

# ImmunoTools *special* Award 2021



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## **The role of n-glycosylation of IgG Fc region in the pathomechanism of rheumatoid arthritis.**

The site-specific n-glycosylation of IgG is a post-translational modification of the protein, which is responsible for the modulation of its effector function. It was observed that the hyposialylation of the glycan in the Fc region enhances the inflammatory response.<sup>1</sup> However, the mechanism behind this is not clarified yet. Individuals suffering from rheumatoid arthritis (RA), an inflammatory autoimmune disease, produce several autoantibodies, which target proteins of the synovium and cartilage, terminally leading to severe bone erosion via osteoclast activation. More than 70 % of RA patients produce anti-citrullinated protein/peptide antibodies (ACPA) that have diagnostic and pathological significance.<sup>2,3</sup> Approximately 1% of the world's adult population suffers from this disease, with a three-fold higher likelihood of occurrence among women. The treatment of such patients mainly consists of administering disease modifying antirheumatic drugs (DMARDs) and biological therapy such as TNF $\alpha$  inhibitors like infliximab.

In our investigations we purified IgG from serum samples of healthy donors and RA patients. From the RA IgG samples we affinity purified ACPA using immobilized citrullinated multi-epitope peptide. Then the IgG from both groups was dimerized with a F(ab')<sub>2</sub> crosslinking two IgG molecules by anti-human F(ab')<sub>2</sub> to form an artificial immune complex, which were then added to previously PMA-activated U937 cells.

This cell line was used as a model of monocytes/macrophages, a major source of inflammatory cytokines. It was observed that the dimers of both ACPA and control IgG bound to the Fc $\gamma$  receptors type I (Fc $\gamma$ RI) on the cell surface, but there was a significant difference in the Fc $\gamma$ RI induced inflammatory cytokine release between the two groups. Namely, the addition of ACPA dimers triggered a significantly higher TNF $\alpha$  production as determined from the supernatants using a sandwich ELISA system. The MS-spectrometry analysis of the trypsin-digested glycopeptides from the samples determined the most abundant glycoforms from each group. It was revealed that there is a difference in the most abundant glycoforms from each group, in the healthy group the glycan bearing one galactose (which harbours the terminal sialic acid) was the most abundant, while in the RA samples the glycoform lacking galactose appeared to be of highest frequency. These results are consistent with the literature in this field.

In our next experiments we are planning to repeat the functional assays (cytokine release tests) with a Siglec-9 (sialic acid binding lectin 9) knockout variant of the cell line used, to determine said receptor's role in the inflammatory process. We also plan to survey primary monocytes/macrophages isolated from peripheral blood of healthy blood donors as well, for this endeavour we plan to utilize a stimulation with GM-CSF and an intracellular staining of TNF $\alpha$ , IL-6, IL-12, and IL-23 while staining the CD14 monocyte marker on the cell surface. IL-12 and IL-23 have a role in altering glycosylation of IgG <sup>1</sup>, if the binding of ACPA has an enhancing effect on the said cytokine's production, it may lead to the downregulation of the sialyl-transferase enzyme responsible for attaching terminal sialic acid to the glycan, leading to less sialylated IgG, increasing its pathogenicity.<sup>4</sup>

#### **References:**

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**ImmunoTools special** AWARD for **Balázs Gyebrovski** includes 10 reagents

PE - conjugated anti-human TNF $\alpha$  (2 units), IFN $\gamma$ , IL-6

PerCP - conjugated anti-human CD14

recombinant human GM-CSF

human ELISA-set (for one 96 plate) TNF $\alpha$

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