Objectives: This study aimed to analyse the development of damage and death in an inception cohort of SLE patients recruited within 1 year of diagnosis with up to 13 years of follow-up.

Methods: This was a prospective multi-centre longitudinal study in the UK of SLE patients recruited within 12 months of achieving 1997 ACR revised criteria for SLE. Data were collected on BILAG-2004, BILAG2004-Pregnancy Index (during pregnancy), SLICC/ACR DI (SDI), cumulative drug exposure and death at every visit. Information on cardiovascular risk factors and antiphospholipid syndrome status were also collected. This study ran from 1st January 2005 to 31st December 2017. Mortality and development of damage were analysed.

Results: There were 273 patients recruited (91.2% female, 59.3% Caucasian, 17.2% African/Caribbean, 17.2% South Asian) with mean age at recruitment of 38.5 years (SD 14.8). 97.8% had no damage at recruitment (2.2% had SDI score of 1). Median follow-up was 73.4 months (range: 1.8, 153.8) with total follow-up of 1767 patient-years.

There were 13 deaths (4.8%): 76.9% female, 84.6% Caucasian, 15.4% South Asian, mean age 62.6 years ($\pm$ SD 15.8) and mean disease duration 3 years ($\pm$ SD 1.8). Causes of death were cancer in 5 (38.5%), infection in 3 (23.1%), ischaemic heart disease in 1 (7.7%) and unknown in 4 (30.8%).

114 new damage items in 83 patients occurred during follow-up. The distribution of damage was musculoskeletal (21, 18.4%), ophthalmic (18, 15.8%), neuropsychiatric (18, 15.8%), renal (14, 12.3%), malignancy (12, 10.5%), cutaneous (7, 6.1%), GIT (7, 6.1%), cardiac (6, 5.3%), pulmonary (4, 3.5%), diabetes mellitus (4, 3.5%) and vascular (3, 2.6%). The rate of development of damage appears to be higher in the first 3 years which subsequently stabilised (Table 1).

Table 1. Incidence rate of development of damage over period of follow-up at 3 yearly intervals

Period of follow-up (year)	Person-years at risk	Number of new items of damage	Incidence rate, per 1000 person-years (95% CI)
0 – 3	753.4	60	79.6 (61.8, 102.6)
3 – 6	534.0	31	58.1 (40.8, 82.6)
6 – 9	321.2	12	37.4 (21.2, 35.8)
9 – 12	152.5	5	32.8 (13.6, 78.7)
> 12	5.9	0	-

Conclusion: Mortality is uncommon during the first 12 years of follow-up for newly diagnosed SLE patients. However, development of damage appears to be higher in the first 3 years before stabilizing to a lower rate subsequently.

Acknowledgements: Versus Arthritis, Vifor Pharma

Disclosure of Interests: Chee-Seng Yee Consultant of: Bristol Myer Squibb, ImmuPharma, Grant/research support from: Vifor Pharma, Vernon Farewell: None declared, Mohammed Akil: None declared, Peter Lanyon: None declared, Christopher John Edwards Consultant of: Glaxo Smith Kline, Roche, Grant/research support from: Glaxo Smith Kline, Roche, David Isenberg: None declared, Anisur Rahman: None declared, Lee-Suan Teh: None declared, Sofia Tosounidou: None declared, Robert Stevens: None declared, Ahtiveer Prabu: None declared, Bridget Griffiths: None declared, Neil McHugh: None declared, Ian N. Bruce: None declared, Yasmeen Ahmad: None declared, Munther Khamashta: None declared, Caroline Gordon Speakers bureau: UCB, Consultant of: Center for Disease Control, Astra-Zeneca, MGP, Sanofi and UCB

DOI: 10.1136/annrheumdis-2021-eular.8

Translating vasculitis

POS0112 CD8+ T-CELL INFILTRATION IS ASSOCIATED WITH LESIONAL GM-CSF OVEREXPRESSION IN GCA

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Background: Giant cell arteritis (GCA) is a large-vessel vasculitis characterized by granulomatous T cell- and macrophage infiltration. Granulocyte-macrophage colony stimulating factor (GM-CSF) is present in GCA-affected vessels where it may be involved in skewing of tissue destructive macrophages (1). Furthermore, a recent phase 2 clinical trial demonstrated that GM-CSF receptor blockade was superior to placebo at 26 weeks in GCA. However, the cellular source of GM-CSF in GCA is still unclear.

