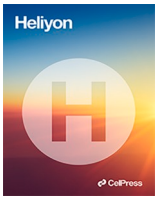
Heliyon 9 (2023) e18037

Contents lists available at ScienceDirect

Heliyon

journal homepage: www.cell.com/heliyon



Immune-dysregulated neutrophils characterized by upregulation of CXCL1 may be a potential factor in the pathogenesis of abdominal aortic aneurysm and systemic lupus erythematosus

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ARTICLE INFO

Keywords:
Abdominal aortic aneurysm
Systemic lupus erythematosus
Neutrophils
Immune cell infiltration analysis
Bioinformatics

ABSTRACT

Background: The abdominal aortic aneurysm (AAA) incidence is closely related to systemic lupus erythematosus (SLE). However, the common mechanisms between AAA and SLE are still unknown. The purpose of this research was to examine the main molecules and pathways involved in the immunization process that lead to the co-occurrence of AAA and SLE through the utilization of quantitative bioinformatics analysis of publicly available RNA sequencing databases. Moreover, routine blood test information was gathered from 460 patients to validate the findings.
Materials and methods: Datasets of both AAA (GSE57691 and GSE205071) and SLE (GSE50772 and GSE154851) were downloaded from the Gene Expression Omnibus (GEO) database, and differentially expressed genes (DEGs) were analyzed using bioinformatic tools. To determine the functions of the common differentially expressed genes (DEGs), Gene Ontology (GO) and Kyoto Encyclopedia analyses were conducted. Subsequently, the hub gene was identified through cytoHubba, and its validation was carried out in GSE47472 for AAA and GSE81622 for SLE. Immune cell infiltration analysis was performed to identify the key immune cells correlated with AAA and SLE, and to evaluate the correlation between key immune cells and the hub gene. Subsequently, the routine blood test data of 460 patients were collected, and the result of the immune cell infiltration analysis was further validated by univariate and multivariate logistic regression analysis.
Results: A total of 25 common DEGs were obtained, and three genes were screened by cytoHubba algorithms. Upon validation of the datasets, CXCL1 emerged as the hub gene with strong predictive capabilities, as evidenced by an area under the curve (AUC) > 0.7 for both AAA and SLE. The infiltration of immune cells was also validated, revealing a significant upregulation of neutrophils in the AAA and SLE datasets, along with a correlation between neutrophil infiltration and CXCL1 upregulation. Clinical data analysis revealed a significant increase in neutrophils in both AAA and SLE patients ($p < 0.05$). Neutrophils were found to be an independent factor in the diagnosis of AAA and SLE, exhibiting good diagnostic accuracy with AUC >0.7.
Conclusion: This study elucidates CXCL1 as a hub gene for the co-occurrence of AAA and SLE. Neutrophil infiltration plays a central role in the development of AAA and SLE and may serve to be a potential diagnostic and therapeutic target.

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https://doi.org/10.1016/j.heliyon.2023.e18037
Received 9 February 2023; Received in revised form 19 June 2023; Accepted 5 July 2023
Available online 13 July 2023

1. Introduction

An abdominal aortic aneurysm (AAA) is one of the most prevalent conditions in vascular surgery, characterized by localized dilatation of the abdominal aorta exceeding the normal diameter by > 50% [1]. The prevalence of AAA is reported to be 9% in elderly men and 1% in women over 65 years of age [2]. Despite the complexity of AAA pathogenesis, increasing evidence supports the essential involvement of vascular smooth muscle cells (VSMCs) in either the onset or advancement of AAA [3]. Infiltration of inflammatory cells is suggested to be a potential contributor to the elimination of VSMCs [4].

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease characterized by the formation of circulating autoantibodies, causing widespread inflammation and damage to multiple organs, including skin, joints, and the central nervous system [5]. The prevalence of SLE varies substantially by geographical region, with a global prevalence ranging from 0 to 241/100, 000, and the male-female prevalence ratio 1: 10–12 [6]. The pathogenesis of SLE is not fully known but is believed to be linked to multiple factors: genetic, infection, endocrine, and environmental. Additionally, defective immunomodulatory mechanisms, such as ineffective clearance of apoptotic cells and immune complexes, are important contributing factors in the occurrence of SLE [5].

A study by Guy et al. reported that patients with SLE exhibited a significantly increased risk of developing AAA compared to non-SLE controls [7]. This was attributable to pathological changes in the aorta, such as atherosclerosis, vasculitis, and cystic medial necrosis in SLE patients [8]. Are there any common mechanisms between AAA and SLE? Currently, very few studies have been conducted in this area. Therefore, it is imperative to investigate the shared mechanisms between AAA and SLE, including the role of inflammation and immune regulation.

In the present study, we screened for common DEGs in AAA and SLE and identified CXCL1 as the hub gene. Overall, identifying common hub genes and pathways will help elucidate the common mechanisms of AAA and SLE. The graphical abstract of this study is illustrated in Fig. 1.

2. Materials and methods

2.1. GEO dataset download

For related gene expression datasets, we used abdominal aortic aneurysm and Systemic lupus erythematosus as keywords from the Gene Expression Omnibus (GEO) database. For AAA, GSE57691 [9], and GSE205071 [10] were included, whereas for SLE, GSE50772 [11] and GSE154851 [12] were included.

2.2. Patients

For this study, forms requesting informed consent were signed by volunteers. The study was approved by the Ethics Committee of The First Affiliated Hospital of Guangxi Medical University. From June 2014 to June 2022, we selected a cohort of 151 AAA patients and 155 SLE patients from The First Affiliated Hospital of Guangxi Medical University. The inclusion criteria for AAA consisted of (a) age >18 years and (b) a diagnosis of AAA based on computed tomography angiography (CTA) test. Exclusion criteria for AAA were (a) active infection, (b) patients diagnosed with abdominal aortic dissection aneurysm, abdominal aortic pseudo aneurysm, thoracic AAA,

