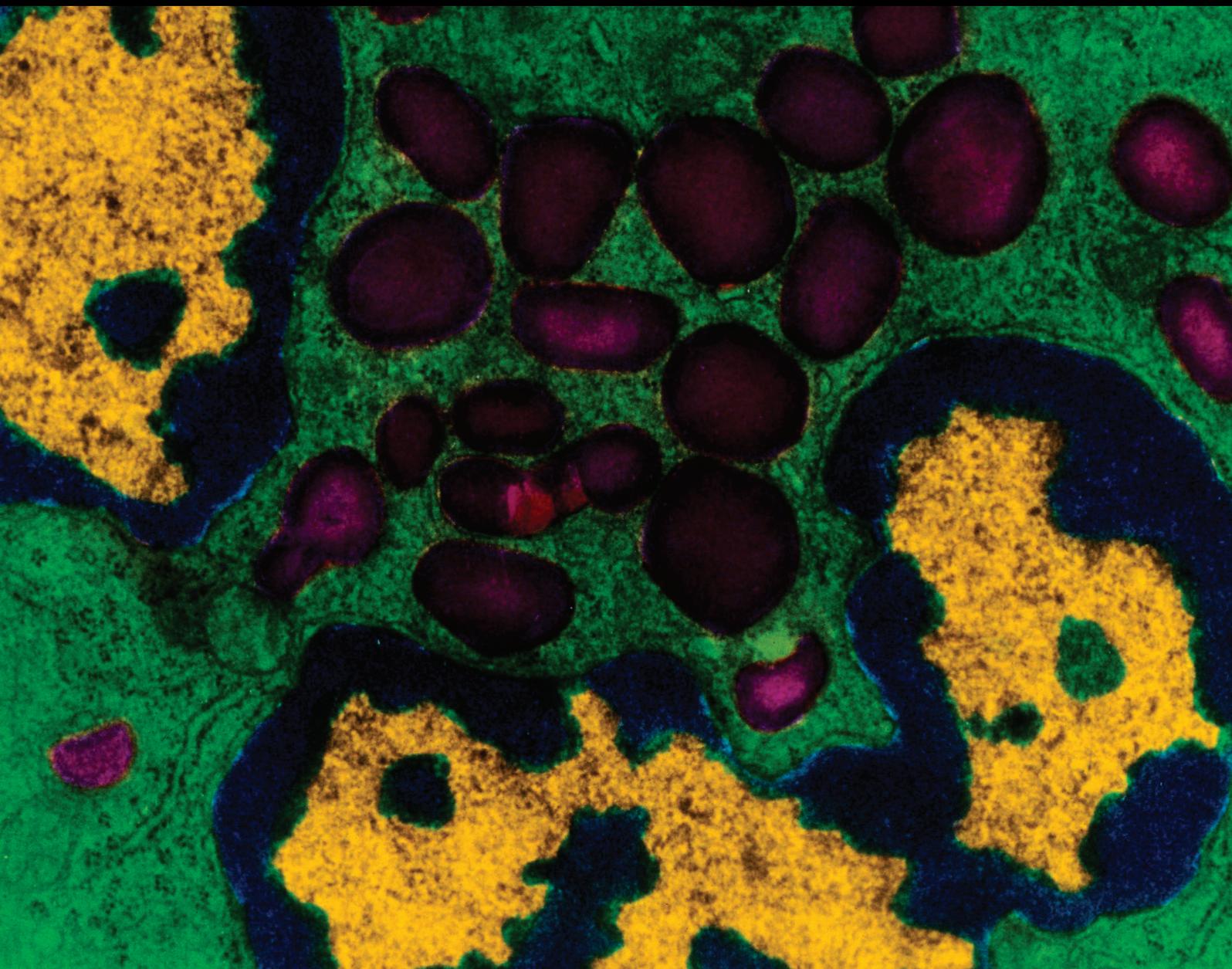


Mediators of Inflammation

Interplay between Hormones, the Immune System, and Metabolic Disorders

Special Issue Editor in Chief: Joilson O. Martins

Guest Editors: Naïma Moustaid-Moussa and Francisco Rios





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Contents

Interplay between Hormones, the Immune System, and Metabolic Disorders

Francisco J. Rios, Naima Moustaid-Moussa , and Joilson O. Martins 

Editorial (2 pages), Article ID 8654212, Volume 2018 (2018)

Role of Histamine in Modulating the Immune Response and Inflammation

Anna Cláudia Calvielli Castelo Branco , Fábio Seiti Yamada Yoshikawa , Anna Julia Pietrobon, and Maria Notomi Sato 

Review Article (10 pages), Article ID 9524075, Volume 2018 (2018)

Impact of Retinoic Acid on Immune Cells and Inflammatory Diseases

Luana de Mendonça Oliveira , Franciane Mouradian Emidio Teixeira , and Maria Notomi Sato 

Review Article (17 pages), Article ID 3067126, Volume 2018 (2018)

Insulin-Like Growth Factor-I as an Effector Element of the Cytokine IL-4 in the Development of a *Leishmania major* Infection

Luiza C. Reis, Eduardo Milton Ramos-Sanchez, Fabricio Petitto-Assis, Audun H. Nerland,

Maria Hernandez-Valladares, Frode Selheim, Lucile Maria Floeter-Winter, and Hiro Goto 

Research Article (17 pages), Article ID 9787128, Volume 2018 (2018)

Intrauterine Malnutrition Reduced Long Leptin Receptor Isoform Expression and Proinflammatory Cytokine Production in Male Rat Pulmonary Endothelial Cells Stimulated by Lipopolysaccharide

Aleksandro M. Balbino, Marina M. Silva, Gabriela A. Azevedo, Noemi L. Gil, Renaide R. Ferreira,

Leila A. dos Santos, Rebéca M. Gasparin, Liliam Fernandes, Maristella A. Landgraf ,

and Richardt G. Landgraf 

Research Article (11 pages), Article ID 8597361, Volume 2018 (2018)

Protective Effect of Sex Hormone-Binding Globulin against Metabolic Syndrome: *In Vitro* Evidence Showing Anti-Inflammatory and Lipolytic Effects on Adipocytes and Macrophages

Hiroki Yamazaki , Akifumi Kushiya, Hideyuki Sakoda, Midori Fujishiro, Takeshi Yamamotoya,

Yusuke Nakatsu, Takako Kikuchi, Sunao Kaneko, Hirotohi Tanaka, and Tomoichiro Asano 

Research Article (12 pages), Article ID 3062319, Volume 2018 (2018)

GLP-1 Analogue Liraglutide Enhances SP-A Expression in LPS-Induced Acute Lung Injury through the TTF-1 Signaling Pathway

Tao Zhu, Changyi Li, Xue Zhang, Chunyan Ye, Shuo Tang, Wei Zhang, Jiayang Sun, Niwen Huang,

Fuqiang Wen , Daoxin Wang , Huojin Deng, Jing He, Di Qi, Wang Deng, and Tao Yang

Research Article (14 pages), Article ID 3601454, Volume 2018 (2018)

Diabetes Mellitus and Liver Surgery: The Effect of Diabetes on Oxidative Stress and Inflammation

Mariana Mendes-Braz , and Joilson O. Martins 

Review Article (11 pages), Article ID 2456579, Volume 2018 (2018)

Wound Healing and Omega-6 Fatty Acids: From Inflammation to Repair

Jéssica R. Silva, Beatriz Burger, Carolina M. C. Kuhl, Thamiris Candreva, Mariah B. P. dos Anjos,

and Hosana G. Rodrigues 

Review Article (17 pages), Article ID 2503950, Volume 2018 (2018)

Rooming-in Reduces Salivary Cortisol Level of Newborn

Giuseppe De Bernardo, Marina Riccitelli, Maurizio Giordano, Fabrizio Proietti , Desiree Sordino, Mariangela Longini, Giuseppe Buonocore , and Serafina Perrone 
Research Article (5 pages), Article ID 2845352, Volume 2018 (2018)

Neutrophils Release Metalloproteinases during Adhesion in the Presence of Insulin, but Cathepsin G in the Presence of Glucagon

Natalia V. Fedorova, Alexander L. Ksenofontov, Marina V. Serebryakova, Vladimir I. Stadnichuk, Tatjana V. Gaponova, Ludmila A. Baratova, Galina F. Sud'ina , and Svetlana I. Galkina 
Research Article (9 pages), Article ID 1574928, Volume 2018 (2018)

Editorial

Interplay between Hormones, the Immune System, and Metabolic Disorders

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Received 5 August 2018; Accepted 5 August 2018; Published 30 September 2018

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This special issue of *Mediators of Inflammation* focuses on diverse research areas related to the interplay between hormones, immune response, and metabolic disorders.

Hormones are metabolic components produced by different cell types, capable of regulating body homeostasis and the cross talk among the endocrine, cardiovascular, and immune systems. In patients with compromised immune response, inflammation may last longer or may be ineffective, leading to recurrent infections or other types of systemic dysfunctions associated with chronic inflammation. In the past few years, it became evident that hormones, neurotransmitters, and dietary factors are specific modulators of cells from the immune system by fine-tuning their activation and key functions. Of note, cells from the immune system present high expression of receptors for different hormones present in the blood circulation, such as aldosterone and glucocorticoids. This in turn might also affect the vascular function leading to cardiovascular diseases. Therefore, the main scope of this edition is to contribute to knowledge in this growing and innovative area, through reviews and original articles that will help to understand the diverse mechanisms by which hormones and/or diet can influence inflammatory response and immune activation.

This special issue covers the most current research aimed at elucidating how metabolites and dietary components such as vitamins, bioactive compounds, or lipid mediators influence inflammatory processes. Articles published in here explore the cell and molecular mechanisms underpinning the endocrine/paracrine networks of regulatory immune

mediators, their targets on immune cell signaling, and how they contribute to metabolic dysregulations in obesity. The current issue also highlights the importance whereby hormones contribute to cellular homeostasis and immune system regulation, and that an imbalance in this well-regulated system can lead to cardiovascular and/or metabolic disorders.

In this edition of *Mediators of Inflammation*, N. V. Fedorova et al. studied the effects of insulin, glucagon, and 17β -estradiol (E2) on the activation of human neutrophils. They reported that hormones influence the activation of neutrophils and induce their adherence to blood vessels in diabetes and metabolic disorders. Extracellular matrix proteins play a crucial role in this process. Moreover, glucagon can contribute to the development of metabolic vascular disorders by initiating the secretion of cathepsin G, an important enzyme present in neutrophils with bactericidal activity. In addition, cathepsin G may promote inflammatory response and stimulate further neutrophil adhesion via proteolysis of cell surface receptors. On the other hand, insulin and E2 can alter the adhesion of neutrophils initiating the secretion of metalloproteinases, which modify extracellular matrix proteins.

In newborns, the developing hypothalamic-pituitary-adrenal axis is activated after exposure to painful and stressful situations as a result of increased glucocorticoid secretion by the adrenal gland cortex. A high concentration of cortisol might also result in an increased risk factor for insulin resistance, hyperlipidaemia, immunologic deficiencies, and

destructive changes in the hippocampus. G. De Bernardo et al. presented a pilot but interesting study showing that a full-time rooming-in (for 24 hrs.) is better than a partial rooming-in (for 14 hrs.) in reducing neonatal stress response in hospitalized newborns. This was supported by their data showing that lower salivary cortisol levels (SCLs) may have long-term positive effects in reducing the risk of metabolic syndrome, high blood pressure, and cognitive and behavioural changes. In addition, in an experimental study, A. M. Balbino et al. evaluated long leptin receptor isoform (OBRb) expression in lung endothelial cells from low birth weight (LBW) rats and examined the production of lipid mediators and cytokines. They found that lung endothelial cells isolated from intrauterine undernourished rats with a LBW exhibit suppressed IL-1 β and IL-6 production after applying inflammatory stimuli. They further demonstrate that these effects may be linked to a lack of OBRb receptor expression and mediated in part by the NF- κ B and p38 MAPK signaling pathways.

Wound healing involves a series of tightly controlled biochemical and cellular events, divided in 3 concomitant and overlapping phases: inflammation, proliferation, and remodeling. Poor wound healing or chronic wounds are characterized by a full thickness in depth and a slow healing tendency. Examples of these include diabetic foot ulcers, venous leg ulcers, and pressure ulcers, and all represent a silent epidemic that affects a large fraction of the world population and represent a major public health problem. J. R. Silva et al. reported that omega-6 (ω -6) fatty acids can improve the wound healing process by modulating cellular responses, through increased endothelial and inflammatory cell migration and function as well as enhanced angiogenesis at the wound site, therefore accelerating the wound healing process.

Sex hormone-binding globulin (SHBG) is a serum protein released mainly by the liver, and a low serum level correlates with a higher risk for metabolic syndrome including diabetes, obesity, and cardiovascular events. H. Yamazaki et al. report that SHBG exhibits anti-inflammatory effects involving macrophages and adipocytes, as evidenced by suppressed mRNA levels for inflammatory cytokines such as IL-6, TNF α , and MCP-1, all known to be highly expressed in adipocytes, with major effects on the chronic low grade inflammation. Additionally, in a review article M. Mendes-Braz and J. O. Martins discuss recent publications addressing the effects of diabetes mellitus (DM) on oxidative stress response and inflammatory processes, which play an essential role in ischaemia-reperfusion injury and impaired hepatic regeneration after liver surgery. Authors highlight the need to expand the knowledge in this area, to benefit patients with DM who undergo surgical procedures that are increasing in clinical practice.

T. Zhu et al. showed that in lipopolysaccharide- (LPS-) induced pulmonary inflammation, there is a reduction in the surfactant protein-A (SP-A) expression, both *in vivo* and *in vitro*. Pulmonary surfactant (PS) is synthesized by type II alveolar epithelial (ATII) cells and plays a crucial role in the maintenance of pulmonary compliance and fluid balance in the lungs, in preventing the lung from collapsing

at the end of expiration, and in regulating the size of alveoli and pulmonary immune defenses. They also reported that the SP-A-enhancing property of liraglutide was most likely mediated via the thyroid transcription factor-1 (TTF-1) signaling pathway.

Leishmania is an obligatory intracellular protozoan that is transmitted vectorially and causes a disease that affects two million people globally each year. This infection results in lesions on the skin, mucosa, or viscera, depending on the specie of the parasite as well as the host response. L. C. Reis et al. reported new insights into the immunology of leishmaniasis by showing that IGF-I is an effector element in cellular responses mediated by IL-4, leading to M2 macrophage polarization. Mechanisms underlying these effects are dependent on the PI3K/Akt pathway during *L. major* infection. In addition, they speculated that individuals in endemic areas might be more susceptible or resistant depending on the expression of basal IGF-I.

Histamine is a biogenic vasoactive amine, which may impact the immune system activation, by acting as a regulatory component to establish homeostasis after injury or preventing the inflammatory process. Histamine is the main mediator responsible for the clinical symptoms in type 1 hypersensitivity reactions and has pleiotropic effects that are dependent on the interaction with histamine receptors. A. C. C. Branco et al. discuss recent findings about histamine effects on inflammation through the activation of intracellular pathways to enhance the production of inflammatory mediators and cytokines in different immune cells. In addition, a review article written by L. M. Oliveira et al. discusses the effects of vitamin A on the innate and adaptive immunity with special emphasis on the inflammatory status, which is becoming a public health concern. Currently, more than 2 billion people are affected by micronutrient deficiency worldwide and vitamin A supplementation is highly effective in reducing mortality from different causes, such as intestinal diseases, neurodegenerative processes, skin aging, and cancer.

In summary, we hope that the original research and the review articles featured in this special issue will enhance the knowledge about the importance of different endocrine systems in inflammatory processes, and help shed light on potential avenues for the development of novel therapies for increasingly prevalent inflammatory and metabolic diseases.

Conflicts of Interest

The authors have no conflict of interest regarding the publication of this editorial.

Acknowledgments

We would like to thank all the authors and reviewers for their valuable contributions to this special issue.

Francisco J. Rios
Naiima Moustaid-Moussa
Joilson O. Martins

Review Article

Role of Histamine in Modulating the Immune Response and Inflammation

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Received 23 February 2018; Revised 15 June 2018; Accepted 4 July 2018; Published 27 August 2018

Academic Editor: Naïma Moustaid-Moussa

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Inflammatory mediators, including cytokines, histamine, bradykinin, prostaglandins, and leukotrienes, impact the immune system, usually as proinflammatory factors. Other mediators act as regulatory components to establish homeostasis after injury or prevent the inflammatory process. Histamine, a biogenic vasoactive amine, causes symptoms such as allergies and has a pleiotropic effect that is dependent on its interaction with its four histamine receptors. In this review, we discuss the dualistic effects of histamine: how histamine affects inflammation of the immune system through the activation of intracellular pathways that induce the production of inflammatory mediators and cytokines in different immune cells and how histamine exerts regulatory functions in innate and adaptive immune responses. We also evaluate the interactions between these effects.

