Table 1. Description of complications

Complications of US-guided CNB	
Patients presenting complications, n/N (%)	11/20 (55%)
Description of transient complications	
Swelling at biopsy site, n	2
Bleeding, n	1
Hematoma, n	1
Local Pain, n	7
Local infection, n	0
Sialocele or fistula, n	0
Anaesthesia/paraesthesia, n	0
Transient facial palsy (< 1 hour), n	1
No persistent complications reported	

All the above specified complications were transient (< 12 weeks). No persistent complications were reported in the follow up.

POST-BIOPSY COMPLICATIONS QUESTIONNAIRE

1. Did you have any swelling at biopsy site? If yes, how long? Physician control	YES NO YES NO
2. Did you have any hematoma at biopsy site? If yes, how long? Physician control	YES NO YES NO
3. Did you have any bleeding at biopsy site? If yes, how long? Physician control	YES NO YES NO
4. Did you have pain at biopsy site? If yes, choose a number from 0 to 10 to describe pain intensity If yes, how long?	YES NO
5. Did you have any local infection? Physician control	YES NO YES NO
6. Did you have any anesthesia / paresthesia in the biopsy area? If yes, how long? Physician control	YES NO YES NO
7. Did you have any sialocele or fistula in the biopsy area? Physician control	YES NO YES NO

Figure 1. Post-biopsy complication Questionnaire

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POS0736

IDENTIFICATION OF MOLECULAR PHENOTYPES AND IMMUNE CELL INFILTRATION IN SYSTEMIC LUPUS ERYTHEMATOSUS PATIENTS ACCORDING TO LONGITUDINAL GENE EXPRESSION

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Background: Systemic lupus erythematosus (SLE) is a chronic autoimmune disease with highly heterogeneous clinical presentation characterized by disease unpredictable flares and multi-systemic involvement^{1,2}. This clinical heterogeneity calls for design a molecular stratification to improve clinical trial design and formulate personalization treatment therapies.

Objectives: This research was conducted to develop a reliable method to stratify SLE patients combined gene expression information and disease status.

Methods: The mRNA expression profile of GSE138458 (contained 307 patients and 23 controls) and GSE49454 (contained 111 patients and 16 controls) were downloaded from the publicly GEO databases. After background adjustment, batch correction, and other pre-processing, obtaining a big gene matrix to identify the differentially expressed genes (DEGs) in SLE compared with healthy controls, which were screened by P value < 0.01. SLE subtypes were identified by non-negative matrix factorization (NMF) based on DEGs. Acquired signature genes in different SLE subtypes were conducted to process pathway enrichment analysis in Metascape. SLEDAI score and immune cell infiltration was also performed between subtypes by software package R (version 4.0.3).

Results: Total 1202 DEGs were imputed to NMF unsupervised machine learning method. Patients with SLE were stratified into two subsets based on 184 signature genes derived from obtained DEGs (Fig.1A, 1B). GO and KEGG enrichment analysis showed that signature genes were mainly involved in negative regulation of innate immune response, toll-like receptor signaling pathway, regulation of immune effector process and so on (Fig.1C). Patients in Sub1 group had severe disease activity measures compared with those in Sub2 (Fig.1D). SLEDAI scores from GSE49454 dataset were also higher in Sub1 compare with Sub2 (Fig.1E). Further, immune cell infiltration results revealed an insufficient of regulatory T cell, CD8 T cells and naive CD4 T cells in Sub1 and neutrophils cells in Sub2 (P<0.05) (Fig.1F).

Conclusion: Our findings indicate that patients with SLE could be stratified into 2 subtypes which had different lymphocyte status and closely related to disease activity. This phenotyping may help us understand the etiology of the disease, inform patient in the design of clinical trials and guide treatment decision.

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Fig.1: (A) NMF consensus clustering of 418 SLE patients based on 1202 differentially expressed genes. Columns and rows represent patients and signature genes, respectively. (B) Heatmap of two clusters defined by signature genes. Colors indicate relative gene expression value, with red for high expression and blue for low expression. (C) GO and KEGG pathway enrichment analysis of signature genes indicate possibly differential pathways. (D) Disease activity distribution in the two subtypes. (E) SLEDAI scores among two subtypes in GSE49454. (F) Violin plot show the fraction of 22 immune cell subpopulations in two subtypes based on CIBERSORT algorithm.

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POS0737

LOW PRECONCEPTIONAL COMPLEMENT LEVEL IS RELATED WITH ADVERSE OBSTETRIC OUTCOME IN A MULTICENTRIC COHORT OF PREGNANCY IN PATIENTS WITH APS AND APL POSITIVITY

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Background: The role of complement in the antiphospholipid (aPL) related pathology has been widely studied in animal models. Antiphospholipid antibodies can induce fetal loss in experimental animals but mice deficient in specific complement components (C4, C3, C5) appear somehow protected. In addition, in pregnant mice injected with aPL, antibody deposition has been found at decidual level causing focal necrosis, apoptosis and neutrophil infiltrates and supporting aPL pathogenetic potential. On the other hand, human studies did find hypocomplementemia associated to pregnancy complications in patients with obstetric antiphospholipid syndrome (APS). These results, however, are not unanimously confirmed and, in addition, some studies only show increased levels of complement activation products (i.e. Bb) and not decreased levels of C3 and/or C4. A recently study focusing on complement level in early pregnancy and before pregnancy showed a significant correlation with pregnancy complications and loss in a large cohort of primary APS.