Objectives: As T cells have been identified as a major source of GM-CSF in other immune-mediated diseases such as multiple sclerosis, we investigated whether T cells are GM-CSF producers in GCA patients, both systemically and locally.

Methods: GM-CSF production capacity by PMA-stimulated PBMCs from newly diagnosed, untreated GCA patients and HCs (N=10 each) was assessed using flow cytometry. Temporal artery biopsies (TABs, N=5) were immunohistochemically stained for CD3, CD8 and GM-CSF. Colocalization of these markers was assessed with immunofluorescence.

Results: Proportions of CD4+ (median GCA=3.1%; HCs=2.76%) and CD8+ (median GCA=5.8%; HCs=5.8%) T cells produced GM-CSF after *in vitro* stimulation, but no significant differences were found between the groups. Immunofluorescence staining confirmed that CD3+ T cells (both CD8+ and CD8-) were positive for GM-CSF in TABs. Interestingly, GM-CSF positivity in TABs correlated strongly with the extent of CD8+ T-cell infiltration ($r=0.74$, $p<0.01$), but not with CD3+ T-cell infiltration ($r=0.38$, $p=0.16$).

Conclusion: Our data imply that T cells are an important source of GM-CSF in GCA lesions. The correlation of the extent of CD8+ T-cell infiltration with GM-CSF positivity suggests that CD8+ T cells are the major source of local GM-CSF overexpression in tissue.

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Disclosure of Interests: William Febry Jiemy: None declared, Rosanne Reitsem: None declared, Ayla Kwant: None declared, Wayel Abdulahad: None declared, Annemieke Boots Consultant of: Grünenthal GmbH until 2017, Peter Heeringa: None declared, Elisabeth Brouwer Speakers bureau: Roche, paid to the UMCG

DOI: 10.1136/annrheumdis-2021-eular.1899

POS0113 BAFF-APRIL-BAFFR PATHWAY ON THE PATHOGENESIS OF IMMUNOGLOBULIN-A VASCULITIS

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Background: BAFF, APRIL and BAFFR are genes that encode cytokines with a key role in the development and survival of B-lymphocytes [1-4]. The B cell-activating factor (BAFF, also known as BlyS), a proliferation-inducing ligand (APRIL) and BAFF receptor (BAFFR), respectively. Previous genetic studies have revealed that the BAFF-APRIL-BAFFR pathway is implicated in the genetic predisposition to several immune-mediated diseases [5].

Objectives: To determine whether the BAFF-APRIL-BAFFR pathway represents a novel genetic risk factor for the pathogenesis of Immunoglobulin-A vasculitis (IgAV), an inflammatory disease in which IgA deposits and B-lymphocytes are crucial [6, 7].

Methods: A functional BAFF polymorphism (rs374039502) and two tag variants within APRIL (rs11552708 and rs6608) and BAFFR (rs7290134 and rs77874543)

were genotyped in 386 Caucasian IgAV patients (the largest series of Caucasian patients with IgAV ever assessed for genetic studies) and 806 sex and ethnically matched healthy controls by TaqMan assays.

Results: No statistically significant differences in the genotype and allele frequencies between patients with IgAV and healthy controls were observed when each genetic variant of *BAFF APRIL* and *BAFFR* was analyzed independently (Table 1). Likewise, no statistically significant differences in genotype and allele frequencies of *BAFF APRIL* or *BAFFR* were found when patients with IgAV were stratified according to the age at disease onset or to the presence/absence of gastrointestinal or renal manifestations. Similar results were disclosed when haplotype frequencies of *APRIL* and *BAFFR* were compared between patients with IgAV and healthy controls as well as patients with IgAV stratified according to the age at disease onset or to the presence/absence of gastrointestinal or renal manifestations.

Conclusion: Our results suggest that the *BAFF-APRIL-BAFFR* pathway does not contribute to the genetic network underlying IgAV.

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Table 1. Genotype and allele frequencies of *BAFF*, *APRIL* and *BAFFR* genes in patients with IgA vasculitis and healthy controls.

