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

Disclosure of Interests: Luciapa Farina: None declared, Gaetana Minnone : None declared, Marzia Soligo : None declared, Luigi Manni : None declared, Gian Marco Moneta: None declared, Ivan Ciaiello: None declared, Luigi Manzo : None declared, Fabrizio De Benedetti Grant/research support from: Abbvie, SOBI, Novimmune, Roche, Novartis, Sanofi, Pfizer, Luisa Bracci-Laudiero: None declared, Marzia Soligo : None declared, Luigi Manni : None declared, Gian Marco Moneta: None declared, Ivan Ciaiello: None declared, Luigi Manzo : None declared, Fabrizio De Benedetti Grant/research support from: Abbvie, SOBI, Novimmune, Roche, Novartis, Sanofi, Pfizer, Luisa Bracci-Laudiero: None declared

DISCUSSION
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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 NetDS Cytoscape 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 splice variant into the parent gene using the RSEM method [3]. The expression enriched at various time points, we combined RPKM values of each individual splice variant into the parent gene using the RSEM method [3]. The expression enrichment analysis was repeated: 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). Comparing 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 those in which syndromes are strongly associated with bone remodeling during radiographic stage of the disease.

Acknowledgement: This work was supported by MH CR 032728, SVV 260373
AZV - 17-33127A

Disclosure of Interests: Hana Hulejova: None declared, Kristyna Bubova: None declared, Klara Pragerová: None declared, Marketa Husakova: None declared, Maria Filkova: None declared, Michal Tomlik: None declared, Kare Pavleka: None declared, Ladislav Šenolt: 1 Institute of Rheumatology, Prague, Czech Republic; 2 Institute of Rheumatology, Department of Rheumatology, 1st Faculty of Medicine, Charles University, Prague, Czech Republic

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 elevated in 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).

Methods: Sixty-one patients who fulfilled the Assessment of SpondyloArthritis international Society (ASAS) classification criteria for axSpA and twenty age and sex-matched HC 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 syndromes (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). Comparing 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 those in which syndromes, which may suggest its role in bone formation during radiographic stage of the disease.

Acknowledgement: This work was supported by MH CR 032728, SVV 260373
AZV - 17-33127A

Disclosure of Interests: Hana Hulejova: None declared, Kristyna Bubova: None declared, Klara Pragerová: None declared, Marketa Husakova: None declared, Maria Filkova: None declared, Michal Tomlik: None declared, Kare Pavleka: None declared, Ladislav Šenolt: Grant/research support from: AbbVie, Bristol- Myers Squibb, Celgene Corporation, Merck Sharp and Dohme, Novartis, Pfizer, Roche, UCB, Amgen, Takeda, Speakers bureau: AbbVie, Amgen, Bristol-Myers Squibb, Celgene Corporation, Eli Lilly, Merck Sharp and Dohme, Novartis, Pfizer, Roche, UCB


AB0064 SERUM TENASCIN-C LEVELS ARE ELEVATED IN PATIENTS WITH AXIAL Spondyloarthritis
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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 elevated in 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).

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Acknowledgement: This work was supported by MH CR 032728, SVV 260373
AZV - 17-33127A

Disclosure of Interests: Hana Hulejova: None declared, Kristyna Bubova: None declared, Klara Pragerova: None declared, Marketa Husakova: None declared, Maria Filkova: None declared, Michal Tomlik: None declared, Kare Pavleka: None declared, Ladislav Senolt: Grant/research support from: AbbVie, Bristol- Myers Squibb, Celgene Corporation, Merck Sharp and Dohme, Novartis, Pfizer, Roche, UCB, Amgen, Takeda, Speakers bureau: AbbVie, Amgen, Bristol-Myers Squibb, Celgene Corporation, Eli Lilly, Merck Sharp and Dohme, Novartis, Pfizer, Roche, UCB