Methods: The case-control pilot study included 143 children (39 with SLE and 103 healthy unrelated volunteers as a control group). Diagnosis of SLE was based on 2012 SLICC criteria. STAT4 rs7574865 G/T polymorphism was investigated using allele-specific real-time polymerase chain reaction (RT-PCR).

Results: The group of pts with SLE consisted of 29 girls and 10 boys, with an average age of 11.8±3.7 years (from 3 to 17 years) and an average disease duration of 4.1±2.4 years. 79.5% pts had acute cutaneous lupus at the onset, 46.1% - non-scarring alopecia, 71.8% - arthritis, 23.1% - oral and nasal ulcers, 23.1% - serositis, 43.6% - renal involvement, 35.9% - neuropsychiatric disorders. Leucopenia/lymphopenia was found in 71.8% of pts, thrombocytopenia - in 23.1%. ANA were detected in 100% pts, anti-dsDNA - in 79.5%, anti-Sm - in 31.6%, antiphospholipid antibodies - in 7.3%, hypocomplementemia - in 61.5%, positive direct Coombs test - in 35.9%. Macrocephalic activation syndrome at the onset was documented in 15.4 % of pts. The distribution of rs7574865 genotypes in the control group showed no significant deviations from the Hardy-Weinberg equilibrium. The distribution of genotype frequencies among pts had statistically significant differences compared to the control ($\chi^2=12.95$, $p=0.0015$): GG-30.8% and 63.1% ($p=0.001$), GT-56.4% and 33.0% ($p=0.018$), TT-12.8% and 3.9% ($p=0.114$), GT+TT - 69.2% and 36.9% ($p=0.0005$). The frequency of the mutant STAT 4 allele T (polymorphism), was significantly higher in the SLE group than in the control group (41% and 20.4%, respectively; $p=0.0007$). We identified an association of the T allele with some clinical, laboratory, and immunological disorders in SLE: arthritis (OR 3.9, $p=0.0002$), acute cutaneous lupus (OR 2.47, $p=0.003$), non-scarring alopecia (OR 3.12, $p=0.002$), renal involvement (OR 2.42, $p=0.022$), leucopenia (OR 2.72, $p=0.003$), thrombocytopenia (OR 4.88, $p=0.002$), anti-dsDNA (OR 2.82, $p=0.0006$), hypocomplementemia (OR 2.34, $p=0.012$), positive direct Coombs test (OR 3.38, $p=0.002$).

Conclusion: Our pilot study confirmed that the STAT4 rs7574865 G/T polymorphism was associated with the risk of SLE in children and some of SLE manifestations.

Disclosure of Interests: None declared

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AB0008

APPLYING WHOLE EXOME SEQUENCING TO FAMILIAL ANTIPHOSPHOLIPID SYNDROME: NEW PLAYERS IN A RARE DISEASE?

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Background: Antiphospholipid Syndrome (APS) is an autoimmune disease whose precise aetiology is still unknown, but the high heterogeneity of its manifestations and clinical course is presumably due to the occurrence of different mechanisms and alterations at different levels and pathways [1]. The first genetic studies in APS focused primarily on the human leukocytes antigen system region, but more recent data highlighted a role of other genes in APS susceptibility, primarily those involved in the immune response and in the haemostatic process.

Objectives: We aimed to deepen the investigation of APS genetic background starting from a case of familial APS, analysing two siblings with thrombotic APS (Table 1), both triple positive for antiphospholipid antibodies (aPL).

Table 1. Main clinical and laboratory characteristics of the patients included in the study.

Patient	Age	aPL Profile	Relevant Clinical History
1 (F)	51	Triple positive (LA, aCL IgG, aβ2GPI IgG)	Two episodes of ischemic stroke, one episode of CAPS (renal thrombotic microangiopathy, visual impairment, ischemic stroke)
2 (M)	47	Triple positive (LA, aCL IgG, aβ2GPI IgG)	Three episodes of deep vein thrombosis, regardless ongoing well conducted therapy vitamin k antagonist and additional retinal vein thrombosis

LA: lupus anticoagulant; aCL: anti-cardiolipin antibodies; aβ2GPI: anti- β2 glycoprotein I antibodies; CAPS: catastrophic APS.

