regulated and involves numerous factors, including calcium deposal and other bone remodelling factors.²

Objectives: The objective of this study was to find a signature of miRs linked both to osteoporotic fracture risk and abdominal aortic calcification (AAC).

The first outcome was the link between miRs levels at baseline and incident osteoporotic fractures (IOF) during 20 years; the second outcome was the link between miRs levels at baseline and the increase in AAC during 17 years.

Methods: Post-menopausal women older than 50 years from the OFELY cohort (Os des Femmes de LYon) were selected if they had available serums at inclusion, and available data for each outcome.

3 miRs selected after literature review because of their impact on vascular calcification and bone turnover (miRs 26a-5p, 34a-5p, and 223-5 p) were measured at baseline. Bioassays of miRs was conducted with miRCURY Biofluids (Exiqon) extraction kit, TaqMan Life Technologies protocol, and QuantStudio 7 flex (Applied Biosystems) for RNA quantification. Results are expressed by relative quantification of Cycle threshold (Ct).

Results: A sample of 434 age-matched women (63 [57–72] years old), 50% with incident osteoporotic fracture during the 20 years of follow-up, was included. 183 women had available data to explore AAC; 93 had an increase in Kauppila score in 17 years (58 [55–61] years old), 90 did not (55 [53–58] years old).

No significant link was underlined between miRs and IOF (miR-26: 1.06 [0.85–1.27] vs 0.99 [0.85–1.17], $p=0.07$; miR-34: 1.15 [0.53–1.87] vs 1.26 [0.60–2.07], $p=0.35$; miR-223: 1.01 [0.68–1.43] vs 1.05 [0.72–1.56], $p=0.32$).

No miR was significantly linked to an increase in AAC (miR-26: 1.09 [0.94–1.28] vs 1.10 [0.89–1.30], $p=0.95$; miR-34: 0.78 [0.46–1.21] vs 0.73 [0.38–1.50], $p=0.90$; miR-223: 0.97 [0.69–1.22] vs 0.78 [0.56–1.22], $p=0.11$).

Conclusions: No association was observed between the 3 tested miRs and IOF or increase in AAC. Larger studies are necessary to select interesting epigenetic pathways reproducible on wider population.

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Disclosure of Interest: None declared

DOI: 10.1136/annrheumdis-2018-eular.5792

AB0009 GENETIC ASSOCIATION OF MITOCHONDRIAL DNA POLYMORPHISMS WITH BEHÇET'S DISEASE IN A KOREAN POPULATION

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Background: Behcet's disease (BD) is an inflammatory multi-genetic disorder with unknown etiology. In the previous study, we sequenced whole mitochondrial nucleotides from blood of 20 BD patients and 10 sex-, age-matched healthy controls, m.248A>G, m.709G>A, m.3970C>T, m.6392T>C, m.6962G>A, m.10310G>A, m.10609T>C, m.12406G>A, m.12882C>T, m.13928G>C, m.16129G>A, and m.16304T>C were more frequently observed in patients group than healthy control without statistical significance. While, m.304C>A, m.3010G>A, m.4883C>T, m.5178C>A, and m.14668C>T were more frequent in control group ($p=0.008$, 0.026, 0.007, 0.007, and 0.026, respectively). m.16182A>C, m.16183A>C, m.16189T>C were associated with uveitis ($p=0.041$, 0.022, and 0.014, respectively).

Objectives: We performed a follow-up study to validate these possible associations in larger groups.

Methods: Whole blood or buffy coat were collected from 98 BD patients from four university hospitals located in Chung-Cheong district of Republic of Korea, 196 age-, sex-matched healthy controls from Konyang University Hospital. Above mentioned 20 targeted mitochondrial DNA (mtDNA) genomes were analysed using MassARRAY[®] system (Agena Bioscience, Inc., San Diego, CA, USA) for m.709, m.3010, m.4883, m.6392, m.6962, m.10310, m.10609, m.12406, m.12882, m.13928, and m.14668; Sanger sequencing for m.248, m.304, m.5178, m.16129, m.16182, m.16183, m.16189, and m.16304; and TaqMan-based genotyping assay (Applied Biosystems, Foster City, CA, USA) for m.3970. Results were compared with the revised Cambridge Reference Sequence (rCRS). Chi square or Fisher's exact test were used to analyse association of mtDNA

alterations between groups and between mtDNA alterations and clinical/laboratory characteristics.