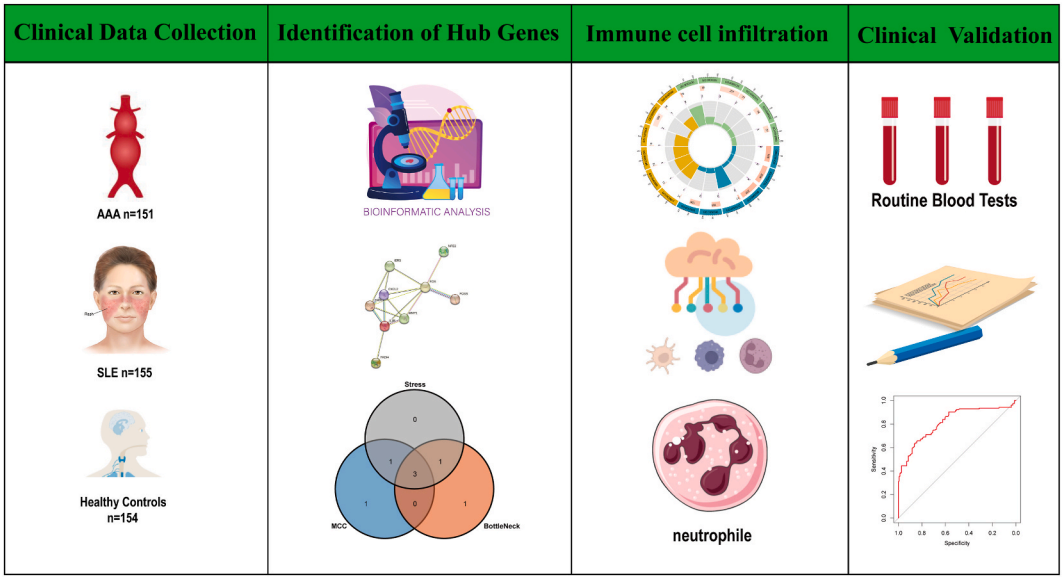

Fig. 1. Graphical abstract of this study.: AAA: abdominal aortic aneurysm; SLE: systemic lupus erythematosus.

or ruptured AAA, and (c) presence of a tumor. The following inclusion criteria were used for SLE: (a) age >18 years and (b) meeting the classification criteria of 2012 Systemic Lupus erythematosus International Collaborating Clinics (SLICC) [13]. Exclusion criteria used for SLE were: (a) active infection and (b) the presence of a tumor or other connective tissue disease.

Between June 2014 and June 2022, a random selection of non-AAA and non-SLE patients was carried out among all outpatients aged 18 years and above, without any current infection or malignancy, at the First Affiliated Hospital of Guangxi Medical University. After identification, 154 eligible patients were enrolled in the study.

2.3. Identification of differentially expressed genes

Series matrix files of datasets were downloaded from GEO. The data were normalized and differentially expressed genes (DEGs) were obtained by the 'limma' package in R software [14]. The fold changes (FCs) were calculated for individual gene expression. Genes meeting specific cutoff criteria of p-value <0.05 and |logFC|>0.585 were defined as DEGs. The R package 'veen' was used to obtain common DEGs [15].

2.4. Gene ontology and Kyoto encyclopedia of genes and genomes pathway enrichment analyses

Gene Ontology (GO) annotation [16] and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis [17] of DEGs were performed using R packages, including clusterProfifiler, org. Hs.eg.db, enrichplot, and ggplot2 to determine the functions of common DEGs [18]. GO enrichment analysis included three main categories: Cellular Component (CC), Biological Process (BP), and Molecular Function (MF). A p-value <0.05 was set as the cutoff criterion.

2.5. Identification of hub genes

The identified common DEGs were imported into the Search Tool for the Retrieval of Interacting Genes Database (STRING) and visualized by Cytoscape 3.9.1 [19]. We set the minimum interaction score to medium confidence (0.400) and utilized CytoHubba, a Cytoscape plug-in that evaluates nodes based on their network characteristics to determine their significance in biological networks, to identify hub genes [20].

2.6. Validation of hub gene expression

The expression levels of the identified hub genes for AAA were validated in GSE47472 [21] and SLE in GSE81622 [22]. The two datasets were compared using the Wilcoxon test, and a p-value <0.05 was considered statistically significant [23]. Additionally, to assess the predictive accuracy of the hub genes, ROC curves were generated using the pROC package in the R language [24].

2.7. Estimation of immune infiltration-related cells and genes

The immune cell composition of the GEO dataset was analyzed to assess immunological infiltration in individuals with AAA and SLE by using CIBERSORT. CIBERSORT is a bioinformatic software that characterizes the composition of immune cells and expresses the immune cell components in a matrix [25]. In order to investigate the correlation between immune cells, AAA, and SLE, a correlation heat map was generated. The statistically significant immune cell differences in AAA and SLE ($p < 0.05$) were considered for subsequent analyses. Furthermore, the relationship between the hub gene and 22 immune cells was analyzed to identify the immune cells associated with the hub gene.

2.8. Validation of immune cells

A total of 460 patients, including 151 AAA patients, 155 SLE patients, and 154 non-AAA and non-SLE patients, were enrolled in this study. Immune cells with statistical differences between AAA and non-AAA patients and between SLE and non-SLE patients were analyzed. Subsequently, univariate and multivariate logistic regression analyses were performed to validate the predictive capability of the key immune cells, and receiver operating characteristic (ROC) curves were generated.

2.9. Statistical analysis

Statistical analysis was performed using IBM SPSS 26.0 software and R software (version 4.2.1). Clinical data were expressed as mean (SD) or median (P25, P75), depending on the normality of the variables. Depending on the data type, we employed Student's t-test, Mann-Whitney U test, or chi-square test, and the significance level was set at p-value <0.05. In addition, the independent predictive factors' performance was assessed using ROC curves.

3. Results

3.1. Identification of common DEGs

We observed that 1615 DEGs were screened between AAA and healthy controls (Fig. 2A), while 410 DEGs in SLE patients compared to healthy controls (Fig. 2B). Considering the intersection of the Venn diagrams (Fig. 2 C, D), we identified 25 common DEGs that exhibited the same expression patterns, comprising 14 common upregulated genes and 11 common downregulated genes. Heat maps of the intersecting DEGs are depicted in Supplementary Figure 1.

3.2. GO and KEGG pathway analyses

GO analysis and KEGG pathway enrichment were performed to further examine the underlying biological data of these common DEGs. The top five entries of Biological Process (BP) in the GO enrichment analysis were observed to be female pregnancy, multi-organism reproductive process, multi-multicellular organism process, response to corticosterone, and neutrophil chemotaxis. Fig. 3A presents the top five entries of Cellular Component (CC) and Molecular Function (MF). The top five CC entries were specific granule, tertiary granule, protein-DNA complex, RNA polymerase II, and transcription regulator. The top five MF entries were CXCR chemokine receptor binding, chemokine activity, cytokine activity, chemokine receptor binding, and SMAD binding. The KEGG pathway enrichment analysis revealed that these genes were mainly enriched in the IL-17 signaling pathway, Rheumatoid arthritis, Lipid and atherosclerosis, TNF signaling pathway, and Osteoclast differentiation (Fig. 3B).

