terms. In the screening for genes regulating maturation of Th1/Th17 cells, CBLB, IRF1, STAT3, SGK1 and TNFSF14 were identified among the genes enriched in RA samples, while EGR3 and ETS1 were enriched only in healthy controls. Additionally, transcription factors Ezh2, Rad21, Ctbp2 and Suz12 were identified as common for both RA and healthy groups genes, associated with significant GO enrichment.

Conclusions: This study confirms the role of survivin as a transcription mediator in CD4 +T cells and is suggested to influence multiple genes involved in RA pathology.

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AB0017 VITAMIN D LEVEL AND MIRNA 22 AND 125b GENE EXPRESSION IN BEHÇET'S DISEASE PATIENTS

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Objectives: To investigate serum levels of vitamin D and its effect on microRNA 22 and 125b gene expression in Behçet's disease (BD) patients and to evaluate their relation to clinical characteristics and disease activity.

Methods: Fifty-one BD patients and 45 matching controls were studied. Disease activity was assessed using BD Current Activity Form (BDCAF). Serum vitamin D3 was measured by ELISA. MicroRNAs were assayed by reverse transcription-quantitative polymerized chain reaction (RT-qPCR).

Results: Patients mean age was 34.3±8.6 years and disease duration 65.3±52.4 months. The BDCAF was 2.4±1.3. Vitamin D level was significantly lower (29.7 ±14.4 ng/ml) in patients than in control (40.1±17.8 ng/ml)(p<0.001) especially males (25.8±7.5 ng/ml) compared to females (48±23.7 ng/ml)(p<0.001). There was no relation between 25(OH)D levels and disease activity or with the presence of clinical manifestations. There was a 3.8±1.5 fold increase in miRNA125b while miR-22 showed no significant difference (0.38±0.46) but was significantly reduced in those receiving steroids (0.21±0.27) compared to those not (0.66±0.58) (p=0.003). There was no significant difference in the frequency of miR-22 or miR-125 expression according to the presence of clinical manifestations, medications received or disease activity. The fold change in miR-125b significantly correlated with vitamin D (r=0.54, p<0.001) but not with BDCAF (p=0.64).

Conclusions: Vitamin D level is decreased in BD patients and significantly correlated with the fold change of miR-125b especially in males thus representing a possible therapeutic target. The miR-22 expression did not change but was notably downregulated by steroids. Further longitudinal studies on a larger sample are recommended to validate the present results.

Disclosure of Interest: None declared

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AB0018 CLINICAL STATUS AND GENE EXPRESSION IN CLASS IV LUPUS NEPHRITIS

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Background: Lupus nephritis (LN) is one of the most frequent and serious complications in the patients with systemic lupus erythematosus. Several studies have identified risk factors for poor kidney prognosis in patients with SLE, including age, sex, hypertension, decreased estimated GFR (eGFR), proteinuria, and renal pathologic types.¹ Biopsy allows classifying the type of renal involvement, assessing its activity, and thus guiding the therapeutic behaviours. It has been shown that structural changes and inflammatory infiltrate associated with LN contribute to a hypoxic state which induces angiogenesis.² Herein, it was hypothesised that differential expression of angiogenic genes could classify Lupus

Nephritis Patients (LNP) with the same histological score but different "clinical status".

Objectives: To investigate if there is a differential angiogenic gene expression in biopsies of LNP under the same histological classification but different "clinical status" measured by eGFR.

Methods: Twenty four kidney biopsies samples classified according to ISN/RPS scoring system as Class IV from 24 LNP were divided into eGFR <60 ml/min (n=10, age: 31.00±10.93, range: 17–46) and eGFR >60 ml/min (n=14, age: 32.64 ±11.34, range: 21–64). RNA was isolated using TRIzol-Chloroform technique and then was reverse-transcribed using random primers. Gene expression level of pro-angiogenic factors: VCAM-1, VEGF, TGF-β and ANGPT-1 were evaluated using Quantitative Real Time PCR (QPCR). The threshold cycle (Ct) scores were averaged for calculations of relative expression values. The Ct scores were normalised by subtracting β2Microglobuline (β2M) control, or ΔCt=Ct, gene- Ct,β2M. To test for differential gene expression between groups, a two sample T-test was performed to compare the ΔCt in the two groups.

Results: ΔCt is inversely proportional to the gene expression level. Significant differences between groups was found in VEGF-A gene (p=0.0326), where the greatest expression corresponding to eGFR <60 ml/min group. However, there were not statistically significant differences in VCAM-1, ANGPT1 and TGF-β expression (table 1). Particularly TGF-β, a proangiogenic and profibrotic gene showed a uniform expression level in both groups.

Abstract AB0018 – Table 1. Levels of gene expression and laboratory parameters in eGFR <60 ml/min and eGFR >60 ml/min expressed as ΔCt values.

Gene	eGFR<60 ml/min n=10	eGFR>60 ml/min n=14	p value
VCAM-1	5,021±1768	6,248±3264	0,3165
VEGF-A	3,414±1161	4,651±1409	0,0326
TGF-β	6,168±1011	6,699±1351	0,3421
ANGPT1	10,330±2294	9,891±2113	0,5007

Conclusions: In the present cross-sectional study, increased levels of VEGF-A were observed in biopsies Class IV from LNP with eGFR <60 ml/min. These findings suggest a differential gene expression that may be associated with an impaired renal function, reflected by eGFR.

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AB0019 THE ROLE OF THE IL2-IL21 RS6822844 POLYMORPHISM IN THE PREDISPOSITION TO THE ERYTHROCYTE SEDIMENTATION RATE ELEVATION IN JUVENILE IDIOPATHIC ARTHRITIS

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Background: Juvenile idiopathic arthritis (JIA) is the most common chronic rheumatic disorder in paediatrics.¹ The erythrocyte sedimentation rate (ESR) is one of the key measures of the JIA activity.² However, in some patients, even in the active disease period, the ESR is not elevated.³

Objectives: The aim of the study was to assess the relationship between the IL2-IL21 rs6822844 locus polymorphic variants and a predisposition to the ESR elevation in JIA patients.

Methods: The study included 255 JIA patients from the Republic of Bashkortostan, Russia. The ESR was considered elevated if its value exceeded the upper limit of the normal range two or more times. Genotyping was performed by real-time PCR, statistical analysis – using the two-tailed Fisher exact test (p) and the odds ratio (OR) with a 95% confidence interval (CI).

Results: The girls/boys ratio was 65.88%/34.12%. The ESR elevation in the active disease period was seen in 70.98% of patients. When studying the IL2-IL21 rs6822844 polymorphic locus, a marginal significance level was noted for the rarer occurrence of the GT genotype in patients with the elevated ESR (14.92%