1. Introduction

Histamine and its receptors represent a complex system of immunoregulation with distinct effects mediated by four GPCRs (G protein-coupled receptors HRs 1–4) and their differential expression, which changes according to the stage of cell differentiation and microenvironmental influences. Several host factors, in addition to genetic factors, may influence histamine/receptor effects, including the microbiota, gender, ageing, autoimmune diseases, inflammatory skin, cancer, gut, and pulmonary diseases.

Inflammatory conditions (e.g., allergy, asthma, and autoimmune diseases) have long been thought to be mainly mediated by the activation of histamine receptor 1 (H1R). However, in the treatment of diseases such as chronic pruritus, asthma, and allergic rhinitis, the use of selective H4R ligands and/or modulation of H1 and H4 receptor synergism may be more effective for such pathophysiological conditions. Recent evidence strongly suggests that H4R ligands might be exploited as potential therapeutics in allergy, inflammation, autoimmune disorders, and possibly cancer.

Overall, exploiting the impact of histamine on innate and adaptive immune responses may be helpful for understanding receptor signaling and trends during inflammation or regulation.

Histamine shows a dichotomous nature, whereby it is able to promote inflammatory and regulatory responses that contribute to pathological processes, such as allergy induction, as well as homeostatic functions, such as intestinal regulation. In this review, we summarize recent findings about the regulation of the immune response by histamine. A general overview of the immune cascades triggered by histamine receptor activation is provided.

2. Histamine and Histamine Receptors

Histamine (2-[3H-imidazol-4-yl]ethanamine) is an important chemical mediator that causes vasodilation and increased vascular permeability and may even contribute to anaphylactic reactions [1]. It also acts on several physiological functions, such as cell differentiation, proliferation, haematopoiesis, and cell regeneration. Synthesis of histamine

occurs through decarboxylation of the amino acid histidine by the enzyme L-histidine decarboxylase (HDC), which is expressed in neurons, parietal cells, gastric mucosal cells, mast cells, and basophils; degradation of histamine is mediated by the enzyme diamine oxidase (DAO) and histamine N-methyltransferase (HNMT), which catalyses histamine deamination [2, 3]. HNMT is expressed in the central nervous system, where it may play a critical regulatory role because its deficiency is related to aggressive behaviour and abnormal sleep-wake cycles in mice [4].

The pleiotropic effects of histamine are mediated by 4 histamine receptors (HRs), H1R, H2R, H3R, and H4R, which are G protein-coupled receptors. The active and inactive conformations of these receptors coexist in equilibrium. Agonists of these receptors stabilize the active conformation, whereas antagonists stabilize the inactive conformation. Curiously, the ageing process impairs expression or activity of HRs, and the enzymes HDC and DAO may contribute to the progression of allergic reactions and various neurodegenerative disorders [5]. Chronic itch in the elderly is a common problem that is often multifactorial due to physiological changes in ageing skin, including impaired skin barrier function, and changes in immunological, neurological, and psychological systems associated with age.

H1R is expressed in various cell types, such as neurons, endothelial cells, adrenal medulla, muscle cells, hepatocytes, chondrocytes, monocytes, neutrophils, eosinophils, DCs, T cells, and B cells. H1R signaling results in the following: synthesis of prostacyclins; activation of platelet factor; synthesis of nitric oxide, arachidonic acid and its metabolites, and thromboxane; and contraction of smooth muscle cells. In addition, H1R activation leads to increased chemotaxis of eosinophils and neutrophils at the site of inflammation, higher functional capacity of antigen-presenting cells (APCs), activation of Th1 lymphocytes, and decreased humoral immunity but the promotion of IgE production [6]. As expected for such biological actions, H1R antagonists, including pyrillamine, fexofenadine, diphenhydramine, and promethazine, are commonly used for the treatment of allergic symptoms.

Signaling via H1R leads to the activation of intracellular transcription factors, such as IP3 (inositol triphosphate), PLC (phospholipase C), PKC (protein kinase C), DAG (diacylglycerol), and Ca^{2+} . Recently, H1R and H4R signaling was implicated in MAPK signaling and cAMP accumulation, leading to increased proinflammatory gene expression [7]. In addition, activation of H1R is important for the generation of Th1 responses, whereas H2R regulates Th2 responses. Mice genetically deficient for H1R (H1R^{-/-}) have an exacerbated Th2 profile due to a decrease in Th1 responses [8]. In addition, H1R was demonstrated in an experimental allergy model to play a critical role together with histamine in orchestrating recruitment of Th2 cells to the site of allergic lung inflammation [9].

H2R is expressed by parietal cells of the gastric mucosa, muscle, epithelial, endothelial, neuronal, hepatocyte, and immune cells. H2R antagonizes some of the effects mediated by H1R and leads to the relaxation of smooth muscle cells, causing vasodilation. H2R activation regulates several of the

functions mediated by histamine, including cardiac contraction, gastric acid secretion, cell proliferation, and differentiation [10]. It also acts as a suppressor molecule in DCs, increasing IL-10 production [11]. One recent study demonstrated that histamine acts on H2R and induces inhibition of leukotriene synthesis in human neutrophils through cAMP-dependent protein kinase (PKA) signaling [12]. In a murine lung inflammation model, H2R loss has an effect on invariant natural killer T (iNKT) cells, aggravating local inflammation [13].

In monocyte-derived DCs from healthy adult subjects, H2R activation counterbalances the Toll-like receptor (TLR) response, leading to inhibition of CXCL10, IL-12, and TNF- α stimulation of IL-10, which is likely associated with Th2 polarization [14]. Mechanistically, inhibition of TLR-associated NF- κ B and AP-1 pathways occurs due to cAMP activation downstream of H2R activation [14].

While the activation H1R and H2R mainly accounts for mast cell- and basophil-mediated allergic disorders [15], H3R functions were identified in the central nervous system and peripheral and presynaptic receptors to control the release of histamine and other neurotransmitters. The asymmetry of histamine via H3R inhibits the acetylcholine released in the mouse cortex, which controls neurogenic inflammation by inhibiting cAMP formation and Ca^{2+} accumulation [16]. H3R knockout mice exhibit an obese phenotype, suggesting that H3R regulates insulin resistance and leptin release, as well as a decrease in homeostatic energy, the cellular process for coordinating homeostatic regulation of food intake (energy inflow) and energy expenditure (energy outflow), as associated with the UCP1 and UCP3 genes [17]. H3R expression may be associated with bronchoconstriction, pruritus (without involvement of mast cells), increased proinflammatory activity, and antigen-presentation capacity [18].

Neuromodulation and the waking state are related to histaminergic neurons. The waking state is maintained by continual activation of aminergics (such as histamine, dopamine, noradrenaline, and acetylcholine). Three subtypes of HRs are widely distributed in the brain, not only on neurons but also on astrocytes and blood vessels. Positive-allosteric modulators of GABA_A receptors acting on histamine neurons in the posterior hypothalamus induce a natural NREM-like sleep [19]. Targeting the histamine and noradrenergic systems may aid in the design of more precise sedatives and, at the same time, may reveal more about the natural sleep-wake circuitry [19]. In fact, there is a potential utility of histamine H3R antagonist/inverse agonists for CNS disorders. An experimental study showed that when subjected to lipopolysaccharide (LPS) challenge, histamine inhibits the injurious effect of microglia-mediated inflammation by protecting dopaminergic neurons, highlighting the down-modulatory ability of histamine and/or HR agonists. This finding may be useful for the development of new therapeutic approaches to treat neurodegenerative disorders [20].

H4R is preferentially expressed in the intestine, spleen, thymus, bone marrow, peripheral haematopoietic cells, and cells of the innate and adaptive immune systems. Expression of H4R is regulated by stimulation with IFN, TNF-

α , IL-6, IL-10, and IL-13, leading to inhibition of cAMP accumulation and activation of MAPK (mitogen-activated protein kinases) by H4R. Activation of this receptor causes chemotaxis in mast cells and eosinophils, leading to an accumulation of inflammatory cells and control of cytokine secretion by DC and T cells. H4R is also involved in increased secretion of IL-31 by Th2 cells [21]. Treatment of mice with the H4R antagonist JNJ7777120 attenuates pruritus in response to histamine, IgE, and compound 48/80, and its inhibitory effect is greater than that observed with H1R antagonists [22]. The use of this synthetic H4R antagonist in a murine encephalomyelitis model resulted in an increase in the clinical and pathological signs of the disease, suggesting a modulatory role [23].

HRs are present on tumour cells, making them sensitive to variations in histamine. High levels of histamine are associated with bivalent behaviour in the regulation of several tumours (i.e., cervical, ovarian, vaginal, uterine, vulvar, colorectal, and melanoma cancers) by promoting or inhibiting their growth [24]. The presence of H3R and H4R in human mammary tissue suggests that H3R may be involved in regulating breast cancer growth and progression [25], emphasizing the possible use of antihistamines as adjuvants in cancer chemotherapy.

In HDC-deficient mice, a decrease in H4R expression on iNKT cells is associated with lower production of IL-4 and IFN- γ by those cells, which demonstrates regulation between these factors [26]. Several studies have shown that histamine is involved in regulating the function of DCs [27], such as by potentiating antigen endocytosis, inducing intracellular Ca²⁺ mobilization, promoting F-actin polymerization in immature DCs derived from monocytes [28], and promoting expression of MHC class II molecules. Strikingly, cross-presentation, the ability to drive MHC II-associated antigens towards the MHC I pathway, is blocked by H3R/H4R antagonists. Histamine also acts on T cell polarization by inhibiting IFN- γ or LPS-driven IL-12 production in a H1R/H2R dependent manner [29]. H4R has a modulatory role in APCs (DCs and monocytes) by exerting anti-inflammatory action and reducing IL-12 and CCL2 production [28, 30].

Asthma is prevalent in males during childhood but is more frequent in females during adolescence and adulthood. Furthermore, allergic diseases are common in women of childbearing age. Both asthma and atopic conditions may worsen, improve, or remain the same during pregnancy. Female hormones, such as estrogen, can modulate the inflammatory response, and histamine receptors can differ between males and females, which might explain the different incidence of allergy between the sexes [31]. For example, H2R and H3R are highly expressed in female compared to male rats and are downregulated in ovariectomized females, whereas H1R is equally expressed in both sexes [32].

The cascades and effects of different histamine receptors are summarized in Figure 1 and Table 1.

3. Histamine Stimulates Inflammation

Inflammatory mediators are molecules produced by activated cells that intensify and prolong the inflammatory

response. Histamine is a potent inflammatory mediator, commonly associated with allergic reactions, promoting vascular and tissue changes and possessing high chemoattractant activity. The binding of histamine to eosinophil H4R induces increased expression of macrophage-1 antigen (Mac1) and ICAM-1 adhesion molecules, in addition to promoting actin filament rearrangement [33, 34]. These events favour the migration of eosinophils from the bloodstream to the site of inflammation. In mast cells, the binding of histamine to this same receptor promotes the intracellular release of calcium and recruitment of mast cells into tissues [35]. Mast cells from H4R-knockout mice lose the ability to migrate against a histamine gradient [35]. Recruitment of these cells to sites of inflammation amplifies the inflammatory reactions mediated by histamine and may favour the establishment of a chronic inflammatory response. In experimental models, histamine drives colitis via HR4 by promoting granulocyte infiltration into the colonic mucosa [36].

Histamine also modulates the inflammatory response by acting on other cellular populations, in human lung macrophages, binding of histamine to H1R induces production of the proinflammatory cytokine IL-6 and β -glucuronidase [37, 38], a marker of exocytosis, and the release of lysosomal enzymes is associated with epithelial damage and rupture of the basement membrane [39]. Together, these events suggest that histamine may contribute to the maintenance of inflammatory conditions in the airways. In contrast, activation of H2R in rat peritoneal macrophages inhibits production of TNF- α and IL-12 when stimulated with LPS [40].

In an animal model of allergic airway inflammation, H4R-knockout mice present lower inflammation, reduced pulmonary infiltrate of eosinophils and lymphocytes and an attenuated Th2 response [41]. The contribution of histamine to the induction of airway inflammation is also due to its effect on nonimmune cells. In nasal fibroblasts, there is a dose-dependent increase in IL-6 production in response to histamine stimulation [42]. This inflammatory mediator increases expression of phosphorylated p38, pERK, and pJNK and induces NF- κ B activation. Treatment with H1R antagonists reduces expression of phosphorylated p38 and NF- κ B and, consequently, IL-6 production.

Blocking H4R in a model of pulmonary fibrosis alleviates the inflammatory response, reducing COX2 expression and activity, leukocyte infiltration, production of TGF- β (profibrotic cytokine), and collagen deposition [43]. Histamine also activates pulmonary epithelial cells. Histamine binding to H1R enhances TLR3 expression in these cells, and treatment with the TLR agonist poly(I:C), along with histamine, potentiates NF- κ B phosphorylation and IL-8 secretion, indicating an increased response of epithelial cells to microbial ligands [44].

In the nervous system, microglial activation is regulated by histamine in a dose-dependent manner, which leads to the production of proinflammatory cytokines, such as IL-6 and TNF- α [45]. This activation is mediated via H1R, and H4R and is dependent on MAPK and PI3K/AKT cascades. In addition to inducing iNOS expression and NO production, histamine promotes the loss of mitochondrial membrane potential and the production of ROS in microglia by

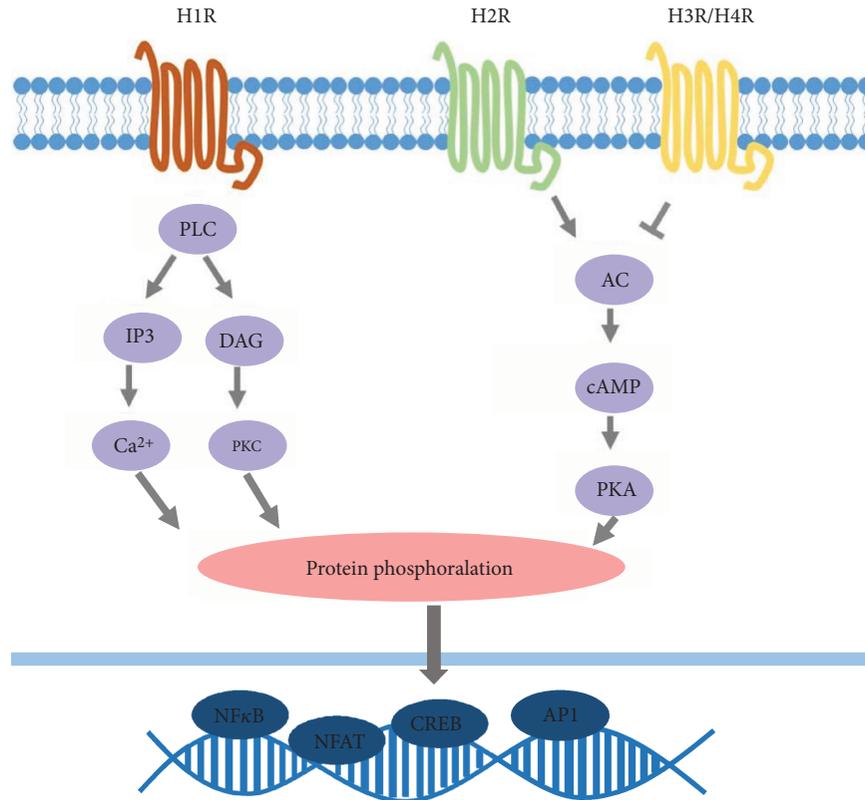


FIGURE 1: Intracellular activation cascades triggered by histamine receptors (HRs). The pleiotropic effects of histamine are mediated by four histamine receptors: H1R, H2R, H3R, and H4R, which are G protein-coupled receptors. Signaling via H1R leads to activation of intracellular transcription factors, such as PLC (phospholipase C), IP3 (inositol triphosphate), PKC (protein kinase C), DAG (diacylglycerol), and Ca²⁺. H2R signaling acts through activation of adenylyl cyclase (AC), which increases cyclic adenosine monophosphate (cAMP) levels and activates protein kinase A (PKA), while H3R and H4R inhibit this cascade. Those intracellular signaling pathways culminate into protein phosphorylation and transcription of nuclear factor such as nuclear factor kappa B (NF-κB), nuclear factor of activated T-cells (NFAT), cAMP response element binding protein (CREB), and activator protein 1 (AP-1).

TABLE 1: Immunological functions mediated by histamine receptors signaling.