3.3. Screening of Hub Genes

Twenty-five common DEGs were imported into the online STRING database. We screened five genes employing three cytoHubba algorithms: MCC, BottleNeck, and Stress (Fig. 4A–C). Finally, we screened out three genes: CXCL1 (C-X-C Motif Chemokine Ligand 1), CXCL2 (C-X-C Motif Chemokine Ligand 2) and FOS (Fos Proto-Oncogene, AP-1 Transcription Factor Subunit) using the intersection of the Venn diagrams (Fig. 4D).

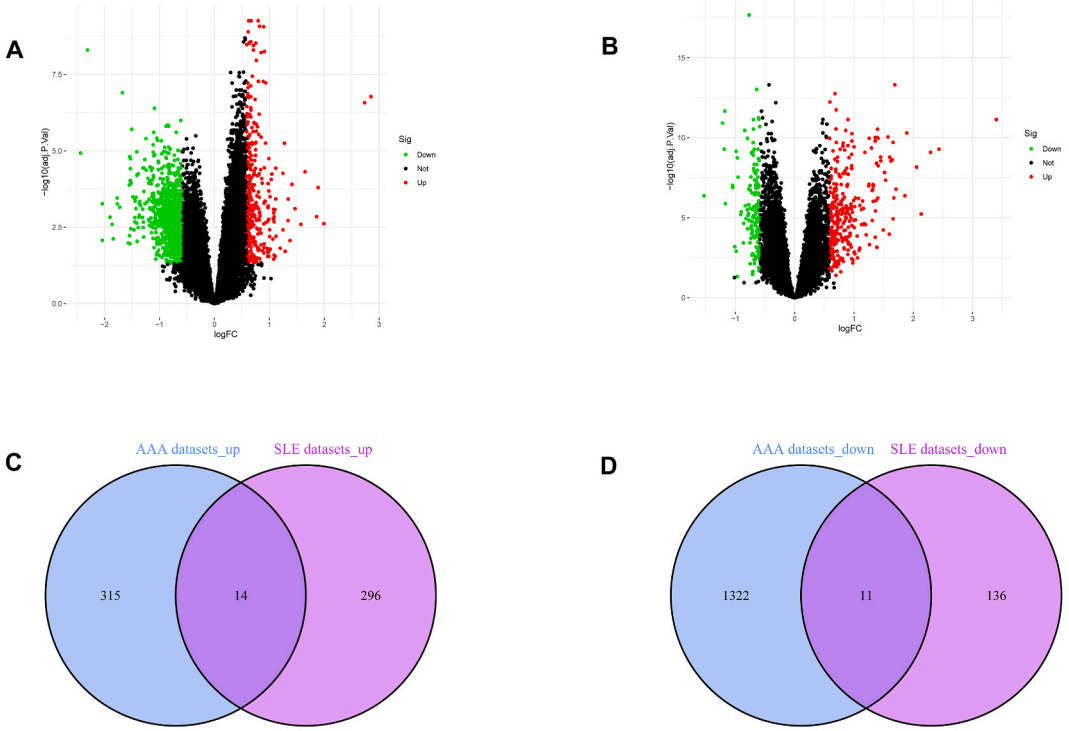

Fig. 2. Identification of common DEGs. (A) Volcano plot revealing 1615 DEGs between the AAA patients and healthy controls. (B) Volcano plot revealing 410 DEGs between SLE patients and healthy controls. (C–D) A total of 25 common DEGs with the same expression trends were found in the datasets, including 14 common upregulated genes and 11 common downregulated genes. AAA: abdominal aortic aneurysm; DEG: differentially expressed gene; SLE: systemic lupus erythematosus.

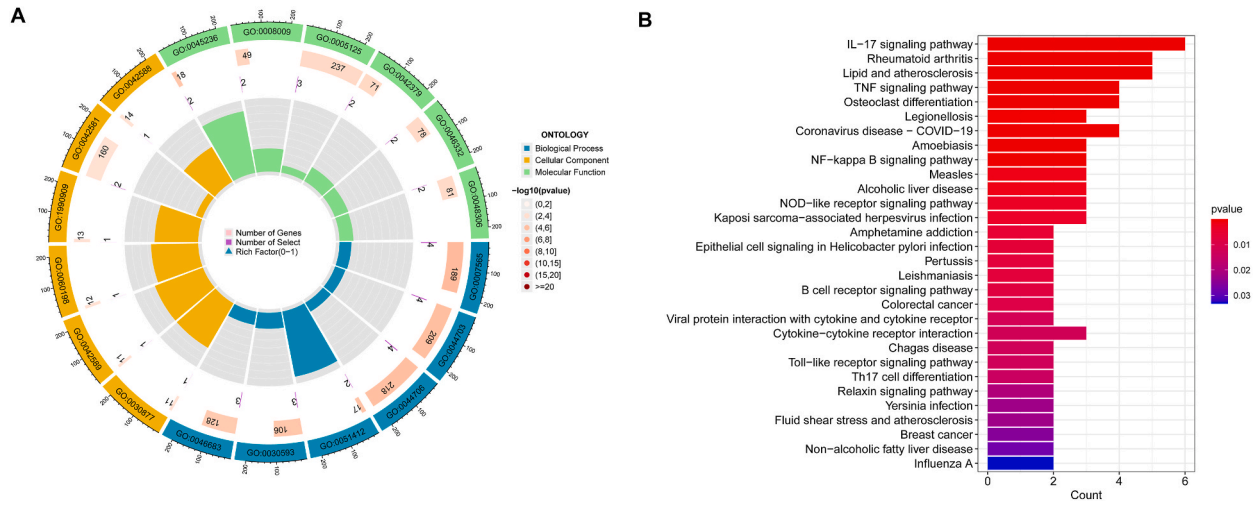

Fig. 3. GO and KEGG pathway enrichment analysis of the common DEGs. (A) GO terms in biological process, cellular component, and molecular function were used for functional enrichment clustering analysis on common DEGs. (B) KEGG pathway analysis was performed on common DEGs.: DEG: differentially expressed genes; GO: Gene Ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes.

