Conclusion: Using target proteome profiling technique, we demonstrated PON1 as a potential biomarker of D2T RA. However, these results have to be validated on a larger cohort.

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AB0064

EVALUATION OF QUALITY OF LIFE IN RHEUMATOID ARTHRITIS USING SF-36 AND HAQ SCALES

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Background: The assessment of health-related quality-of-life (HRQoL) in rheumatoid arthritis (RA) is becoming a common tool in clinical practice. The medical outcomes survey short form 36 (SF-36) is one of the most widely used tools for measuring HRQoL in RA as well as the HAQ scale.

Objectives: The aim of our study is to evaluate the impact of the RA in the quality of life (QoL) of our patients using the SF-36 and the HAQ questionnaires.

Methods: This is a cross-sectional study during a period of the year 2020, including 70 patients followed in the department of Rheumatology in Mahdia, Tunisia. All patients were diagnosed with RA based in ACR 1987/EULAR 2010. We evaluated for each patient, the mean global scale and the eight domains of SF-36 (physical functioning (PF), role physical (RP), bodily pain (BP), general health (GH), vitality (VT), a social functioning (SF), role emotional (RE) and mental health (MH)), scored from 0 (worst) to 100 (best).

Results: Our study included 70 patients (59 females/11males) with an age ranged from 21 to 76 years. The mean age was 54 ± 12 years. The mean duration of the disease was 11 ± 10 years [1-40]. The mean number of tender joints was 9.7 ± 9.4 and swollen joints were 4.2 ± 6.1. The mean disease activity score (DAS28) was 4.6 ± 1.9 [1.2-8.4]. The mean HAQ score was 1.5 ± 1.3, 47.1% of patients had specific joint deformations, 82.9% had radiologic involvement and 31.4% had osteoporosis. The biologic analysis showed that the mean ESR was 46.7 ± 30.5 and the CRP was 15.8 ± 23.3. Rheumatoid factors were positive in 42.9% of cases, the ACPA were positive in 50% of cases. 84.3% of RA patients were treated by methotrexate, 4.3% were treated by salazopyrin and 11.4% were treated by biologic treatments.

The SF-36 global score was 50.4 ± 26.3 [15.3-92.8]. 46 patients (65.7% of cases) had impaired QoL (SF-36 < 66.7). The means of different domains (PF, RP, BP, GH, VT, SF, RE, MH) were respectively 51; 41.4; 51.4; 50; 51.2; 57.7; 41.9; 59.2. The most severely impacted domains were the RP and RE.

Our study showed a significant correlation between the SF-36 global score and the number of tender joints (p=0.002), the DAS28 (p=0.017) and the HAQ (p=0.000).

Conclusion: Our study showed that 65.7% of RA patients presented impaired QoL (SF-36 < 66.7), which is associated with high disease activity. So it's important to jugulate the disease, in order to ameliorate the quality of life of our patients.

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AB0065

HGF/C-MET SIGNALING PROMOTE ANGIOGENESIS THROUGH CXCL16 IN RHEUMATOID ARTHRITIS

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Background: Hepatocyte growth factor (HGF) binds to the receptor tyrosine kinase c-Met and is a multifunctional cytokine that promotes processes such as cell proliferation, survival, differentiation, migration and angiogenesis [1]. We previously reported that HGF is produced by inflammation in the RA synovium, and activates monocyte migration to the synovium and promotes bone destruction through its own chemotactic effect and enhanced chemokine production in the synovium [2].

Objectives: Therefore, we next aimed to determine the role of HGF in RA angiogenesis.

Methods: The expression of HGF / c-Met in the serum and synovial tissues (STs) of RA patients and controls and human umbilical vein endothelial cells (HUVECs) was evaluated by ELISA and immunostaining. The effect of HGF/c-Met signaling on the promotion of CXCL16 production from HUVECs and RA fibroblast-like synoviocytes (FLSs) was determined by ELISA. To examine the role of HGF in angiogenesis, we performed in vitro Matrigel assays using HUVECs treated with HGF.

Results: HGF in serum in treatment-naïve RA patients was significantly higher than that in controls and HGF in serum in treatment-resistant RA showed a significant positive correlation with CXCL16. c-Met were expressed on vascular endothelial cells of RA STs and HUVECs. Stimulation of HUVECs with HGF dose-dependently increased CXCL16 production. c-Met signal inhibition by SU11274 suppressed TNF- α stimulation-enhanced CXCL16 production by RA FLSs in a dose-dependent manner. Furthermore, HGF induced HUVEC tube formation by 1.8-fold.

Conclusion: HGF is produced by inflammation in the RA synovium, and activates angiogenesis through its own potent angiogenic effect and enhanced production of CXCL16 in the synovium. These results indicate that a strategy targeting c-Met signalling may be important for resolving treatment-resistant RA.

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AB0066

MECHANISMS OF TOTAL SAPONINS OF PANAX JAPONICUS MITIGATES COLLAGEN-INDUCED ARTHRITIS

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Background: Total saponins of *Panax japonicus* (TSPJ) are extracted from *Panax japonicus* (T.Nees) C.A.Mey and have achieved a good therapeutic effect in the treatment of rheumatoid arthritis (RA). Unfortunately, the mechanism of TSPJ acting on RA is not clear.

Objectives: To investigate the potential mechanisms and key targets of TSPJ on RA.

Methods: The raw data were downloaded from the Gene Expression Omnibus (GEO) database, and the RStudio3.6.1 software was used to identify differentially expressed genes (DEGs). The potential targets of active compounds from TSPJ were predicted by the PharmMapper and SwissTargetPrediction databases. Based on the overlapping genes, we used Cytoscape 3.7.2 software to construct a protein-protein interactions (PPI) network and to determine the mechanisms of the treatment by Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis. Collagen-induced arthritis (CIA) model was established and treated with different doses of TSPJ. Arthritis index (AI) and histology score were used to evaluate the symptoms of CIA. The levels of vascular endothelial growth factor (VEGF), hypoxia-inducible factor 1 (HIF-1), IL-1 β , and IL-17A tested by enzyme linked immunosorbent assay and real time-quantitative Polymerase Chain Reaction.