Receptor	Expression	Intracellular signaling	Immunological activity
H1R	Endothelial cells, nerve cells, epithelial cells, neutrophils, eosinophils, monocytes, macrophages, DCs, and T and B cells	PLC, PIP ₂ , DAG, IP ₃ , Ca ²⁺ , and PKC	Allergic reactions and inflammation, histamine release, eosinophil and neutrophil chemotaxis, antigen presentation ability, Th1/IFN-γ activity, and recruitment of Th2 cells; decreases humoral immunity and IgE production
H2R	Endothelial cells, nerve, epithelial, neutrophils, eosinophils, monocytes, macrophages, DCs, and T cells and B	Adenyl cyclase, cAMP, PKA, CREB, and EPAC	Increases IL-10 production and humoral immunity; decreases cellular immunity; inhibits Th2 cells and cytokines, chemotaxis of eosinophils, and neutrophils; suppresses IL-12p70 of MoDCs
H3R	Histaminergic neurons, monocytes, eosinophils	Inhibitor of adenyl cyclase and cAMP; increases levels of Ca ²⁺	Control of neurogenic inflammation, increased proinflammatory activity, and antigen presentation capacity
H4R	Eosinophils, DCs, Langerhans cells, neutrophils, T cells, basophils, and mast cells	Inhibitor of adenyl cyclase and cAMP; increases levels of Ca ²⁺	Affects pDC and mDC functions, Th1/Th2 differentiation, eosinophil and mast cell chemotaxis, IL-6 production, leukotriene B ₄ , and migration of Tγ/δ cells; increases IL-17 secretion by Th17 cells, and regulatory T recruitment; suppresses IL-12p70 of MoDCs

binding to these same receptors [46, 47]. Overall, the accumulation of these cytokines and proinflammatory molecules can be deleterious, leading to nerve damage.

Histamine also modulates the response of DCs. Stimulation of immature DCs induces expression of CD86, CD80, and MHC class II, increasing the efficiency of T cell activation [11]. In the presence of histamine, DCs exhibit a higher production of IL-6, IL-8, and CCL2 as well as induced expression of IL-1 β , CCL5, and CCL4. However, the H2R pathway promotes IL-10 production and inhibits IL-12 synthesis by immature DCs, favouring the development of a Th2 response profile [29]. This modulation of cytokine production, suggests that histamine indirectly alters the Th1/Th2 balance through the stimulation of DCs. In a food allergy model, simultaneous blockage of H1R and H4R inhibited the development of intestinal inflammation and diarrhoea when the animals were exposed to the allergen by suppressing histamine-mediated DC antigen presentation and chemotaxis [48].

The Th1/Th2 balance is directly regulated by histamine, as described above. Th1 cells display higher H1R expression, and their binding to histamine promotes activation of Th1 responses, potentiating IFN- γ production [49]. In contrast, Th1 and Th2 responses are inhibited by histamine stimulation via H2R. Histamine also alters the response of other subpopulations of lymphocytes. Activation of CD8+ T cells via H4R induces secretion of IL-16, a chemoattractant molecule for CD4+ cells such as monocytes and DCs [50]. In addition, histamine stimuli induces IL-17 production in human Th17 cells, suggesting the contribution of this inflammatory mediator to the activation of lymphocytes present in skin lesions in atopic dermatitis and psoriasis [51].

Other evidence, indicates that histamine plays an important role in inflammatory skin diseases. When stimulated via H4R, the NK cells present in skin lesions, increase expression of the chemokines CCL3 and CCL4, favouring cell recruitment to injured tissue [52]. As H4R knockout mice display a lower influx of inflammatory cells and less cell proliferation at the lesion sites, H4R is associated with the inflammatory response in atopic dermatitis [53]. H4R is also involved in NK cell recruitment and induction of CCL17 production by DCs at lesion sites in murine models of atopic dermatitis, contributing to increased local inflammation [54]. In an experimental model of pruriginous dermatitis, H4R blockage decreases itching because the activation of this receptor is involved in increased IL-31 secretion by Th2 cells [21, 55]. Moreover, blocking H4R improves skin lesions and reduces the number of mast cells at lesion sites [55].

Within the context of vascular inflammatory diseases, histamine produced by the tunica intima stimulates the monocytes present in atherosclerotic plaques to express CCL2 and its receptor CCR2, via activation of H2R [56]. Furthermore, higher production of IL-6 and adhesion molecules, such as ICAM-1 and VCAM-1, occurs in endothelial cells stimulated by histamine, thereby favouring progression of the disease [56, 57]. In an experimental model, the absence of H1R reduced the development of atherosclerosis, whereas the absence of H2R exerted the opposite effect [58].

4. Regulatory and Immunomodulatory Functions of Histamine

As discussed above, the pleiotropic effects of histamine are a consequence of the existence of four different receptors that belong to the same family of G-coupled proteins and trigger different signaling cascades; these receptors are differentially distributed across tissues and cells [59]. Therefore, in addition to its classical roles in the inflammatory process, histamine is recognized as a key player in immune regulation.

Although histamine is commonly associated with skin inflammation processes, for example, allergic dermatitis [60], it may play a regulatory role in other clinical conditions such as psoriasis, which is a multifactorial Th1/Th17-driven inflammation of the skin [61]. In a murine psoriasis-like model induced by imiquimod administration, Kim et al. showed that the H4R agonist 4-methylhistamine ameliorated the clinical scores of psoriatic mice due to repression of Th1 cytokines and simultaneous induction of Treg cells [62]. These findings suggest that histamine targeting has pharmacological potential. In addition, histamine participates in the wound-healing process by increasing the viability of rat wound fibroblasts and promoting the production of TGF- β in an H1R-dependent manner [63].

The contribution of histamine to inflammatory neurological diseases, such as multiple sclerosis, is controversial: although H1R and H2R appear to favour the inflammatory response in brain lesions [64], H3R dampens neuroinflammation, mainly by modulating the production of chemokines and maintaining the integrity of the blood-brain barrier [65] in a murine model of multiple sclerosis, experimental autoimmune encephalomyelitis (EAE). Pharmacological blockage of H4R exacerbates EAE, as observed by increased recruitment of inflammatory mediators, larger lesion areas, and enhanced activation of T cells, indicating that H4R also plays a regulatory role in a neurological context [23]. In a murine model of the motor neuron disorder amyotrophic lateral sclerosis (ALS), microglia from SOD1-G93A mice, which spontaneously develop an ALS phenotype, appear to be responsive to histamine through H1R and H4R, leading to a reduction in the inflammatory state. The findings suggest deregulation of the histaminergic pathway in ALS patients [66].

Regardless, the role of histamine in gut homeostasis maintenance is clearly essential, as exemplified in a murine model of HDC deficiency. Yang et al. showed that HDC^{-/-} mice were prone to develop inflammation and had a higher tumour burden at mucosal sites (intestine and skin) in models of chemically induced carcinogenesis but that their phenotype was attenuated by histamine administration [67]. Most HDC expression in these tissues was found in immature myeloid cells (IMCs), rather than in resident mast cells; curiously, histamine administration, acting through H1R and H2R, was required to promote terminal differentiation of IMCs into monocytes and neutrophils [67].

Expression levels of HDC and H2R are positively associated with increased survival in colorectal cancer patients [68], and some epidemiological studies support the association of atopy with the reduced incidence of some cancers

[69, 70], reinforcing a possible role of histamine in blocking tumour development.

In addition to tumour biology, histamine has a regulatory function in gut inflammatory diseases, such as in a murine trinitrobenzene sulfonic acid- (TNBS-) induced model of colonic inflammation, which promotes a delayed hypersensitivity reaction that resembles the phenotype [71]. By employing H4R-deficient mice, Wunschel et al. demonstrated that histamine protects animals from an exacerbated inflammatory reaction in the colon, as illustrated by enhanced production of chemokines/cytokines and loss of intestinal architecture, which ultimately leads to death [72]. Strikingly, Schirmer et al. reported the opposite effect using a similar mouse background (H4R^{-/-} mice), whereby histamine worsened dextran sodium sulfate- (DSS-) induced colitis and pharmacological inhibition of H4R ameliorated the health of the mice [73]. Differences between the models, such as the chemical stimulation used and the route of administration, may account for the opposite results. Overall, the response that prevails in humans requires further investigation.

Recently, the microbiota was revealed to be very important for gut pathophysiology. Indeed, the microbial community in the intestine shapes the health status of the host and its susceptibility to a broad range of local and systemic diseases [74]. The microbiota supplies the host with a number of metabolites, such as short-chain fatty acids, tryptophan metabolites and histamine [75, 76], and a recent work highlights the key role of microbe-derived histamine in the host response.

For example, histamine-secreting bacteria (*Escherichia coli*, *Lactobacillus vaginalis*, and *Morganella morganii*) are found at higher frequency in faecal samples from asthmatic patients, with a possible contribution to their atopic phenotype [76, 77], as microbial-derived histamine is indistinguishable from the human-produced form.

Lactobacillus reuteri is a member of the gut microbiota that belongs to the Firmicutes family; HDC gene expression by this commensal bacterium confers the ability to produce histamine from histidine [78]. Microbial histamine modulates the inflammatory response of the human monocyte cell line THP-1, mainly by acting through H2R, to promote activation of the cAMP/PKA cascade and block of ERK signaling [79]. *L. reuteri*-derived histamine relies on H2R to promote its regulatory function in the intestine [80]. Interestingly, histamine modulates the response of myeloid and plasmacytoid DCs to LPS, favouring IL-10 production over the secretion of inflammatory cytokines [14] and enhancing their ability to phagocytose soluble antigens and upregulate expression of the costimulatory molecules CD86 and inducible costimulator ligand (ICOS-L) [81]. Although the effects depend on H2R and cAMP, histamine requires the participation of exchange proteins activated by cAMP (Epac) in DCs, as opposed to PKA in monocytes, indicating that these signaling cascades are cell type specific [14].

In addition to H2R agonism, *L. reuteri* simultaneously blocks H1R signaling by secreting the enzyme diacylglycerol kinase (DGK). H1R leads to the production of inflammatory mediators by triggering PKC-dependent NF- κ B activation

[82]. PKC activation, in turn, requires the cofactor diacylglycerol (DAG); DGK degrades DAG into phosphatidic acid. Thus, *L. reuteri*-derived DGK interrupts H1R signaling and blocks the inflammatory effects of histamine but preserves H2R-associated immunomodulation [83].

L. reuteri administration protects HDC-deficient mice from colon tumours in a model of intestinal carcinogenesis with azoxymethane/dextran sodium sulfate (AOS/DSS) administration. *L. reuteri* produces or restores the histamine pool in the intestine, lowering recruitment of immature myeloid cells and production of inflammatory cytokines, which blocks tumour development [68]. Importantly, *L. reuteri* only produces histamine; therefore, it exerts regulatory activity regardless of whether the precursor (histidine) is exogenously provided, for example, by food intake [80]. This highlights the critical interplay between the host immune response, the microbiota, and environmental (dietary) influences on biological outcomes.

In addition to *L. reuteri*, other bacteria have probiotic potential. Another lactobacilli, *Lactobacillus rhamnosus*, is a source of histamine that promotes a regulatory Foxp3-T cell response profile in intestinal Peyer patches while dampening Th1 polarization in an H2R-dependent fashion [14].

The lung is a classical mucosal site under histamine control. Although histamine is associated with deleterious inflammation in asthmatic patients, triggering airway hyper-responsiveness and remodelling [84, 85], recent evidence suggests that the contribution of histamine to pulmonary homeostasis is not straightforward and depends on the receptor and cell type involved. H1R antagonism is well known for its beneficial effects in asthma management [86]; however, H2R deficiency or pharmacological blockade worsens lung inflammation in OVA-sensitized mice due to increased activation of iNKT cells, which promotes recruitment of macrophages and neutrophils and production of IL-4, IL-17, and IFN- γ by T cells [13].

Although the regulatory properties of histamine reveal a promising therapeutic potential, histamine may also exert deleterious effects in some clinical conditions. For example, histamine immunomodulation might contribute to higher susceptibility to sepsis in diabetic mice. Mast cell-derived histamine is increased in diabetic settings and reduces neutrophil recruitment due to repression of CXCR2 [87]. In addition, histamine may impair the oxidative burst of neutrophils [88]. Because neutrophils produce histamine once stimulated [89], a negative feedback loop is established, attenuating the microbicidal mechanism against invading bacteria.

5. Conclusion

Histamine research is an attractive perspective for the potential therapeutic exploitation of new drug targets. The main actions of histamine in controlling the immune response are summarized in Figure 2. The pleiotropic actions of histamine due to the different natures of its receptors allow this simple molecule to exert broad and oppose effects on the immune system, highlighting the importance of a fine-tune control that promotes a homeostatic environment in the

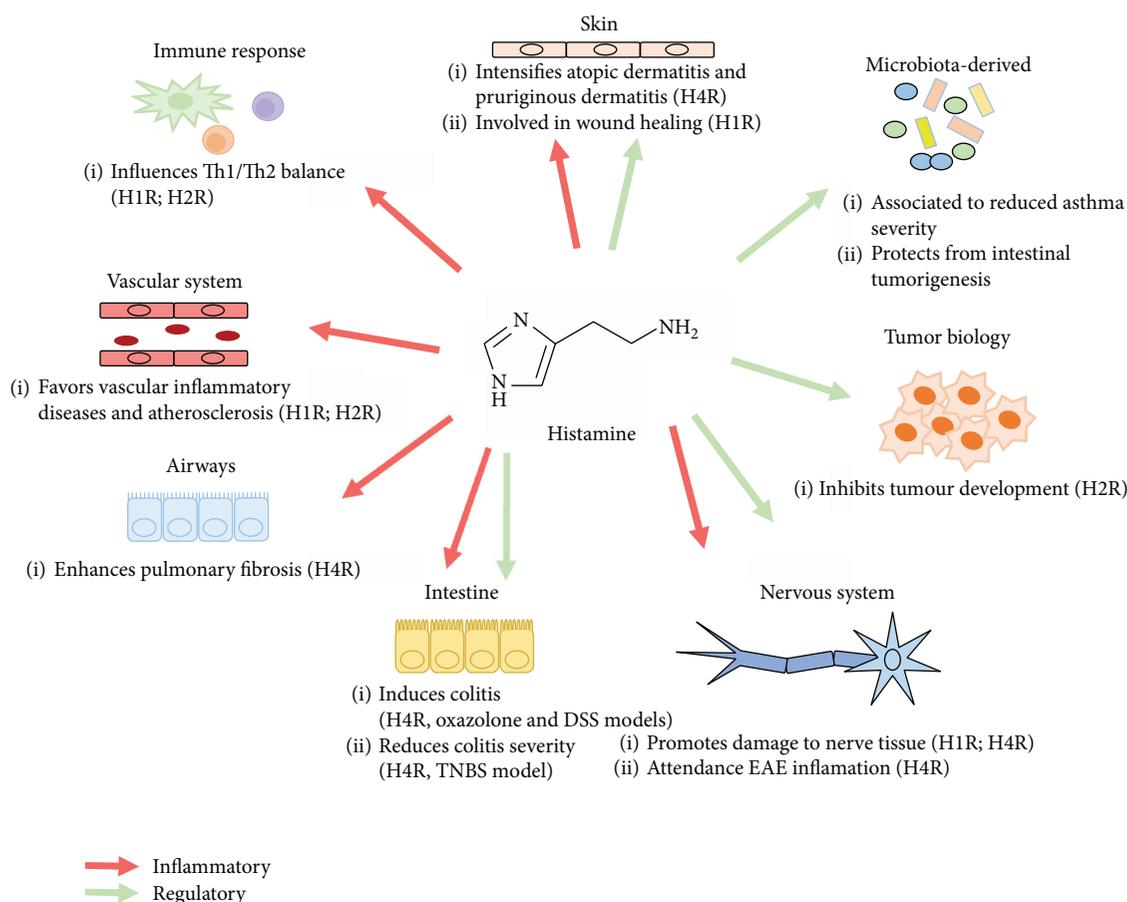


FIGURE 2: Inflammatory and regulatory functions of histamine on different body sites. Histamine plays dual functions according to the cell type and the receptor. As an inducer of inflammation, histamine can contribute to pulmonary fibrosis, cardiovascular diseases and atherosclerosis, atopic dermatitis, central nervous system damage, and colitis in some experimental models, besides favoring the polarization of the immune response to a Th1 profile. On the other hand, histamine can regulate inflammation in models of experimental autoimmune encephalomyelitis (EAE) and colitis, favor wound healing in skin lesions, and inhibit tumour development. Also, microbiota-derived histamine can regulate the inflammatory picture of asthma. Red arrows indicate proinflammatory action; green arrows indicate regulatory action of histamine.

body, balancing important inflammatory reactions to host protection as well as immunomodulation. The findings about the role of histamine in carcinogenesis, allergic regulation, and even behavioural regulation underscore histamine as a remarkable therapeutic target. However, as HRs are widely expressed in the body and change during cell differentiation and ageing and even differ between sexes, complex histamine/receptor agonism/antagonism should be exploited for therapeutic approaches with caution. New insight about the role of histamine in different body sites and cell types may result in more targeted therapies. Overall, recent findings about the microbial contribution to histamine homeostasis add a new layer of complexity to the picture. Ideal histaminergic therapy should be composed of a mixture of agonists and antagonists that would avoid deleterious side effects. Future studies may improve our understanding of the histamine network in organisms and its paradoxical nature.

Conflicts of Interest

There are no conflicts of interest to declare.

Acknowledgments

This work was supported by the Fundação de Amparo à Pesquisa do Estado de São Paulo under Grant 2012/16524-6 and the Laboratório de Investigação Médica, Unidade 56.

