Research Article

Exosome Derived from Human Umbilical Cord Mesenchymal Cell Exerts Immunomodulatory Effects on B Cells from SLE Patients

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1. Introduction

Systemic lupus erythematosus (SLE) is a chronic systemic autoimmune disease of unknown etiology, affecting predominantly women of reproductive age [1]. Conventional SLE therapies, such as immunomodulatory agents and immunosuppressive drugs, remain limited, and the inflammatory milieu is only temporarily effectively controlled when the lupus disease is under flaring condition. Long-term immunosuppression is often required; however, these immunosuppressive drugs can potentially induce infection, secondary malignancy, and organ failure [2]. Therefore, finding effective therapeutic options with mild side effects and enduring immunosuppressive effects is urgent.

Due to the immunomodulatory potential, human umbilical cord mesenchymal stem cells (hucMSCs), extracted from donor sources through noninvasive procedures, exerting immunosuppressive and hematopoiesis-supportive effects [3], have been increasingly investigated in the context of SLE and other immunologic diseases [4]. They can block specific effector cells in SLE [5], the generation of regulatory T cell subset, and release various anti-inflammatory cytokines, including interleukin-10 (IL-10) and transforming growth factor (TGF)β1 [6], indicating that hucMSCs are a promising approach to controlling SLE disease. However, this creates a concern about a potential
tumorigenic effect after MSC implantation [7]. Compared with hucMSCs-based therapy, human umbilical cord mesenchymal stem cell-derived exosomes (hucMSCs-Exo) based cell-free treatment has the advantages of nontumorigenicity, high stability, and no vascular obstruction [8]. Up to now, whether and how hucMSCs-Exo regulates SLE immune response is still unknown.

Recent studies have shown that exosomes exert critical regulatory effects on the physiological functions of recipient cells via regulating miRNAs [9]. To date, miR-155, a highly conserved miRNA among mammals serving as a critical regulator of cell proliferation [10], is one of the most highly implicated miRNAs in autoimmunity. Available data demonstrated that miR-155 has a robust regulatory function in B cells [11]. SLE’s immune response hallmark is the autoantibodies’ production by autoreactive B cells reacting to self-antigens and triggering an overwhelming inflammatory response, resulting in multifaceted immune modulation, including deficiency and hyperactivity of the immune system [12]. Although the therapeutic efficacy of hucMSCs-Exo has not been discussed in the context of SLE, the anti-inflammatory, immunomodu latory, and other potentials of hucMSCs-Exo have been demonstrated in many other diseases. Therefore, it is reasonable to hypothesize that hucMSCs-Exo may attenuate inflammation and regulate the immune response of B cells in SLE patients by regulating miR-155 and its target gene.

To confirm our hypothesis, we first demonstrated the immunomodulatory effects of hucMSCs-Exo on SLE patients’ B cell proliferation, apoptosis, activation, and inflammation in an in vitro cell experiment. Then, we explore and characterize the underlying biological mechanism of the immunomodulatory effect of hucMSCs-Exo through coculture inhibition of miR-155 and hucMSCs-Exo.

2. Materials and Methods

2.1. Patients and Controls. Twenty-eight SLE patients with no history of corticosteroids or immunosuppressive drug use were recruited from the General Hospital of the Central Theater Command from January 2022 to May 2022. All the enrolled SLE patients had not taken glucocorticoids or immunosuppressive agents when they came to our hospital for diagnosis and treatment. The SLE patients fulfilled the 1997 SLE classification criteria revised by the American College of Rheumatology [13]. Twenty-two ethnically, age- and sex-matched healthy controls (HC), who had no history of autoimmune or inflammatory diseases themselves and in their families, were also recruited into the present study. All participants signed written informed consent, and the Ethics Committee approved the study of the General Hospital of Central Theater Command (approval no. [2021]065-02).

2.2. Sample Collection and Preparation. Peripheral blood of SLE patients and healthy controls were collected. The blood of SLE patients was collected prior to therapy with glucocorticoids and immunosuppressive agents. Diluted with equal proportion phosphoric acid buffered brine (PBS). Peripheral blood mononuclear cells (PBMCs) were prepared by Ficoll-Plaque (Multi-Sciences Biotech, China) density gradient centrifugation (2,000 rpm, 23°C, 30 min), washed in PBS (Biosharp, China) twice, and then resuspended in RPMI 1640 culture medium (Gibco, USA) at a concentration of 2 × 10^6 cells/mL. Further, 10% fetal bovine serum Premium (PAN FBS, Germany) and 1% penicillin/streptomycin were supplemented with cells at 37°C with 5% CO_2.