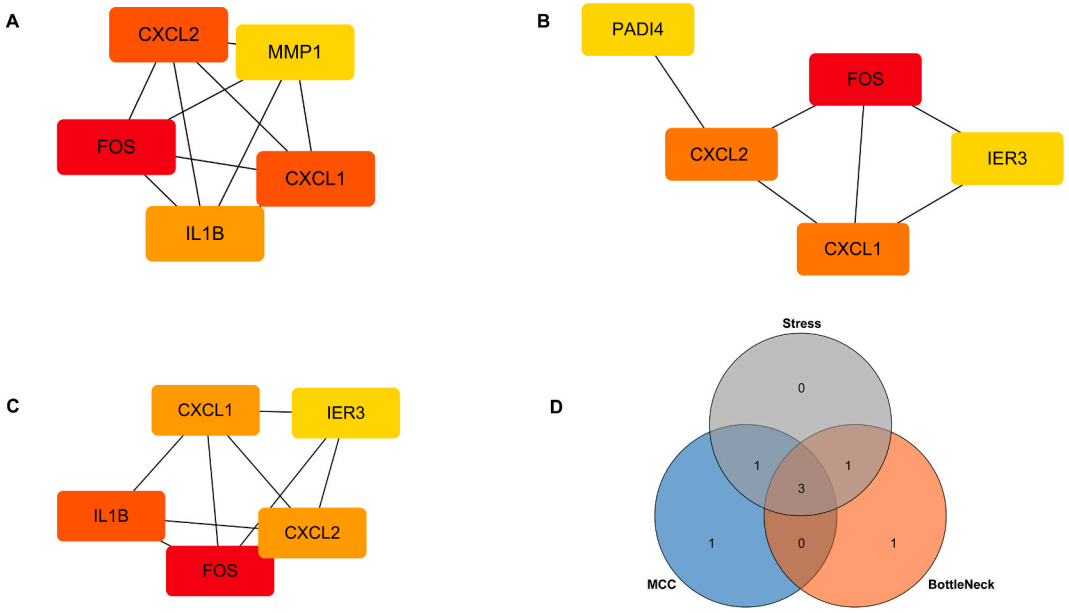

Fig. 4. Screening of Hub Genes. (A) Top 5 genes utilizing MCC algorithm. (B) Top 5 genes utilizing BottleNeck algorithm. (C) Top 5 genes utilizing Stress algorithm. (D) Three overlapping genes were filtered using venn diagram.

3.4. Validation of hub genes

Validation was performed in GSE47472 for AAA and GSE81622 for SLE from the GEO database. The results showed that in both AAA and SLE, only CXCL1 was significantly upregulated when compared to normal tissues (Fig. 5A–F). The hub gene was identified as CXCL1. We acquired the expression level of the hub gene and used the pROC package in R language to produce ROC curves and evaluate the accuracy of the diagnostic features (Fig. 6A–D). The AUC values for CXCL1 were greater than 0.7 in all datasets, indicating the hub gene's exceptional predictive abilities. CXCL1 can be regarded as a potential marker for the diagnosis of AAA and SLE.

3.5. Association between the hub gene and immune infiltration

The relationship between the hub gene and immune cells was investigated using the CIBERSORT software. The bar plot depicts the correlation between the 22 immune cells and the GEO datasets of AAA and SLE (Supplementary Figure 2). The violin plot of immune

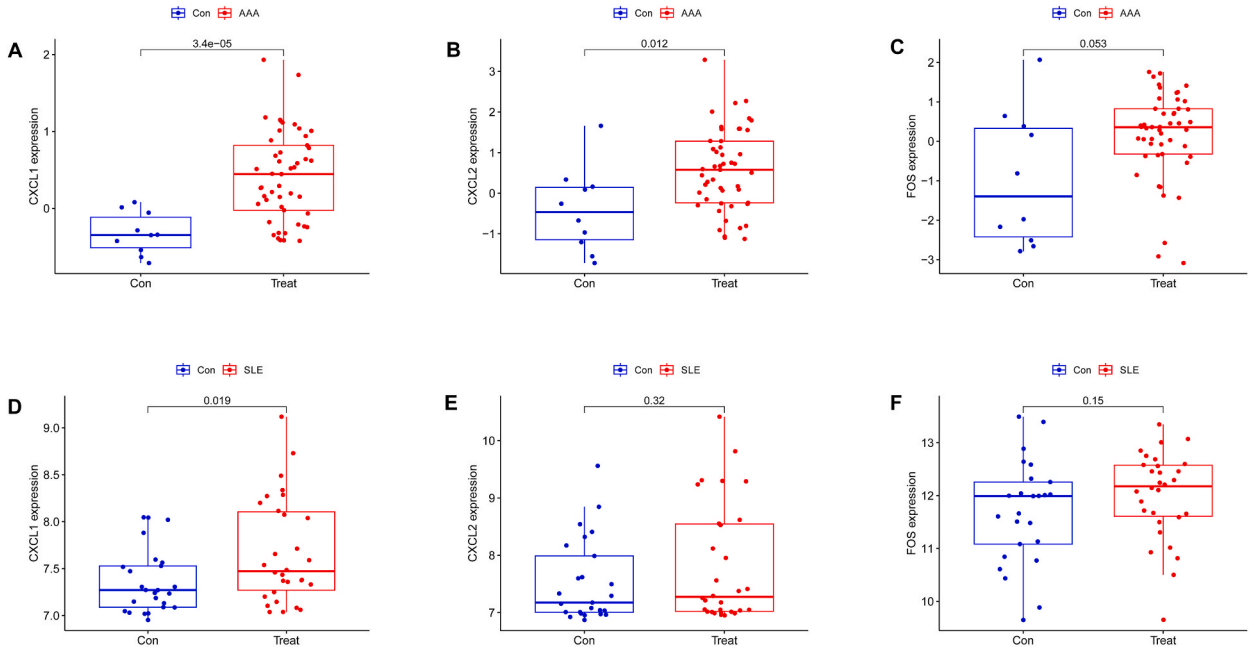

Fig. 5. Validation of hub genes. (A–C) CXCL1, CXCL2 and FOS were validated in GSE47472. The boxplots show that the expression level of the CXCL1 is higher in AAA samples. (D–F) CXCL1, CXCL2 and FOS were validated in GSE81622. The boxplots show that the expression level of the CXCL1 is higher in SLE samples.AAA: abdominal aortic aneurysm; SLE: systemic lupus erythematosus.

cell components showed that patients with AAA and SLE had a significantly higher level of monocytes and neutrophils (Fig. 7A and B). In the AAA datasets, we found a significant correlation between CXCL1 and neutrophils and monocyte activation ($p < 0.001$) (Fig. 8 A, B). Similarly, the correlation of CXCL1 with neutrophil activation was observed to be significant in SLE datasets ($p < 0.001$), while the correlation between monocyte activation and CXCL1 was not significant (Fig. 8C). The lollipop plot was used to illustrate the correlation coefficient of CXCL1 and immune cells (Fig. 9A and B). Overall results suggest a significant correlation of neutrophil activation with both AAA and SLE, as well as CXCL1.

