiation. This study demonstrates that the peripheral immune profile in PD is not typical for older donors. We found that there is no replicative senescence of T-cells (CD3+CD56-CD57+). However, in the group of PD and OHD in the population of T-lymphocytes (CD3+) at different stages of differentiation, no differences were found.

Keywords: Ageing, biomarkers, immune senescence, memory**Acknowledgments:** The reported study was funded by RFBR, project number 20-315-90072.

P-0952

Severity of allergic rhinitis symptoms is associated with ceruloplasmin levels and a deficiency of microbial strains that sequester ironSebastian Alexander Jensen¹, Lisa Marie Petje¹, Tina Bartosik³, Petra Pjevack⁵, Bela Hausmann⁴, Karin Hufnagel¹, Gerold Besser³, Julia Eckl Dorna³, Sheriene Mousa Afify⁶, Claus Georg Krenn⁷, Georg Roth⁸, Stephan Hann⁹, Elisa Rivelles¹⁰, Erika Jensen Jarolim¹¹, Franziska Roth Walter²¹The Interuniversity Messerli Research Institute of the University of Veterinary Medicine Vienna, Medical University Vienna and University Vienna, Vienna, Austria²Institute of Pathophysiology and Allergy Research, Center of Pathophysiology, Infectiology and Immunology, Medical University of Vienna, Vienna, Austria³Department of Otorhinolaryngology, Head Neck Surgery, Medical University of Vienna, Vienna, Austria⁴Joint Microbiome Facility of the Medical University of Vienna and the University of Vienna, Vienna, Austria⁵University of Vienna, Centre for Microbiology and Environmental Systems Science, Department of Microbiology and Ecosystem Science, Division of Microbial Ecology, Vienna, Austria⁶Laboratory Medicine and Immunology Department, Faculty of Medicine, Menoufia University, Egypt⁷Department of Anesthesiology, General Intensive Care and Pain Medicine, Medical University of Vienna, Vienna, Austria⁸Department of Anesthesiology and Intensive Care, Franziskus Spital, Vienna, Austria⁹Department of Chemistry, University of Natural Resources and Life Sciences (BOKU), Vienna, Austria¹⁰Department of Laboratory Medicine, Medical University Vienna, Vienna, Austria¹¹Biomedical Int. R+D GmbH, Vienna, Austria

Since allergy is associated with iron deficiency, we sought to determine whether iron and microbial parameters correlate with the clinical response of allergic rhinitis subjects during nasal provocation. Female allergic subjects donated blood, and stool samples before they underwent a graded nasal provocation ($n=38$) with birch or grass pollen extract. Total nasal symptom scores (TNSS), visual analogue scale (VAS) and weight of nasal fluids were recorded. Complete blood cell counts and iron metabolism markers were determined. Stool samples were subjected to 16S rRNA amplicon sequencing. Serum hepcidin was assessed by ELISA. LegendPlex assay analysis was utilized to define levels of IgE, ceruloplasmin, lipocalin2 and cytokines in nasal fluids. Trace elements in serum and aqueous stool extracts were determined via inductively coupled plasma-mass spectrometry. Nasal and serum ceruloplasmin was the sole protein marker that positively correlated with all assessed symptom parameters (TNSS, VAS and nasal fluid weight), VAS scores in addition correlated with serum transferrin, haptoglobin and nasal IgE-levels. A positive correlation to symptoms was confirmed for serum copper, whereas gut iron and cobalt showed an inverse relationship to clinical symptoms. Particularly members of the order Bacteroidales and members of the genus Ruminococcus seems protective against TNSS and correlate well with the presence of gut iron. For the first time, we show that essential parameters in iron homeostasis, such as the copper-containing ferroxidase ceruloplasmin, correlate with the allergic outcome. Additionally, commensal bacteria sequestering iron seem to play a beneficial role against hay fever in adults.

Keywords: Allergic disorders, drugs for immune modulation, microbiome and environmental factors

P-0953

Overexpression of galectin 3 in pancreatic beta cells amplifies beta cell apoptosis and islet inflammation in type 2 diabetes in miceIvica Petrović¹, Nada Pejnović², Biljana Ljujić³, Sladjana Pavlović⁴, Marina Miletić Kovacević⁵, Ilija Jeftić¹, Aleksandar Djukić¹, Dragica Selaković⁶, Nevena Draginić⁷, Marijana Andjić⁸, Nemanja Jovčić⁹, Miodrag L. Lukić⁴¹Department of Pathophysiology, Faculty of Medical Sciences, University of Kragujevac, Serbia²Department of Immunology, Sinisa Stanković Institute for Biological Research, University of Belgrade, Serbia³Department of Genetics, Faculty of Medical Sciences, University of Kragujevac, Serbia⁴Center for Molecular Medicine and Stem Cell Research, Faculty of Medical Sciences, University of Kragujevac, Serbia⁵Department of Histology and embryology, Faculty of Medical Sciences, University of Kragujevac, Serbia⁶Department of Physiology, Faculty of Medical Sciences, University of Kragujevac, Serbia⁷Department of Pharmacy, University of Kragujevac, Faculty of Medical Sciences, Kragujevac, Serbia

During obesity hematopoietic cells-derived galectin 3 induces insulin resistance. While the role of galectin 3 expressed in islet invading immune cells in both type of diabetes has been studied, the importance of expression of this molecule on the target pancreatic beta cells is not defined. We have used 10-12 weeks old C57/BL6 male mice (WT) and C57/BL6 mice with transgenically enhanced Gal-3 expression in pancreatic β cells (TG). Obesity was induced with 16 weeks high fat diet regime. Pancreatic beta cells were tested for susceptibility to apoptosis induced by non-esterified fatty acids and cytokines as well as parameters of oxidative stress. The overexpression of galectin 3 increases beta cells apoptosis in HFD conditions and increases the percentage of proinflammatory F4/80+ macrophages in islets that express galectin 3 and TLR4. In isolated islets, we have shown that galectin 3 overexpression increases cytokine and palmitate-triggered beta cells apoptosis and also increases NO₂- induced oxidative stress of beta cells. Also, in pancreatic lymph nodes, macrophages were shifted towards proinflammatory TNF- α producing phenotype. By complementary approach *in vivo* and *in vitro*, we have shown that galectin 3 overexpression facilitates beta cell damage, enhances cytokine and palmitate-triggered beta cells apoptosis and also increases NO₂- induced oxidative stress in beta cells. Further, the results suggest that increased expression of galectin 3 in the pancreatic beta cells affects the metabolism of glucose and glycoregulation in mice on HFD, affecting the fasting glycemic values, as well as glycemia after glucose loading.

Keywords: Animal models, cytokines and mediators, diabetes, effector molecules