Results: Presence of m.248A>G, m.304C>A, m.709G>A, m.3010G>A, m.3970C>T, m.4883C>T, m.5178C>A, m.6392T>C, m.6962G>A, m.10310G>A, m.10609T>C, m.12406G>A, m.12882C>T, m.13928G>C, m.14668C>T, m.16129G>A, and m.16304T>C were not differentiated by the groups. However, m.16812A>C was more frequently observed in the patient group than control [22 (22.4%) vs. 24 (12.2%), $p=0.061$], and it was significantly associated with HLA-B51 positivity ($p=0.011$), arthralgia ($p=0.043$) and methotrexate use ($p=0.02$), and was not associated with uveitis in the follow-up study. Among clinical and laboratory characteristics in BD patients, thrombosis was more frequently observed in male patients than female patients [7 (22.6%) vs. 0 (0%), $p<0.001$], and WBC counts were lower in female patients [3642.3±3413.6 vs. 5200.8±3912.7, $p=0.048$].

Abstract AB0009 – Table 1

RCRS position	Alteration	BD (n=98)	HC (n=196)	p-value	OR* (95% CI)
248	A del	12 (12.2%)	23 (11.7%)	1.000	1.050 (0.499–2.209)
304	C>A	0 (0%)	0 (0%)	NA	NA
709	G>A	24 (24.5%)	35 (17.9%)	0.236	1.492 (0.929–2.686)
3010	G>A	19 (19.4%)	50 (25.5%)	0.307	0.702 (0.387–1.273)
3970	T>C	14 (14.3%)	19 (9.7%)	0.327	1.553 (0.743–3.246)
4883	C>T	25 (25.5%)	59 (30.1%)	0.494	0.795 (0.460–1.374)
5178	C>A	25 (25.5%)	59 (30.1%)	0.494	0.795 (0.460–1.374)
6392	T>C	14 (14.3%)	19 (9.7%)	0.327	1.553 (0.743–3.246)
6962	G>A	12 (12.2%)	18 (9.2%)	0.540	1.380 (0.636–2.993)
10310	G>A	16 (16.3%)	24 (12.2%)	0.434	1.398 (0.705–2.774)
10609	T>C	12 (12.2%)	16 (8.2%)	0.361	1.570 (0.711–3.463)
12406	G>A	12 (12.2%)	17 (8.7%)	0.447	1.469 (0.672–3.213)
12882	C>T	12 (12.2%)	16 (8.2%)	0.361	1.570 (0.711–3.463)
13928	G>C	14 (14.3%)	19 (9.7%)	0.327	1.553 (0.743–3.246)
14668	C>T	19 (19.4%)	49 (25.0%)	0.353	0.722 (0.398–1.310)
16129	G>A	23 (23.5%)	42 (21.4%)	0.804	1.124 (0.631–2.005)
16182	A>C	22 (22.4%)	24 (12.2%)	0.061	2.062 (1.089–3.906)
16183	A>C	32 (32.7%)	42 (21.4%)	0.092	1.766 (1.026–3.040)
16189	T>C	42 (42.9%)	64 (32.7%)	0.112	1.547 (0.939–2.548)
16304	T>C	15 (15.3%)	18 (9.2%)	0.170	1.787 (0.859–3.720)

Conclusions: We performed a follow-up study to validate possible associations between BD and 20 mtDNA alterations. m.16812A>C could be associated with BD and its several clinical or laboratory characteristics a Korean population.

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Acknowledgements: The current study was supported by the National Research Foundation of Korea funded by the Korean Government (grant no. NRF-2017R1C1B2008199).

Disclosure of Interest: None declared

DOI: 10.1136/annrheumdis-2018-eular.1714

AB0010 EVALUATION OF SENSITIVITY TO DNA DAMAGING AGENTS AND EFFICIENCY OF DNA REPAIR IN HUMAN PERIPHERAL BLOOD MONONUCLEAR CELLS FROM PATIENTS WITH DERMATOMYOSITIS AND POLYMYOSITIS

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Background: Idiopathic inflammatory myopathies (IIM) being one of the connective tissue diseases are a group of diseases with not fully understood pathology. The common features are production of autoantibodies, abnormal immune response against self-antigens and inflammatory process leading to destruction of muscle cells and internal organ involvement. Patients with inflammatory myopathies have higher risk of developing cancers. One of the processes that can

attribute to increased risk of cancers can be genomic instability and impaired DNA repair.