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Review Article

Impact of Retinoic Acid on Immune Cells and Inflammatory Diseases

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Received 29 March 2018; Revised 16 June 2018; Accepted 28 June 2018; Published 9 August 2018

Academic Editor: Naïma Moustaid-Moussa

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Vitamin A metabolite retinoic acid (RA) plays important roles in cell growth, differentiation, organogenesis, and reproduction and a key role in mucosal immune responses. RA promotes dendritic cells to express CD103 and to produce RA, enhances the differentiation of Foxp3⁺ inducible regulatory T cells, and induces gut-homing specificity in T cells. Although vitamin A is crucial for maintaining homeostasis at the intestinal barrier and equilibrating immunity and tolerance, including gut dysbiosis, retinoids perform a wide variety of functions in many settings, such as the central nervous system, skin aging, allergic airway diseases, cancer prevention and therapy, and metabolic diseases. The mechanism of RA is interesting to explore as both a mucosal adjuvant and a combination therapy with other effective agents. Here, we review the effect of RA on innate and adaptive immunity with a special emphasis on inflammatory status.

1. Introduction

Vitamins are essential components of diet and are essential for the maintenance of various biological processes. For example, vitamin A, through its active metabolite, retinoic acid (RA), acts in several biological conditions, such as embryonic development, hormone function, the maintenance and modulation of the immune response, and the homeostasis of epithelial tissues and mucosa [1, 2].

Vitamin A is obtained through diet, and its deficiency, especially in childhood, increases the morbidity and mortality risk from infectious diseases, especially diseases of the gastrointestinal and pulmonary tracts, causes blindness and anemia, and impairs vaccine responses [1, 3]. In low-income countries, children receive insufficient amounts of vitamin A during breastfeeding and childhood, making vitamin A deficiency a public health problem. Studies have shown that vitamin A supplementation reduces the mortality rate by 24% among children aged 6 months to 5 years [4].

For this reason, the World Health Organization (WHO) recommends vitamin A supplementation for infants and children aged 6–59 months in underdeveloped countries [5].

Indeed, after the absorption and metabolization of vitamin A into RA in the gut, RA plays critical roles in the mucosal immune response as a regulatory signal in the intestinal mucosa by promoting Foxp3 regulatory T cell differentiation [6] and immunoglobulin (Ig) A production [7]. In addition, RA induces the homing of innate immune cells, such as innate lymphoid cells (ILCs) [8] besides regulatory and effector T and B cells, to the gut [9–11]. During infections, RA can induce the production of proinflammatory cytokines by dendritic cells (DCs), promoting the differentiation of effector T cells and the protection of the mucosa [12]. Thus, RA is crucial for maintaining homeostasis at the intestinal barrier and equilibrating immunity and tolerance. Due to the extensive role of RA in immune cells and the immune response, reducing mortality in children by vitamin A supplementation may be possible [4].

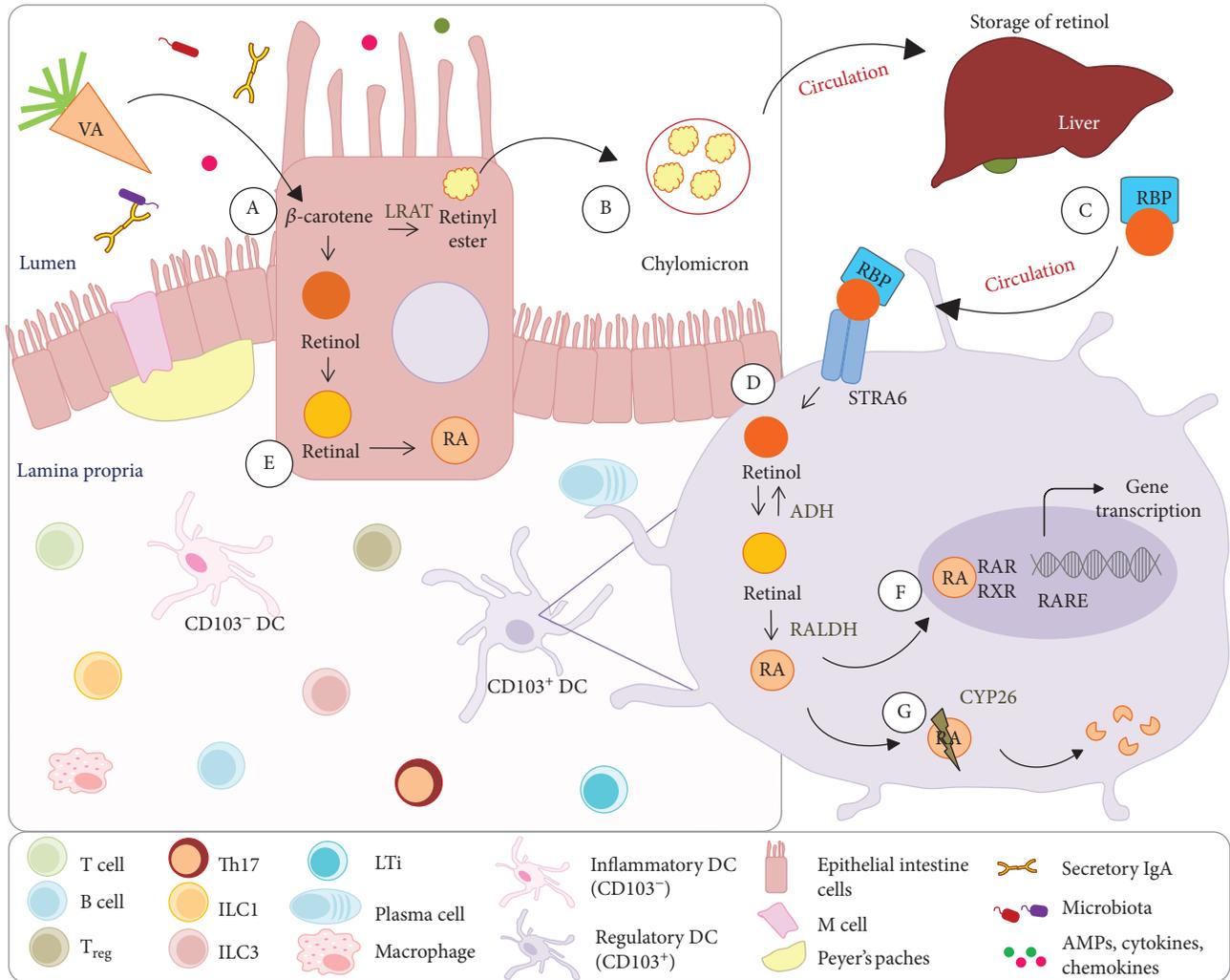


FIGURE 1: RA metabolism and signaling. (A) Vitamin A and its precursors (β -carotene) obtained from diet are absorbed by intestinal epithelium cells and esterified in retinyl esters by the enzyme lecithin retinol acyltransferase (LRAT). (B) Retinyl esters are packed with chylomicrons and enter general circulation where they are captured by hepatocytes and stored as retinol. (C) The retinol binds to retinol binding protein (RBP) in the liver and is carried through the bloodstream. This complex is recognized via the stimulated by retinoic acid 6 (STRA6) receptor, which mediates the absorption of extracellular retinol to cytosol. (D) After uptake, RA is generated from retinol by two sequential reactions. First, retinol is oxidized into retinal by enzyme alcohol dehydrogenase (ADH). Subsequently, in CD103⁺ DCs, retinal is oxidized by the enzyme retinal dehydrogenase (RALDH) to generate RA. (E) Intestinal epithelium cells can also metabolize vitamin A after absorption into retinal and RA, which can be directly released into the intestinal mucosa. (F) RA interacts with nuclear receptors, such as the retinoic acid receptor (RAR) and retinoid receptor X (RXR), to regulate the transcription of several target genes by binding the retinoic acid-responsive elements (RAREs) in DNA. (G) Control of the RA concentration in tissues is performed by a group of enzymes that belong to the cytochrome P450 family 26 (CYP26), which catalyzes RA present in the cytosol to generate the oxidized forms.

In addition, due to its regulatory activity, RA has been shown to play an important role in the control of inflammatory diseases not only in the intestine [13, 14] but also in other tissues, such as the central nervous system [15–17] and pulmonary mucosa [18, 19].

Therefore, the roles of RA in the immune system, that is, both maintaining mucosal and epithelial homeostasis and contributing to anti-inflammatory function, are addressed in this review. The focus is on the role of RA in inflammatory responses, such as responses to inflammatory skin, intestinal, and airway diseases and its impact on immune cells.

However, first, we discuss the metabolism of vitamin A into RA and its signaling pathways.

2. RA Metabolism and Signaling

Vitamin A is obtained from diet through the consumption of foods containing vitamin A precursors (mainly β -carotene) and vitamin A in the form of retinyl esters, which are derived from plant and animal food, respectively [20]. Vitamin A and its precursors are absorbed in the intestine by intestinal epithelium cells, and the vitamin A precursors are esterified

in retinyl esters by the enzyme lecithin retinol acyltransferase (LRAT). Retinyl esters are packed with chylomicrons and enter general circulation [21] (Figure 1). In the systemic circulation, the chylomicrons undergo the action of the lipoprotein lipase enzyme, resulting in their capture by hepatocytes and hydrolysis to retinol. Retinol is stored in the liver, mostly in hepatic stellate cells (HSCs) [1].

When RA is needed by the organism, the formed retinol binds retinol-binding protein (RBP) in the liver and is carried through the bloodstream [22]. This complex is recognized via the stimulated by retinoic acid 6 (STRA6) receptor, which mediates the absorption of extracellular retinol to cytosol [23]. However, the STRA6 receptor is only essential for maintaining RA homeostasis in the eye; therefore, other mechanisms are likely involved in the uptake of retinol into other tissues [24, 25].

After uptake, RA is generated from retinol by two sequential reactions. In the first reversible reaction, retinol is oxidized into retinal by the ubiquitously expressed enzyme alcohol dehydrogenase (ADH) [20]. Subsequently, in intestinal epithelium cells, DCs and macrophages associated with mesenteric lymph nodes (mLNs) and Peyer's patches (PPs), retinal is oxidized by the enzyme retinal dehydrogenase (RALDH) to generate RA [1]. There are three isoforms of RALDH (RALDH1, RALDH2, and RALDH3) [21], and their expression is tightly regulated and limited in the cells mentioned above. Thus, RALDH is considered the main enzyme that defines the populations of cells that are capable of producing RA [20]. Intestinal epithelium cells can also metabolize vitamin A after absorption into retinal and RA, which can be directly released into the intestinal mucosa [21].

RA can be generated in multiple forms as *all-trans*, *9-cis*, and *13-cis* RA [26, 27]; however, *all-trans* RA (atRA) is physiologically the most abundant [28]. RA interacts with nuclear receptors, such as the retinoic acid receptor (RAR) and retinoid receptor X (RXR), to regulate the transcription of several target genes [10, 29] by binding the retinoic acid-responsive elements (RAREs) in DNA [30]. These receptors form heterodimers; RAR comprises three major isoforms (α , β , and γ) that interact with all forms of RA, whereas RXR, which also has the α , β , and γ isoforms, mainly interacts with *9-cis* RA [31]. RA can also signal through peroxisome proliferator-activating receptor beta (PPAR- β) when it forms a heterodimer with RXR, which may be important for lipid metabolism and glucose homeostasis [1]. In addition, chicken ovalbumin upstream promoter-transcription factor II (COUP-TFII) [32] and hepatocyte nuclear factor 4 (HNF-4) [33] receptors can form a heterodimer with RXR and become low-affinity retinoic acid receptors. Similar to PPAR- β , their signals are important for lipid metabolism and glucose homeostasis [32].

Control of the RA concentration in tissues is performed by a group of enzymes that belong to the cytochrome P450 family 26 (CYP26), including subfamilies A1, B1, and C1 (CYP26A1, CYP26B1, and CYP26C1), which catalyze RA present in the cytosol to generate the oxidized forms (*5,8-epoxy* RA, *4-oxo* RA, *4-hydroxy* RA, and *18-hydroxy* RA) [34, 35]. The action of these enzymes prevents RA accumulation in the organism and maintains

optimal physiological RA concentrations for the best performance.

3. Effects of RA on Immune Cells

RA can act on different cells of both the innate and adaptive immune systems (Figure 2), exerting local action at mucosal sites, mainly in the intestinal mucosa, and systemic action. In addition, RA plays a key role in the maintenance of immune homeostasis during inflammatory responses.

3.1. Tolerogenic Effect of RA on DCs and Macrophages. The balance between tolerance and effector responses is mainly regulated by antigen-presenting cells (APCs), especially DCs [36]. DCs in peripheral organs are characterized by the expression of CD103 and CD11b molecules [37]. RA can regulate the differentiation of bone marrow DC precursors (pre-DCs) into premucosal DC (pre- μ DCs) by expression of gut-trafficking receptor $\alpha 4\beta 7$ and gives rise to intestinal CD103⁺CD11b⁺ DC, in mice [38].

Tolerogenic CD103⁺ DCs, which are located mainly in the lamina propria of the small intestine and gut-associated lymphoid tissue (GALT), such as PPs and mLNs [39, 40], are responsible for the maintenance of homeostasis. This type of DC can promote the generation of Foxp3⁺ regulatory T cells and the migration of regulatory and effector cells to the GALT [9–11]. The migration of T and B cells is mediated by CD103⁺ DCs due to their ability to synthesize RA [10, 41] as these cells have a high expression of the RALDH1 and RALDH2 enzymes, which are responsible for the conversion of retinal to RA; thus, these cells are the main synthesizers of RA [42].

Other RALDH⁺ DC populations that also produce RA are mainly located at mucosal interfaces, such as the skin, the lungs, and the corresponding draining lymph nodes [43, 44]. At the moment of antigen presentation in secondary lymphoid organs, RALDH⁺ DCs (mainly CD103⁺ DCs) release RA, which can freely diffuse across the cell membrane of the target cell. Then, RA signaling via the RAR α receptor regulates the transcription of the promoter regions of the $\alpha 4$ gene subunit of $\alpha 4\beta 7$ integrin and the CC chemokine receptor 9 (CCR9) gene on target cells [10], promoting the synthesis and expression of gut-trafficking receptors $\alpha 4\beta 7$ and CCR9 in the cellular membrane. $\alpha 4\beta 7$ and CCR9 can interact with mucosal vascular addressin cell adhesion molecule 1 (MAdCAM-1) and CC chemokine ligand 25 (CCL25), respectively [41, 45]. MAdCAM-1 is present in the venules of mLNs and PPs, while CCL25 is produced by intestinal epithelial cells; thus, RA imprints gut-homing specificity on immune cells [8, 40, 41, 45, 46].

However, not all DCs express the RALDH enzyme, such as inflammatory DCs, which can infiltrate or develop in the gut during inflammation due to chemokines and cytokines secreted by resident cells during the inflammatory process [47, 48]. In contrast to CD103⁺ DCs, the proinflammatory CD103⁻ DC population promotes the differentiation of interferon-gamma- (IFN- γ -) producing T cells and produces proinflammatory cytokines, such as tumor necrosis factor-alpha (TNF- α) and interleukin- (IL-) 6, suggesting that these