A typical panel of markers used to identify the significant subset of lymphocytes included CD3 (clone: UCHT1), CD4 (clone: RPA-T4), CD8 (clone: RPA-T8), CD19 (clone: HIB19), and CD16 + 56 (clone: 3G8). The isolated PBMCs were resuspended with appropriate amount of PBS. For the staining of surface antigens, cells were incubated with FITC-conjugated anti-CD3, APC-conjugated anti-CD4, PE-conjugated anti-CD8, APC-conjugated anti-CD19, and PE-conjugated anti-CD16 + 56 (all from BioLegend Bioscience, USA). Mouse anti-human FITC-, PE-, and APC-conjugated IgG1 were used as isotype controls. The samples were detected by flow cytometry (Agilent NovoCyte, Model number: D2040, China) and analyzed by NovoExpress software. The supernatant of PBMC was taken, and IL-6, IL-10, IFN-γ, IL-17, IL-4, and TNF-α were detected by flow cytometry with multiple microspheres according to the manufacturer’s instructions and analyzed by LEGENDplex software.

2.3. Preparation and Identification of hucMSCs. hucMSCs were provided by the Basic Medical Laboratory of the General Hospital of the Central Theater Command. hucMSCs at passage 3 were resuscitated, then cultured in α-MEM complete medium (10% fetal bovine serum + 1% double antibody + α-MEM basal medium), incubated in 5% CO_2 and 37°C. The protocol for preparation and identification of huMSCs was published previously [14]. Briefly, cells were observed under an inverted microscope and were in good condition. The cells were collected and centrifuged, and the concentration of cells was adjusted to 1 × 10^6 cells/mL in PBS. According to Biolegend instructions, huMSCs labeled with flow cytometry were stained for immunophenotype characterization. The antibody contains three positive markers (FITC-CD73, PE-CD90, and FITC-CD105) and five negative cocktails (APC-CD34, PerCP-CD45, PE-CD11b, APC-CD19, and PerCP-HLA-DR) [14], as well as their isotype controls. Analysis was performed in a flow cytometer (Agilent NovoCyte, China). huMSCs at passage 3 were cultured in stem cell osteogenic and adipogenic differentiation media (Stemcell, Canada) to identify the differentiation properties. To identify differentiation characteristics, huMSCs of the third generation were cultured in stem cell osteogenic and adipogenic differentiation medium (Stemcell, Canada) for 23 days according to the manufacturer’s protocol. huMSCs were fixed and dyed with Alizarin red for osteogenic cells and Oil red for adipose cells. Cells cultured in normal medium served as controls.

2.4. Extraction and Identification of hucMSCs-Exo. The huMSCs were cultured with a fusion rate of 60%–70%. After being replaced with serum-free MEM medium (α-MEM, TBD, China) for 48 hr, the cell supernatant was collected and centrifuged at 300 g successively for 10 min, another 10 min at 2,000 g, followed by 30 min at 20,000 g, all at 4°C. Finally, the supernatant was centrifuged at high speed at...
120,000 g for 70 min at 4°C. The precipitate was resuspended with aseptic PBS buffer solution at 4°C, then centrifuged at 120,000 g for 70 min, and an appropriate amount of aseptic PBS was resuspended, filtered by a 0.22 μm filter, and frozen at −80°C for later use.

Transmission electron microscope was used to observe the characteristic morphologies of the exosomes. (HITACHI Transmission Electron Microscope HT7700). The distribution of particle size of hucMSCs-Exo was analyzed using a nanoparticle tracking analysis system (Particle Metrix, Meerbusch, Germany). Surface markers of exosomes, including CD63 (PE, Biolegend, USA) and CD81 (APC, Biolegend, USA), were detected by flow cytometry.

2.5. Coculture of PBMCs with hucMSCs or hucMSCs-Exo. hucMSCs were plated in six-multiwell flat bottom culture plates (NEST, China) at 5 × 10⁴ cells/well density and cultured in basal medium supplemented with FBS (10%). After 6 hr for cell adhesion, the medium was aspirated and replaced with fresh PBMCs at 5 × 10⁵ cells/well, corresponding to a ratio of hucMSCs/PBMC 1 : 10. To assess apoptosis, PBMCs were collected after coculture using Annexin V-FITC/PI apoptosis kit (MULTI Sciences, China) according to the manufacturer’s instructions, centrifuged at 1,500 rpm for 5 min, washed with PBS, and resuspended in 500 μL 1× binding buffer. B cells were sorted by sequentially adding 5 μL CD19 (APC, Biolegend, USA), then incubated with FITC and PI for 15 min at room temperature and then analyzed by flow cytometry (Agilent NovoCyte, Model number: D2040, China).

The concentration of purified hucMSCs-Exo was measured via BCA protein concentration Assay Kit (Solarbio, China). To select the optimal concentration of hucMSCs-Exo for the subsequent experiments, a series of concentrations of hucMSCs-Exo, including 20, 50, 100, and 200 μg/mL, was prepared. The optimal concentration was determined according to the minimum concentration that could promote cell apoptosis.