Methods: Genomic DNA was extracted from peripheral blood and the samples underwent Whole Exome Sequencing (WES). Sequencing was done on a 100X coverage, and reads have been aligned to the human reference genome (GRCh37/hg19 assembly) using the Burrows-Wheeler Alignment tool (BWA). The mean sequencing depth on target regions was 170X for patient 1, 205X for patient 2, moreover, 99.50% of the targeted bases had at least 10X coverage for all the three donors. The resulting single nucleotide polymorphisms (SNPs) have been analysed through a step-by-step process based on their frequency population (using Genome Aggregation Database), their predicted effects on the protein (using VarSome) and a literature research about the genes carrying them. Moreover, genes previously associated with a pro-thrombotic tendency and with APS have been analysed in the two patients.

Results: Starting from more than 120000 SNPs for each patients, the analysis led to reduce the list of SNPs of interest to 27 missense mutations. The complete literature research regarding the genes carrying these mutations allowed to further reduce the number of selected genes, focusing on those that exert a role potentially involved in APS pathogenesis and development. In particular, these genes (*PLA2G6*, *HSPG2*, *BCL3*, *ZFAT*, *ATP2B2*, *CRTC3* and *ADCY3*) take part in the immune response and the vascular homeostasis. The list of the DNA missense variants of interest found in our cases of familial APS is resumed in Figure 2.

GENE	FULL NAME	SNP	CHR	COORDINATE	TRANSCRIPT	VARIANT EFFECT
CROCC	Clary novel coiled-coil domain	c1144279934 (A/T)	1	17238697	NSM 014075.1	Missense variant (p. Arg570His)
HSPG2	Heparan sulfate proteoglycan 2	c276663773 (C/T)	1	22207915	NSM 005528.5	Missense variant (p. Arg570His)
KIF14	Kinesin family member 14	c371895990 (C/T)	1	20593037	NSM 014375.2	Missense variant (p. Arg570His)
ADCY3	Adenylyl cyclase 3	c584085662 (C/T)	2	25606928	NSM 004063.3	Missense variant (p. Val789Met)
CR3P1	Chlamydomonas reinhardtii receptor 1	c1140137679 (A/C)	3	5943419	NSM 014343.2	Missense variant (p. Tyr107Phe)
SRGAP3	SLIT-ROBO GTPase activating protein 3	c762133718 (C/T)	3	914644	NSM 014350.3	Missense variant (p. Arg130Gln)
ATP2B2	A P2-type plasma membrane Ca ²⁺ transporting 2	c581257856 (G/A)	3	10382352	NSM 00101331.2	Missense variant (p. Ala305Val)
OSXNAD1	Oxidoreductase NAD binding domain containing 1	c1140137679 (A/C)	3	16343175	NSM 130317.1	Missense variant (p. Phe139Gln)
PDZD2	PDZ domain containing 2	c1140137679 (A/C)	5	22097311	NSM 176140.2	Missense variant (p. Pro2737Ala)
FAT2	FAT atypical cadherin 2	c762133718 (C/T)	5	150915618	NSM 001447.2	Missense variant (p. Arg495Gln)
ORF1	Orf1 domain family 2 subfamily F member 1	c777034277 (T/C)	7	114367370	NSM 012369.2	Missense variant (p. Phe103Leu)
ZFAT	Zinc finger and AT hook domain containing	c584085662 (C/T)	8	135894714	NSM 020663.2	Missense variant (p. Arg390Cys)
ITIH3	Interleukin-13 receptor alpha 1	c3383427	9	51229335	NSM 021258.2	Missense variant (p. Tyr119Ile)
ZNF462	Zinc finger protein 462	c326AAT	9	109664419	NSM 021254.4	Missense variant (p. Asn757Val)
MRPL48	Mitochondrial ribosomal protein L48	c743995190 (G/T)	11	73555903	NSM 016055.5	Missense variant (p. Arg487Val)
LYBP2	Lysine binding protein 2 factor beta binding protein 2	c1131094102 (G/A)	14	54991233	NSM 000428.2	Missense variant (p. Asp74Glu)
CRTC3	CRTC3 regulated transcription coactivator 3	c1483C-T	15	91083301	NSM 022508.4	Missense variant (p. Leu555Phe)
USP32	Ubiquitin specific peptidase 32	c1140137679 (A/C)	17	58311560	NSM 025282.3	Missense variant (p. Leu390Phe)
BNIP2	Birc2 domain containing protein 2	c1140137679 (A/C)	18	12009990	NSM 014214.2	Missense variant (p. Val103Asn)
MYC10	Myosin 10	c260952932 (C/T)	19	96057604	NSM 025096.2	Missense variant (p. Glu650Val)
CC2D4A	Coiled-coil and C2 domain containing 1A	c794G-T	19	11028928	NSM 017721.4	Missense variant (p. Arg265Ile)
MAP3K10	Mitogen-activated protein kinase kinase kinase 10	c338G-A	19	46098296	NSM 002446.3	Missense variant (p. Glu120Lys)
BCL3	BCL2 transcription coactivator	c747455076 (C/A)	19	45262863	NSM 004918.4	Missense variant (p. Met101Asn)
MRMR	Mitochondrial ribosomal maintenance 8 homologous recombination repair factor	c768426146 (G/A)	20	5933350	NSM 00121521.1	Missense variant (p. Arg415Met)
PLA2G6	Phospholipase A2 group VI	c780423461 (C/G)	22	38528920	NSM 003568.2	Missense variant (p. Cys322Ser)

