Furthermore, the rhythm of *PER3* was present exclusively in RA patients, but not in healthy participants.

Conclusion: Taken together, we conclude that the circadian rhythms of immune cells in RA patients are different from that in healthy individuals. The alteration can be observed on both cellular and RNA level. We postulate that the alterations in circadian rhythms may contribute to disease manifestations and may have impact for optimizing diagnosis and therapy in RA. Further analysis is required to expand the data set. It is also of interest to investigate the functionality of circadian clock genes in immune cells.

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SAT0069

PROTECTIVE EFFECT OF PROTOCATECHUIC ACID RICH FRACTION OF TRIANTHEMA PORTULACASTRUM AGAINST COLLAGEN INDUCED RHEUMATOID ARTHRITIS VIA GUT MICROBIOTA MODULATION

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Background: Rheumatoid arthritis, a chronic inflammatory joint disease affects people all over the world. *Triantema portulacastrum* (TP) has been traditionally utilized for the treatment of rheumatism.

Objectives: The current study was envisaged to evaluate the effect of protocathechuic acid rich fraction of TP on type II collagen induced rheumatoid arthritis, inflammation and microbial population of gut by using rodent model.

Methods: Hydroethanolic extract of TP was fractionated with three different solvents (ethyl acetate, chloroform and n-butanol) and quantitatively analyzed with HPLC-DAD method which revealed n-butanol fraction of TP (BFTP) is rich in protocathechuic acid along with other phenolic compounds. Animals were randomly divided into five groups. Four groups were injected with bovine type-II collagen (BTC-II; 100µg) in Freund's complete adjuvant (0.1 ml) intradermally. On day 21, animals were again treated with BTC-II along with booster incomplete Freund's adjuvant injection. After 24 hrs, animal groups were administered intraperitoneally with their respective drug treatment, i.e., vehicle, BFTP (100, 200 and 400 mg/kg b.w.) and methotrexate (3 mg/kg b.w.), respectively once in a day for next 21 days. At the end of experiment serum level of pro-inflammatory cytokines was determined, and gut microbiota was analyzed by using Illumina HiSeq.

Results: Results revealed BFTP preadministered group exhibited significantly reduced level of paw swelling and arthritis score as compared to vehicle group. Inflammatory markers (IL-1β, IL-6, IL-7, IL-23 and TNF-α) of rheumatoid arthritis were also significantly alleviated by BFTP. Histological studies of mice ankle soft tissue also support the protective effect of BFTP. Additionally, BFTP repair altered gut microbial communities by reducing relative loads of inflammatory microbes such as *Mucispirillum*, *Helicobacter* and *Lachnospiraceae*.

Conclusion: The results conclude that BFTP possess beneficial anti-inflammatory response in arthritic model and can be used as a potential anti-arthritic agent for the management of arthritis.

Disclosure of Interests: None declared

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Rheumatoid arthritis – prognosis, predictors and outcome

SAT0070

PROTEOMIC SPECTRUM PROFILE IN INFLAMMATORY AND DEGENERATIVE ARTHRITIS

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Background: The identification and quantification of protein biomarkers present in tissues and body fluids is a new area of interest in the clinical management of rheumatic diseases. Proteomics may identify novel biomarker(s) which assist in understanding the pathogenesis of rheumatic disorders with diagnostic and prognostic implications. In addition, proteomic techniques in RA may be helpful to identify newer autoantibodies and inflammatory acute phase proteins.

Yet, the integration of potential biomarkers resulting from rheumatic proteomics analyses in differential diagnosis of rheumatologic disorders is not yet fully established and so several studies are needed to confirm the efficacy of these approaches.

Objectives: The purpose of this study was to use Matrix Assisted Laser Desorption Ionization – Time of Flight – Mass Spectrometry (MALDI-TOF-MS) to identify differentially expressed disease-related and condition-specific peptide in serum of patients with Rheumatoid arthritis (RA) and osteoarthritis (OA).

Methods: Hundred participants were divided into three groups as following: RA group (35 patients with Rheumatoid arthritis representing patients with inflammatory arthritis); OA group (35 patients with Osteoarthritis representing patients with non-inflammatory arthritis); healthy control group (30 healthy volunteers). All participants were subjected to full history taking; clinical examination; and clinical Assessment of disease activity in RA patients using Disease activity score 28 (DAS-28); routine laboratory investigations; Acute phase reactants; serological tests; plain x-ray of affected joints, as well as serum proteomic profile using Magnetic beads (MB) separation and (MALDI – TOF – MS).^[1] Using the spectral data from the three groups, three different classification models for the three groups were generated using GA, SNN and QC algorithms. The GA model showed the best sensitivity and specificity in the three trials (RA versus control, OA versus control, and RA versus OA).

Results: In comparing RA versus control group; the results revealed 101 peaks that discriminated the RA from the control group; 53 were significant (PWKW p>0.05) and 48 nonsignificant. Three peaks (14;25;62) were significant and 2 were nonsignificant (43;53).

Regarding OA versus control group; 95 peaks were identified that discriminated the OA from the control group; 38 were significant (PWKW p>0.05) and 57 nonsignificant. Three peaks (18;3;14) were significant and peak 75 and 23 were nonsignificant.

Finally the RA group was discriminated from the OA group, the trial showed 113 peaks 73 were significant (PWKW p>0.05) and 40 nonsignificant. Five peaks were integrated (75:7767.82 40:2953.29 41:2991.59 48:4054.75 68:6434.51), and all integrated peaks were significant. The integrated peaks showed that all peaks were downregulated except peak 40 was upregulated.

Conclusion: Data obtained from proteomic analysis allow differentiation between RA, OA, and healthy subjects. Because of its simplicity and accuracy, (MALDI-TOF-MS) is a promising method for identifying differentially expressed inflammatory versus degenerative disease-related peptide.

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