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Disclosure of Interest: None declared
DOI: 10.1136/annrheumdis-2017-eular.1083

FRI0083 REDUCED INCREASE OF ACPA IGG-FC GALACTOSYLATION DURING PREGNANCY IN COMPARISON TO TOTAL IGG: AN EXPLANATION WHY AUTOANTIBODY POSITIVE RA-PATIENTS IMPROVE LESS DURING PREGNANCY?

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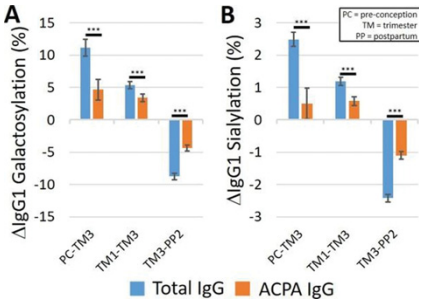
Background: Rheumatoid arthritis (RA) disease activity (DAS28-CRP) improves less during pregnancy in autoantibody positive patients.[1] The most specific autoantibodies for RA are anti-citrullinated protein antibodies (ACPAs), which mainly occur as the immunoglobulin (Ig) G isotype. An association with DAS28-CRP and the pregnancy-associated improvement is well established for the Fc glycosylation of total IgG, in particular for galactosylation (Gal) and sialylation (SA).[2] The Fc glycosylation of ACPAs – mainly present as IgG – has been reported to be different from the total IgG Fc glycosylation.[3]
Objectives: We sought to determine whether the change in ACPA IgG glycosylation during pregnancy is different from that of total IgG, and whether this relates to the improvement of RA during pregnancy.
Methods: ACPA positive patient sera (*n*=152) were obtained within the framework of the PARA cohort, a prospective study designed to investigate pregnancy-associated improvement of RA. ACPA IgG was isolated using microscale affinity chromatography. Trypsin digested ACPA IgG was measured using nano-liquid chromatography mass spectrometry, and compared to total IgG.
Results: Pregnancy-associated changes in the levels of glycosylation were observed for all ACPA IgG subclasses. Pregnancy-associated glycosylation changes were less pronounced during pregnancy and after delivery in ACPA IgG (Gal +5%; SA +0.5%) compared to total IgG (Gal +11%; SA +2.5%; Figure 1), but – for total IgG – not different between ACPA+ and ACPA- patients. No association of the change in DAS28-CRP with the change in ACPA IgG or total IgG galactosylation was observed for ACPA+ patients, whereas a strong association of total IgG galactosylation was observed for ACPA- patients.



Conclusions: During pregnancy the increase in galactosylation of ACPA IgG was less pronounced than that of total IgG, whereas the increase in the galactosylation of total IgG was not different between ACPA+ and ACPA- patients. Since it is known that changes in IgG galactosylation are associated with improvement of RA during pregnancy and since ACPA is thought to be of pathogenic significance in RA, our data might provide an explanation why ACPA+ RA patients are less likely to improve during pregnancy.
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Acknowledgements: This project is funded by the Dutch Arthritis Foundation (NR 10–1-411) and by the European Union's Seventh Framework Program (FP7-Health-F5–2011) under grant agreement no°278535 (HighGlycan). We thank Dr Jan Wouter Drijfhout (LUMC, Leiden) for providing the CCP2 peptide.
Disclosure of Interest: None declared
DOI: 10.1136/annrheumdis-2017-eular.6229

FRI0084 THE TONSIL MICROBIOME IS INVOLVED IN RHEUMATOID ARTHRITIS

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Background: Rheumatoid arthritis (RA) is a prevalent systemic autoimmune disease characterized by the production of autoantibodies[1]. The tonsil has been demonstrated to be a site of citrullination, and tonsillectomy has been reported to be a potential treatment of RA, suggesting the possibility that the tonsil could be a site of autoimmunity generation in RA[2,3]. The dysbiosis of gut microbiome and the associated host immune response has been implicated in the initiation and progression of RA[4–6]. However, there is no in-depth studies on the role of tonsil microbiota in RA. Thus, studies of the characteristics of tonsil microbiome in RA patients, the underlying mechanisms, as well as specific markers for the diagnosis and therapeutic evaluation for RA, are critical for the early diagnosis and prevention of RA.
Objectives: Therefore, we aimed to define the association of RA with tonsil microbiome as well as a microbial and metabolite profile that could predict disease status.
Methods: 16S rRNA gene sequencing was utilized on 220 tonsil swab samples (121 RA patients and 99 healthy controls) as well as 78 fecal samples (68 RA and 10 controls). Analysis of microbial taxa and metabolic pathway were performed to characterise and compare the tonsil microbiome of RA patients and healthy subjects
Results: Results showed that the tonsil harbored a unique microbiome relative to that present in the fecal samples. Patients with RA exhibited different tonsil microbiome from controls. A taxon-level analysis suggested that the relative abundance of 26 microbial clades were significantly altered, with 7 taxa increased and 19 taxa decreased in RA samples. Noticeably, we observed an expansion of rare microbial lineages as well as an alteration in microbial cladogenesis within RA patients. RA tonsil microbiota was associated with smoke, anti-peripheral factor, rheumatoid factors, disease duration and activity. Furthermore, we identified that 86 genes associated with bacterial metabolic pathway were enriched in RA tonsil microbiome.
Conclusions: Our results demonstrated that the RA tonsil microbiome differs from that of healthy controls, which correlates with systemic autoimmune changes and may potentially drives initiation of RA.
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Disclosure of Interest: None declared
DOI: 10.1136/annrheumdis-2017-eular.4707

FRIDAY, 16 JUNE 2017

Rheumatoid arthritis - prognosis, predictors and outcome

FRI0085 NUMBER OF PEPTIDE-SPECIFIC ANTI-CITRULLINATED PEPTIDE ANTIBODIES IN SYNOVIAL FLUID AND IN SYNOVIAL FLUID IMMUNE COMPLEXES ASSOCIATE WITH DEGREE OF RADIOLOGICAL DESTRUCTION AND RESPONSE TO TRIAMCINOLONE HEXACETONIDE FOR KNEE SYNOVITIS IN RHEUMATOID ARTHRITIS

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Background: We have described a planar microarray for the determination