Figure 2. List of DNA missense variants of interest found in patient 1 and 2. Genes potentially involved in APS pathogenesis and development are highlighted in bold.

No mutations on genes known to be associated with a pro-thrombotic state (*F5*, *F2*, *MTHFR*, *F13A1*, *PROC*, *PROS1*, *FGB* and *SERPINE1*), or on genes previously associated with APS (*B2GPI*, *PF4V1*, *SELP*, *TLR2*, *TLR4*, *GP1a*, *GP1BA*, *F2R*, *F2RL1*, *TFPI*, *F3*, *VEGFA*, *FLT1*, and *TNF*) have been found in the WES analysis.

Conclusion: To some extent, this can be seen as a proof of concept of the complexity of APS. Efforts to interpret the genetic risk factors involved in the heterogeneous clinical features of the syndrome, for instance, the integration of WES and network-based approaches might help to identify and stratify patients at risk of developing APS.

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AB0009

ASSOCIATION OF STAT4 RS7574865, RUNX1 RS9979383, IL6 RS1800795, IL6R RS2228145, IL6R RS4845618 WITH SYSTEMIC LUPUS ERYTHEMATOSUS SUSCEPTIBILITY AND SOME LUPUS MANIFESTATIONS IN BELARUSIAN POPULATION

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Background: Systemic lupus erythematosus (SLE) has a significant genetic predisposition. Many genetic variants of susceptibility to SLE have been published and analyzed, but the clinical and functional significance of the various genotypes has not yet been clearly defined [1].

Objectives: To estimate the association between some of non-HLA gene polymorphisms such as STAT4 rs7574865, RUNX1 rs9979383, IL6 rs1800795, IL6R rs2228145, IL6R rs4845618 and susceptibility to SLE in Belarusian population as well as some disease manifestations.

Methods: We examined 383 healthy blood donors and 54 SLE patients (18-72 years old, median age 35) classified according to the 1997 American College of Rheumatology (ACR) revised classification criteria [2]. Deoxyribonucleic acid was extracted from peripheral blood samples by phenol-chloroform method. Genotyping was performed by real-time PCR with fluorescent probes. Differences of distribution of all the single nucleotide polymorphism (SNP) genotypes and their associations with secondary antiphospholipid syndrome (APS) and lupus arthritis were analyzed using Pearson χ^2 (χ^2) and two-way Fisher exact test ($F_{p,2}$). Diagnostic odds ratio (dOR), likelihood ratio of positive (LR⁺) and negative (LR⁻) tests and corresponding 95% confidence intervals (CI) were also calculated.

