Table. Risk of herpes zoster: Results of adjusted regression analyses with and without inverse probability weights

	Multivariate Analysis without IPW		Multivariate Analysis with IPW	
	Adjusted HR (95% CI)	P Value	Adjusted HR (95% CI)	P Value
Female sex	1.42 (1.12-1.82)	0.0042	1.21 (0.96-1.53)	0.1095
Age per 10 years	1.23 (1.13-1.33)	<.0001	1.31 (1.2-1.43)	<.0001
Glucocorticoids, 5-10 vs 0 mg/d	1.16 (0.95-1.41)	0.1577	1.23 (1-1.52)	0.0501
Glucocorticoids, >10 vs 0 mg/d	1.58 (1.02-2.46)	0.0417	1.92 (1.27-2.92)	0.0022
<i>csDMARD treatment</i>	<i>Reference</i>		<i>Reference</i>	
Monoclonal TNFi antibodies	1.55 (1.20-2.00)	0.0009	1.63 (1.25-2.12)	0.0003
Soluble TNF receptors	1.32 (0.98-1.77)	0.0683	1.34 (0.98-1.83)	0.0631
T-cell co-stimulation modulator	1.41 (0.97-2.05)	0.0746	1.69 (1.17-2.45)	0.0048
B-cell targeted therapies	1.45 (1.07-1.97)	0.0156	1.66 (1.19-2.3)	0.0026
IL-6 inhibitors	1.31 (0.97-1.77)	0.0737	1.55 (1.15-2.09)	0.0045
JAK inhibitors	3.55 (2.33-5.41)	<.0001	5.01 (3.45-7.28)	<.0001

Acknowledgments: RABBIT is supported by a joint, unconditional grant from AbbVie, Amgen, BMS, Fresenius Kabi, Hexal, Lilly, MSD, Mylan, Pfizer, Roche, Samsung Bioepis, Sanofi-Aventis and UCB

Disclosure of Interests: Anja Strangfeld Speakers bureau: AbbVie, BMS, Pfizer, Roche, Sanofi-Aventis, Imke Redeker: None declared, Jörn Kekow Speakers bureau: BMS, MSD, Pfizer, Roche, Gerd Rüdiger Burmester Consultant of: AbbVie Inc, Eli Lilly, Gilead, Janssen, Merck, Roche, Pfizer, and UCB Pharma, Speakers bureau: AbbVie Inc, Eli Lilly, Gilead, Janssen, Merck, Roche, Pfizer, and UCB Pharma, Juergen Braun Grant/research support from: Abbvie (Abbott), Amgen, BMS, Boehringer, Celgene, Celltrion, Centocor, Chugai, Eli Lilly and Company, Medac, MSD (Schering Plough), Mundipharma, Novartis, Pfizer (Wyeth), Roche, Sanofi-Aventis, and UCB Pharma, Consultant of: Abbvie (Abbott), Amgen, BMS, Boehringer, Celgene, Celltrion, Centocor, Chugai, EBEWE Pharma, Eli Lilly and Company, Medac, MSD (Schering-Plough), Mundipharma, Novartis, Pfizer (Wyeth), Roche, Sanofi-Aventis, and UCB Pharma, Speakers bureau: Abbvie (Abbott), Amgen, BMS, Boehringer, Celgene, Celltrion, Centocor, Chugai, EBEWE Pharma, Eli Lilly and Company, Medac, MSD (Schering-Plough), Mundipharma, Novartis, Pfizer (Wyeth), Roche, Sanofi-Aventis, and UCB Pharma, Angela Zink Speakers bureau: AbbVie, Amgen, BMS, Gilead, Hexal, Janssen, Lilly, MSD, Pfizer, Roche, Sanofi-Aventis, UCB

DOI: 10.1136/annrheumdis-2020-eular.3171

Preclinical models of arthritis and bone disease

OP0239

WHY DOES ALCOHOL INHIBIT ARTHRITIS? - AN EXPLANATION OF THE MECHANISM OF ARTHRITIS INHIBITION BY ETHANOL

V. Azizov¹, M. V. Sokolova¹, K. Sarter¹, V. Temchura², U. Steffen (Née Harre)¹, M. Herrmann¹, G. Schett¹, M. Zaiss¹. ¹Department of Internal Medicine 3, Erlangen, Germany; ²Institute of Virology, Erlangen, Germany

Background: Alcohol consumption has emerged as consistent protective factor for the development of autoimmune diseases such as rheumatoid arthritis (RA). The underlying mechanism for this tolerance-inducing effect of alcohol, however, is unknown.