2.6. Cell Apoptosis, Cell Proliferation Assays, and B Cell Activation Detection Assays. Cell apoptosis was detected by Annexin V-FITC/PI apoptosis kit, flow cytometry, and NovoExpress analysis. The apoptosis rate of B cells was detected by flow cytometry. PBMCs were isolated from SLE participants and had no further stimulation with anti-CD3 and anti-CD28. In addition to healthy controls, all PBMCs were collected after 72 hr and analyzed by Agilent NovoCyte flow cytometer and NovoExpress software.

To assess the proliferative stimulatory activity of hucMSCs and their exosomes, we labeled 1 × 10⁵ PBMCs with cell tracking CFSE (Beyotime Biotechnology, China), which were cocultured with hucMSCs or hucMSCs-Exo isolated from passages 3, 6, and 9, as described in the manufacturer’s instructions. These PBMCs were isolated from SLE participants and had no further stimulation with anti-CD5 and anti-CD28. In addition to healthy controls, all PBMCs were collected after 72 hr and analyzed by Agilent NovoCyte flow cytometer and NovoExpress software.

Table 1: Primers sequences for qRT-PCR.

<table>
<thead>
<tr>
<th>Primers</th>
<th>Sequences (5’ to 3’)</th>
</tr>
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<tbody>
<tr>
<td>mir-155-5p F</td>
<td>GGGTTAATGCTAATGCTGAT</td>
</tr>
<tr>
<td>mir-155-5p R</td>
<td>CAGTGCGTGCTCAGTGGGT</td>
</tr>
<tr>
<td>mir-155-5p R</td>
<td>GTCGTATCCCAGTGCTGTCGAGTC</td>
</tr>
<tr>
<td>SHIP-1 F</td>
<td>CATCTACAGGCTTCTCACCC</td>
</tr>
<tr>
<td>SHIP-1 R</td>
<td>TCACGTCCTGCTTCCAAPA</td>
</tr>
<tr>
<td>U6 F</td>
<td>CTGGCTTTCGGCAGCACAAA</td>
</tr>
<tr>
<td>U6 R</td>
<td>AAGCCTTACAGAAATTGGGT</td>
</tr>
<tr>
<td>GAPDH F</td>
<td>GGAGTCACACTGGGGCTTCAC</td>
</tr>
<tr>
<td>GAPDH R</td>
<td>GTCTAGAGTCTTCTCCAGATACC</td>
</tr>
</tbody>
</table>

PBMC was cocultured with huc-MSCs and hucMSCs-Exo for 0, 4, 12, 24, and 36 hr, and PBMC was collected to evaluate B cell activation. CD19- (APC, Biolegend, USA) labeled B cells and CD69 (PE, Biolegend, USA) were used to detect B cell activation, which was protected from light for 15 min, and analyzed by flow cytometry and NovoExpress software.

2.7. RNA Extraction and qPCR Analysis. Total RNA was extracted from PBMCs using Trizol Reagent (TaKaRa, Japan). First, proper amount of chloroform was added and centrifuged. A new enzyme-free EP tube was taken out and 400 μL isopropl alcohol was added. After centrifugation, proper amount of RNA from the upper layer was taken and added to it. RNA was reverse-transcribed into cDNA using Thermo Scientific ReverTaid RT kit (Thermo Scientific, USA). qRT-PCR was performed using TB Green Premix Ex Taq II (Tli RNaseH Plus, TaKaRa, Japan), followed by testing using the LightCycler 96 PCR instrument (Roche, Tusem, China). U6 or GAPDH was used as internal parameters, and the relative expression levels of miRNAs or mRNAs were calculated by 2−ΔΔCt. Primer sequences were acquired from Big Tech Solutions (Beijing Liuhe, China) (Table 1).

2.8. Cell Transfection. PBMCs were transfected with the indicated miRNA antagonirs or NCs using Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA) following the manufacturer’s instructions. Twenty-four hours after transfection, cells were collected for subsequent coculture with hucMSCs-Exo to detect B cell apoptosis, proliferation, activation, and cytokines. Antagomir-155 and antagonir-NC were designed and synthesized by RiboBio Biotechnology (Guangzhou, China).

2.9. Plasmid Construction and Luciferase Reporter Assay. The possible miRNA-binding sites on the SHIP-1 were predicted using the TargetScan, miRDB, and miRWalk databases. BrieFLY, the miR-155-binding sites in the SHIP-1 3'-UTR sequence were cloned into a psiCHECK-2 vector (YouBiao, Hunan, China). For the luciferase reporter assay, 293T cells were cotransfected with the luciferase reporter plasmids combined with miR-155 mimics or controls, respectively. After 24 hr of transfection, the cells were lysed and measured for luciferase activities using the chemiluminescence immune analyzer (Compson, Shijiazhuang, China) following the manufacturer’s protocols.

