improvement of the gut barrier and growth inhibition of a translocating *Lactobacillus* strain. This *Lactobacillus sp*. was shown to drive lupus-related pathology in mice via the type I interferon pathway, and its genus was also enriched in a subset of SLE patients. Whether diet enriched in RS have similar effects in patients is unknown. We aimed to understand how dietary RS content influences gut microbial community structures in SLE and SLE-related antiphospholipid syndrome (APS) patients with well-defined microbiomes.[3,4]

Methods Stools and dietary information were collected from 12 SLE (n=28), 15 APS (n=44) patients and 20 control subjects (n=48) for up to 3 visits (0, 4 and 8 weeks) as previously described (3,4). Microbiota composition was defined by 16S rRNA V4 region sequencing. The FDA reference list was used to calculate the RS content. Patients' diets were classified as low RS content if less than 2.5 g per day, medium RS if 2.5 to 15 g, and high RS above 15 g.

Results *Lactobacillus spp*. were significantly enriched in SLE patients (p=0.002) compared to non-disease controls. APS patients showed a similar trend (p=0.06), but SLE patients displayed higher relative abundance compared to APS (p=0.011). No significant association was observed between low-to-medium RS content and *Lactobacillus*. High RS content was not achieved in routine diets of SLE and APS patients in these cohorts. However, medium RS was associated with an outgrowth of *Bifidobacterium* in SLE patients (p=0.016). Also, medium RS correlated in APS patients with a reduction of cardiolipin-synthesizing bacteria from the *Coriobacteriaceae* family (p=0.011) including *Collinsella* (p=0.009) and *Slackia* genera (p=0.033), previously linked to APS.[5,6]

Conclusions The content of RS in patients` regular diets has a distinct impact on the gut microbiota composition depending on the autoimmune disorder. Medium levels of dietary RS were associated in SLE with increased *Bifidobacterium*, short-chain fatty acid producing bacteria known to promote immune homeostasis, and with decreased cardiolipin-producing commensals in APS. It remains to be tested in an interventional trial if high RS content corrects the outgrowth of *Lactobacillus* in these patients, but moderate levels of RS may provide already beneficial effects on other taxa potentially involved in the pathogenesis of these disorders.

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Trial Registrations ClinicalTrials.gov Identifiers: NCT02394964 (The Human Microbiome in Immune-Mediated Diseases) and NCT01787305 (Pilot Study of Gut Commensals in Antiphospholipid Syndrome).

1505 GENETICS: FLIPONS AND THE ROLE OF THE LEFT-HANDED Z-RNA CONFORMATION IN INTERFERONOPATHIES

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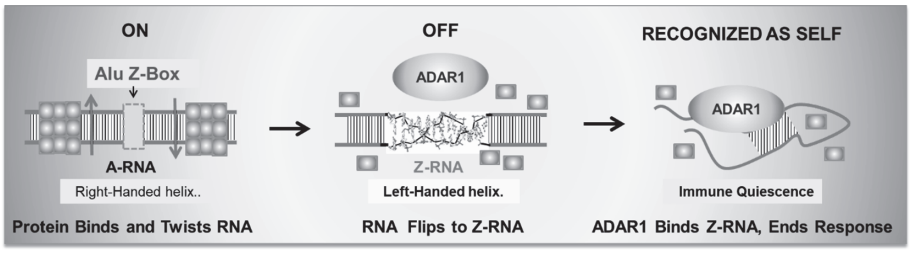
Background In 1979, the first ever DNA crystal that was solved led to the surprising discovery of the left-hand Z-DNA conformation This structure forms from the right-handed classical B-DNA by flipping the bases over. The first protein shown to bind Z-DNA with high affinity was the double-stranded RNA editing protein ADAR1, but exactly why was uncertain for many years. A Proline to Alanine substitution at position 193 of ADAR1 (P193A) and an Asparagine to Serine substitution at position 173 (N173S), both in the Zα domain have been reported in families with Aicardi Goutières Syndrome type 6 , but also in the general population. Aicardi Goutières Syndrome causes severe neurological disease marked by dystonia with very few individuals surviving childhood. Disease is associated with a type I interferon signature.

Materials and Methods Structural and Genetic Analysis of ADAR1 biology

Results Evidence that P193A and N173S variants of the Z-RNA binding domain, Zα, of the RNA editing enzyme ADAR1 are causal for the Type I Interferonopathy Aicardi Goutières syndrome will be presented. The disease outcomes are driven by double-stranded RNAs derived from endogenous Alu inverted repeat retrotransposons. The Alu elements contain a Z-box with Z-RNA forming sequences that are normally bound by the Zα domain of ADAR1 to prevent activation of the double-stranded RNA sensor to MDA5 that drives the interferon response. The Alu elements mark host-transcripts as self, preventing auto-reactivity.

Conclusions The regulation of type I Interferon responses by Z-RNA is the first time that a biological role for flipons has been conclusively confirmed. The P193A variant



Abstract 1505 Figure 1 Double-stranded A-RNA (dsRNA) formed by Alu RNA elements is twisted and shortened as the helicase MDA5 engages it. If the right-handed dsRNA (helical length =2.46 nm) contains a Z-Box, then the tension generated is relieved by flipping the sequence to the longer left-handed Z-RNA conformation (helical length = 4.56 nm). The flip causes the immune proteins to fall off the RNA. The Z-RNA formed engages the editing enzyme ADAR1. ADAR1 modifies dsRNA, producing single-stranded RNA that does not cause immune activation. The Z-Box sequences are called flipons.