3.6. Clinical data analysis

Clinical data of enrolled patients are presented in Tables 1 and 2. This study included patient variables like age, BMI, and gender. Immune cell data from routine blood tests were also obtained. We found a significant difference in gender, age, BMI, and neutrophils between patients with AAA and patients without AAA ($p < 0.05$) (Table 1). Table 2 shows a significant discrepancy in gender, age, BMI, white blood cells, erythrocytes, hemoglobin, platelets, and neutrophils between patients with and without SLE ($p < 0.05$). Next, we conducted univariate and multivariate binary logistic regression analyses on the variables that exhibited significant differences between the disease and control groups. Our data further revealed that gender, age, BMI, and neutrophils were correlated with AAA (Table 3). On the other hand, age, BMI, white blood cells, platelets, and neutrophils were correlated with SLE (Table 4).ROC curves were plotted to validate the predictive capability of neutrophils (Fig. 10A and B). The AUC values for neutrophils exceeded 0.7 in both AAA and SLE cases. To conclude, neutrophils demonstrated remarkable predictive abilities and were significantly distinctive in AAA and SLE patients as compared to non-AAA and non-SLE patients.

4. Discussion

Recent studies have shown that patients with SLE have an increased risk of developing AAA (7). However, the mechanism of comorbidity between AAA and SLE is still unclear. This study used bioinformatic analysis to explore the common hub genes and pathways associated with AAA and SLE in the GEO database. Our observation revealed a significant upregulation of CXCL1 in both AAA and SLE patients, showing the strongest correlation with neutrophil cells. Additionally, the relationship between neutrophil infiltration and the co-occurrence of AAA and SLE was further confirmed by routine blood tests of 460 patients. Neutrophils also exhibited good accuracy in predicting AAA and SLE. We, therefore, concluded that CXCL1 might play an important role in immune processes by affecting neutrophil infiltration during the progression of AAA and SLE.

CXCL1, also known as GRO alpha, NAP-3, or MGSA, belongs to the sub-family of CXC chemokine, and plays a major role in neovascularization, inflammatory response, wound healing, and tumor formation [25,26]. CXCL1 is expressed by macrophages, neutrophils, and epithelial cells, and its expression is known to increase during inflammatory responses, contributing to the process of inflammation [27]. CXCL1 acts as a key chemoattractant for neutrophils by binding specifically to its corresponding G-protein-coupled

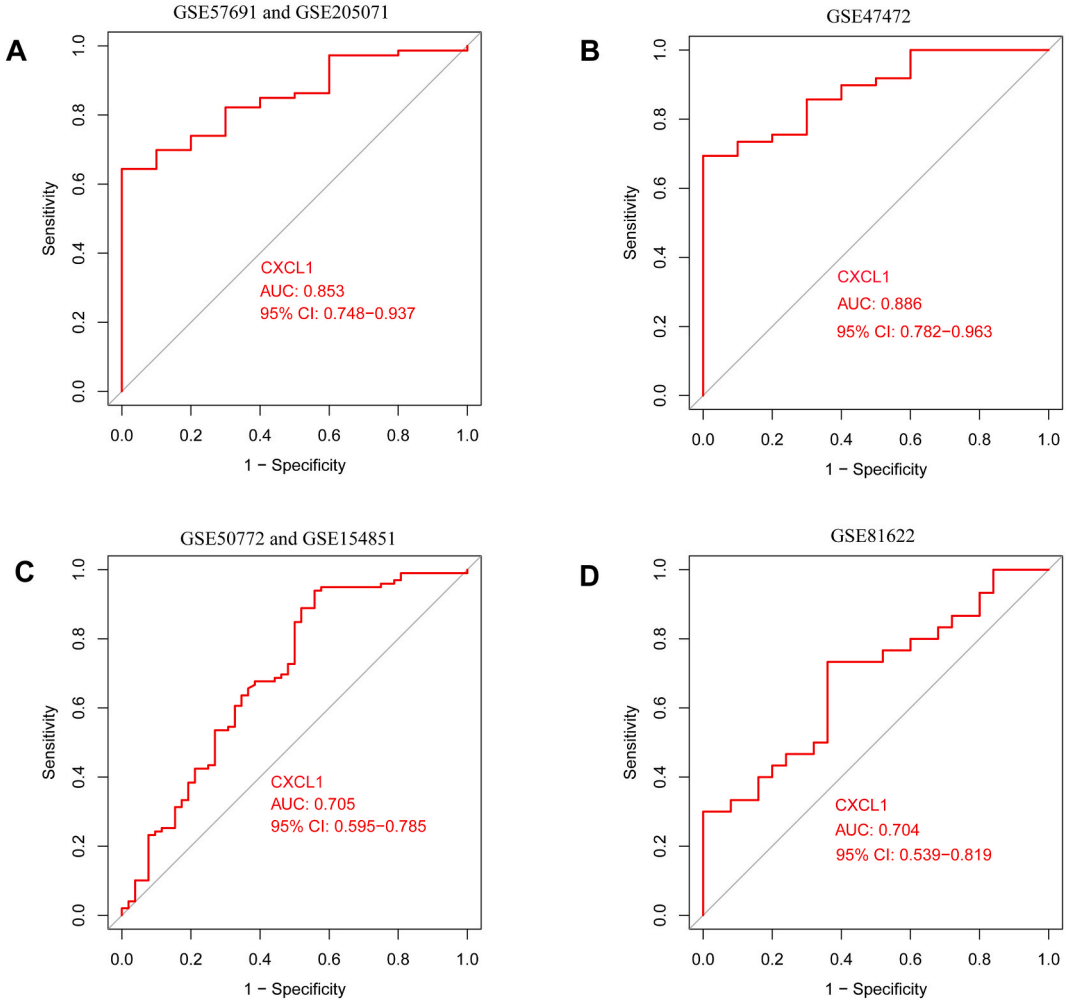

Fig. 6. ROC curves of hub gene in AAA and SLE. ROC curves were drawn to evaluate the accuracy of the hub gene in diagnosing AAA (A, B) or SLE (C, D).AAA: abdominal aortic aneurysm; AUC: area under curve; CI: confidence interval; SLE: systemic lupus erythematosus.

receptor, C-X-C Motif Chemokine Receptor 2 (CXCR 2), and promoting its recruitment to the site of injury or infection, thereby playing a crucial role in regulating immune and inflammatory responses [28,29]. The infiltration of neutrophils, monocytes, and macrophages into the arterial wall can cause the release of reactive oxygen species (ROS) and other pro-inflammatory mediators, leading to additional damage to blood vessels. This process can result in myocardial infarction, ischemia/reperfusion injury, atherosclerosis, and hypertension [30,31].