2.10. Western Blotting Analysis. Cultured cells were collected and centrifuged for 5 min at 1,500 rpm, cell lysate containing...
protease and phosphorylase (Beyotime, China) was added, and total protein was extracted by lysis on ice. Sample handling and concentration determination were carried out according to the instructions in the BCA protein Quantification kit (Beyotime, China). After protein denaturation, gel making, load sample, separated by electrophoresis, transferred to PVDF membrane (Millipore, MA, USA), and blocked with 5% skim milk powder. For primary antibodies, antibody β-tubulin was diluted 1 : 50,000, and SHIP-1, p-ERK, and ERK were diluted 1 : 1,000 according to the manufacturer’s instructions and incubated with membranes overnight at 4°C. Next, the cells were incubated with the corresponding secondary antibody (HRP-conjugated goat anti-rabbit antibodies, 1 : 600, Beyotime, A0208).

2.11. Statistical Analysis. Data were analyzed using GraphPad Prism Version 8.0. All data were presented as mean ± standard deviation (SD). Differences between the two data sets were statistically analyzed using the Student t-test while comparisons between multiple groups were done by one-way analysis of variance. Statistically significant level was set at $P$ value <0.05.

3. Results

3.1. Absolute Numbers of CD19+ B Cells Increased in SLE Patients. A total of 28 patients diagnosed with SLE and 22 healthy controls were included. Compared with healthy controls, the absolute numbers of CD3+ T cells (Figure 1(a)), CD4+ T cells (Figure 1(b)), and NK cells (Figure 1(c)) were significantly downregulated. In contrast, the absolute numbers of CD19+ B cells (Figure 1(d)) increased in SLE patients, and the levels of IL-6, IL-10, and TNF-α in SLE patients significantly increased. The levels of IL-4 decreased (all $P < 0.05$) (Figure 1(e)). The demographic information and some other clinical manifestations of enrolled participants are also detailed in Table 2.

3.2. Isolation and Identification of hucMSC and hucMSC-Exo. hucMSCs were cultured for 2 weeks after being successfully isolated. hucMSCs around the tissue block showed fibroblast-like morphology and were attached to the surface of the culture flask. After passage, hucMSCs proliferated and arranged in a spiral pattern (Figure 2(a)). Osteogenic and adipogenic differentiation of hucMSCs were confirmed using alizarin red staining (Figure 2(b)) and Oil red O staining (Figure 2(c)). Flow cytometry results demonstrated that the positive markers, including CD73, CD90, and CD105, were highly expressed. Furthermore, the negative markers (CD11b, CD19, CD34, CD45, and HLA-DR) were not expressed (Figure 2(d)).

The supernatant of the third to seventh passages of hucMSC-Exo was selected and purified by continuous ultrahigh-speed centrifugation. hucMSCs-Exo is purified from the serum-free supernatant of hucMSCs by continuous ultrahigh-speed centrifugation. Transmission electron microscope results showed...
spherically shaped vesicles within a size range of exosomes (Figure 2(e)). The sizes of exosomes were characterized by a nanoparticle tracking analysis system which tracks the dynamics of particle movement and approximates it with Brownian motion to obtain size information. The average size of exosomes was approximately 130 nm in diameter (Figure 2(e)). The sizes of exosomes were characterized by a spherically shaped vesicles within a size range of exosomes.

3.3. hucMSCs-Exo Promoted B Cell Apoptosis, Inhibited Proliferation, and Prevented Overactivation and Inflammation.

To assess the effects of hucMSCs-Exo on B cells in vitro, we cocultured PBMC of SLE patients with hucMSCs-Exo, then sorted B cells by CD19 after coculture. Although this study focused on exosomes, hucMSCs were also included as a control group to compare the effects of hucMSCs-Exo and hucMSCs. We found that miR-155 expression was significantly enhanced in isolated hucMSCs-Exo compared with the control group. This result is consistent with previous studies showing that miR-155 promotes B cell apoptosis.

The proapoptotic rate of B cells in the hucMSCs-Exo group was the highest, followed by the hucMSC and untreated B cell groups (Figure 3(b)). Flow cytometry showed that hucMSCs and hucMSCs-Exo could promote B cell proliferation compared with the control group. Still, hucMSCs-Exo had a better effect in promoting B cell proliferation (Figure 3(c)).