Polymorphism	Locus	1/2	Data set	1/1	1/2	2/2	1	2
rs374039502	BAFF	T/A	Patients	91.9 (353)	8.1 (31)	0	95.9 (737)	4.1 (31)
			Controls	91.5 (733)	8.1 (65)	0.4 (3)	95.6 (1531)	4.4 (71)
rs11552708	APRIL	G/A	Patients	78.1 (299)	20.6 (79)	1.3 (5)	88.4 (677)	11.6 (89)
			Controls	77.9 (625)	20.4 (164)	1.6 (13)	88.1 (1414)	11.9 (190)
rs6608	APRIL	C/T	Patients	71.9 (277)	26.0 (100)	2.1 (8)	84.9 (654)	15.1 (116)
			Controls	70.0 (561)	27.6 (221)	2.5 (20)	83.7 (1343)	16.3 (261)
rs7290134	BAFFR	A/G	Patients	58.0 (224)	36.3 (140)	5.7 (22)	76.2 (588)	23.8 (184)
			Controls	57.2 (459)	36.4 (292)	6.5 (52)	75.3 (1210)	24.6 (396)
rs77874543	BAFFR	G/C	Patients	82.7 (316)	16.0 (61)	1.3 (5)	90.7 (693)	9.3 (71)
			Controls	83.0 (666)	16.6 (133)	0.4 (3)	91.3 (1465)	8.7 (139)

Acknowledgements: This study was supported by European Union FEDER funds and "Fondo de Investigaciones Sanitarias" (grant PI18/00042) from 'Instituto de Salud Carlos III' (ISCIII, Health Ministry, Spain). DP-P is a recipient of a Río Hortega programme fellowship from the ISCIII, co-funded by the European Social Fund (ESF, 'Investing in your future') [grant number CM20/00006]; SR-M is supported by funds of the RETICS Program co-funded by the European Regional Development Fund (ERDF) [grant number RD16/0012/0009]; VP-C is supported by a pre-doctoral grant from IDIVAL [grant number PREVAL 18/01]; BA-M is a recipient of a 'López Albo' Post-Residency Programme funded by Servicio Cántabro de Salud; LL-G is supported by funds of IDIVAL [grant number INNVAL20/06]; RL-M is a recipient of a Miguel Servet type I programme fellowship from the ISCIII, co-funded by the European Social Fund (ESF, 'Investing in your future') [grant number CP16/00033].

Disclosure of Interests: Diana Prieto-Peña Speakers bureau: Abbvie, Pfizer, Roche, Bristol-Myers, Janssen and MSD, Consultant of: Abbvie, Pfizer, Roche, Bristol-Myers, Janssen and MSD, Grant/research support from: Abbvie, MSD and Roche, Sara Remuzgo Martínez: None declared, Fernanda Gené: None declared, Verónica Pulito-Cueto: None declared, Belén Atienza-Mateo: None declared, Belén Sevilla: None declared, Javier Llorca: None declared, Norberto Ortego: None declared, Leticia Lera-Gómez: None declared, Maite Leonardo: None declared, Ana Peñalba: None declared, J. Narváez: None declared, Luis Martín-Penagos: None declared, Jose Alberto Miranda-Fillooy: None declared, LUIS CAMINAL MONTERO: None declared, PAZ COLLADO: None declared, Javier Sanchez Perez: None declared, Diego de Argila: None declared, Esteban Rubio-Romero: None declared, MANUEL LEON LUQUE: None declared, Juan María Blanco-Madriral: None declared, E. Galindez: None declared, Javier Martín Ibanez: None declared, Santos Castañeda: None declared, Ricardo Blanco Speakers bureau: Abbvie, Pfizer, Roche, Bristol-Myers, Janssen and MSD, Consultant of: Abbvie, Pfizer, Roche, Bristol-Myers, Janssen and MSD, Grant/research support from: Abbvie, MSD and Roche, Miguel A González-Gay Speakers bureau: Pfizer, Abbvie, MSD, Grant/research support from: Pfizer, Abbvie, MSD, Raquel López-Mejías: None declared

DOI: 10.1136/annrheumdis-2021-eular.707

POS0114 ABERRANT MONOCYTE SUBSETS IN PATIENTS WITH BECHET'S DISEASE

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Background: Behçet's Disease (BD) is a systemic vasculitis of unknown etiology[1]. Monocytes closely related to inflammation potentially contribute to BD's pathogenesis. They are classified into three subsets: classical monocytes (CM), intermediate monocytes (IM) and non-classical monocytes (NCM). Abnormalities of monocyte subsets have been reported in many infectious, inflammatory and autoimmune diseases[2-6], but their implication in BD remains elusive.

