cells. In PDT, a light-sensitive molecule is delivered to a target cell and activated with light of a specific wavelength. This causes cell death through the production of reactive oxygen species.

Methods The anti-FAP antibody 28 H1 was conjugated with the photosensitizer IRDye700DX (28H1-700DX). *In vitro* PDT assays were performed with 3 T3 fibroblasts stably transfected with FAP. 3T3-FAP cells were incubated with 28H1-700DX or a control conjugate for 4 hours, and exposed to varying 690 nm light doses. Subsequently, cell viability was measured using the CellTiter-Glo assay. For *in vivo* biodistribution, 5 days after onset of antigen-induced arthritis (AIA) C57Bl6 mice were injected with 28H1±700 DX labelled with radioactive Indium for quantification purposes (expressed as% injected dose per gram tissue (%ID/g)). For the PDT treatment experiment, arthritic mice were injected at day 5 of AIA with 28H1-700DX or PBS and exposed to 50 or 90 J/cm^2 light 24 hours post injection. Joints were isolated at day 10 for histological analysis.

Results To assess PDT efficacy, we applied 13.7 J/cm2 light exposure to 3T3-FAP cells incubated with 6.67 pM 28H1-700DX, which significantly reduced cell viability (89.27% ±2.48 compared to control ($p<0.001$)). No cell death was observed with the control 700DX-conjugate.

Conjugating the anti-FAP antibody to 700DX changed the *in vivo* biodistribution of the antibody, with a higher accumulation in the liver (27,06±0,95%ID/g vs. 6,08±0,42%ID/g with control ($p<0,001$)) and lower blood levels (5,32±0,36% ID/g vs. 12,72±0,80%ID/g with control ($p<0,001$)). Accumulation in the arthritic joints was not significantly different. Histological analysis of the PDT-treated mouse knee joints is ongoing.

Conclusions We have demonstrated fibroblast-specific cell death using 700DX-conjugated 28 H1 PDT, indicating FAP-based PDT as a promising new tool in treating RA. Furthermore, we demonstrated that adding 700DX results in faster liver clearance of the antibody, but does not affect uptake in the inflamed knee joint. Future research will further elucidate the applicability of our conjugate for PDT in animal models of RA.

Disclosure of interest None declared

P108 EXPLORING THE MOLECULAR BASIS OF GENDER BIAS IN SYSTEMIC LUPUS ERYTHEMATOSUS (SLE)

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Background/objectives SLE features a substantially greater frequency in females than in males (ratio ranging 7:1–15:1). By contrast, males tend to suffer from more severe disease.[1–3] Understanding the molecular basis of SLE variability and sexual dimorphism may advance our understanding of disease pathogenesis and assist the development of personalized treatments. We performed full transcriptome analysis (RNA-seq) to monitor for differentially expressed genes (DEGs) between male and female SLE patients that are not differentially expressed between male and female healthy subjects, thus identifying a gender-biased molecular signature specific for the disease.

Materials and methods Whole blood RNA was extracted from SLE patients and healthy individuals. Paired-end mRNA sequencing was performed using the Illumina HiSeq2000 platform. A list of DEGs in SLE males versus females were generated using 5% false discovery rate (FDR). To increase the specificity of our results, we generated a similar list of DEGs in healthy males versus females using a 50% and 90% FDR cut-off, and the two lists were intersected.

Results We studied 142 SLE patients with diverse levels of disease activity/severity (120 SLE females, 22 SLE males) compared to 58 matched healthy volunteers (48 healthy females, 10 healthy males). We identified 39 genes which were significantly differentially expressed in SLE males versus females. Notably, 6 of these genes were not differentially expressed in healthy males versus females at either 50 or 90% FDR, highlighting a potential role in disease sexual dimorphism. The proteins encoded by these genes are implicated in various biological processes such as transcriptional regulation and DNA damage repair (SMC1A), lipoprotein particles catabolism (APOE), glutathione biosynthesis and metabolism (OPLAH), correct composition of bone and cartilage matrix (ARSD), whereas 2 of these genes do not code for proteins (MTCO2 and FRG1B). Further validation of these genes is in progress.

Conclusions A gender-biased molecular signature specifically associated with SLE was unraveled. Further investigation of the molecular pathways which are associated with these genes will give us insights for the molecular basis of gender bias in SLE and lead to novel, more effective treatments tailored for male and female patients.

REFERENCES

1. Margery-Muir AA, *et al*. Gender balance in patients with systemic lupus erythematosus. *Autoimmun Rev* 2017;16(3):258–268.
2. Boodhoo KD, Liu S, Zuo X. Impact of sex disparities on the clinical manifestations in patients with systemic lupus erythematosus: A systematic review and meta-analysis. *Medicine (Baltimore)* 2016;95(29):e4272.
3. Gergianaki I, *et al*. Epidemiology and burden of systemic lupus erythematosus in a Southern European population: Data from the community-based lupus registry of Crete, Greece. *Ann Rheum Dis* 2017.

P109 CLINICAL DEVELOPMENT OF A NOVEL STRATEGY TO MITIGATE BIOLOGIC IMMUNOGENICITY: MONTHLY DOSING OF A PEGYLATED URICASE WITH SVP-R ENABLES SUSTAINED REDUCTION OF SERUM URIC ACID (SUA) LEVELS BY MITIGATING FORMATION OF ANTI-DRUG ANTIBODIES (ADAS)

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Introduction Pegylated uricases are a promising but highly immunogenic therapy for severe gout. Preclinical studies have shown the ability of synthetic vaccine particles containing rapamycin (SVP-R) to inhibit the formation of ADAs against pegsiticase, a pegylated uricase.[1] Here we report initial data on the safety, immunogenicity and activity of an ongoing Phase 2 study of SEL-212, a novel combination therapy consisting of pegsiticase and SVP-R.

Objectives Evaluate the ability of monthly doses of SEL-212 to mitigate the immunogenicity of pegsiticase and enable sustained control of sUA in gout patients.