Objectives: To understand the anti-arthritogenic effect of alcohol

Methods: The immune-regulatory properties of alcohol consumption in vivo were tested in the collagen-induced arthritis (CIA) and serum-induced arthritis (SIA) model as well as after immunization with T cell-dependent (NP-CGG) and independent (TNP-FICOLL) antigens. Additional experiments in vivo experiments in these models were done with acetate- the metabolite of ethanol. The models were analysed for T-cell lineage and plasma cell differentiation, germinal centre formation and IgG levels and sialylation. Molecular expression of T follicular helper cell (TFH) activation such as IL-21, Bcl-6 and PD-1, as well as TFH: B cell conjugates were also assessed. Furthermore, TFH cells were generated in vitro, exposed to ethanol or acetate and tested for IL-21 production, PD1 expression and conjugate formation with B cells.

Results: Ethanol exposure significantly inhibited arthritis in the active adaptive immunity-driven model of arthritis (CIA) but not in the passive innate immunity-driven model (STA) suggesting that the immune suppressive effect of alcohol is based on interference of T- and B- cell activation. In line ethanol and even more its metabolite acetate, suppressed T cell dependent antibody formation after NP-CGG immunization, while T cell independent antibody formation after TNP-FICOLL immunization was not suppressed. Ethanol, as well as its metabolite acetate, specifically altered the functional state of T follicular helper (TFH) cells in vitro and in vivo, thereby exerting immune regulatory and tolerance-inducing properties. Alcohol-exposed mice showed reduced Bcl6 and PD-1 expression as well as interleukin (IL)-21 production by TFH cells, preventing proper spatial organization of TFH cells to form TFH: B cell conjugates in the germinal centre. This effect of alcohol on TFH cells was associated with impaired autoantibody formation, higher sialylation of autoantibodies and less arthritis. In addition, overexpression of IL-21 in vivo completely reversed the immune regulatory effects of alcohol.

Conclusion: In summary, these data provide a new mechanistic explanation for the immune regulatory and tolerance-inducing effect of alcohol consumption in arthritis.

Acknowledgments: Funded by DFG-FOR2886, DFG-CRC1181, Staedtler foundation, Johannes und Frieda Marohn-Stiftung, Else Kröner-Fresenius foundation, Interdisciplinary Centre for Clinical Research, Erlangen, BMBF-MAS-CARA, IMI funded project RTCure.

Disclosure of Interests: Vugar Azizov: None declared, Maria V Sokolova: None declared, Kerstin Sarter: None declared, Vladimir Temchura: None declared, Ulrike Steffen (née Harre): None declared, Martin Herrmann: None declared, Georg Schett Speakers bureau: AbbVie, BMS, Celgene, Janssen, Eli Lilly, Novartis, Roche and UCB, Mario Zaiss: None declared

DOI: 10.1136/annrheumdis-2020-eular.4116

OP0240

A MULTIMODAL MASS SPECTROMETRY APPROACH REVEALS SPECIFIC CARTILAGE MOLECULAR PROFILES ASSOCIATED TO TYPE 2 DIABETIC PATIENTS

M. Eveque¹, P. Emans², B. Claes¹, F. Bouwman³, R. M. A. Heeren¹, B. Cillero-Pastor¹. ¹Maastricht MultiModal Molecular Imaging (M4I) Institute, Division of Imaging Mass Spectrometry, Maastricht, Netherlands; ²Maastricht University Medical Center, Department of Orthopedic Surgery, Maastricht, Netherlands; ³Maastricht University Medical Center, Department of Human Biology, NUTRIM School of Nutrition and Translational Research in Metabolism, Maastricht, Netherlands

Background: Osteoarthritis (OA) is mainly characterized by the progressive deterioration of articular cartilage. Recent studies support that type 2 diabetes (TD2) is a risk factor to develop OA [1, 2]. However, the molecular cartilage profile of patients combining these two diseases remains unclear, and a better understanding of the different OA phenotypes should be considered for the development of personalized medicine.

Matrix-assisted laser desorption/ionization (MALDI) mass spectrometry imaging (MSI) is used to investigate the bimolecular distribution of proteins, lipids or metabolites through the *in-situ* analysis of tissue sections. Bottom-up proteomics focuses on the relative quantification of proteins. The combination of both technologies could be considered to reveal specific molecular profiles and help for patient classification.

Objectives: The main goal of this study is to apply a multimodal mass spectrometry approach on cartilage to reveal specific lipidomic and proteomic profiles associated to TD2 patients.

Methods: Human cartilages from OA (n_a=10) and OA/TD2 human patients (n_b=10) were obtained from donors undergoing total knee joint replacement. Cartilage punches of 8*8mm were sectioned at 12 µm thickness for MALDI-MSI and bottom-up proteomics.

For MALDI-MSI experiments (n_a=6; n_b=6), norharmane matrix was sprayed over the samples for the detection of lipids. Experiments were then performed in positive ion polarity at 50 µm of lateral resolution using a RapifleX MALDI