To analyze the hyperactivation of B cells, we cocultured PBMC with hucMSC and hucMSCs-Exo. B cells were sorted by flow cytometry with CD19, followed by evaluation of B cell activation with CD69. Compared with healthy controls, B cells in SLE patients peaked at hour 4 and gradually decreased until 36 hr, whereas the exosome group reduced significantly. The cytokines IL-6, IL-10, and TNF-α are known to be elevated in SLE patients, which is also confirmed in Figure 1. After coculture, the levels of cytokines IL-6, IL-10, INF-γ, IL-17, IL-4, and TNF-α were detected by flow cytometry. Compared with the control group, IL-6, IL-10, and TNF-α levels significantly decreased in the exosome group (Figure 3(e)). In contrast, the level of IL-6 in the hucMSCs group was significantly higher than in the control group. It may be that these B cells themselves secrete IL-6 when paracrine, leading to a significant increase in IL-6 levels after coculture.

3.4. MiR-155 Targets SHIP-1. To investigate whether miR-155 is involved in SLE immune response, we used qPCR to detect its expression. We found that miR-155 expression significantly increased in SLE patients’ B cells compared with healthy controls (Figure 4(a)).
To illustrate the role of miR-155 in the pathogenesis of SLE, the TargetScan, miRDB, and miRWalk databases were used to predict the target genes of miR-155 (Figure 4(b)). Subsequently, we analyzed the possible targets of miR-155 in cells to reveal the molecular mechanism of miR-155 affecting the apoptosis, proliferation, and activation of B cells. The bioinformatics analysis revealed that the 3′-UTR of SHIP-1 (the SH2 domain-containing inositol 5′-phosphatase 1) mRNA contains a complementary binding site in the seed region of miR-155, which is conserved across species (Figure 4(c)). Second, the
FIGURE 2: Isolation and identification of hucMSCs and hucMSC-Exo. (a, b) Osteogenic differentiation of hucMSCs was performed in the differentiation medium, while the control cells were grown in a regular medium. Both were dyed with Alizarin Red S staining. Most hucMSCs were Alizarin red-positive. (c) Oil red O staining was used to stain hucMSCs after adipogenic differentiation, showing the Oil red O-positive lipid droplets (bar = 100 μm). (d) Flow cytometry analysis of the phenotypic markers of hucMSCs showed that hucMSCs were positive for CD73, CD90, and CD105 and negative for CD34, CD45, and human leukocyte antigen (HLA)-DR. (e) Transmission electron microscopic images of typical hucMSC-Exo. Scale bar = 100 nm. (f) The size distribution of the hucMSC-Exo was determined using a nanoparticle tracking analysis. hucMSC-Exo had an original concentration of 2.0e + 10 particles/mL, a mean size of 145.1 nm with a peak of 137.7 nm. (g) Expression of positive markers, CD63 and CD81, was mainly expressed in hucMSC-Exo using flow cytometry analysis.

FIGURE 3: Continued.
expression of SHIP-1 was analyzed by GEO chip GSE4588 (Figure 4(d)). The genes related to SHIP-1 were screened for GO analysis, which showed they were related to the MAPK/ERK pathway (Figure 4(e)). We examined its expression using qPCR and found that mRNA SHIP-1 expression significantly increased in SLE patients’ B cells compared with healthy controls (Figure 4(f)).

We carried out luciferase reporter assays to provide direct evidence that SHIP-1 is a target of miR-155. The results showed that miR-155 mimics significantly decreased the luciferase activity for wild-type 3′-UTR of SHIP-1 but did not inhibit the mutated 3′-UTR of SHIP-1 (Figure 4(g)). In conclusion, miR-155 inhibits SHIP-1 expression in B cells by directly targeting the 3′-UTR of SHIP-1 mRNA.

3.5. MiR-155 Modulates SHIP-1 Expression and the Downstream ERK Kinase Pathway after BCR and FcγRIIB Coligation. The SH2 domain-containing inositol 5′-phosphatase 1 (SHIP-1) phosphatase acts downstream of inhibitory cell-surface receptors, including the IgG inhibitory receptor FcγRIIB (FcγRIIB), which is essential in opposing B-cell activation signals in mice and humans [15]. After collating the FcγRIIB with the B-cell receptor (BCR), FcγRIIB recruits SHIP-1 to the plasma membrane, which negatively regulates cell survival, Ca2+-dependent effector functions, and ERK activation, thus controlling cell proliferation, anergy, and apoptosis [16, 17]. MiR-155 has been reported to regulate SHIP-1 expression in mammalian myeloid and malignant B cells [18]. At present, it is unclear whether the regulation of SHIP-1 by miR-155 affects the autoimmune response of SLE. We found that the level of miR-155 was significantly increased in the B cells of SLE patients. As detected by Western blotting, the SHIP-1 level in B cells treated with hucMSCs and Exo was significantly higher than that in the untreated control group (Figure 5(a)). We also found that miR-155-inhibited B cells had a 1.7-fold increase in SHIP-1 levels after coordinated hucMSCs-Exo intervention (Figure 5(b)).