The molecular mechanism of AAA lesions and whether CXCL1 contributes to their formation and progression are currently unknown, and its related research is scarce. This study proposed that the chemotaxis of CXCL1 to neutrophils might mediate the occurrence and development of AAA. In the past decade, it has been regarded that macrophages and metalloproteinases play an important role in the development of AAA [32,33]. However, recent research has shed light on neutrophils' significance in AAA, which are known to play a pivotal role in several processes, such as oxidative stress, proteolytic degradation of the media layer, inflammation of adventitia, and intraluminal thrombus formation [34]. An animal study by Huang et al. found that neutrophil recruitment and the neutrophil cytokines, CXCL1/CXCL2, were suppressed in apo(*a*)tg mice in the abdominal aortic aneurysm model [35]. In apo(*a*)tg mice, reconstitution of CXCL1 or CXCL2 is reported to restore neutrophil recruitment. In a separate study, Pope et al. investigated the impact of D-series resolvin (RvD) on AAA murine models. The results showed that several pro-inflammatory cytokines, including CXCL1, were elevated in non-treated animals when compared to RvD-treated animals RvD treatment in animals with small AAA demonstrated a 25% reduction in AAA size, suggesting its protective role in AAA pathogenesis [36].

Although the role of CXCL1 in autoimmune diseases is unclear, its involvement in the pathogenesis of SLE has been widely accepted [37]. In addition, several reports suggest that neutrophils may contribute significantly to promoting innate and adaptive aberrant autoimmunity and tissue damage in SLE. Kanapathippillai et al. stated that CXCL1 was among the elevated chemokines in primary mesangial cells of (NZBxNZW)F1 (B/W) mice with SLE, activated by either nucleosomes alone or nucleosome-IgG complexes. This activation caused the infiltration of neutrophils, macrophages, and T and B cells [38]. A study by Wang et al. [39] in a murine model of

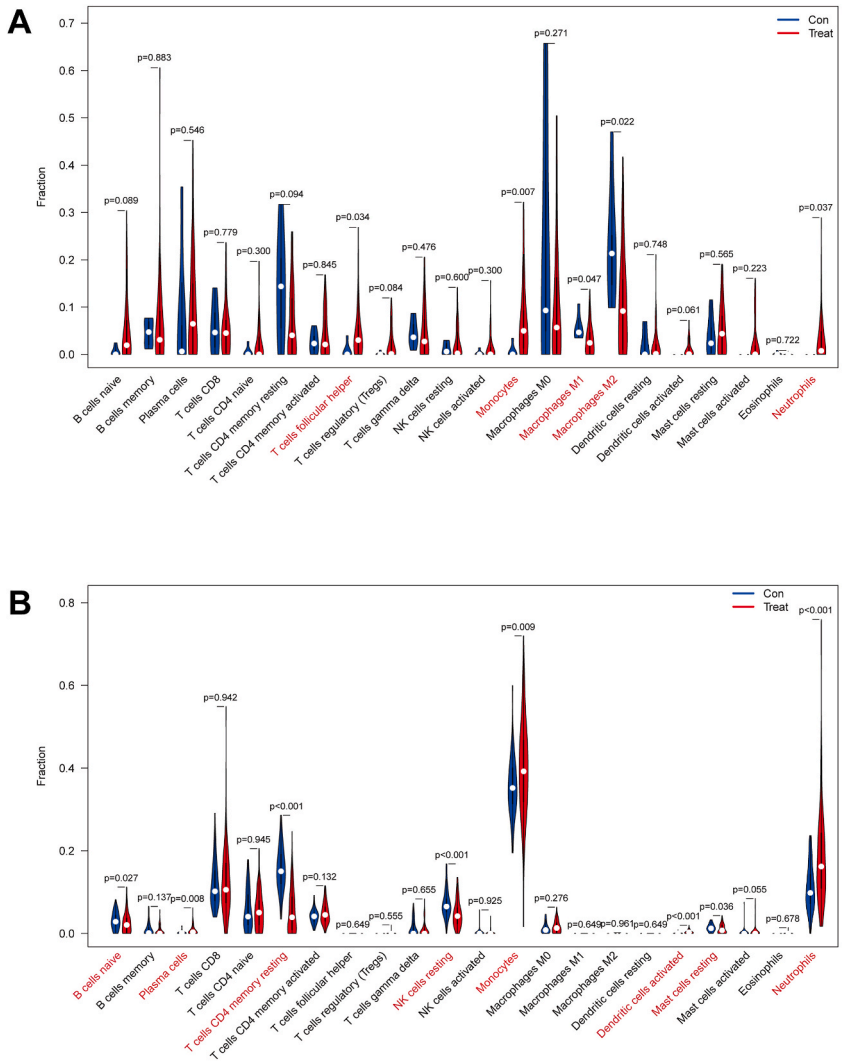

Fig. 7. Immune cells violin plot of AAA and SLE datasets. (A) Indicates the differences in the composition of the 22 immune cells based on AAA datasets. (B) Indicates the differences in the composition of the 22 immune cells based on SLE datasets.

lupus reported elevated levels of CXCL1, MCP-1, antisnRNP, and *anti*-dsDNA in pristane-treated wild-type (WT) mice compared to untreated mice. These findings confirmed that CXCL1 might be involved in developing SLE and regulating active neutrophils' recruitment into inflamed tissue.

Recent studies have reported the significance of neutrophil extracellular traps (NETs) in AAA and SLE. NETs are extracellular networks of DNA, histones, and granule proteins formed by neutrophils in the presence of pathogens and as a response to an inflammatory stimulus. This process of programmed cell death is different from apoptosis and necrosis and is known as NETosis [40]. Recent research suggests that high-density lipoprotein (HDL) can undergo modifications by active oxidative enzymes that are externalized in NETs. As a result, HDL loses its anti-inflammatory and vasoprotective properties, and its capacity to mediate reverse cholesterol transport is impaired [41]. McMahon et al. discovered that SLE patients display pro-inflammatory forms of HDL, and they implicated that NETs may play a key role in the proatherogenic lipoprotein modification in lupus [42]. This finding suggested that NETs may play an important role in the development of AAA in patients with SLE.

In our investigation, we employed bioinformatics techniques to identify differentially expressed genes (DEGs) in AAA and SLE and recognized CXCL1 as the hub gene. Subsequently, we confirmed the significant upregulation of neutrophils in AAA and SLE datasets and their regulation by CXCL1. Our results were further strengthened by clinical data analysis, thereby increasing the reliability of our findings. Our study provides novel insights into the pathogenesis of abdominal aortic aneurysm and systemic lupus erythematosus by highlighting a common factor: immune-dysregulated neutrophils, which are characterized by the upregulation of CXCL1. This discovery offers potential opportunities for research and development of targeted treatments for both diseases, ultimately improving patient outcomes and enhancing their quality of life.