(rs145588689) is present in 0.2% of the world population and in 0.3~04% of non-Finnish Europeans. It seems likely that the variant underwent selection during the period of urbanization during the Middle Ages. The increased interferon responses may have enhanced survival against pandemic viruses. Whether P193A increases risk of systemic lupus erythematosus is unknown.

1506 A HUMAN SLE VARIANT NCF1-R90H PROMOTES KIDNEY DAMAGE AND MURINE LUPUS THROUGH ENHANCED TFH2 RESPONSES INDUCED BY DEFECTIVE EFFEROCYTOSIS OF MACROPHAGES

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Background We previously identified a p.Arg90His (p.R90H) hypomorphic variant of neutrophil cytosolic factor 1 (*NCF1*, a regulatory subunit of phagocyte NADPH oxidase 2 complex, NOX2) predisposes to multiple autoimmune diseases including systemic lupus erythematosus (SLE). We established a C57BL/6 (B6) mouse model with a knock-in (KI) H90 variant in the *Ncf1* locus by CRISPR/Cas9 editing to study how this common *NCF1* variant promotes the development of lupus manifestations.

Materials and Methods Wild type (WT) and KI littermates were assessed either for spontaneously-developed or pristane-induced immune profiles and lupus-like features. Efferocytosis was assessed using irradiated WT thymocytes or Jurkat cells as apoptotic cells (AC) to co-culture with murine bone marrow-derived macrophages or human circulating monocyte-derived macrophages, respectively. Disease activity and renal damage of SLE patients were assessed by SLEDAI and renal items of SLICC, respectively.

Results Compared to WT littermates, 5-week-old homozygous KI mice had reduced oxidative burst, splenomegaly, elevated type I interferon (IFN-I) scores, increased ratios of splenic follicular T helper 2 (Tfh2) to either T follicular regulatory (Tfr) or Tfh1 cell numbers, increased ANA^+ follicular, germinal center B cells and plasma cells, but no spontaneous kidney disease up to one-year of age. Pristane treatment induced kidney disease development in 36-week-old H90 KI B6 female mice, exhibiting increased Tfh2 coupled with decreased Tfr and Tfh1 proportions, robust germinal center formation and IgG autoantibody production. Decreased efferocytosis of macrophages derived from KI mice and homozygous H90 SLE patients promoted elevated ratios of Tfh2/Tfr and Tfh2/Tfh1 as well as dysregulated humoral responses due to reduced Hv1-dependent acidification of phagosome pH to neutralize the decreased electrogenic effect of the H90 variant, resulting in impaired maturation and proteolysis of phagosome. SLE patients carrying homozygous H90 genotype had elevated circulating Tfh2/Tfr and Tfh2/Tfh1 ratios, positive correlations of circulating Tfh2 percentage with plasmablast frequency and disease activity, deposition of IgG and complement C3 in kidney biopsies, and increased kidney damage in multiple ethnic populations.

Conclusion The same links between the NCF1 H90 hypofunctional genotype to lupus-like phenotype in a mouse model and SLE patients demonstrates it is the causal variant in the NCF1 locus associated with SLE.

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1507 THE RELATIONSHIP BETWEEN DNA METHYLATION PATTERNS AND DISEASE ACTIVITY IN A LONGITUDINAL MULTI-ANCESTRAL COHORT OF LUPUS PATIENTS

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Background Epigenetic dysregulation is implicated in the pathogenesis of lupus. We performed a longitudinal analysis of DNA methylation in lupus patients and assessed epigenetic changes over time and across disease activity status. Combining genetic and epigenetic analyses, we also examined ancestry-specific DNA methylation and DNA methylation changes influenced by genetic variants across the genome.

Methods A total of 54 female lupus patients, including 32 European-American and 22 African-American, were followed for up to 4 years. Blood samples were obtained at routine follow up visits and during disease flares, with a total of 229 samples collected. Disease activity at each blood draw was determined by SLEDAI. Granulocytes were isolated and DNA extracted. Genotyping was performed using the Infinium Global Screening Array v2.0, and genome-wide DNA methylation was assessed at each time-point using the Infinium MethylationEPIC array. Ancestry-specific DNA methylation changes and methylation quantitative trait loci (meQTL) were identified. A linear mixed effects model was implemented to identify DNA methylation alterations that vary with disease activity and the development of lupus nephritis during follow up.

Results We identified 487 hypomethylated and 420 hypermethylated CpG sites in African-American compared to European-American lupus patients, annotated to 391 and 316 unique genes, respectively. Differentially methylated genes include type I interferon-response genes such as *IRF7* and *IFI44,* and genes related to the NFkB pathway. After adjusting for age, medications, and genetic background, DNA methylation levels in 142 (15.7%) differentially methylated sites were found to be allele-specific and influenced by at least one genetic variant located within 1kb. *TREML4*, which plays a vital role in toll-like receptor signaling, was hypomethylated in African-American patients and demonstrated a strong *cis*-meQTL association (R^2=0.91). The associated genetic variant (rs9369265) significantly differs in allele frequencies between