Results: We revealed significant difference in STAT4 rs7574865 genotypes in SLE patients and healthy donors ($\chi^2=8.27$, $p=0.016$) with significant increase of TT genotype frequency in SLE patients vs healthy donors ($\chi^2=6.83$, $p=0.009$; $p_{2-1}=0.020$; dOR=3.78 (CI_{95%} 1.36-10.55); LR⁺=3.44 (CI_{95%} 1.35-8.71); LR⁻=0.91

($CI_{95\%}$ 0.83-0.98)). Lupus arthritis was more common in risk TT-genotype SLE carriers than in other SLE patients ($\chi^2=5.902$ $p=0.015$; $p_{2-1}=0.027$). We revealed significant increase of CT genotype (RUNX1 rs9979383) in healthy donors vs SLE patients ($\chi^2=4.14$; $p=0.042$; $dOR=0.53$ ($CI_{95\%}$ 0.29-0.98); $LR^+=0.69$ ($CI_{95\%}$ 0.45-0.99); $LR^- =1.3$ ($CI_{95\%}$ 1.01-1.56)). Lupus arthritis was more common in SLE CT-genotype carriers than in other SLE patients ($\chi^2=4.66$ $p=0.031$; $p_{2-1}=0.058$).

Significant differences in IL6 rs1800795, IL6R rs2228145 and IL6R rs4845618 genotypes distribution between studied groups were not found (χ^2 , $p=0.427$, $p=0.559$ and $p=0.407$, correspondingly) but GG-genotype (IL6 rs1800795) carrier-ship in SLE patients was associated with increased APS frequency ($\chi^2=4.45$, $p=0.035$; $dOR=0.19$ ($CI_{95\%}$ 0.04-0.9); $LR^+ =0.28$ ($CI_{95\%}$ 0.07-0.93); $LR^- =1.41$ ($CI_{95\%}$ 1.03-1.64).

Conclusion: Our data suggest the susceptibility to SLE in TT genotype of STAT4 rs7574865 polymorphism, protective role of CT genotype of RUNX1 rs9979383 for SLE and association between GG-genotype of IL6 rs1800795 and APS in SLE patients in Belarusian population. Lupus arthritis was associated with TT genotype of STAT4 rs7574865 and CT genotype of RUNX1 rs9979383.

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AB0010 ASSOCIATION OF SAA1 GENE POLYMORPHISM -13T/C (RS12218) WITH ANKYLOSING SPONDYLITIS IN RUSSIAN POPULATION

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Background: Ankylosing spondylitis is a chronic systemic inflammatory disease. Inflammation and high levels of serum amyloid A (SAA) protein are predisposing factors for secondary AA amyloidosis. The role of SAA1 gene polymorphisms in AS is not well understood.

Objectives: To investigate the association of SAA1 gene polymorphism -13T/C (rs12218) with ankylosing spondylitis and to evaluate the influence of this polymorphism on SAA protein concentration.

Methods: 123 AS patients (72 males, 51 females; age - M (SD) 37.51 (12.77) years; disease duration - 14.28 (11.22) years; BASDAI - 5.59 (1.13); B27-positive - 111 (90.2%) pts) and 95 gender, age matched healthy individuals (control group) were included in this study. SAA1 gene polymorphism -13T/C was genotyped using allele-specific RT-PCR assay. SAA protein concentration was measured using nephelometry in AS patients.

Results: The distribution of genotypes TT, TC and CC differed statistically between AS and control groups (24.4%, 56.1%, 19.5% and 41.1%, 44.2%, 14.7% respectively, $\chi^2=6.9$, $p=0.03$).