Our study had a few limitations. At first, patients with only AAA or SLE, not both diseases, were used to validate the hub gene of

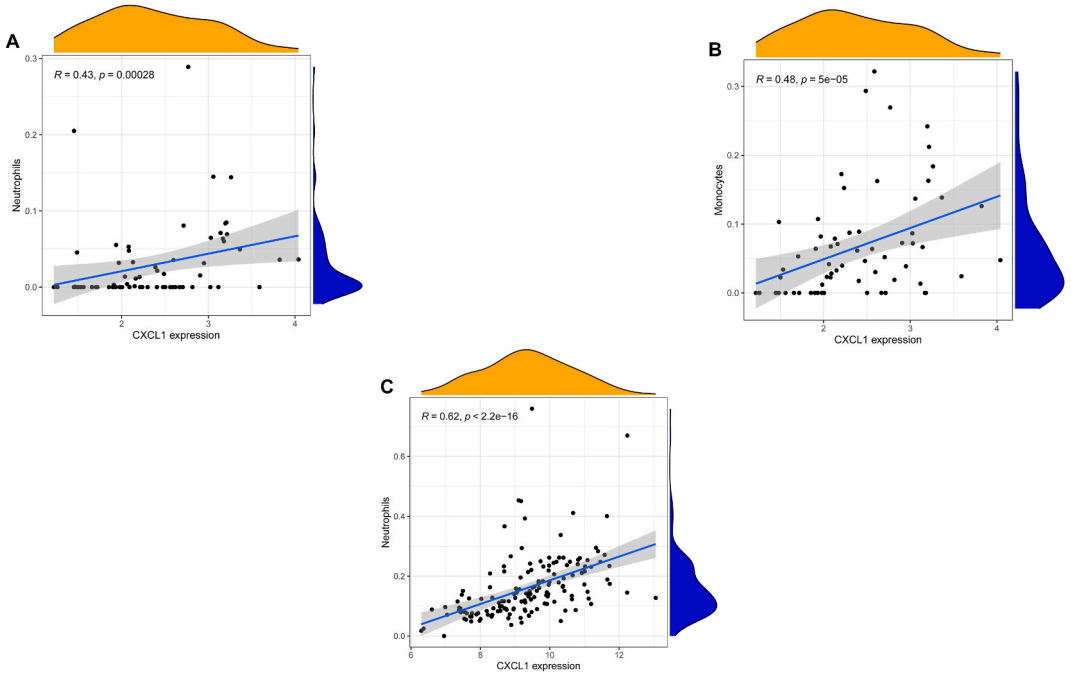

Fig. 8. (A–B) Correlation plot of CXCL1 with neutrophils and monocytes activation in AAA datasets. (C) Correlation plot of CXCL1 with neutrophils activation in SLE datasets.

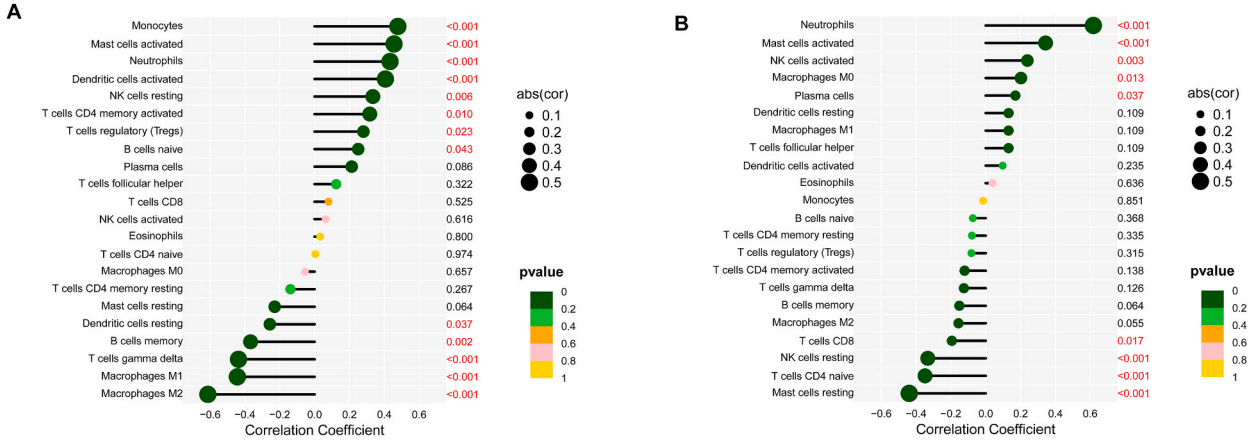

Fig. 9. (A) Correlation coefficient of CXCL1 with 22 immune cells in AAA datasets. (B) Correlation coefficient of CXCL1 with 22 immune cells in SLE datasets.

AAA and SLE. The lack of datasets at the present time, including patients in AAA combined with SLE, made the validation unattainable. Second, due to the unavailability of related cases, we did not have enough clinical data on patients in AAA combined with SLE; hence, patients with only AAA or SLE were enrolled in this study. However, we would collect clinical data of patients with both AAA and SLE in multi-centers and establish a diagnostic model of AAA combined with SLE in future studies. Third, the hub gene and the key pathway identified in the present study have not been validated in laboratory experiments. Fourth, the GEO datasets lacked information on SLE disease activity. Therefore, this study could not thoroughly explore the impact of SLE activity on AAA development. We hope to examine this relationship in greater depth in future research.

5. Conclusion

This bioinformatics research highlights CXCL1 as the hub gene for the co-occurrence of AAA and SLE. The infiltration of neutrophils is a critical element in the progression of AAA and SLE and could be considered as a prospective diagnostic and therapeutic target.

Table 1
Baseline characteristics between AAA patients and non-AAA patients.

Characteristics	levels	AAA (N = 151)	Non-AAA (N = 154)	p
Gender	Male	101 (66.9%)	79 (51.3%)	0.01
	Female	50 (33.1%)	75 (48.7%)	
Age	Median (IQR)	70.00 (63.00–75.00)	52.00 (42.00–65.00)	<0.001
BMI	Median (IQR)	22.49 (20.56–24.45)	24.13 (21.78–26.45)	<0.001
White blood cells	Median (IQR)	6.85 (5.73–9.52)	7.96 (6.15–10.19)	0.05
Erythrocytes	Mean ± SD	4.14 ± 0.73	4.26 ± 0.77	0.14
Hemoglobins	Median (IQR)	120.20 (104.05–132.55)	122.00 (105.60–133.50)	0.56
Platelets	Median (IQR)	224.50 (184.80–268.45)	230.05 (172.00–296.80)	0.68
Neutrophils	Median (IQR)	6.51 (4.28–8.69)	3.54 (2.83–4.78)	<0.001
lymphocytes	Median (IQR)	1.47 (1.06–1.88)	1.53 (1.16–1.90)	0.32
Monocytes	Median (IQR)	0.49 (0.43–0.62)	0.52 (0.43–0.65)	0.12
Eosinophils	Median (IQR)	0.18 (0.07–0.27)	0.14 (0.08–0.25)	0.24
Basophils	Median (IQR)	0.03 (0.02–0.05)	0.03 (0.02–0.04)	0.58

BMI: body mass index.