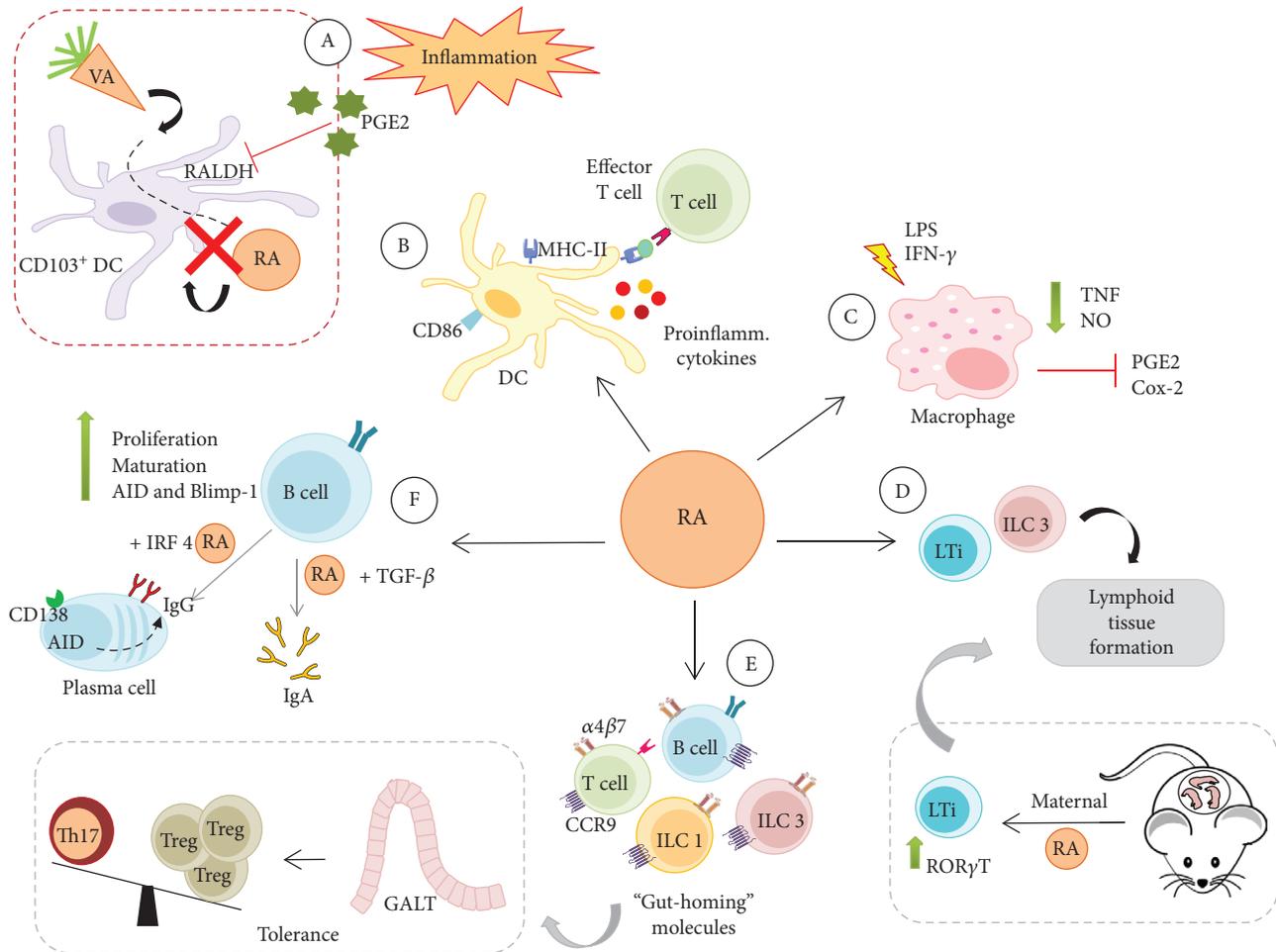


FIGURE 2: Role of RA in immune cells. RA can act on different cells of both the innate and adaptive immune systems exerting local action at mucosal sites and systemic action, which simultaneously, depending on where the RA-producing cells, mainly CD103⁺ DCs, are located when it releases the RA. (A) However, in an inflammatory environment (red box), PGE2 released during the inflammatory response inhibits the RALDH enzyme that is required for RA synthesis. When RA is released, it acts as follows: (B) RA together with proinflammatory cytokines contributes to the activation of DCs and the generation of effector T cells; (C) RA promotes macrophage modulation, inhibiting inflammatory mediators and the release of TNF and NO; (D) RA also activates ILC3, especially LTi cells, which are required for the formation of lymphoid tissue, including during fetal development; (E) RA induces expression of the molecules $\alpha 4\beta 7$ and CCR9 in lymphocytes and ILCs and the homing of these cells into the intestine and promotes the balance of Th17/Treg cells in the GALT, assuring tolerance, but is also able to induce Th17 in the presence of infection and inflammation; and (F) RA promotes the activation of B cells and their differentiation into Ab-secreting plasma cells.

subsets of DCs can play a distinct role in promoting effector T cell response in the gut [36, 49].

Some inflammatory factors may influence RALDH expression, such as prostaglandin E2 (PGE2), which is produced by peripheral stromal cells and suppresses the differentiation of RA⁺ DCs by directly antagonizing RALDH expression [50]. In addition, DCs that infiltrate the gut during inflammation do not acquire RALDH activity, which is required for RA synthesis. These inflammatory DCs express E-cadherin and the CD103 receptor, accumulate in the mesenteric lymph nodes and the inflamed colon, exhibit high expression of Toll-like receptors (TLRs) and produce cytokines IL-6 and IL-23, enhancing inflammation [47].

Mice with a vitamin A-deficient diet (VAD) exhibit reduced expression and activity of the RALDH enzyme in intestinal DCs, which is essential for the regulation of

immune and inflammatory responses [51]. Other factors, including GM-CSF, IL-4, IL-13, and TLR ligands 2 and 5, may induce the *in vitro* expression of RALDH [52, 53], suggesting that the local microenvironment is able to modulate RA synthesis.

In infections, RA signaling may also induce the production of proinflammatory cytokines by DCs, promoting the differentiation of effector T cells [12] and enhancing the cellular activation state, in addition to the promotion of the formation of tertiary lymphoid structures [10]. These structures are formed in response to nonresolving inflammation generating lymphoid aggregates that drive adaptive immune reactions [54, 55]. RA also influences the maturation of monocyte-derived DCs (MoDCs) by increasing the expression of major histocompatibility complex (MHC) class II and CD86 and regulating the survival of DCs via the

RAR α /RXR pathway [56]. In parallel to the activation of the innate immune response, RA promotes human DCs to induce IL-10-producing T cells to control inflammation and the maintenance of tissue homeostasis [57].

There are other sources of RA, such as lamina propria stromal cells, intestinal epithelial cells, and macrophages. Intestinal macrophages express RALDH1 and RALDH2, but that expression is dependent on external stimuli, such as cytokines and TLR ligands, whereas in CD103⁺ DCs, the expression of these enzymes appears to be related to dietary vitamin A [51, 58]. In contrast, atRA treatment upregulates CD103 expression in human MoDCs, increasing the ability of the DCs to synthesize RA [59] and inducing tolerogenic DCs.

Mucosal macrophages, which constitute the most abundant population of phagocytic cells in the gut, show inflammatory anergy, avoiding inflammation in normal intestinal mucosa despite proximity to immunostimulatory microbiota [58]. RA also acts directly on macrophages at both mucosal sites and other immunological sites. atRA modulates peritoneal macrophage activation by endotoxin and IFN- γ by suppressing TNF production and nitric oxide (NO) synthesis [60]. In addition, atRA inhibits the expression of PGE2 and COX-2 and the release of TNF, which are induced by bacterial lipopolysaccharide (LPS) in murine peritoneal macrophages [61].

Retinoid treatment inhibits IL-12 production in LPS-activated macrophages by inhibiting nuclear factor kappa B (NF κ B)-DNA interactions and the competitive recruitment of transcription integrators between NF κ B and RXR [62]. atRA also inhibits the LPS-induced production of the proinflammatory cytokines TNF- α and IL-12 and potentiates IL-10 production in the THP-1 monocyte/macrophage cell line and human cord blood mononuclear cells (CBMCs) [63]. Plasma factors, such as transforming growth factor-(TGF- β) and PGE2, in combination with RA, act synergistically with IL-4 synthesized by basophils to increase the sensitivity of macrophages to IL-4, which contributes to M2 macrophage polarization and the regulation of the inflammatory process in mice [64].

Tissue-resident macrophages are highly heterogeneous in terms of their functions and phenotypes as a consequence of adaptation to different microenvironments [65]. Monocyte-derived inflammatory macrophages can be converted into the resident tissue phenotype in a vitamin A-dependent manner [66]. VAD mice fail to convert tissue-resident macrophages during infection, which may lead to a deregulated inflammatory process [66].

In general, the impact of RA on macrophages suggests that RA inhibits the production of inflammatory cytokines and favors the generation of tolerance.

3.2. Modulation of Innate Lymphoid Cells (ILCs) by RA. ILCs constitute a group of tissue-resident innate immune cells that can regulate inflammation and repair tissues in multiple anatomical compartments, particularly on the barrier surfaces of the skin, airways, and intestine [67]. ILCs are derived from the same DNA-binding 2- (Id2-) dependent precursor and are characterized by the expression of the IL-7 receptor [68].

These cells are subdivided into the following three main groups: group 1 ILCs (ILC1), which include natural killer (NK) cells, are induced by transcription factor T-box expressed in T cells (T-bet) and produce IFN- γ ; ILC2 require the GATA-binding protein 3 (GATA3) transcription factor and produce IL-5 and IL-13; and ILC3 depend on the transcription factor retinoic acid receptor-related orphan nuclear receptor gamma (ROR γ t) and secrete IL-17 and IL-22 [69].

ILC1 are accumulated during chronic inflammation in the gut (inflammatory bowel disease) and lung (chronic obstructive pulmonary disease), where they contribute to IFN- γ -mediated inflammation; ILC2 are mainly found in the lung but can also be present in the skin and gut, are related to helminth defense, and are mostly involved in tissue repair, allergy, and asthma, and ILC3 are implicated in gut barrier defense and skin inflammation [70].

In addition, ILC3 include lymphoid tissue-inducing cells (LTi) that contribute to the formation of secondary lymphoid organs [71]. RA during gestation is necessary for the development of fetal LTi cells during the embryonic stage, since maternal RA upregulates the ROR γ t transcription factor and favors the formation of lymphoid tissue, promoting greater efficiency in the immune responses of adult offspring [72]. Similarly, RA is required during the postnatal phase for the generation of intestinal ILC3 and LTi cells in adult mice, since its deficiency or the blockade of RA-RAR signaling reduces the development of enteric lymphoid tissue [73].

RA also induces the expression of α 4 β 7 and CCR9 in ILCs 1 and 3, which is crucial during antiviral and antibacterial responses in the intestinal mucosa; this effect is not observed in ILC2 since the homing receptors expression of these cells is determined during development in the bone marrow [8]. RA associated with IL-2 *in vitro* contributes to the synthesis of IL-5 and IL-13 by ILC2 and IFN- γ by ILCs 1 and 3, which are important for the functional maintenance of ILCs in allergic and inflammatory diseases [74].

Intestinal tolerance induced by RA could be obtained by modulating ILC3 function in the GALT by increasing IL-22 production during colon inflammation induced by dextran sulfate sodium (DSS) or pathogenic bacteria, in mice [75]. In addition, the RAR receptor, which acts as a transcription factor, is able to bind the IL-22 promoter and directly promote its transcription. Moreover, human intestinal ILC1 can differentiate into ILC3 *in vitro* in response to IL-2, IL-23, IL-1 β , and RA [59], which is important for tolerance.

In NK cells, RA acts tolerogenically and suppresses the human NK cell cytotoxicity activated by IFN- α [76]. NK cells are cytotoxic cells that act against tumor cells and virus-infected cells by a complex process of signaling mediated by activating and inhibitory receptors [77]. Additionally, antibody-dependent cellular cytotoxicity (ADCC) directs the cytotoxicity of NK cells toward antibody-coated target cells [78]. RA can influence the activity of NK cells by inhibiting ADCC and its natural cytotoxicity *in vitro* [79]. In addition, high concentrations of atRA inhibit NF κ B signaling in NK cells, negatively regulating the secretion of IFN- γ , which is important for granzyme B release [80]. *In vitro* treatment with 13-*cis* RA also regulates NK cell activity by increasing CD158b, which is a killer inhibitory receptor [81].

On the other hand, RA increases the expression of MHC class I chain-related proteins A and B (MICA and MICB) in tumor cells that bind the natural killer group 2D (NKG2D) receptor in NK cells, promoting their activation [82]. In addition, the number of circulating NK cells in humans is positively regulated by the level of retinol stocks [83]. Thus, RA exerts a bidirectional effect on NK cells, which may contribute to its inhibition or activation.

3.3. Effect of RA on B Cell Differentiation. RA plays an important role in the humoral response and is essential for B cell production of IgA antibodies playing a multifactorial role in mucosal immunity [10, 84]. Oral administration of RA in VAD mice proved to be efficient in reestablishing IgA production after influenza vaccination [7]. In addition, vitamin A and zinc deficiency leads to a decrease of serum IgA and a drastic reduction of humoral mucosal immunity [85]. During vaccination, the association with RA potentiates the immune response in both adult and neonatal mice, suggesting an important role of RA as a vaccine adjuvant, especially during the early stages of life [86, 87].

Retinoids are described as important cofactors for the stimulation and proliferation of B cells, accelerating B cell lymphopoiesis [88, 89]. RA increases the number of peripheral B cells in the spleen while decreasing lymphoid progenitors in the marrow; these effects are mediated by an increase of the early B cell factor 1 (EBF1) and paired box protein-5 (Pax-5) transcription factors, which are crucial for B cell development [89]. Moreover, RA accelerates the maturation of human B cells and their differentiation into plasma cells [90].

The development of an effective long-lasting humoral response requires the formation of germinal centers (GCs) in the lymphoid follicles, where interactions between B cells and follicular helper T cells guarantee the development of memory B cells and long-lived plasma cells [91]. Thus, B cells undergo somatic hypermutation and immunoglobulin class-switching recombination as a part of the GC reactions mediated by the activation-induced cytidine deaminase (AID) enzyme [92]. RA may increase more differentiated B cell phenotypes by upregulating the expression of AID and B lymphocyte-induced maturation protein-1 (Blimp-1) and increasing the expression of CD138 and IgG in splenic B cells [93]. RA also induces the expression of interferon regulatory factor 4 (IRF4), which is involved in the generation of plasma cells and RA-mediated IgG production, favoring AID expression [94]. In addition, RA may increase IgM and IgG syntheses in human B cells from CBMCs and adult peripheral blood mononuclear cells (PBMCs), respectively [95].

The microenvironment may directly affect the modulation of the humoral response. The combined effects of bacterial products and RA on the intestinal mucosa trigger signaling cascades via TLRs and RAR, respectively, activating follicular dendritic cells (FDCs) [96]. This process enhances the synthesis of CXC chemokine ligand 13 (CXCL13), which is a chemoattractant of B cell follicles in lymphoid tissues, and increases the expression of B cell-activating factor (BAFF), which is an important factor for B cell survival and TGF- β [96]. Collectively, RA favors the migration and

survival of B cells and leads to the preferential generation of IgA in the intestine [84]. Other components present in the mucosa contribute to the generation of IgA, such as lactoferrin [97], which, together with RA, leads to the production of IgA by peritoneal B-1 cells [98].

On barrier surfaces, the humoral response is the main effector response to frequent microbial challenges from both the host microbiota and the external environment. RA plays a key role in the modulation of mucosal inflammatory responses by contributing to the synthesis of antibodies, especially IgA, ensuring immunity and tolerance.

3.4. Effects of RA on the T Cell Population. The effects of RA on the balance of Th1/Th2 responses are controversial. Some studies indicate that high levels of RA can promote the differentiation of naïve T cells into Th2 cells by inducing IL-4 gene expression [1]. In addition, RA modulates IL-12 production by APCs, inhibiting Th1 cell differentiation [99], and induces the expression of GATA3 and signal transducer and activator of transcription 6 (STAT6), which is important for the maintenance of the Th2 response [1, 36]. RXR agonists and 9-*cis* RA also favor the development of Th2 cells [100]. However, an experimental ovalbumin-induced asthma murine model suggests that vitamin A deficiency is related to increased pulmonary inflammation by inducing type 2 cytokines [101]. In addition, some studies have shown that oral vitamin A treatment (vitamin A supplementation diet) indirectly reduces pulmonary inflammation as a result of the anti-inflammatory effects of RA on other immune cells and Treg cell generation in the lung without directly affecting the Th2 population [18, 19].

Although RA inhibits Th1 responses, it is essential for the stability and maintenance of Th1 cells, repressing transcription factor ROR γ t, which is important for the induction of Th17 cells [102]. Furthermore, RA plays an important role in the maintenance of Th1 responses since VAD mice exhibit a negative Th1 response after infection with *Toxoplasma gondii* [12].

The impact of RA on the Th17/Treg balance has a known mechanism. Small intestinal lamina propria DCs synthesize RA and have the ability to generate Tregs in the presence of TGF- β [6]. Thus, elevated levels of TGF- β promote the generation of Tregs from naïve CD4 T cells by an RA-dependent mechanism [9, 39, 103, 104] in which atRA promotes the acetylation of histones on the promoter of the Foxp3 gene. In addition, atRA, which activates STAT6 through IL-4 signaling, also promotes the acetylation of histones on the Foxp3 gene promoter, increasing its expression in the cell [105, 106].

At the steady state, RA inhibits the differentiation of naïve T cells into Th17 cells by blocking IL-23 and IL-6 signaling [107]. RA also indirectly induces Treg conversion by inhibiting the CD44^{hi}CD4⁺ T cell population of memory cells, which blocks the differentiation of naïve T cells into Tregs via the secretion of IL-4, IL-21, and IFN- γ [108]. In addition, RA controls the generation of T cells with an inflammatory profile in the GALT, suppressing the differentiation of naïve T cells into Th17 cells in the mucosa to maintain tolerance [45]. In contrast, IL-6 inhibits the generation of Tregs, favoring the expansion of Th17 cells in colitis [105, 109].

Th17 cells are generated in the presence of IL-6 and IL-21 and low levels of TGF- β in the intestinal mucosa, mainly during chronic inflammation [109, 110]. These cells can secrete cytokines, such as IL-17A, IL-17F, IL-21, and IL-22, which can control bacterial and fungal infections at mucosal sites [10]. Although RA inhibits Th17 generation, during infection of the intestinal mucosa, low concentrations of RA produced by TLR5⁺ lamina propria DCs induce the generation of Th17 cells, potentiating the protective response in the mucosa [111]. In addition, RA is essential for the *in situ* generation of Th17 cells in the intestinal mucosa during infection caused by *Toxoplasma gondii* [12].

