weightlessness in the water. The warmer pool temperature was stated as a reason for the benefits obtained.

Reported benefits of hydrotherapy are illustrated in graph 1:

Conclusions: This survey suggests variability in utilisation of hospital hydrotherapy services by a national AS patient group in the UK, with barriers to access, lack of promotion and pool closures. Similar benefits of hydrotherapy to those stated in the NICE guidance were experienced.¹ Future service recommendations which focus on flexible access for flare management, 'Pay as you Go' schemes, group exercise and self-management may increase utilisation, optimise experience and reverse decline. Research to assess the benefits of these service recommendations in a clinical population is needed.

REFERENCE:

[1] <http://www.nice.org.uk/guidance/ng65>

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OP0280-HPR PHYSICAL ACTIVITY IN ESTABLISHED RA AND VARIABLES ASSOCIATED WITH PHYSICAL ACTIVITY MAINTENANCE OVER A SEVEN YEAR PERIOD

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Background: Interventions to promote a healthy lifestyle also in patients with rheumatoid arthritis (RA) have been in focus over the last years. Physical activity (PA) defined as moderate-to-vigorous physical activity (MVPA) has the possibility to reduce disease burden in RA and may contribute to improved quality of life (QoL). It is well known that a large number of patients with RA have a sedentary life style and are less active than their healthy peers. However, less information is known about the long term change of MVPA and possible associated variables.

Objectives: To study self-reported change of MVPA over seven years in a well-defined RA cohort.

Methods: A lifestyle questionnaire was sent twice to patients in the BARFOT cohort, in 2010 (n 1525) and in 2017 (n 1046) with a response rate of 73% and 68% respectively and 950 patients responded to both questionnaires. All patients fulfilled the ACR criteria for classification of RA and had a disease duration at inclusion (1992 to 2006) of ≤ 12 months. Patients were dichotomized as being active on recommended levels of MVPA (MVPA_{rec}; physically active on a moderate level ≥ 150 min/week (MPA) or on an intense level ≥ 75 min/week (VPA)) or not (sedentary). The patients reported body mass index, smoking habits, tender (TJC) and swollen joint count (SJC, 28-joints), patient global assessment (PatGA), pain intensity (NRS) and distribution (pain mannequin), fatigue (NRS), physical function (HAQ), health related QoL (EQ5D), comorbidities and medical treatment. Possible associated variables with meeting MVPA_{rec} at both time points or not (dependent variable) was studied by using a logistic regression analysis. All variables were adjusted for age, gender and smoking habits.

Results: Forty-one percent (n 389) of the patients met MVPA_{rec} at both occasions, and they reported better EQ5D scores compared with the sedentary group (mean 0.77 (SD 0.18) vs 0.68 (0.27)). The patients who met MVPA_{rec} were younger, (mean age (SD) 59¹³ years vs 62¹³ years, $p < 0.001$) and were to higher extent never smokers 46% vs 38%, $p = 0.021$. There was a negative association

with meeting MVPA_{rec} and being overweight (OR 0.58, 95% CI: 0.43 to 0.96) or obese (OR 0.38, 95% CI: 0.25 to 0.59), the presence of cardiovascular (OR 0.56, 95% CI: 0.41 to 0.75) and pulmonary diseases (OR 0.51, 95% CI: 0.31 to 0.85), TJC (OR 0.98, 95% CI: 0.95 to 0.995), high pain intensity (OR 0.99, 95% CI: 0.987 to 0.998), and pain distribution (OR 0.93, 95% CI: 0.90 to 0.96), worse fatigue (OR 0.99, 95% CI: 0.998 to 0.997) and a worse physical function (HAQ, OR 0.58, 95% CI: 0.45 to 0.76). Patients with higher values in QoL (EQ5D, OR 3.1, 95% CI: 1.52 to 6.2) were positively associated with meeting MVPA_{rec}. In 2010 there were no differences in medical treatment between the groups, $p = 0.377$. In 2017 the group meeting MVPA_{rec} included a lower number of untreated patients compared to 2010 (25% vs 34%, $p = 0.017$).

Conclusions: Only four out of ten patients with established RA reported to maintain recommended levels of PA over a seven year period. Experiencing high quality of life seems to be important for PA maintenance together with lower levels of pain, fatigue and better physical function. Health care professionals need to take the patient perspective into account and support maintenance of physical activities accordingly.

Disclosure of Interest: None declared

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OP0281-HPR PREFERENCES OF PATIENTS WITH RHEUMATOID ARTHRITIS REGARDING DISEASE MODIFYING ANTI-RHEUMATIC DRUGS: A DISCRETE CHOICE EXPERIMENT

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Background: Adherence to disease modifying anti-rheumatic drugs (DMARDs) is suboptimal in rheumatoid arthritis (RA) patients. Adherence rates vary from 30% to 90%, which may be partly due to patients' preferences regarding treatment benefits and drawbacks of DMARD therapy. Tailoring treatment options to these preferences might motivate patients to adhere to their drugs and eventually improve adherence.

Objectives: The primary objective is to identify subgroups in RA patients based on their preferences towards DMARD characteristics. The secondary objective is to identify characteristics associated with subgroup membership.

Methods: A discrete choice experiment (DCE) based on a literature review, expert recommendations and focus groups was used to elicit preferences in RA patients. Patients were asked to state their choice over two different hypothetical treatment options, which were described by seven DMARD characteristics and three levels within each characteristic (e.g. route of administration with the levels: oral, subcutaneous and intravenous). Patients were eligible to participate if they were diagnosed with RA according to the ACR/EULAR 2010 criteria, current user of at least one DMARD, and aged ≥ 18 years. Latent class analysis was used to identify subgroups based on stated preferences towards DMARD characteristics and multinomial logistic regression was used to identify characteristics (i.e. beliefs about medicines, patient- and disease-related variables) associated with subgroup membership.

