Conclusion: In addition to inducing p75NTR up-regulation, inflammatory stimuli increase the release of proNGF in arthritis SFs. Autocrine proNGF binds to p75NTR and further enhances pro-inflammatory cytokine production, creating a vicious circle that amplifies the inflammatory response. Blocking the binding of endogenous proNGF to its receptor p75NTR strongly reduces the production of inflammatory mediators and prospects the use of p75NTR inhibitors as a new therapeutic approach to chronic arthritis.

REFERENCES
[2] AB0063 A SYSTEMS APPROACH TO INVESTIGATE INFLAMMATION RESOLUTION BY MULTICOMPONENT MEDICINAL PRODUCT TR14
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Background: Acute inflammation is a nonlinear, spatio-temporal process for the removal of invading pathogens and the repair of damaged tissues to re-establish homeostasis. If not resolved, it leads to chronic inflammatory clinical phenotypes. The current medical paradigm is based on using single-molecule inhibitors aiming to block certain molecular pathways involved in inflammation. Complex diseases, where large number of feedback mechanisms play a central role, require multi-target interventions [1]. Dynamics of feedback mechanisms associated with multiple therapeutic checkpoints require systems biology approaches.

Objectives: The objective of our study was to construct a comprehensive molecular interaction map (MIM) of acute inflammation and its resolution. We further aimed to understand the effect of Traumeel (TR14), a multicomponent drug, on inflammation resolution, by mapping previously published TR14 transcriptomics data [2] from a wound healing murine model onto the MIM.

Methods: We constructed a comprehensive MIM using damage-, and pathogen-associated molecular patterns (DAMPs and PAMPs) and established disease genes from selected acute inflammatory clinical phenotypes as seed molecules. From the MIM, we identified feedback loops (FBLs) with the NetDysCytoscape plugin using our previously published methodology [1]. All FBLs were merged to create a core regulatory network responsible for the overall dynamics of acute inflammation initiation, transition and resolution.

Using TR14 transcriptomics data to identify acute inflammatory processes enriched at various time points, we combined RPKM values of each individual gene from selected acute inflammatory clinical phenotypes as seed molecules. Further, the fold change expression profile for each gene was calculated keeping nodes with absolute fold change expression of ≥ 1.5 and a p-value < 0.05.

Results: The MIM has, as of January 2019, 3300 interactions, which are divided at each time point using the Cytoscape ClueGo app.

Conclusion: By mapping previously published TR14 transcriptomics data [2] from a wound healing murine model onto the MIM, we identified enrichment of inflammatory regulated genes at early time points. Using TR14 treated vs untreated mice. These data were mapped to the core regulatory network, and time point-specific sub-networks were identified by keeping nodes with absolute fold change expression of ≥ 1.5 and a p-value < 0.05.

AB0064 SERUM TENASCIN-C LEVELS ARE ELEVATED IN PATIENTS WITH AXIAL SPONDYLOARTHROSIS
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Background: Tenascin-C (TNC) is a pro-inflammatory extracellular matrix glycoprotein that is synthesized in various pathological conditions. TNC induces inflammatory activity and promotes damage of joints. Its expression in adults is restricted to sites of tissue injury, particularly during phases of inflammation and active tissue remodelling. Only a few studies have described elevated serum TNC levels in ankylosing spondylitis (AS) compared to healthy controls (HC).

Objectives: The aim of this study was to examine the levels of serum TNC among different axial spondyloarthritis (axSpA) subsets and whether TNC levels are related to disease activity measures or other clinical features.

Methods: Sixty-one patients who fulfilled the Assessment of SpondyloArthritis international Society (ASAS) classification criteria for axSpA and twenty age and sex-matched HC were included in this study. Based on imaging, patients were further classified as AS (n = 45) and as nr-axSpA (n = 16). Patients with AS were further divided into two subsets based on the absence (n=22) or presence of syndesmophytes (n=23).

TNC serum levels were determined using ELISA. The following data were collected: clinical and laboratory disease activity measures; demographic status; disease-related factors such as the Bath Ankylosing Spondylitis Disease Activity Index (BASDAI) and CRP levels. Statistical analyses were performed with GraphPad Prism 5.1. The data are presented as the median and interquartile range.

Results: TNC serum levels were elevated in axSpA patients (535.3 (457.7-677.2) ng/mL) compared to HC (432.1 (329.1-565.9) ng/mL, p= 0.007). Dividing axSpA into nr-axSpA and AS subsets the difference was observed only between AS patients and HC (535.3 (434.5-677.2) vs. 432.1 (329.1-565.9) ng/mL, p=0.022). TNC serum levels did not correlate with disease activity biomarkers (serum CRP or BASDAI) in patients with axSpA. Although we have not observed correlation between TNC and mSASSS radiographic score, weak correlation with disease subsets was found (r=0.25, p=0.025).

Conclusion: We demonstrated here elevated serum TNC levels in patients with axSpA, particularly in those with syndesmophytes, which may suggest its role in bone formation during radiographic stage of the disease.

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AB0065 PATIENTS WITH AXIAL SPONDYLOARTHRITIS
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Background: Axial spondyloarthritis (axSpA) is defined as enthesitis-related inflammatory disorders affecting axially related joints. AxSpA is classified as either ankylosing spondylitis (AS) or non-radiographic axial spondyloarthritis (nr-axSpA) according to the classification criteria of the ASAS. nr-axSpA is characterized by axial symptoms and documented inflammatory back pain with a radiographic absence of syndesmophytes. TR14 modulates multiple network components at early time points, which can be linked to inflammation resolution.

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