Objectives: To investigate if the simple detection of low C3 and/or C4 could be considered a risk factor for adverse pregnancy outcome in APS and aPL carriers pregnancies.

Methods: We performed a multicentric study including patients from 10 Italian and 1 Russian Centers. Data on pregnancies in women with primary APS (n=434) and asymptomatic carriers with persistently positive aPL but not fulfilling clinical criteria for APS (n=218) were retrospectively collected. Serum C3 and C4 levels were evaluated by nephelometry; hypocomplementemia was defined by local laboratory reference values. Statistical analysis was performed using GraphPad.

Results: Preconceptional complement levels and gestational outcome were available for 107 (25%) pregnancies in APS out of 434 and for 196 (90%) pregnancies in aPL carriers women out of 218. In pregnancies with low preconceptional C3 and/or C4, a significantly higher prevalence of pregnancy losses was observed (p=0.019). A subgroup analysis focusing on triple aPL positive patients was also performed. Preconceptional low C3 and/or C4 levels were found to be associated with an increased rate of pregnancy loss (p = 0.027) in this subgroup also. Otherwise, adverse pregnancy outcomes in single or double aPL positive women were not related to preconception complement levels (p = 0.44) (Table 1). Of note, all the pregnancy losses in the triple positive group occurred in patients treated with low dose aspirin and low molecular weight heparin from the time of positive pregnancy test.

Conclusion: Our findings confirm that decreased complement levels before pregnancy are associated with increased risk of adverse outcome. This has been seen only in women with triple aPL positivity, indeed single or double positivity does not show this trend. Complement levels are cheap and easy to be measured therefore they could represent a useful aid to identify patients at increased risk of pregnancy loss. test positivity.

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Table 1.

	Triple aPL positivity		p	Single or double aPL positivity		p
	Low C3/C4 (n=49)	Normal C3/C4 (n=17)		Low C3/C4 (n=57)	Normal C3/C4 (n=165)	
Gestational outcome						
Term live birth (>37w)	15 (31%)	6 (35%)	ns	34 (60%)	110 (67%)	ns
Preterm live birth (≤37w)	22 (45%)	11 (65%)	ns	15 (26%)	38 (23%)	ns
Pregnancy losses (abortion and miscarriages)	12 (24%)	0 (0%)	0.027	8 (14%)	17 (10%)	ns

Disclosure of Interests: None declared

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POS0738 BLUNTED CEREBRAL OXYGENATION DURING EXERCISE IN NON-NEUROPSYCHIATRIC SYSTEMIC LUPUS ERYTHEMATOSUS

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Background: Systemic lupus erythematosus (SLE) is a chronic autoimmune disease affecting multiple organs, including the central nervous system. Sub-clinical brain lesions have been reported in SLE patients, even without overt neuropsychiatric manifestations (non-NPSLE). Studies using PET/MRI, examining structural or functional brain abnormalities in SLE, have been previously performed, either at rest or during a mental task (1–3). Exercise can be used to identify early alterations in brain oxygenation that might not detectable during resting conditions (4).

Objectives: Our study aimed to examine possible differences in cerebral oxygenation during a handgrip exercise test between SLE patients without neuropsychiatric manifestations and age-matched controls.

Methods: Fifty-two participants (26 non-NPSLE and 26 controls), following evaluation of handgrip strength, underwent a protocol involving a seated rest (baseline), a 3-min handgrip exercise (at 30% of maximal strength), and a 3-min recovery. Continuous-near-infrared-spectroscopy (NIRS) was used to monitor changes in cerebral-oxygenated hemoglobin (O2Hb), de-oxygenated (HHb) and total-hemoglobin (tHb). Beat-by-beat blood pressure (Finapres) was continuously monitored.

Results: There were no differences between the two groups in age, body mass index, blood pressure, and smoking status. Median SLE duration was 7.5 (3.0 – 16.0) years. During exercise, cerebral -O2Hb increased in both groups; however, non-NPSLE exhibited a significantly lower increase in O2Hb vs. controls (average response: 1.20±0.89 vs. 2.33±1.61µM, respectively, p<0.005) and lower tHb responses (p<0.05), with no differences in HHb.

Conclusion: Our data show, for the first time, that SLE patients even without overt neuropsychiatric manifestations exhibit a blunted increase in cerebral-O2Hb during a submaximal exercise stimulus compared to age-matched controls. Examining brain oxygenation during a simple exercise task may assist in identifying patients with early alterations in cerebral function.

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