Results: A total of 1317 RA patients were invited to participate in this study with an overall response rate of 24.8% (n=326). Three subgroups with segment sizes of 46.5% (SG1), 24.6% (SG2) and 28.9% (SG3) were found. SG1 was most strongly influenced by chance of efficacy, which contributed for 43.6% in their choice for a DMARD. In contrast with SG1, route of administration, risk of cancer and frequency of administration contributed most in SG2 (relative importance (RI) of 22.3%, 17.0% and 16.2% respectively). In SG3, route of administration (RI: 38.2%) contributed most in their choice for a DMARD with a strong preference for tablets/capsules. Current and previous use of other cDMARDs (i.e. leflunomide, azathioprine, ciclosporin or gold therapy) and indifferent (low necessity, low concerns) beliefs were significantly associated with assignment to SG2 (Relative Risk Ratio (RRR) 6.03, $p = 0.0012$, RRR=3.64, $p = 0.013$ and RRR:14.91, $p = 0.003$ respectively). Current and previous use of sulfasalazine, other cDMARDs, medium educational level and (early) retirement were significantly associated with assignment to SG3 (RRR:3.91, $p = 0.009$; RRR:0.34, $p = 0.010$, RRR:3.38, $p = 0.020$, RRR:3.12, $p = 0.005$ and RRR:0.358, $p = 0.034$).

Abstract OP0281-HPR – Figure 1 Relative importance of attributes for each subgroup

Conclusions: DCE data revealed that RA patients had different preferences for DMARD characteristics, which resulted in the identification of three subgroups. Integrating preferences of these subgroups in patient-tailored treatment decisions and the effect on medication adherence should be part of future research.

REFERENCE:

- [1] Pasma A, et al. *Arthritis Res Ther* 2015;1–10. doi:10.1186/s13075-015-0801-4

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From gene to function

OP0282 NEW SYSTEMIC SCLEROSIS RISK LOCI IDENTIFIED THROUGH A META-GWAS STRATEGY

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Background: In systemic sclerosis (SSc), previous GWASs have identified several loci associated with the disease, but their rate of discovery has been limited due to modest sample sizes. Extensive collaborative efforts have enabled us to gather the largest cohort of SSc patients. In the present study, we have performed a large meta-GWAS taking advantage of our well-powered cohort.

Objectives: To continue unravelling the complex genetic component of SSc.

Methods: The complete set of individuals enrolled for this study comprised a total of 26 679 genome-wide genotyped individuals of European ancestry. PLINK and EIGENSTRAT were used for quality control and population stratification adjustments. Genotype imputation was performed with IMPUTE2 and the 1000 Genome Project Phase 3 as reference panel.

Results: Twenty-three loci reached the genome-wide significance level (p -value $< 5 \times 10^{-8}$) in our large-scale meta-analysis. Twelve out of the total significant signals represented new associations and involved novel pathways in the pathophysiology of the disease. Significant enrichment was observed for epigenetic marks of active promoters and active enhancers in critical cell types for the disease. In addition many of the interrogated variants correlated with eQTLs thus altering gene expression.

Conclusions: Using a large meta-GWAS, we have identified twelve novel associations for SSc susceptibility and confirmed several previously reported risk loci. These results considerably increase our understanding of the genetic basis of SSc and shed light on the pathogenesis of the disease providing important information to discover new therapeutic targets genetically validated.

Disclosure of Interest: None declared

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OP0283 CROSS-DISEASE META-ANALYSIS IN FOUR SYSTEMIC AUTOIMMUNE DISEASES TO IDENTIFY SHARED GENETIC ETIOLOGIES

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Background: Cross-disease genome-wide association studies (GWAS) in autoimmune diseases (AIDs) has become a powerful tool to expose new genetic variants associated with disease susceptibility and to reveal shared biological mechanisms in the pathophysiology of these conditions.

Objectives: The goal of our study was to identify shared genetic etiologies by performing a large-scale meta-analysis of four systemic AIDs in individuals from European-descent populations, including rheumatoid arthritis [4595 cases and 3372 controls], systemic lupus erythematosus [3154 cases and 8775 controls], systemic sclerosis [2255 cases and 4407 controls] and myositis [1674 cases and 3150 controls]

Methods: PLINK and EIGENSTRAT were utilised for quality control and population stratification adjustments. Genotype imputation was performed using Minimac in the Michigan Imputation Server and the Haplotype Reference Consortium as reference panel.

Results: We meta-analysed ~6.5 million single nucleotide polymorphisms (SNPs) ($MAF > 1\%$, $Rsq > 0.3$) across the four diseases and were able to identify 27 genome-wide significant independent loci with at least two diseases leading the association. Our new findings include five unreported shared risk loci: *NAB1*, *KPNA4-ARL14*, *DGQK*, *LIMK1*, and *PRR12*. The results from the meta-analysis were functionally enriched in transcription factor binding sites, promoter and enhancer histone marks and DNase cleavage hotspots in immune cell lines, as well as in epithelial and epidermal cell lines. This is consistent with the clinical manifestations across diseases related to the immune system and the connective tissue. Interestingly, several associated variants were able to modify the expression of the nearest genes and constitute shared expression quantitative trait loci across diseases.

Conclusions: These studies offer the opportunity to uncover new biological pathways, address patient classification based on their molecular taxonomy and provide an opportunity for drug repositioning by targeting shared mechanisms across diseases.

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