The presence of the C allele was associated with the development of AS ($OR=1.55$ [CI 1.04-2.33], $p=0.03$). The SAA1 -13T/C polymorphism tended to be associated with SAA protein value in AS patients: TT+TC genotypes -13.8mg/l [4.2; 91.0], CC genotype -7.8mg/l [1.6; 29.6], $p=0.07$. ESR, CRP and BASDAI values did not correlated with SAA1 -13T/C polymorphism ($p=0.6$, $p=0.4$, $p=0.4$ respectively).

Conclusion: The results of our study demonstrated for the first time that SAA1 gene polymorphism -13T/C (rs12218) is associated with susceptibility to AS. It is also shown that this polymorphism can affect the SAA protein level. Our findings need to be verified in AS patients with high levels of SAA protein in various ethnic and population groups.

Disclosure of Interests: None declared

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AB0011 EXPRESSION PROFILE AND POTENTIAL FUNCTION OF CIRCRNAS IN PERIPHERAL BLOOD MONONUCLEAR CELLS FROM PATIENTS WITH PRIMARY GOUT

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Background: Autophagy is a phenomenon of "self-phagocytosis" in eukaryotic cells, which maintains cell homeostasis by transporting intracellular materials to lysosomes for degradation and recycling. In recent years, studies have shown that autophagy may be involved in the pathogenesis of rheumatoid arthritis(RA) [1], but its specific mechanism is still unclear.

Objectives: The expression levels of autophagy-related genes(ATG) unc-51-like kinase 1(ULK1), ATG13, ATG17, microtubule associated protein 1 light chain 3 (LC3), and P62 in peripheral blood mononuclear cells (PBMC) of patients with RA were detected, and their role and clinical significance in the pathogenesis of RA were explored.

Methods: Real-time fluorescent quantitative PCR was performed to detect the expression levels of ULK1, ATG13, ATG17, LC3, and P62 in PBMCs of 50 RA patients, 50 healthy controls (HC), and 25 moderate to severe RA patients before and after treatment. Then, t test, χ^2 test, Mann-Whitney U test, Pearson test were used for statistical analysis.

Results: 1.The levels of hsCRP, white blood cell(WBC), neutrophils(GR), platelet(PLT) and plateletcrit(PCT) in RA group were higher than those in HC group ($P <0.05$). Lymphocytes (LY), red blood cell(RBC), hemoglobin(HGB), hematocrit(HCT), mean corpuscular hemoglobin(MCH), mean red blood cell volume(MCV) and mean red blood cell hemoglobin concentration(MCHC) in RA group were lower than those in HC group ($P <0.05$). 2.The expressions of ULK1, ATG17, and LC3 in RA group were higher than those in HC group, while the expressions of P62 was lower than those in HC group($P <0.05$) (Figure 1). The correlation analysis suggested that ATG17 was positively correlated with tender joint count (TJC), swollen joint count (SJC), and health assessment questionnaire (HAQ) ($P <0.05$); ULK1 and HAQ were negatively correlated ($P <0.05$). 3. Compared with before treatment with TNFi, ATG17, HAQ, DAS-28, ESR, hsCRP, WBC, GR, PLT and PCT were significantly reduced after treatment ($P <0.05$); the expressions of RBC, HCT, MCV and MCH were significantly increased after treatment, ($P <0.05$); ULK1, ATG13, LC3, P62 and other related clinical and laboratory indicators were not significantly different before and after treatment with TNFi ($P >0.05$).

Figure 1. The expression levels of ATGs in HC and RA groups.

Conclusion: There is abnormal expression of autophagy genes in the peripheral blood of RA patients. ULK1, ATG17, LC3 and P62 may be related to the pathogenesis of RA, among them, ATG17 may regulate the pathogenesis of RA by participating in the TNF- α pathway.

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AB0012 THE EFFECTS OF COMMON THERAPEUTICS ON AIRE METHYLATION STATUS AND THE LEVELS OF IL-16, IL-1B, AND IFN- γ IN LPS-INDUCED MACROPHAGE CELLS CAN SULPHASALAZINE'S INFLUENCE ON METHYLATION STATUS OF AIRE EXPLAIN ITS AUTOIMMUNE SIDE EFFECTS?

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