**Figure 3**: hucMSCs-Exo promoted B cell apoptosis, inhibited proliferation, and prevented overactivation and inflammation. (a) Different concentrations of Exo were cocultured with B cells from SLE. (b) B cell apoptosis was determined using Annexin V-FITC kit (c) B cell proliferation was determined using the CFSE kit. (d) The expression of B cell activation marker CD69. (e) Cytokine expression levels after coculture with hucMSCs and exosomes compared with control. Exosomes were isolated from hucMSC. Data are expressed as the mean ± SEM. *P<0.05, **P<0.01, ***P<0.001.
Control Relative expression of miR-155 SLE

(a)

miR-155

miRDB

miRWalk

(b)

Targets

miR-155

Human INPP5D 3’UTR

Gene Human INPP50 3’UTR length:1188

Conserved sites for conserved miRNA families

miR-155

(c)

predicted pairing of target region (top) and miRNA (bottom)

Position 500-526 of INPP5D 3’ UTR

hsa-miR-155

(d)

Figure 4: Continued.
FIGURE 4: miR-155 targets SHIP-1. (a) qPCR was used to detect the expression of miRNA-155 in B cells of the control group and SLE patients (n = 3 per group). U6 snRNA was used as an endogenous control. (b) The potential targets of miR-155 were predicted by integrating the results of three databases (TargetScan, miRDB, and miRWalk). (c) Conservation of the miR-155 target sequence in SHIP1 3'-UTR among different species and conservation of the miR-155 sequence among different species. (d) GEO chip GSE4588 analyzed the expression of SHIP-1. (e) The SHIP-1-related genes were screened for GO analysis and showed to be related to MAPK/ERK pathway. (f) The SHIP-1 expression was determined by qPCR (n = 3 per group). GAPDH snRNA was used as an endogenous control. (g) The dual-luciferase reporter assay was performed in 293 T cells. Cells were cotransfected with the wild- or mutant-type SHIP-1, 3'-UTR luciferase reporter plasmids, and miR-155 mimics or mimics-NC. The ratio of Renilla activity: Firefly activity represents luciferase activity. Data are expressed as the mean ± SEM. *P<0.05, **P<0.001.

FIGURE 5: MiR-155 modulates SHIP-1 expression and the downstream ERK kinase pathway after BCR and FcγRIIB coligation. (a) Western blot analysis was used to detect the protein level of SHIP-1 after coculture with hucMscs and exosomes. β-tubulin was used as an internal control. (b) Western blot analysis was used to detect the protein level of SHIP1 after transfection with agomir-155 or agomir-NC after intervention with hucMSCs-Exo. β-Tubulin was used as an internal control. After incubation with hucMSCs-Exo and transfection with agomir-155 or agomir-NC, whole-cell lysates were probed with antiphosphorylated ERK, stripped, and reprobed with anti-total ERK. β-Tubulin was used as an internal control. Ratio: p-ERK/total ERK determined by Bio-Rad Quantity One software.
above results indicated that SHIP-1 protein expression was low in unstimulated B cells, possibly because miR-155 was highly expressed in B cells.

In contrast, inhibition of miR-155 in B cells combined with hucMSCs-Exo intervention significantly increased SHIP-1 levels in B cells. Therefore, inhibition of miR-155 can restore the expression level of SHIP-1 in B cells of SLE patients. In this context, miR-155 is at least partly responsible for the low expression of SHIP-1 in B cells. The results also showed that inhibition of miR-155 in B cells maintained SHIP-1 at a high level, thus making B cells less susceptible to activation.

Next, we investigated how ERK activation was affected by dysregulation of SHIP-1 expression in miR-155-inhibited B cells. P-ERK activation was inhibited in B cells with the combined effects of antagoni-155 and hucMSCs-Exo. At the same time, ERK levels did not change significantly (Figure 5(b)). These results suggest that the inhibition of miR-155 expression level attenuates the ERK signaling pathway by reducing the activation of ERK. The recovery of SHIP-1 activity can promote B cell apoptosis, inhibit B cell proliferation, prevent B cell overactivation, and reduce inflammation in SLE patients by inhibiting ERK/SHIP-1 signaling pathway, thereby slowing down the disease. These data suggest that the miR-155 SHIP-1 axis may also be essential in regulating B-cell activation and survival.