Oral supplementation with RA in mice with chronic inflammation in the ileum may attenuate inflammation by restoring the balance between the Th17 and Treg populations, increasing the number of CD103⁺ DCs and RALDH2 expression by a positive feedback mechanism [45, 109]. Microbial stimuli, such as the TLR-2 receptor ligand in mice, also increase RALDH2 expression and RA production, promoting regulatory T cells and inhibiting the generation of Th17 cells [42, 52]. Thus, RA balances the generation of subsets of T cells depending on the conditions and factors of the microenvironment to maintain homeostasis.

4. Immunomodulatory Effect of RA during Inflammatory Processes

Inflammation during immune responses is an important way to remove tissue injuries and promote restoration. Inflammation can occur as a physiological process in which dead cells are removed from tissues, keeping the tissues healthy, but it can also be caused by several other stimuli, such as pathogen infections, damaged cells, toxic compounds, or irradiation [112].

Typically, organisms undergo acute inflammatory responses in which molecular and cellular interactions resolve injury and infections without tissue damage, contributing to the restoration of tissue homeostasis. However, uncontrolled acute inflammation or nonresolution of infection may generate chronic inflammation, contributing to a variety of chronic inflammatory diseases [113, 114].

Simultaneously, some components of the diet act as anti-inflammatory mediators by attenuating acute and chronic inflammatory processes, promoting homeostasis and, thus, ameliorating the harmful effects of inflammatory responses. Here, we focus on how RA modulates the inflammatory response at different mucosal sites and different tissues (Figure 3).

4.1. Intestinal Mucosa. Inflammatory bowel disease (IBD), which is mainly referred to as Crohn's disease and ulcerative colitis, is a result of chronic inflammation characterized by excessive innate immune cells activation, tissue damage, and the induction of adaptive immune responses against the intestinal microbiota. Gut dysbiosis, mainly among commensal bacteria, initiates an exacerbated inflammatory response. This disorder can be caused by multiple factors, including abnormal immune responses, genetic susceptibility,

infection, dietary habits, and the administration of antibiotics [115, 116].

RA has been shown to regulate immune responses and restore the Th17/Treg balance, mainly in the intestinal mucosa, showing that RA plays an important role in intestinal mucosal homeostasis [45, 109]. Vitamin A impairs the reprogramming of inducible Tregs (iTregs) into Th17 cells during intestinal inflammation induced in a T cell-dependent colitis model [13, 14]. In addition, DCs were more efficient for Treg differentiation after the restoration of intestinal RA by diet in intestinal tumor models [14].

In an experimental model of DSS- or pathogenic bacteria-induced colitis, RA was shown to attenuate inflammation by increasing IL-22 production by ILC3 and T γ δ cells and, consequently, increasing the synthesis of antimicrobial peptides [75] or by decreasing TNF levels and NF κ B activation [115]. Moreover, in inflamed intestinal tissues from Crohn's disease patients, the number of CD127⁺ ILC1 increased at the cost of ILC3 [59]; however, ILC1 can be differentiated into ILC3 *in vitro* and *in vivo* upon IL-2, IL-23, and IL-1 β stimulation and this process was enhanced in the presence of RA, reducing inflammation [117]. In addition, *in vitro* atRA treatment of inflamed colonic mucosa from patients with ulcerative colitis and colitis-associated cancer modulates the LPS/TLR4/NF κ B signaling pathway and decreases nitric oxide synthase 2 (NOS2) and TNF- α expression [118]. This finding suggests that RA may be a target for future colorectal cancer treatments.

The absence of RA in VAD mice makes them more susceptible to the development of DSS-induced colitis and colon cancer due to worsening of chronic inflammation in the intestine [119]. In this context, CYP26B1, which is responsible for the catabolism of RA [35], has been shown to regulate the differentiation and function of CD4 T cells during experimental colitis, driving the cells towards an inflammatory profile. The passive transfer of naïve cytochrome p450 family 26 subfamily b1-deficient (Cyp26b1^{-/-}) mice CD4 T cells into recombination-activating gene 1-deficient (Rag1^{-/-}) mice resulted in a significantly reduced disease state in a model of T cell-dependent colitis [120].

In humans and murine models of ulcerative colitis associated with colorectal cancer, alterations of atRA metabolism mediated by microbiota-induced intestinal inflammation, with increasing levels of CYP26A1, another atRA-catabolizing enzyme, reduced colonic atRA and promoted tumorigenesis [121]. Supplementation with atRA reduced the tumor burden, and this effect was mediated by cytotoxic CD8 T cells activated by MHC I upregulation on tumor cells [121]. In a case-control study with 898 colon cancer cases, 501 rectal cancer cases, and 1399 matched controls, an association between higher plasma retinol concentrations and a lower risk of colon cancer was observed, mainly in proximal colon cancer [122]. This evidence suggests a role of RA in the prevention of colon cancer.

Serum retinol levels in adults and children with Crohn's disease are lower than those in healthy people probably due to a deficiency in nutrient absorption [123, 124]; similar results were reported for ulcerative colitis [125]. Considering the tolerogenic role of RA in the intestinal mucosa and the

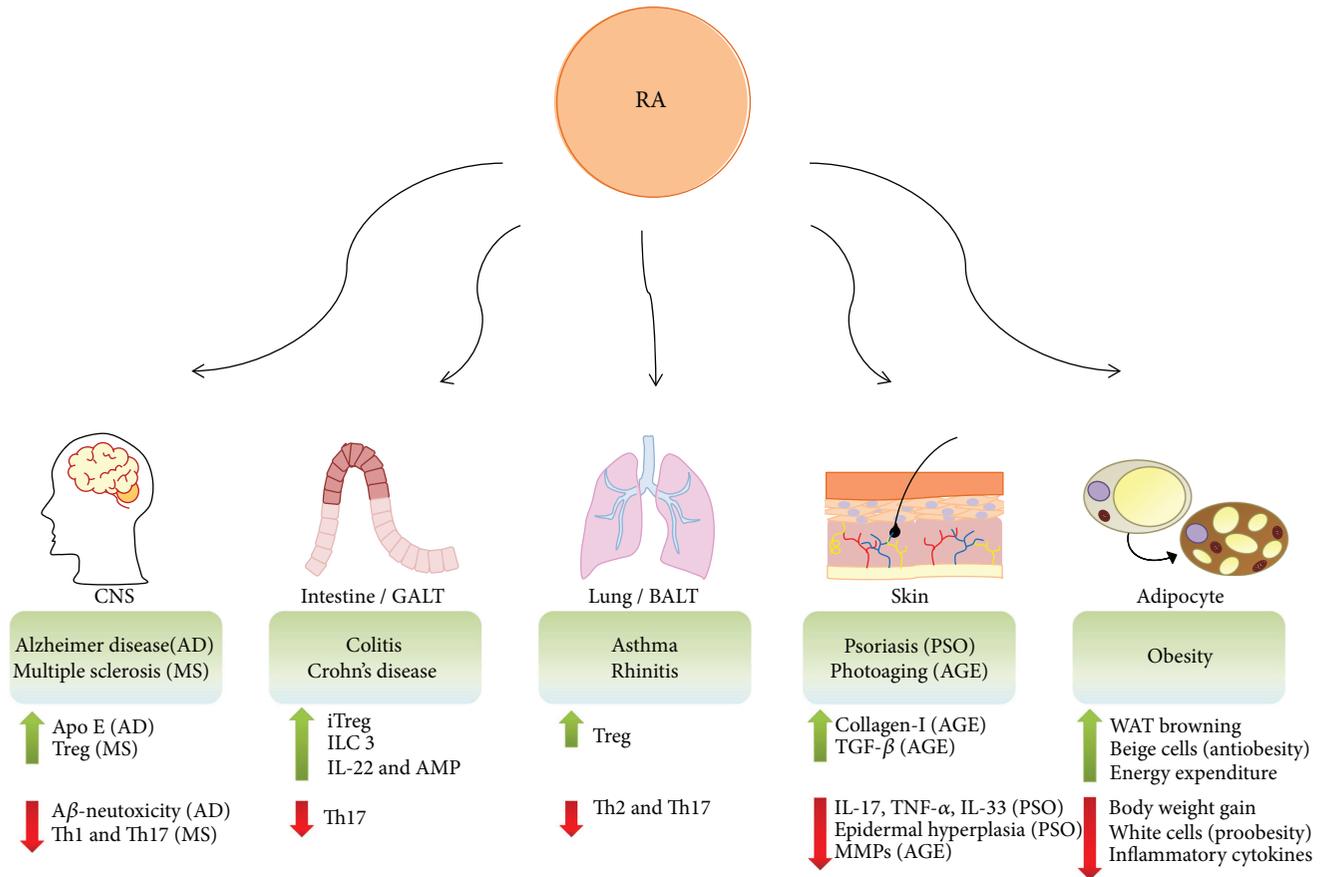


FIGURE 3: Potential anti-inflammatory effects of RA. RA can decrease inflammatory processes, promoting homeostasis and attenuating harmful inflammatory responses in mucosa and tissues. RA shows immunosuppressive effect on Th1/Th17 cells in multiple sclerosis (MS) and induces Apo E in microglia, protecting from the neurotoxic effects mediated by amyloid β (A β) in Alzheimer disease (AD), contributing to neuronal homeostasis. RA is crucial for intestinal tolerance, by inducing Treg, cytokines IL-10 and IL-22, and antimicrobial peptide (AMP) synthesis, which may lead to Th17 inhibition. RA modulates inflammatory airway diseases (asthma and rhinitis) by inhibiting Th2/Th17 response and enhancing Treg cells. Retinoids increases type I collagen and TGF- β , reducing matrix metalloproteinase (MMPs) in photoaging (AGE), and reduces IL-1 family cytokines (IL-17 and TNF- α), IL-33, and epidermal hyperplasia in psoriatic (PSO) lesions. RA also has effects in adipocytes, promoting white adipose tissue (WAT) browning by differentiation into beige cells (antiobesity) instead of white cells (proobesity). The formation of brown adipocytes within WAT enhances energy expenditure and reduces obesity. In addition, RA can repress the expression of inflammatory chemokines and cytokines, inhibiting inflammatory responses triggered by obesity.

fact that IBD patients have low levels of serum retinoids, RA administration should be an adjuvant treatment for inflammatory diseases.

Moreover, we must consider that RA also plays an important role during intestinal inflammation caused by pathogen infection, as observed during *Salmonella typhimurium*-mediated gastroenteritis in mice [126] and during *Vibrio cholera* infection after pretreatment with RA prior to immunization [127].

Overall, RA displays an important anti-inflammatory activity in the control of inflammation in the intestinal mucosa, but more studies are necessary to better understand the role of RA in inflammatory processes.

4.2. Airways and the Lung. Inflammatory airway diseases, such as asthma and allergic rhinitis, have a high prevalence around the world. Airway inflammation is mediated by Th2 cells that characteristically produce IL-4, IL-5, and IL-13

[128]. Moreover, in chronic airway inflammatory diseases, the massive infiltration of eosinophils is mediated by allergen-specific Th2 cells and neutrophils also participate in chronic obstructive pulmonary disease mediated by Th17 cells [129].

The role of RA in the pulmonary mucosa is controversial. Supplementation with vitamin A has been shown to increase the severity of asthma in experimental models with high levels of IgE and IgG1 antibodies and pulmonary inflammation [29]. In addition, RA has the ability to induce Th2 responses and inhibit Th1 responses [99, 100]. In contrast, oral administration of Net-41B, an RXR partial agonist, suppressed aryl hydrocarbon receptor (AHR) and inflammatory cell accumulation in the airways and attenuated TNF- α levels in the lung and IL-5, IL-13, and NO levels in bronchoalveolar lavage fluid from mice [130]. The RXR partial agonist Net-41B may be a promising candidate for the treatment of allergic airway inflammation.

Moreover, vitamin A deficiency has been related to an increased asthma incidence in children due to damage to the pulmonary mucosa and to the maintenance of the airway epithelium [131]. During vitamin A deficiency, a mouse asthma model revealed the induction of Th2 cytokines, such as IL-5 and IL-13, and an increase in pulmonary inflammation [101]. The administration of RA may attenuate inflammation by increasing the population of regulatory T cells in the lung and decreasing the tissue damage caused by inflammation [18, 19]. The association between RA and ovalbumin in oral tolerance in a murine model of bronchial asthma efficiently inhibited the inflammatory response and decreased eosinophilic infiltration besides Treg cells induction in the lung [132]. Treatment with atRA was able to attenuate airway inflammation by inhibiting Th2 and Th17 cytokines and downregulating the expression of the GATA3 and ROR γ t transcription factors in the lung [128]. Similar results were observed in a murine model of allergic rhinitis [133]. Interestingly, lung-resident tissue macrophages that coexpress TGF- β and retinal dehydrogenases (RALDH1 and RALDH2) are able to induce Treg cells at a steady state, favoring airway tolerance [134].

In human studies, the retinoid concentrations in the serum were significantly lower in patients with asthma than those in healthy control subjects and were even lower in patients with severe asthma than those in patients with mild asthma [135, 136], highlighting the importance of equilibrating physiological RA concentrations in airway diseases.

4.3. Central Nervous System. Although the brain is an immunologically privileged site, in pathologic conditions of the central nervous system (CNS), an organized immunologic response can develop within the CNS to eliminate inflammation without tissue damage [137]. However, in some cases, a persistent inflammatory response develops during neurodegenerative processes, such as multiple sclerosis (MS) and Alzheimer's disease (AD).

MS is an autoimmune disease characterized by recurrent episodes of demyelination and axonal lesions mediated by Th1 and Th17 cells, macrophages, and immune inflammatory mediators [138]. Taking into account the immunosuppressive role of RA for Th1/Th17 cells and macrophages, it is not unreasonable to think that RA may exert beneficial effects in MS.

Indeed, treatment with atRA alone or in combination with calcitriol (an active vitamin D metabolite) in murine autoimmune encephalomyelitis (EAE), which is an experimental model of MS, increased the expression of the Foxp3 and TGF- β genes in splenocytes while reducing ROR γ t gene expression [139]. PBMCs from patients with MS who were supplemented with vitamin A for 6 months also showed an upregulation of TGF- β and Foxp3 gene expression [15] and a reduction in IFN- γ and T-bet gene expression [16]. RA treatment also suppresses T γ δ cell pathogenic activity by decreasing IL-17 production, which is important for the maintenance of EAE [17]. Moreover, the combination of atRA and atorvastatin, which is a lipid-lowering agent with anti-inflammatory, immunomodulatory, and neuroprotective properties, causes the regression of the clinical and

neuropathological features of EAE with reduced secretion of IL-17 and increased production of IL-10 and Foxp3⁺ Treg cells in splenocytes [140].

In MS, activated astrocytes participate in promoting lesion progression by secreting proinflammatory mediators and chemokines. In cocultures with inflamed endothelial cells, primary astrocyte-derived RA attenuated oxidative stress [141]. In addition, murine astrocytes that were stimulated with LPS and treated with atRA expressed no or very low levels of CCL and CXCL chemokines [142].

All these data suggest that retinoids are candidates for the treatment of neuroinflammation. Indeed, the use of RA-loaded polymeric nanoparticles (RA-NPs) modulates the murine microglial response towards an anti-inflammatory and neuroprotective phenotype (M2-like) in organotypic hippocampal slice cultures [143]. Recently, the intravenous administration of RA-NPs was shown to prevent ischemic injury in the immature brains of 2-day-old mice, demonstrating the role of RA in the control of neuroinflammation [144].

RA also has neuroprotective activity and is capable of increasing barrier tightness in human-induced pluripotent stem cell-derived brain endothelial cells by RAR α , RAR γ , and RXR α activation [145]. In addition, treatment with RA in experimental models of AD and *in vitro* was beneficial.

AD is a progressive neurodegenerative disease characterized by neuroinflammation with reactive microglia, astrogliosis, proinflammatory cytokines, amyloid- β (A β) peptide deposition, and progressive memory loss [146]. Treatment with RA in an experimental model of AD was beneficial by inhibiting microglial activation in the hippocampus and improving the proliferation of stem cells [147], as well as increasing the synthesis of apolipoprotein E (Apo E) in human macrophages [148]. Apo E acts on microglia, protecting them from the neurotoxic effects of amyloid β , and contributes to neuronal homeostasis [149].

Oral coadministration of Am80 (an RAR- α / β agonist) and HX630 (an RXR agonist) reduced the level of insoluble A β peptide in the brain by promoting the differentiation of IL-4-responsive M2-like microglia and increasing their activity for the clearance of oligomeric A β peptides in an experimental model of AD. This finding showed that combination treatment with RAR and RXR agonists could be an effective approach for AD therapy [146].

atRA administration prevents LPS-induced neuroinflammation, NO production, amyloidogenesis, and memory impairment in aged rats [150]. PBMCs from patients with AD in cultures with atRA showed downregulated spontaneous NO production and iNOS expression, which was associated with a reduction in IL-17A production and increased IL-10 release [151].

All these data suggest that RA may be a potential target in both MS and AD treatments.