Table 2
Baseline characteristics between SLE patients and non-SLE patients.

Characteristics	levels	SLE (N = 155)	Non-SLE (N = 154)	p
Gender	Male	39 (25.2%)	79 (51.3%)	<0.001
	Female	116 (74.8%)	75 (48.7%)	
Age	Median (IQR)	33.00 (21.00–43.00)	52.00 (42.00–65.00)	<0.001
BMI	Median (IQR)	20.83 (19.05–23.09)	24.13 (21.78–26.45)	<0.001
White blood cells	Median (IQR)	5.32 (4.10–7.45)	7.96 (6.15–10.19)	<0.001
Erythrocytes	Mean ± SD	3.89 ± 0.78	4.26 ± 0.77	<0.001
Hemoglobins	Mean ± SD	104.57 ± 22.55	119.18 ± 21.48	<0.001
Platelets	Median (IQR)	163.20 (119.80–245.00)	230.05 (172.00–296.80)	<0.001
Neutrophils	Median (IQR)	6.65 (4.54–8.64)	3.54 (2.83–4.78)	<0.001
lymphocytes	Median (IQR)	1.56 (0.90–1.85)	1.53 (1.16–1.90)	0.30
Monocytes	Median (IQR)	0.43 (0.22–0.74)	0.52 (0.43–0.65)	0.11
Eosinophils	Median (IQR)	0.13 (0.08–0.18)	0.14 (0.08–0.25)	0.10
Basophils	Median (IQR)	0.02 (0.02–0.04)	0.03 (0.02–0.04)	0.17

BMI: body mass index.

Table 3
Univariate and multivariate logistic regression used for identifying independent diagnostic factors to distinguish AAA patients from healthy controls.

Variables	Univariate analysis		Multivariate analysis	
	OR (95%CI)	p-value	OR (95%CI)	p-value
Gender	0.52 (0.33–0.83)	0.006	0.51 (0.26–0.96)	0.040
Age	1.11 (1.08–1.14)	<0.001	1.11 (1.08–1.15)	<0.001
BMI	0.90 (0.84–0.96)	0.001	0.90 (0.82–0.99)	0.027
Neutrophils	1.65 (1.45–1.90)	<0.001	1.66 (1.42–1.97)	<0.001

BMI: body mass index.

Table 4
Univariate and multivariate logistic regression used for identifying independent diagnostic factors to distinguish SLE patients from healthy controls.

Variables	Univariate analysis		Multivariate analysis	
	OR (95%CI)	p-value	OR (95%CI)	p-value
Gender	3.13 (1.95–5.11)	<0.001	1.95 (0.88–4.39)	0.100
Age	0.93 (0.91–0.94)	<0.001	0.94 (0.91–0.96)	<0.001
BMI	0.78 (0.72–0.84)	<0.001	0.83 (0.74–0.93)	0.001
White blood cells	0.78 (0.71–0.85)	<0.001	0.75 (0.65–0.86)	<0.001
Erythrocytes	0.54 (0.40–0.73)	<0.001	0.67 (0.31–1.40)	0.302
Hemoglobins	0.97 (0.96–0.98)	<0.001	0.99 (0.96–1.02)	0.487
Platelets	0.99 (0.99–1.00)	<0.001	0.99 (0.99–1.00)	0.003
Neutrophils	1.78 (1.56–2.06)	<0.001	1.84 (1.53–2.27)	<0.001

BMI: body mass index.

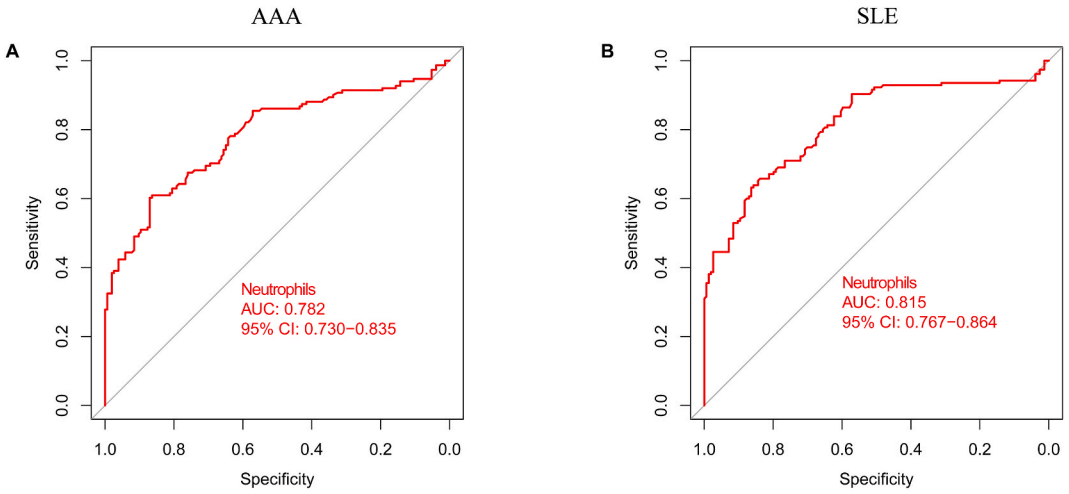

Fig. 10. ROC curves of neutrophils in AAA and SLE.

Ethics statement

This study was approved by the Ethics Committee of The First Affiliated Hospital of Guangxi Medical University. Informed consent forms were signed by the volunteers who participated in this study. The approval number: 2023-E019-01.

Author contribution statement

Lin Zhang: Conceived and designed the experiments; Wrote the paper.
Que Li: Conceived and designed the experiments; Wrote the paper.
Chenxing Zhou: Conceived and designed the experiments; Wrote the paper.
Zhanman Zhang: Analyzed and interpreted the data.
Jiangfeng Zhang: Contributed reagents, materials, analysis tools or data.
Xiao Qin: Contributed reagents, materials, analysis tools or data; Wrote the paper.

Data availability statement

Data included in article/supp. material/referenced in article.

Funding statement

The funding source of this study is the National Natural Science Foundation of China: 81960091, and Prof. Xiao qin from the First Affiliated Hospital of Guangxi Medical University is the recipient.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

The authors are very grateful to Prof. Xiao Qin(Vascular Surgery Ward, The First Affiliated Hospital of Guangxi Medical University) for support in all stages of this study.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.heliyon.2023.e18037.
AAA: abdominal aortic aneurysm; AUC: area under curve; CI: confidence interval; SLE: systemic lupus erythematosus.

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