Objectives: The aim of the study was to assess the processes of endogenous and exogenous DNA damage and its repair in patients with IIM as compared to healthy controls.

Methods: The study included 10 patients (9 men and 1 woman, mean age 46.6 ±16.5) with idiopathic inflammatory myopathies (dermatomyositis or polymyositis) as well as 7 healthy control individuals (4 men and 3 women, mean age 33.8±9.8). DNA damage and repair were investigated by the comet assay. To perform the comet assay human peripheral blood mononuclear cells (PBMCs) were isolated and incubated with tert-butyl hydroperoxide (t-BOOH) or bleomycin. Both compounds are common DNA damaging agents – t-BOOH induces oxidative DNA lesions whereas bleomycin induces also DNA double strand breaks (DSBs). To test the DNA repair capability, PBMCs were allowed to recover for 2 hour. The level of endogenous DNA lesions was also investigated.

Results: The levels of endogenous DNA damage were not statistically significantly different between tested groups (IIM-3.3±3.6% vs 3.2±3.8% in control; $p=0.648$). The extent of the DNA damage induced by bleomycin (IIM-23.3 ±19.5% vs 9.8±5.9% in control) as well as oxidative stress (IIM-14.7±16.2% vs 10.4±7.4% in control) was significantly higher in PBMCs derived from IIM patients than in healthy counterparts ($p<0.001$). Kinetic curves of DNA repair are different but the background mechanism underlying observed differences in the repair curve between healthy subjects and patients need to be evaluated further.

Conclusions: Understanding the etiology of this phenomena in these diseases may provide insight into disease pathogenesis and explain the increased susceptibility of patients to malignancies. Finding the patients with increased DNA instability could potentially serve as a biomarker and indicate the group of patients who should be carefully screened for neoplastic disorder.

Disclosure of Interest: None declared

DOI: 10.1136/annrheumdis-2018-eular.5973

AB0011 EVALUATION OF SALIVARY MIRNAS IN PATIENTS AFFECTED BY SJÖGREN'S SYNDROME AND CORRELATION WITH CLINICAL AND ULTRASONOGRAPHIC OUTCOMES

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Background: It has been demonstrated that miRNAs expressed in PBMCs and salivary glands of patients affected by Sjögren's Syndrome (SS) could be involved in the epigenetic control of the disease.

Objectives: We aimed to compare the concentration of miRNA-146a/b, 16, 17–92 cluster and 181a in salivary and plasmatic samples collected from SS patients and healthy controls and to evaluate the associations with clinical, laboratory and ultrasound findings.

Methods: We collected plasmatic and salivary samples from 28 patients (27 females, mean age 64.4±10.1 years, mean disease duration 10.7±6.9 years) affected by primitive SS according to ACR 2012 and/or 2016 criteria and 23 matched healthy controls. In the group of patients, the following data were recorded: ESS-DAI and ESSPRI scores, anti-SSA and anti-SSB status and laboratory data, Schirmer's test, ultrasound scores of the four major salivary glands according to Cornec et al. and concomitant treatments. The following miRNA were extracted, retro-transcribed and quantified: miR16–5 p, miR17–5 p, miR18a–5p, miR19a–5p, miR19b–1–5 p, miR20a, miR92–5 p, miR146a–5p, miR146b–5p, miR181a–5p.

Results: The concentration of miRNAs evaluated in plasma and saliva did not significantly match both in patients and in controls, underlining a different modulation in their expression according to the corporeal district. In patients and controls miRNAs16, 17 and 20 were hyper-expressed and miRNA146b and 181 hypo-expressed in salivary samples compared to plasmatic ones. Salivary miRNAs 18a and 146a were hyper-expressed in patients and hypo-expressed in controls, when compared to plasmatic concentrations.

Comparing salivary and plasmatic patients' miRNAs concentrations to those of healthy subjects, plasmatic miRNA16 and 181a were significantly more expressed in patients than in controls (two-tailed Wilcoxon test and Student's T test for unpaired samples).