4.4. The Skin. The skin is the primary barrier that provides protection against microbial pathogens and physical and chemical insults to organisms [152]. The skin is composed of the following layers: epidermis, basement membrane, dermis, and subcutaneous fatty region. Each layer has several

structures, such as hair follicles, sweat glands (in humans but not mice), sebaceous glands, nerves, blood vessels, and lymphatics. The epidermis and dermis have a variety of cell types, including immune cells. Together, these cells form an orchestrated defense against invading pathogens [153]. In the epidermis, in addition to melanocytes that produce melanin and keratinocytes, there are Langerhans cells, which are the main skin-resident immune cells, and are more involved in tolerogenic than inflammatory responses [154]. The other types of immune cells, such as DC subpopulations, macrophages, ILC2, NK, and B and T cells, reside in the dermis [155].

In the epidermis, keratinocytes also play an important role in defense against pathogens. Epidermal keratinocytes are proinflammatory effector cells with a large production of antimicrobial peptides (AMPs), proinflammatory cytokines, and chemokines [155]. Keratinocytes also express TLRs [156], which are crucial for promoting skin immune responses and Th1 responses [152]. However, an imbalance in the immune response and microbiota or persistent infections can generate skin inflammations, causing several diseases.

The use of retinoids has long been established for the treatment of immune-mediated skin diseases. In dermatological treatment, retinoids are typically classified into three generations according to how they were developed [157]. The first-generation retinoids are the naturally occurring nonaromatic retinoids, including retinol, retinal, isotretinoin (*13-cis* RA), tretinoin (atRA), and alitretinoin (*9-cis* RA). The second-generation retinoids are the monoaromatics (etretinate, acitretin, and motretinate). The third-generation retinoids are the polyaromatics (bexarotene, adapalene, and tazarotene) [157, 158].

Photoaging is a process mainly triggered by ultraviolet radiation from chronic sun exposure that leads to DNA damage and the production of reactive oxygen species, which both promote inflammation [159] and result in increased matrix metalloproteinases (MMPs) and collagen degradation [160]. Retinoids have demonstrated efficacy in the treatment of the photoaged skin. The effects of RA include the inhibition of the expression of MMPs [161]; inhibition of tyrosinase activity, which increases epidermal cell turnover and leads to increased shedding of melanin-laden keratinocytes; reduction of inflammatory cytokine production; and enhancement of type 1 collagen and TGF- β [162]. All these effects contribute to the improvement of symptoms in photoaging.

In addition to aging/photoaging, the application of retinoids in skin diseases is very diverse and retinoids have been used in treatments for acne, rosacea, psoriasis, lichen planus, basal cell carcinoma, and so on [158]. Acne vulgaris is a common chronic inflammatory cutaneous disease that involves the pilosebaceous unit with abnormal keratinization leading to follicular plugging [163]. Retinoids act by increasing the turnover of follicular epithelial cells and accelerating the shedding of corneocytes, which helps normalize keratinization. Retinoids also exert a sebum-suppressive effect following oral isotretinoin administration [164]. The use of isotretinoin also induces the

remission of acne by normalizing the innate immune response to the commensal bacterium *P. acnes* [165]. This remission occurs due to decreased monocyte TLR-2 expression and the subsequent inflammatory cytokines response to *P. acnes*. Combining retinoids with other components and antibacterial agents can decrease irritation and increase the efficacy of retinoid treatment [163, 166]. Importantly, retinoids regulate the transcription factor AP-1, resulting in the inhibition of MMPs, which are responsible for scar formation in acne [165].

Psoriasis is a prototype inflammatory skin disease characterized by marked keratinocyte hyperproliferation and altered differentiation associated with dermal and epidermal infiltration of leukocytes [166]. Tazarotene is the most commonly used retinoid for topical treatment [167–169] and is usually used in combination with phototherapy, corticosteroids, vitamin D, and other treatments [170–172]. Tazarotene acts by reducing plaque elevation and inflammation probably due to its anti-inflammatory role in immune cells [158].

In general, the use of retinoids in immune-mediated skin diseases has been highly beneficial for the patients.

4.5. Obesity. Obesity is a global health issue, and overnutrition and excess bodyweight are associated with an increased risk of developing metabolic disorders, such as diabetes and cardiovascular diseases. Several inflammatory markers have been consistently associated with obesity, suggesting that persistent low-grade inflammation is present in obesity [173, 174].

RA also plays an important role in the modulation of inflammatory processes at other sites and in other tissues. In human adipocytes, atRA represses chemokine and inflammatory cytokines expression by inhibiting NF κ B signaling. Since inflammatory responses triggered by obesity play a major role in the onset of insulin resistance, atRA supplementation may represent a preventive nutritional strategy for controlling obesity and its complications [175].

Besides the liver, adipose tissue contains a substantial amount of retinol and its metabolites [176]. The RARs are highly expressed in adipose tissues; therefore, the RARs are directly influenced by atRA [177]. atRA and *9-cis* RA, *in vitro*, inhibit proliferation and induce apoptosis in a human preadipocyte cell lineage [178]. In addition, RA enhances lipid oxidation and inhibits lipid's biosynthesis capacity [178], as well as, decreases body weight gain in an obese rat model independent of Stearoyl-CoA desaturase 1 (SCD1) gene regulation, which is an enzyme involved in the biosynthesis of monounsaturated fatty acids [179].

RA also promotes the remodeling of white adipose tissue (WAT) [180], which is associated with metabolic disorders. In a VAD model, a marked increase in adiposity and hypertrophy of WAT was observed [181]. In addition, RA induces white adipose tissue browning by increasing adipose vascularity, which promotes the differentiation into beige cells (antiobesity) instead of white cells (proobesity) [182]. The formation of brown adipocytes within WAT enhances energy expenditure, reduces obesity, and could help improve metabolic health [183].

RA treatment of obese mice induces RAR target genes involved in the regulation of lipid homeostasis, leading to the suppression of obesity and insulin resistance [184].

Moreover, in an experimental obesity model, RA produced by DCs and macrophages upon IL-13 stimulation from IL-33-activated islet-resident ILC2 cells induced insulin secretion by β cells [185]. The IL-33-ILC2 axis was activated after acute β cell stress but was defective during chronic obesity. However, the fact that RA increases insulin secretion shows its potential modulatory role in metabolic diseases.

5. Conclusion and Future Perspectives

Globally, more than 2 billion people are affected by micronutrient deficiency and at least half of children aged 6 months to 5 years worldwide suffer from one or more micronutrient deficiencies. Vitamin A deficiency is a public health concern, and vitamin A supplementation in children is highly effective in reducing mortality from all causes. In adults, the anti-inflammatory effects of RA, which favor immune homeostasis, are a treatment strategy alone or in association with other drugs for inflammatory intestinal diseases, neurodegenerative processes, skin aging, and cancer. Furthermore, alterations of serum RA levels are not only indicators of homeostasis disequilibrium but also biomarkers for the intestinal inflammatory process. An uncontrolled vitamin supply and micronutrient deficiencies reinforce the need to better understand the effects of RA on the immune system and inflammatory diseases.

Conflicts of Interest

No conflicts of interest are declared.

Acknowledgments

This work was supported by the Laboratório de Investigação Médica, Unidade 56, Department of Dermatology, School of Medicine, University of São Paulo, Brazil and Fundação de Amparo à Pesquisa do Estado de São Paulo.

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Research Article

Insulin-Like Growth Factor-I as an Effector Element of the Cytokine IL-4 in the Development of a *Leishmania major* Infection

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Received 16 February 2018; Revised 11 May 2018; Accepted 8 July 2018; Published 29 July 2018

Academic Editor: Naïma Moustaid-Moussa

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Certain cytokines modulate the expression of insulin-like growth factor- (IGF-) I. Since IL-4 and IGF-I promote growth of the protozoan *Leishmania major*, we here addressed their interaction in downregulating the expression of *Igf-I* mRNA using small interfering RNA (siRNA) in *Leishmania major*-infected macrophages. Parasitism was decreased in the siRNA-treated cells compared with the nontreated cells, reversed by the addition of recombinant IGF-I (rIGF-I). In IL-4-stimulated macrophages, parasitism and the *Igf-I* mRNA amount were increased, and the effects were nullified upon siRNA transfection. IGF-I downregulation inhibited both parasite and macrophage arginase activation even in IL-4-stimulated cells. Searching for intracellular signaling components shared by IL-4 and IGF-I, upon siRNA transfection, phosphorylated p44, p38, and Akt proteins were decreased, affecting the phosphatidylinositol-3-kinase (PI3K)/Akt pathway. In *L. major*-infected C57BL6-resistant mice, the preincubation of the parasite with rIGF-I changed the infection profile to be similar to that of susceptible mice. We conclude that IGF-I constitutes an effector element of IL-4 involving the PI3K/Akt pathway during *L. major* infection.

1. Introduction

Certain physiological processes are reciprocally controlled by the immune and endocrine systems, where the actions of cytokines and hormones efficiently regulate these processes [1–3]. In this context, the observation that certain cytokines modulate the expression of the hormone insulin-like growth factor- (IGF-) I [4–6] led us to explore this cross talk in the interaction of the *Leishmania* parasite with host cells since the essential roles of different cytokines and the effect of IGF-I on the development of *Leishmania* infection are known [7].

Leishmania is an obligatory intracellular protozoan that is transmitted vectorially and causes diseases called leishmaniases that affect two million people globally each year. These infections result in lesions on the skin, mucosa, or viscera, depending on the parasite species and the host response and features [8].

Leishmania infection leads to specific activation of the host cellular immune response, in which macrophages that harbor the parasite play a fundamental role in infection progression. Cytokines and growth factors, including IGF-I, act on macrophage leishmanicidal or parasite growth-promoting

mechanisms. The metabolic products of L-arginine exert primary roles in these processes. Nitric oxide (NO), a main leishmanicidal element, is generated through the oxidation of L-arginine catalyzed by the inducible nitric oxide synthase (NOS2). In contrast, polyamines are essential nutrients for the growth of *Leishmania*, which are generated through the hydrolysis of L-arginine by arginase [9–11].

We began studying the role of IGF-I in *Leishmania* infection based on the observation that IGF-I is produced by different cell types, including macrophages, and is present in the skin, which is the tissue where the parasite initiates infection [12]. The addition of extrinsic recombinant IGF-I to cultures at a physiological concentration induces the proliferation of various species of *Leishmania* promastigotes and axenic amastigotes [13–15], promotes an increase in macrophage arginase-1 (ARG1) expression as well as in *Leishmania* arginase (*Larg*), *in vitro* [16, 17], and induces a significant increase in the lesion size and the number of viable parasites at the lesion site in experimental models [18]. Furthermore, macrophages contain endogenous IGF-I in the cytoplasm, which interacts with intracellular *Leishmania* parasites [19].

The initial data on the adaptive immune response in different mouse strains infected with *L. major* have shown that the susceptibility or resistance to this infection is related to the production of certain cytokines of the Th1 or Th2 profile, respectively, IFN- γ , or IL-4 and IL-13 [20–24]. Nevertheless, studies have indicated changes in the simplicity of this model with time. The production of IL-4 in resistant mice does not alter the evolution towards progressive disease, as expected. C3H mice that were treated with IL-4 or anti-IL-12 early in the infection developed a strong but transient increase in IL-4 level, with no change in their resistant phenotype [25–27]. Furthermore, the transfer of BALB/c cells with the high expression of IL-4 to genetically resistant chimeric mice on a C57BL/6 background did not result in susceptibility [28]. The findings from these studies thus suggest that the profiles of resistance and susceptibility are not exclusively due to Th1 and Th2 cytokines. Considering our previous results revealing an important role for IGF-I in the development of *Leishmania* infections and considering the differences in IGF-I expression in different strains of mice [29], IGF-I may emerge as a factor that could explain these differences. Furthermore, IFN- γ stimulation decreases IGF-I levels, whereas IL-4 and IL-13 stimulation increase IGF-I expression [4–6].

In the present work, we evaluated the role of intrinsic IGF-I in *L. major*-infected macrophages *in vitro* and its participation in modulating the effects of cytokines by silencing the expression of the *Igf-I* mRNA using a small interfering RNA. We studied the effects on parasitism and the L-arginine pathway upon cytokine stimulation. We next evaluated the effect on lesion development upon the injection of *L. major* promastigotes preincubated with recombinant IGF-I (rIGF-I) into the footpads of BALB/c and C57BL/6 mice, which differ in basal *Igf-I* mRNA amount.

Focusing on immune-endocrine cross talk, we are the first to observe a process in which a growth factor (i.e., IGF-I) acts as an effector element for the cytokine IL-4 in

the induction of susceptibility to *L. major* infection since the expected parasite growth upon IL-4 stimulation was halted by silencing the IGF-I mRNA. The mechanism was directly related to the expression and activation of arginase and by the activation of the phosphatidylinositol-3-kinase (PI3K)/Akt pathway in macrophages. Furthermore, the injection of *L. major* promastigotes preincubated with rIGF-I into resistant C57BL/6 mice rendered the animals susceptible to the infection. The data thus suggest an essential role for IGF-I in the effect of IL-4 on the alternative macrophage activation pathway during *L. major* infection.

2. Materials and Methods

2.1. Mice. Six- to 8-week-old inbred BALB/c and C57BL/6 mice were obtained from the Animal Facility of the Faculdade de Medicina, Universidade de São Paulo (USP), and maintained in the animal facility of the Instituto de Medicina Tropical de São Paulo, USP.

2.2. Parasites. *L. major* LV39 (MRHO/Su/59/P) was maintained through regular passaging in BALB/c mice, and promastigotes were derived from amastigotes purified from the footpad lesions of BALB/c mice and expanded and maintained in 199 medium (Cultilab, Brazil) supplemented with 10% heat-inactivated fetal calf serum (FCS) (Cultilab, Brazil) at 26°C. The promastigotes used in the experiments were in the stationary phase of growth and had undergone no more than four passages in culture. All procedures were approved by the institutional guidelines for animal care and use and by the ethics committee of the institution.

2.3. Evaluation of the Effect of IGF-I on Promastigotes in Culture. *L. major* promastigote cultures (5×10^5 /mL) were established in 24-well plates (Corning Costar, USA) in 199 medium (Cultilab, Brazil) supplemented with 2% heat-inactivated fetal calf serum (FCS) (Cultilab, Brazil) at 26°C, and parasites were stimulated with or without 50 ng/mL IGF-I (R&D Systems, USA). Parasites were counted daily under a light microscope (Carl Zeiss, Gottingen, Germany), and the result was expressed as the number of parasites $\times 10^7$ /mL followed for 10 days of culture.

2.4. Infection of Macrophages with *L. major*. The RAW 264.7 macrophage cell line (ATCC) and BALB/c and C57BL/6 peritoneal macrophages were grown in Dulbecco's modified Eagle's medium (DMEM) supplemented with 0.5% bovine serum albumin (BSA, insulin-free, Sigma, USA). Cells (5×10^5 or 2×10^6) were dispensed onto round 13 mm² glass cover slips, which were placed in the wells of 24-well plates (Corning Costar, USA) and incubated for 30 minutes at 37°C in a humid atmosphere with 5% CO₂ to allow adhesion. Thereafter, the wells were washed twice with culture medium to remove nonadherent cells. Then, the amastigote or promastigote suspensions (eight parasites per cell) were dispensed into the wells, and infection was allowed to occur for 4 hours at 33°C in a humid atmosphere with 5% CO₂. After incubation, the noninternalized parasites were washed away. In one set of experiments, macrophages were treated with the Th1 cytokine IFN- γ (200 U/mL) or the Th2

cytokines IL-4 (2 ng/mL) and IL-13 (5 ng/mL), both separately and in combination. In other experiments, recombinant IGF-I (50 ng/mL; rIGF-I, R&D Systems, Minneapolis, MN, USA) was added. The culture was then maintained for 48 hours at 37°C in a humid atmosphere with 5% CO₂.

2.5. Parasite Load in Macrophages. Cover slips were removed from the plates, and the slides were stained with Giemsa dyes, mounted, and processed to evaluate parasitism under a light microscope (Carl Zeiss, Germany). 600 cells per group were counted. The data are presented as the number of parasites per 100 cells [(number of parasites/number of infected cells) × (number of infected cells/total number of cells) × 100]. The analysis was performed by two independent observers who were blinded to the experimental conditions.

2.6. NO Production. Nitrite (NO₂) accumulation in the cell culture supernatants was used as an indicator of NO production and was determined using the Griess reaction [30]. Fifty microliters of the culture supernatant was reacted with 50 μL of Griess reagent (1% sulfanilamide, 0.1% N-(1-naphthyl)ethylenediamine dihydrochloride, and 2.5% phosphoric acid in bidistilled water) for 10 min at room temperature. The absorbance was measured at 540 nm using a Multiskan MCC/340 P version 2.20 plate reader (Labsystems), and the nitrite concentration was calculated using a standard curve for sodium nitrite (NaNO₂). The tests were run in triplicate.