3.6. Inhibiting B Cell Activation and Inflammation by Upregulating the Target Genes of miR-155. To determine whether miR-155 promotes B cell apoptosis, inhibits proliferation, prevents excessive activation of B cells, and inhibits inflammation level, we transfected B cells with antagoni-155 (a miR-155 inhibitor) and compared with antagoni-155 negative control (NC) (Figure 6(a)), inhibition of miR-155 promoted B cells apoptosis as measured by flow cytometry with Annexin V-FITC Apoptosis kit. To further verify the effect of hucMSCs-Exo and miR-155 inhibitor, B cells were incubated with hucMSCs-Exo at high concentration in the presence of antagoni-155, which promoted the apoptosis of B cells compared with the negative control. Antagomir-155 synergies with hucMSCs-Exo and promotes B cell apoptosis better. Similarly, the proliferation of B cells was detected by flow cytometry with an SCFE kit. The inhibition of miR-155 could promote the proliferation of B cells, and antagoni-155 synergized with hucMSCs-Exo had a better effect in promoting the proliferation of B cells (Figure 6(b)).

Next, we used CD69 to detect the overactivation of B cells. Flow cytometry results showed (Figure 6(c)) that the inhibition of miR-155 could inhibit the overactivation of B cells. The synergistic effect of the inhibitor and hucMSCs-Exo was more evident than the inhibitor alone. To determine whether miR-155 can inhibit the inflammation level of SLE patients, we transfected PBMC cells with antagoni-155, incubated them for a specific time, collected the cells, and centrifuged them. The supernatant was collected, and the cytokine was detected by multipellet flow immunofluorescence luminescence assay (IL-6, IL-10, INF-γ, IL-4, TNF-α) (Figure 6(d)). Compared with the control group, inhibition of miR-155 could reduce IL-6 and TNF-α. The synergistic effect of inhibitor and hucMSCs-Exo can also reduce IL-6 and TNF-α inflammation levels. Still, the synergistic effect is not as good as the effect of inhibiting miR-155 alone. This step needs to be further studied.

Taken together, by coculture hucMSCs-Exo with B cells of SLE patients, B-cells apoptosis can be promoted, B-cells proliferation can be inhibited, overactivation of B-cells can be prevented, inflammation can be alleviated, and disease progression can be slowed by reducing miR-155-targeting SHIP-1 in B-cells (Figure 7).

4. Discussion

Variable groups have reported different results of lymphocyte subsets. For example, increased, decreased, or normal CD4+ and CD8+ T cell counts have been observed. However, the percentage of B cells is increased in almost all studies. Our data showed a decrease in CD4+ T cells and normal CD8+ T cells while an increase in CD19+ B cells in SLE patients. Hence, lymphocyte subsets are unbalanced in SLE patients, and abnormal B cell function is a critical player in the pathogenesis of SLE because autoantibodies are essential for diagnosis. In addition, B cells exhibit important immunological functions pertinent to SLE, such as the expression of autoantigens and the secretion of proinflammatory cytokines. Therefore, studying B lymphocytes can potentially unravel important pathogenic mechanisms of SLE and thus help develop more specific therapies to improve treatment efficacy and tolerability.

Whether hucMSCs-Exo regulates B lymphocytes in SLE patients is an interesting topic. Our in vitro coculture results showed that hucMSCs-Exo with a 50 μg/mL concentration promoted B cell apoptosis, inhibited proliferation, and prevented overactivation and inflammation. The used dose of exosomes in most studies is approximately 10–100 μg/mL. Our data showed that there was no significant difference between the lower dose (20 μg/mL) and untreated PBMC (P>0.05). No significant difference was observed in the inhibitory effect of 50 and 100 μg/mL doses on B cell apoptosis. Additionally, doses higher than 100 μg/mL were impractical because of inadequate exosome preparation. Based on the results, a series of concentration experiments are recommended in such research.

Another interesting topic is how to explain the immunomodulatory effects of hucMSCs-Exo on B cells from SLE patients. Recently, a study concentrated on the effect of exosome-derived miR-155 on acute lung inflammation demonstrated that exosomes mediate different biological functions and can regulate physiological and pathological processes in vivo. It is confirmed that miR-155 is a highly conserved and important miRNA that can regulate the inflammatory response, and the use of miR-155 inhibitors can significantly reduce inflammatory damage [19]. The pathogenicity of miR-155 is regulated by controlling the immune cell response. It has been shown that miR-155 significantly increases in whole spleen cells and spleen B and T cells in MRL-lpr mice, a mouse model of lupus [20]. In addition, miR-155 was also detected in SLE patients’ serum and urine supernatant. Interestingly, the
serum miR-155 level was higher than the liquid phase of the urine supernatant [21]. The rise or fall of miR-155 levels may be attributed to the effects of immunosuppressive drugs. Elevated levels of miR-155 have been reported in B cells in patients with SLE [22], but it is unclear whether miR-155 controls the expression of autoimmune responses and related pathologies. We found elevated levels of miR-155 in B cells of untreated SLE patients compared with healthy controls. This is consistent with previous reports, suggesting that elevated levels of miR-155 promote the pathogenesis of immune cells. Therefore, we hypothesized that hucMSCs-Exo inhibited miR-155 in lupus patients’ B cells.