In SS patients, salivary miRNA 181 and 146a were significantly increased in older subjects ($p=0.01$ and $p=0.04$ respectively). Spearman's correlation revealed that salivary miRNA146b was significantly hyper-expressed in patients with worse ESSPRI scores ($p=0.02$); on the contrary, salivary miRNA17, 146b and plasmatic miRNA17 were reduced in patients with higher scores at ultrasound evaluation ($p=0.01$, $p=0.01$ and $p=0.04$ respectively). Plasmatic concentration of miRNA18a was increased in patients with less lachrymal production at Schirmer's test ($p=0.01$) and plasmatic concentration of miRNA17 was reduced in patients with

higher ESR values ($p=0.01$). Salivary miRNA18a was significantly increased in patients with anti-La/SSB ($p=0.04$; Mann-Whitney U test for unpaired samples). Salivary and plasmatic miRNAs did not correlate with disease duration and concomitant therapies.

Conclusions: Our data show that the expression of salivary miRNAs 17, 18a and 146b may be altered in SS patients and associated with worse ultrasound and ESSPRI scores and anti-La/SSB positivity.

Disclosure of Interest: None declared

DOI: 10.1136/annrheumdis-2018-eular.4876

AB0012 ALLELE AND GENOTYPE FREQUENCY OF SOME GENE POLYMORPHISMS DIFFERS IN VARIOUS JUVENILE IDIOPATHIC ARTHRITIS SUBTYPES

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Background: In spite of the fact that chronic arthritis has been the core of paediatric rheumatology, etiology and pathogenesis of juvenile idiopathic arthritis (JIA) are still unclear. It is important to ascertain genetic nature of such a heterogeneous disease.

Objectives: The aim of the study was to assess the role of some SNPs of six genes implicated in immune and inflammatory responses: *TNFA* (rs1800629, rs361525), *PTPN22* (rs2476601), *MIF* (rs755622, rs5844572), *TRAF/C5* (rs3761847), *CTLA4* (rs5742909, rs231775), *STAT4* (rs7574865); as well as homozygous deletions of xenobiotic biotransformation genes *GSTT1* and *GSTM1*.

Methods: 206 patients diagnosed with JIA (mean age 8.87±4.92), and 218 hospital controls with no signs of autoimmune or inflammatory diseases (mean age 13.88±2.72) were recruited for the study. The JIA patients were divided into subgroups according to IAR classification criteria; the majority of them (125 patients) had oligoarthritis, 42 children developed RF-negative polyarthritis and 27 patients were diagnosed with systemic arthritis. Genomic DNA was extracted from peripheral blood samples by means of the phenol-chloroform method. SNPs were genotyped using PCR-RFLP, Real-Time PCR or fragmental analysis.

Results: The allele frequencies for all SNPs in the hospital control group were similar to those in European populations. The allele and genotype frequency distribution for all SNPs was identical in patients and controls. However, when comparing distinct subtypes of JIA, *STAT4* polymorphism demonstrated higher frequencies of minor T allele (30.5% vs. 17.8%, $p=0.01$, OR=2.03, 95% CI [1.14–3.6] and G/T genotype (46.3% vs. 25.6%, $p=0.03$, OR=2.51, 95% CI [1.2–5.24]) in RF-negative polyarthritis than in oligoarthritis. On the contrary, Δ *GSTT1* appeared to prevail in oligoarthritis (23.7% vs. 7.9% in RF-negative polyarthritis, $p=0.03$, OR=3.6, 95% CI [1.03–12.7]). As to systemic arthritis, it was shown, that minor G allele of *TRAF/C5* was more frequent in comparison with oligoarthritis ($p=0.037$, OR=2.43, 95% CI [1.05–5.6]).

Conclusions: The results obtained can be considered as evidence for distinct genetic nature of the different JIA subtypes.

Disclosure of Interest: None declared

DOI: 10.1136/annrheumdis-2018-eular.5087

AB0013 EXPRESSION LEVELS OF MIR-124 IN THE PLASMA OF RHEUMATOID ARTHRITIS PATIENTS

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Background: Micro-ribonucleic acids (microRNAs) comprise a class of small non-coding RNAs that regulate gene expression on post transcriptional level. Levels of miR-124 have been found to be decreased in rheumatoid arthritis (RA) synoviocytes and *in vivo* studies have shown that treatment with pre-miR-124 suppresses the progression of joint damage¹.

Objectives: To evaluate the expression levels of miR-124–3 p in plasma of RA patients and to determine its possible role as biomarker for diagnosis and disease activity.

Methods: 34 RA patients according to the 1987 ACR criteria were included in the study. Expression levels of miR-124–3 p in the plasma were determined by PCR