treatment withdrawal is contemplated. Until improved blood or urine biomarkers have been developed, repeat biopsy will remain a useful tool for the clinic.

REFERENCES

Acknowledgements The Hopkins Lupus Cohort is supported by NIH Grant RO1 AR 69572.

O2 EFFECT OF TREATMENT ON ANTI PHOSPHOLIPID ANTIBODIES IN SLE

Michelle Petri, 1Laurence S Magder, 1Daniel W Goldman. 1Medicine, Rheumatology, Johns Hopkins University School of Medicine, Baltimore; 2Dept. Epidemiology, University of Maryland, School of Medicine, Baltimore, USA

Background Unlike primary antiphospholipid syndrome patients, most SLE patients with antiphospholipid antibodies are on one or more treatments for their SLE that might affect levels of their antiphospholipid antibodies. We examined the effect of prednisone and hydroxychloroquine on antiphospholipid antibodies in an SLE longitudinal cohort.

Methods 943 SLE patients, who were tested for each anticardiolipin isotype (aCL IgG, IgM and IgA; INOVA) and lupus anticoagulant (LAC; dRVVT with further confirmatory testing) for at least 10 quarterly clinic visits, were included. We compared visits positive for antiphospholipid antibodies (aCL>20 and aCL>40; dRVVT>45) to visits negative for antiphospholipid antibodies, with respect to treatment, using conditional logistic regression and conditioning on the patient.

Results Prednisone treatment significantly reduced the levels of aCL IgG isotypes (aCL IgG>40 and some prednisone but less than 10 mg/day, OR 0.61 95% CI 0.46–0.80 p=0.0004), but not aCL IgM, IgA, or LAC. Hydroxychloroquine treatment significantly reduced aCL IgG (aCL IgG>40, OR 0.35 95% CI 0.22–0.55 p<0.0001), aCL IgM and (aCL IgM>40, OR 0.56 95% CI 0.36–0.87 p=0.010) and LAC (OR 0.71 95% CI 0.58–0.86 p=0.007) but not aCL IgA.

Conclusions Prednisone does not reduce IgM or IgA isotypes of anticardiolipin, or LAC. These results explain why prednisone does not reduce thrombosis in SLE. Hydroxychloroquine, on the other hand, significantly reduces all antiphospholipid types except for the IgA isotype of anticardiolipin. This may explain why IgA isotypes are more common in SLE. It may also explain why hydroxychloroquine leads to only a 50% reduction in thrombosis, as IgA isotypes do confer some risk of thrombosis.

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O3 CHANGES IN GUT MICROBIOTA AFTER SYMBIOTIC SUPPLEMENTATION IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS: A RANDOMISED, DOUBLE-BLIND, PLACEBO-CONTROLLED TRIAL

11,2 Akhina Widhani, 13Samsuridjal Djausti, 2Franciscus D Suyatna, 3Beti Ernawati Dewi, 4MelvaLouisa, 1AndiYasmon, 5SusanRahaya. 1Allergy and Clinical Immunology Division, 2Dept. of Internal Medicine, Faculty of Medicine, Universitas Indonesia, Jakarta; 3Dr. Cipto Mangunkusumo National General Hospital, Jakarta; 4Doctoral Program in Biomedical Science, Faculty of Medicine, Universitas Indonesia, Jakarta; 5Dept. of Pharmacology and Therapeutic, Faculty of Medicine, Universitas Indonesia, Jakarta; 7Dept. of Microbiology, Faculty of Medicine, Universitas Indonesia, Jakarta; 8Molecular Biology Unit, Integrated Laboratory, Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia

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**Background**
Systemic lupus erythematosus (SLE) is a chronic multiorgan autoimmune disease with high morbidity. The pathogenesis is multifactorial. Gut dysbiosis plays a role in the pathogenesis of systemic lupus erythematosus (SLE). It can cause systemic inflammation.

**Methods**
We conducted a randomized, double-blind, placebo-controlled trial to investigate whether synbiotic supplementation could improve gut microbiota composition and function in patients with SLE.

**Results**
Forty-six SLE patients were randomized to two groups: the synbiotic group received synbiotic capsule (Lactobacillus helveticus R0052 60%, Bifidobacterium infantis R0033 20%, Bifidobacterium bifidum R0071 20% and 80 mg fructo-oligosaccharides) for 60 days and placebo group. In the synbiotic-supplemented group, 21 patients completed the intervention. In the placebo group, one was excluded from the final analysis because she needed antibiotic treatment for 33 days. We analysed 16s rRNA microbiome data from 89 faecal samples of the 46 patients. We found increases in the Firmicutes to Bacteroidetes ratio, butyrate metabolism and nitrotoluene degradation after synbiotic supplementation. We also found a decrease in potentially pathogenic species and an increase in beneficial species.

**Conclusion**
Synbiotic supplementation affect the composition and functions of gut microbiota in patients with systemic lupus erythematosus.

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**Abstract 04 Table 1**
Number of STAT-related genes whose variation has statistically significant association to SLEDAI-2K variation

<table>
<thead>
<tr>
<th>STAT</th>
<th>Week</th>
<th>Number of downstream genes</th>
<th>Number of downstream genes with FDR &lt; 0.1</th>
<th>Number of downstream genes with P &lt; 0.05</th>
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<tr>
<td>STAT1</td>
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<td>30</td>
<td>45</td>
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<tr>
<td>STAT1</td>
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<td>STAT1</td>
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<td>135</td>
<td>0</td>
<td>1</td>
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<td>13</td>
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Spearman rank coefficient correlations between variation in SLEDAI-2K (from baseline) and variation in log2 expression (from baseline) of genes were computed at weeks 2, 4, 12, and 24 with baricitinib 4-mg treatment and tested for statistically significant differences from zero. Genes analyzed were downstream of STAT1, STAT2, or STAT4 as selected from the MetaCore Database. The number of selected downstream genes for each STAT is shown, along with the number of statistically significant genes. FDR=false discovery rate; SLEDAI-2K=Systemic Lupus Erythematosus Disease Activity Index-2000; STAT=signal transducer and activator of transcription.