**FIGURE 6:** Inhibiting B cell activation and inflammation by upregulating the target genes of miR-155. (a) B cell apoptosis was detected by Annexin V-FITC after transfection of antagomir-155 and antagomir-NC. (b) SCFE was used to detect the proliferation of B cells after transfection of antagomir-155 and antagomir-NC. (c) antagomir-155 and hucMSCs-Exo were cocultured with PBMC cells, and B cells were sorted by CD19. Then the activation of 0–36 hr B cells was detected by flow cytometry using CD69. (d) antagomir-155 and hucMSCs-Exo were cocultured with PBMC for a certain time. After centrifugation, the supernatant was collected, and the cytokine levels were detected by multipellet flow immunofluorescence luminescence assay. Exosomes were isolated from hucMSC. Data are expressed as the mean ± SEM. *P < 0.05, **P < 0.01, ***P < 0.001.
We further explored whether the regulation of miR-155 by exosomes could block the continuous activation of autoreactive B cells, thereby alleviating lupus-like diseases. We found that inhibition of miR-155 in B cells of SLE patients can promote B cell apoptosis, prevent B cell overactivation, and inhibit B cell proliferation. Antagomir-155 had a better synergistic effect with hucMSCs-Exo, which confirmed that exosomes could regulate SLE autoimmunity.

MiRNAs are thought to regulate many complex physiological processes by inhibiting the expression of target genes with related functions [23]. KEGG analysis showed that miR-155 target genes were significantly enriched in immune and proliferation-related pathways. Through the database, we found that SHIP-1 is a potential target of miR-155. SHIP-1 is a tumor suppressor widely recognized to inhibit the proliferation of many tumor cells [10]. In terms of mechanism, we found that miR-155 partially controlled the expression of SHIP-1 in B cells, and the coaggregation of BCR and FcγRIIB led to the increase of SHIP-1 protein and impaired ERK activation of miR-155 in B cells. We found that under the combined effects of antagomir-155 and hucMSCs-Exo, p-ERK activation in B cells was inhibited compared with the control, while the ERK level was not significantly changed. These results suggest that the inhibition of miR-155 expression level attenuates the ERK signaling pathway by reducing the activation of ERK. The recovery of SHIP-1 activity can promote B cell apoptosis, inhibit B cell proliferation, prevent B cell overactivation, and reduce inflammation in SLE patients by inhibiting ERK/SHIP-1 signaling pathway, thereby slowing down the disease. These data suggest that the miR-155-SHIP-1 axis may also be essential in regulating B-cell activation and survival.

There are also some limitations in this paper. First, as SLE is an autoimmune disease easily affected by drugs or other factors, immune cell imbalance makes it more difficult to collect samples and separate and purify B cells, so labeled B cells after PBMC isolation are used for research. Second, exosomes have become potential biomarkers and therapeutic agents for autoimmune diseases in recent years, and further studies are needed to clarify what specific substances in exosomes have immunomodulatory properties. Therefore, continued research into the underlying mechanisms and applications will make this field more promising. Despite the rapid growth of exosome research, isolation, and purification techniques are still slow and irregular. Various techniques have been introduced, but these affect recovered exosomes' yield, diversity, and function. Once these limitations are overcome, new biomarkers can be identified to characterize exosomes and used for diagnostic applications. In addition, developing artificial exosome mimics with low side effects may be a new concept for achieving clinical-scale production of nanocarriers.

5. Conclusion

In conclusion, the application of exosomes offers excellent potential for preventing and treating human autoimmune diseases, especially SLE. Despite the above limitations, our study revealed that SHIP-1 regulates B-cell activation through the ERK signaling pathway, targeting miR-155 in B-cells and blocking the sustained activation of switch autoreactive B-cells, thereby alleviating lupus-like disease. Our results provide insight into how hucMSCs-Exo regulates autoimmunity
in patients with lupus and suggest targeting miR-155 for autoimmunity while protecting immunity [24].

Data Availability

The data used to support the findings of this study are included in the article. Any other required data are available from the corresponding author or first author on reasonable request. miR-155 targets were predicted by TargetScan (https://www.targetscan.org/cgi-bin/targetscan/mamm_31/view_gene.cgi?txid=9606&gs=INPP5D&members=miR-155). The SHIP-1-related genes were screened for GO (https://metascape.org/gp/index.html#/main/step1) analysis and showed to be related to the MAPK/ERK pathway.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors’ Contributions

Ying Zhao and Bo Diao were responsible for the concept and design of the study. Ying was responsible for project development, experiments, data analysis interpretation, and manuscript writing. Yueping Liu was in charge of revising the manuscript. All the authors have contributed to the article and have approved the final manuscript. Ying Zhao and Wenbin Song contributed equally to this study.

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