Innate immunity in rheumatic diseases

**MECHANISM AND SIGNIFICANCE OF COMPLEMENT C3 RECEPTOR IN COLLAGEN-INDUCED RHEUMATOID ARTHRITIS MICE MODEL**

L. Dan1, L. Ke2, 1 Department of Rheumatology and Immunology, Xi’an No. 5 Hospital, 2 Core Research Laboratory, he Second Affiliated Hospital of Xi’an Jiaotong University, Xi’an, China

**Background:** Rheumatoid arthritis (RA) is a kind of chronic autoimmune disease, mainly manifested as small joint synovitis. Disease progression appears joint swelling, bone and cartilage damage, deformity and activity limited. The etiology of RA is still unclear and is generally considered to be an immune-mediated inflammatory disease. The activation pathway and regulation function of the complement system have become the hotspot of the research of RA pathogenesis. Previous studies have found that C3-/- mice had lower levels of antibodies to collagen in the Type II collagen-induced rheumatoid arthritis (CIA model), and the molecular mechanism is unclear. The small fragment C3a and large segment iC3b produced by C3 activation are the main effect products, and their biological effects are performed by combining with the specific receptor, C3aR and CD11b respectively.

**Objectives:** To investigate the mechanism of C3a and C3b, the cleavage products of C3 in rheumatoid arthritis, binding to their corresponding receptors, the signalling pathway of complement activation and the effect on arthritic conditions.

**Methods:** This study was intended to establish a CIA model on C3aR knockout and CR3 knockout mice (C3aR-/-or CD11b-/-) to investigate the effect of complement C3a-C3aR signalling and iC3b-CR3 signalling on rheumatoid arthritis. Methods using C57BL6 background transgenic mice (Gifted by King’s College London), Mice were divided into 3 groups according to the experimental mouse strains: C3aR-/- group, CD11b-/- group and WT control group. The clinical score of the joints in each group was measured after the establishment of the CIA model through collagen induction. Moreover, joint specimens were collected for pathology grading. Besides, the level of CD4+ T cell, CD8+ T cell, Th17/Treg ratio and the level of IFN-gamma of NK cell in mouse spleen were detected by flow cytometry.

**Results:** The clinical score of C3aR-/- group was slightly lower than that of WT group, and the clinical score of CD11b-/- group was significantly higher than that of WT group; 2. Pathological score (12 points): The CIA scores of CD11b-/- group, C3aR-/- group and WT control group were 9.35±0.75, 4.81±0.63 and 5.85±0.55 respectively. The CIA scores of CD11b-/- group was significantly higher than that of WT group, which were consistent with clinical score; 3. Through the flow cytometry detection, compared with the WT group, CD4+ T cell, CD8+ T cell and Th17/Treg percentage increased significantly, and Treg cell decreased. In addition, the secretion of IFN-gamma of Splenic NK cell was significantly reduced.

**Conclusions:** iC3b as well as C3a could bind to their respective complement receptor, and express different influence in the immune mechanism of RA. The iC3b-CD11b signalling has a protective effect in RA, while the C3a-C3aR signalling has a protective effect in RA, which were consistent with clinical score; 3. Through the flow cytometry detection, compared with the WT group, CD4+ T cell, CD8+ T cell and Th17/Treg percentage increased significantly, and Treg cell decreased. In addition, the secretion of IFN-gamma of Splenic NK cell was significantly reduced. In summary, iC3b produces by C3 activation are the main effect products, and their biological effects are performed by combining with the specific receptor, C3aR and CD11b respectively.

**Disclosure of Interest:** None declared

**DOI:** 10.1136/annrheumdis-2018-eular.2192

---

**SYNOVIAL TISSUE CD1C+ DENDRITIC CELLS IN RHEUMATOID ARTHRITIS EXPRESS HIGH LEVELS OF THE EPIGENETIC REGULATOR OF INFLAMMATION, MICRORNA-155 AND INFLAMMATORY CYTOKINES**

A. Einesmar1, S. Alivemini2, B. Tolusso3, L. Bui1, D. Vaughan1, M.R. Gigante2, F. Fredonico1, G. Ferracuce3, G. Guarneri4, I.B. Miller5, A.M. Kuroska6, Stolarski4, 1 Institute of Infection, Immunity, and Inflammation, University of Glasgow, Glasgow, UK; 2 Division of Rheumatology, Fondazione Policlinico Universitario A. Gemelli, Catholic University of the Sacred Heart; 3 Institute of Pathology, Fondazione Policlinico Universitario A. Gemelli – Catholic University of the Sacred Heart, Rome, Italy; 4 Rheumatoid Arthritis Pathogenesis Centre of Excellence (RACE), Glasgow, Birmingham, Newcastle, UK

**Background:** Dendritic cells (DCs) direct the immune response against pathogens while maintaining self-tolerance by instructing T/B cells in lymphoid organs and tissue. These cells have the potential to induce tolerance as well as to trigger an inflammatory autoimmune response. Based on the distinct transcriptomics, function and distribution, DCs can be broadly categorised as plasmacytoid and myeloid (conventional) DCs. Based on recent single cells sequencing and secretome data, can be divided into CD141+ DCs (DC1), DC2_A (DC2) defined as CD1c+CD303D30LIdC2BD4CD163+ or DC2_B (DC3) as CD1c+CD303C30LIdC2BD4CD163+. In addition, populations of CD1c+CD141+CD16+ (named DC4), that shares some gene expression with CD16+ monocyte and inflammatory DC (intDC). Most to date studies on Rheumatoid Arthritis patients investigated DCs in circulation or in synovial fluid (SF). This provided important insight into epigenetic changes in DC-precursors before they enter synovial tissue, e.g. RA blood CD1c+have deregulated miRNA-34a driven epigenetic control of anti-inflammatory Axl pathway1 or into the influence of inflammatory milieu on DCs, respectively. However, neither (peripheral blood) PB or SF are major sites for DC regulated T/B cell activation; instead, DCs control immune responses in the appropriate structures of lymph organs and tissues.

**Objectives:** In this study, we sought to investigate myeloid DCs in synovial tissue with the prospect of better understanding their role in driving autoimmunity in RA.

**Methods:** We developed a flow cytometry sorting strategy to characterise the phenotype of distinct myeloid DC subsets in multiple biological compartments (PB, SF and synovial tissue). Synovial tissue (ST) biopsies (RA n=9; Psoriatic arthritis n=3) were digested with liberase prior the analysis. Peripheral blood DCs (RA n=19, Psoriatic arthritis n=16, healthy donors n=12), and SF DC (n=3) were used as comparators. Synovial tissue, SF and PB DCs were sorted and microRNAs, pro-inflammatory and regulatory cytokine expression analysed by amplified qPCR. In addition, DCs were mapped in synovial tissue in RA (n=8), PsA (n=7) and control non-inflammatory OA (n=5) by immunohistochemistry.