Objectives: To investigate the distribution, phenotypes and functions of monocyte subsets in BD and explore their roles in BD pathogenesis.

Methods: The frequencies and phenotypes of monocyte subsets in BD and healthy controls (HC) were determined by flow cytometry, and their correlation with clinical parameters was analyzed. Intracellular cytokines and phosphorylated signal proteins [phosphorylated p65(p-p65) and phosphorylated p38(p-p38)] were determined in LPS-activated monocyte subsets by flow cytometry. Monocyte subsets of BD and HC were sorted and co-cultured with naïve CD4 + T cells, and Th1 cell frequencies were measured on day 5.

Results: A higher IM (9.0±3.6% vs. 4.5±2.0%, p<0.01) and lower NCM (2.6±1.2% vs. 4.2±2.0%, p<0.01) population in BD patients were noted. BD IM were positively correlated with CRP (r=0.5456, p<0.05), ESR (r=0.4683, p=0.05), and the serum level of TNF-α (r=0.7372, p<0.001) and IL-6 (r=0.5013, p<0.05). BD NCM were negatively correlated with CRP (r=0.4822, p<0.05) and the serum level of IgM (r=-0.7830, p<0.001). Moreover, BD IM decreased (12.3±3.8% vs. 5.7±3.6%, p<0.05), while BD NCM increased (2.6±1.3% vs. 3.5±1.5%, p<0.01) after BD patients achieved remission. CD11b and CD64 expression on CM, IM and NCM in BD were enhanced. BD CM promoted TNF-α (61.0±11.4% vs 48.3±9.9%, p<0.05) and IL-6 (7.2±5.4% vs 1.9±1.7%, p<0.05) production and facilitated Th1 differentiation. BD IM promoted IL-6 production (6.2±3.8% vs 2.6±1.6%, p<0.05). Furthermore, we demonstrated a higher level of p-p65 (12.8±2.9% vs 3.3±1.1%, p<0.01) in BD CM and increased p-p65 (3.2±0.6% vs 0.01±0.01%, p<0.01) and p-p38 (1.1±0.6% vs 0.03±0.01%, p<0.01) in BD IM.

Conclusion: To our knowledge, our study is the first study on monocyte subsets in BD. Our data highlighted the aberrant populations of IM and CM in BD, potentially implicated in BD pathogenesis.

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Disclosure of Interests: None declared

DOI: 10.1136/annrheumdis-2021-eular.1157

POS0115 RISK FACTORS FOR CORONARY HEART DISEASE AND ATHEROSCLEROSIS IN PATIENTS WITH BECHET'S DISEASE

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Background:

Objectives: To evaluate traditional risk factors for clinically manifest and asymptomatic atherosclerosis in pts with BD.

Methods: Traditional risk factors for atherosclerosis were evaluated in 95 pts with Bechet's disease (BD) and 40 healthy age and gender matched controls. The male-to-female ratio was 3.7:1, pts' mean age was 29.7 (23-35) y, the mean age at the disease onset - 19.9 (14-25) y, and mean disease duration - 9.6 (4-15) y. The common carotid artery intima-media thickness (IMT) was evaluated by high resolution B-mode ultrasonography. A plaque was defined as a local intima-media thickening ≥1.2mm, with reference IMT thickness <0.9mm. Serum concentration of high-sensitivity C-reactive protein (hs CRP) was measured by immunonephelometric assay (BN-100 Analyzer; Dade Behring). Lipid profile evaluation included total cholesterol, TGs, HDL, LDL and atherogenic index.

Results: Traditional risk factors for atherosclerosis (one or more) were found in 85.3% of BD pts, dyslipidemia was the most common risk factor and was present in 76.84% of pts, mostly due to increased total cholesterol (TC) and