2.7. Arginase Activity. Cells and infected cells were removed from the culture, lysed, and used to determine arginase activity [31]. Briefly, 50 μL of lysates was treated with the same volume of 10 mM MnCl₂ and 50 mM Tris-HCl, pH of 7.4 at 56°C for 10 min to activate arginase. Then, 25 μL of 0.5 M L-arginine at a pH of 9.7 was added to 25 μL of the activated lysate and incubated at 37°C for 60 min. The reaction was stopped with 400 μL of H₂SO₄/H₃PO₄/H₂O (1/3/7, v/v/v). The urea concentration was measured at 540 nm using a spectrophotometer Multiskan MCC/340 P version 2.20 plate reader (Labsystems, Vantaa, Finland) after the addition of 25 μL of 9% α-isonitrosopropiophenone in 100% methanol and incubation 100°C for 45 min. One unit of enzyme activity is defined as the amount of enzyme that catalyzes the formation of 1 μmol of urea per minute.

2.8. RNA Extraction and Reverse Transcription. Total RNA was extracted from 2 × 10⁶ cells using TRIzol (Invitrogen, USA), according to the manufacturer's protocol. RNA integrity was verified by agarose gel electrophoresis/ethidium bromide staining and spectrophotometry (OD₂₆₀/280 absorption ratio greater than 1.8). Total RNA (1 μg) was reverse transcribed using the High Capacity cDNA Reverse Transcription kit (Applied Biosystems, USA) following the manufacturer's protocol and then stored at -20°C.

2.9. Quantitative qPCR. For real-time quantitative qPCR, we used the corresponding primer pairs for mouse sequences (*Igf-I*: 5' TAC TTC AAC AAG CCC ACA GG 3' and 5' AGT CTT GGG CAT GTC AGT GT 3'; *Arg1*: 5' AGC ACT GAG GAA AGC TGG TC 3' and 5' CAG ACC

GTG GGT TCT TCA CA 3'; *Larg*: 5' CAA CAC CAT GTC TGG TAC GGT CTC 3' and 5' CAC AGC ACG TAG ACC AAT GTA GGC 3'; *Nos2*: 5' AGA GCC ACA GTC CTC TTT GC 3' and 5' GCT CCT CTT CCA AGG TGC TT 3'; *Cat-2b*: 5' TAT GTT GTC TCG GCA GGC TC 3' and 5' GAA AAG CAA CCC ATC CTC CG 3'; *β-actin*: 5' GCC TTC CTT CTT GGG TAT GGA ATC 3' and 5' ACG GAT GTC AAC GTC ACA CTT CAT 3'; and *GAPDH*: 5' AAC GAG AAG TTC GGC ATA GTC GAG 3' and 5' ACT ATC CAC CGT CTT CTG CTT TGC 3'). Reactions including master mix (SYBR® Green; Applied Biosystems, USA), 0.3 μM of each primer, and 1 μg of cDNA templates were run in triplicate on a PCR system (StepOne; Applied Biosystems, USA). The PCR conditions were the same for all primer combinations: 95°C for 10 min and 40 cycles of 92°C for 2 min, 57.5°C for 30 s, and 70°C for 30 s. After amplification, a melting curve was used to confirm the specificity of the target product. The relative expression data were quantified using the 2^{-ΔΔCt} method [32].

2.10. siRNA. Small interfering RNAs (siRNAs) targeting murine IGF-I were designed using GenBank (NM_010512) and IDT SciTools RNAi Design (Integrated DNA Technologies) (*sense* 5' AAA GGA GAA GGA AAG GAA GUA CAT T 3' and *antisense* 5' AAU GUA CUU CCU UUC CUU CUC CUU U 3'). Universal scrambled siRNAs were employed as controls (Invitrogen, USA). Macrophages were grown in DMEM supplemented with 0.5% bovine serum albumin (insulin-free BSA, Sigma, USA) in a 24-well plate and were transiently transfected with a 150 μM siRNA duplexes using Lipofectamine™ 2000, according to the manufacturer's instructions (Invitrogen, Carlsbad, CA, USA). Cells transfected with IGF-I siRNA were used after 48 h. The transfection efficiency was confirmed by real-time PCR and confocal microscopy. The inhibition percentage (% KD) for the IGF-I mRNA was calculated using the formula % KD = ([1 - 2^{-ΔΔCt}] × 100) [32].

2.11. Confocal Microscopy. For immunofluorescence staining, cells infected with *L. major* promastigotes were grown on glass slides. Twenty-four hours after infection, cells were fixed with 4% paraformaldehyde, washed with 0.001 M phosphate-buffered saline (PBS; pH 7.2), blocked for one hour with 2% BSA/PBS, and then incubated overnight with a monoclonal goat anti-mouse IGF-I antibody (1:75, R&D Systems, USA) and a polyclonal mouse anti-*Leishmania* antibody (1:400) produced in our laboratory. Alex Fluor 546-conjugated donkey anti-goat IgG (1:200, Invitrogen, USA) and Alex Fluor 488-conjugated donkey anti-mouse IgG (1:400, Invitrogen, USA) were used as secondary antibodies. Fluorescence imaging analyses were performed using a Zeiss LSM 510 Meta laser-scanning confocal microscope. As a negative control, the primary antibodies were omitted from the reaction.

2.12. SDS-PAGE and Western Blot. Cell lysates (20 μg of protein in 20 μL) were separated on a denaturing gradient 4–12% Bis-Tris NuPAGE gel (Invitrogen, USA) according to the

manufacturer's instructions. Briefly, the separated proteins were blotted onto iBlot™ 2 Transfer Stack PVDF mini-membranes using an iBlot Dry Blotting System (Invitrogen, USA). Membranes were blocked with TBS-T buffer (150 mM NaCl, 20 mM Tris, 0.01% Tween 20, pH of 7.4) containing 5% fat-free milk for 1 h. Membranes were reacted with a 1:2000 dilution of a primary anti-phospho-Akt (Ser473) antibody, a 1:2000 dilution of a rabbit anti-p44/42 MAPK (137F5) mAb, and a 1:2000 dilution of a rabbit anti-p38 MAPK (D13E1) XP® mAb (Cell Signaling Technology, USA) overnight at 4°C and incubated with 1:1000 dilutions of a peroxidase-conjugated polyclonal anti-rabbit IgG and HRP-conjugated anti-biotin antibody (Cell Signaling Technology, USA) for 1 h at room temperature. Biotinylated protein molecular weight markers (Cell Signaling Technology, USA) were used. Bound antibodies were detected with an ECL chemiluminescence kit LumiGLO® Reagent (Cell Signaling Technology, USA) according to the manufacturer's instructions. An evaluation of the phosphorylation kinetics was conducted at different time points (0, 5, 10, 20, 30, and 60 minutes) after adding the stimulus (data not shown), and we chose the time of 30 minutes to present the results. Subsequently, protein bands were quantified by densitometry using AlphaEaseFC™ software 3.2 beta version (Alpha Innotech Corporation, San Leandro, CA, USA), and the results are expressed in arbitrary units, which were calculated by integrating the intensity of each pixel over the spot area and normalizing to the gel background.

2.13. Development of Footpad Lesions in Mice. Stationary-phase promastigotes (1×10^6) that had been preincubated with or without 50 ng/mL of recombinant human IGF-I (R&D Systems, USA) for 5 min and then washed were injected into the footpads of BALB/c and C57BL/6 mice. In the opposite footpad, we injected RPMI 1640 medium as a control. For six weeks, we measured the thickness of the foot to indicate the growth of the lesions using a micrometer (Mitsutoyo, Japan), and the difference between the infected and noninfected footpads in millimeters was considered the lesion size.

2.14. Statistical Analysis. Statistical analyses were performed with GraphPad Prism 5 software (GraphPad Software Inc., San Diego, CA, USA). Data were subjected to analysis of variance (ANOVA) and Tukey's posttest and were considered significant when $P < 0.05$.

3. Results

3.1. The Effect of IGF-I on *L. major* in Culture and within Macrophages. We first verified the effect of IGF-I on parasite growth *in vitro*. In the cultures stimulated with rIGF-I, we observed a larger number of parasites that reached the stationary phase earlier than nonstimulated cultures (Figure 1(a)).

When we evaluated the effect of IGF-I on the parasite burden in *L. major* promastigote- or amastigote-infected macrophages, we observed a significant increase in the number of parasites in macrophages stimulated with rIGF-I

compared with that in nonstimulated macrophages (Figure 1(b)). Similar results were observed when amastigotes were used (Figure 1(c)).

3.2. The Effects of *Leishmania* Infection and Th1 and Th2 Cytokines on IGF-I Expression. We analyzed the effects of *Leishmania* infection and Th1 and Th2 cytokines on the amount of the *Igf-I* mRNA. Infection of RAW 264.7 cells and BALB/c mouse peritoneal macrophages with promastigotes decreased the amount of *Igf-I* mRNA compared with that of the uninfected control cells. When promastigote-infected RAW 264.7 cells were stimulated with IFN- γ , we observed a 15-fold decrease in the amount of *Igf-I* mRNA. When cells were simultaneously stimulated with IL-4 and IL-13, we observed a 2.45-fold increase in the amount of *Igf-I* mRNA compared to that in the nonstimulated controls. When cells were stimulated with either IL-4 or IL-13, we observed a 2.9- or 4.8-fold increase in the amount of *Igf-I* mRNA, respectively (Figure 2(a)).

Upon amastigote infection of RAW 264.7 cells, we observed different amounts of *Igf-I* mRNA that increased in all infected cells compared with that in uninfected controls. A 2.2-fold increase in the amount of *Igf-I* mRNA was observed upon amastigote infection, a 1.2-fold increase was observed following stimulation with IFN- γ , and an 8.7-fold increase was observed when cells were simultaneously stimulated with IL-4 and IL-13. When cells were stimulated with either IL-4 or IL-13, we observed a 9.2- or 2.5-fold increase in the amount of *Igf-I* mRNA, respectively (Figure 2(a)). A similar profile was observed in BALB/c peritoneal macrophages (Figure 2(b)).

We confirmed these results using confocal microscopy. In *Leishmania* promastigote-infected macrophages, we observed a decrease in IGF-I immunostaining upon stimulation with IFN- γ compared with that in control cells. When cells were simultaneously stimulated with IL-4 and IL-13 or with IL-4 alone, we observed an increase in immunostaining, indicating increased IGF-I expression (Figure 2(c)).

3.3. Inhibition of IGF-I Expression Using an IGF-I siRNA. Silencing IGF-I expression with siRNA resulted in an approximate 70% decrease in the mRNA amount in promastigote-infected RAW 264.7 cells (Figure 3(a)) and 78% in infected BALB/c peritoneal macrophages (Figure 3(b)). Using confocal microscopy, we observed a significant reduction in IGF-I immunostaining after siRNA transfection. Moreover, infection with *L. major* promastigotes alone inhibited IGF-I expression. A nonspecific double-stranded RNA (scrambled siRNA) was used as a negative control (Figure 3(c)). We observed similar results in cells infected with amastigotes (data not shown).

3.4. The Effect of IGF-I siRNA on Parasitism. Following infection with both promastigotes and amastigotes, we observed a significant increase in parasitism in cells exposed to Th2 cytokines ($P < 0.05$), as expected. In Th1 cytokine-stimulated cells, we noted a significant reduction in parasitism compared with that in the respective control ($P < 0.05$) (Figure 4).

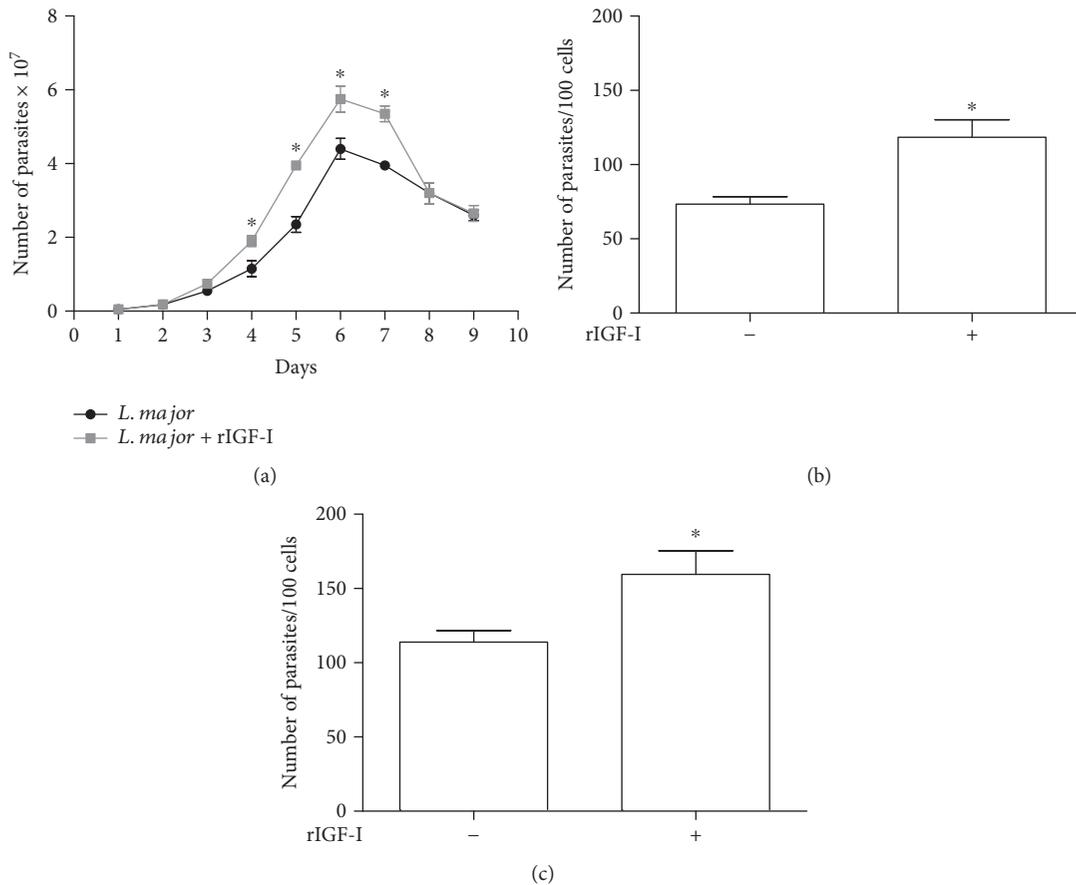


FIGURE 1: The effects of IGF-I on the growth of *L. major* in culture and within macrophages (mean \pm standard deviation). (a) The effect of IGF-I on the growth of *Leishmania* promastigotes in culture maintained in 199 medium supplemented with 2% heat-inactivated FCS at 26°C is shown. *Leishmania* promastigotes were maintained with (gray line) or without (black line) 50 ng/mL rIGF-I. (b and c) The effect of IGF-I on the growth of *Leishmania* within macrophages is shown. RAW 264.7 cells were infected with *L. major* promastigotes (b) or amastigotes (c) treated with or without 50 ng/mL rIGF-I and incubated for 48 h. * $P < 0.05$ (one-way ANOVA and Student's *t* test) compared to the control without rIGF-I.

Upon silencing IGF-I expression with an siRNA in *L. major* promastigote-infected RAW 264.7 cells, we observed a decrease in the parasite number from 79 parasites (median number in the control) to 57 parasites per 100 cells. In amastigote-infected cells, the parasite number was reduced from 139 to 91 parasites per 100 cells ($P < 0.05$). When we analyzed the involvement of Th1 and Th2 cytokines in parasitism following IGF-I silencing, all cells transfected with the siRNA showed a significant decrease in parasitism compared with that in the controls lacking siRNA following infection with both promastigotes and amastigotes (Figures 4(a) and 4(b)). The parasite load did not increase, even in Th2 cytokine-stimulated cells.

We observed similar results in *L. major*-infected BALB/c peritoneal macrophages to those obtained in *L. major*-infected RAW 264.7 cells, reinforcing the findings obtained from the RAW 264.7 cells (Figures 4(c) and 4(d)).

Experiments were performed to restore IGF-I activity after knockdown to ascertain the role of IGF-I. After transfection with siRNA, rIGF-I (50 ng/mL) was added to replace the loss of intracellular IGF-I, followed by an evaluation of parasitism. After the addition of rIGF-I to all cells transfected

with siRNA, parasite numbers increased to the levels similar to the control cells lacking siRNA (Figure 4). We did not observe differences in parasitism in control cells treated with Lipofectamine or transfected with the scrambled siRNA compared with that in control cells. Infections with amastigotes or promastigotes produced similar results (Figures 4(e) and 4(f)).

3.5. The Effects of IGF-I siRNA on the mRNA Amount of *Nos2*, *Arginase (Arg1)*, and *Cationic Amino Acid Transporter 2 (Cat-2B)* in Macrophages and *Leishmania Arginase (Larg)* mRNA Expression and Enzyme Activity. We analyzed the effects of IFN- γ and IL-4 and/or IL-13 in combination with levels of IGF-I on L-arginine metabolism. IL-4 stimulation produced a significant increase in both *Arg1* (Figure 5(a)) and *Larg* mRNAs (Figure 5(b)), as well as an increase in arginase activity (Figure 5(d)). However, IL-13 stimulation did not show an increase in *Arg1* mRNA or arginase activity (Figures 5(a) and 5(d)) but showed an increase in *Larg* mRNA (Figure 5(b)). A significant increase in the amount of *Cat-2B* mRNA (Figure 5(c)) was observed after treatment with IL-4 ($P < 0.05$) compared to that in the control group.

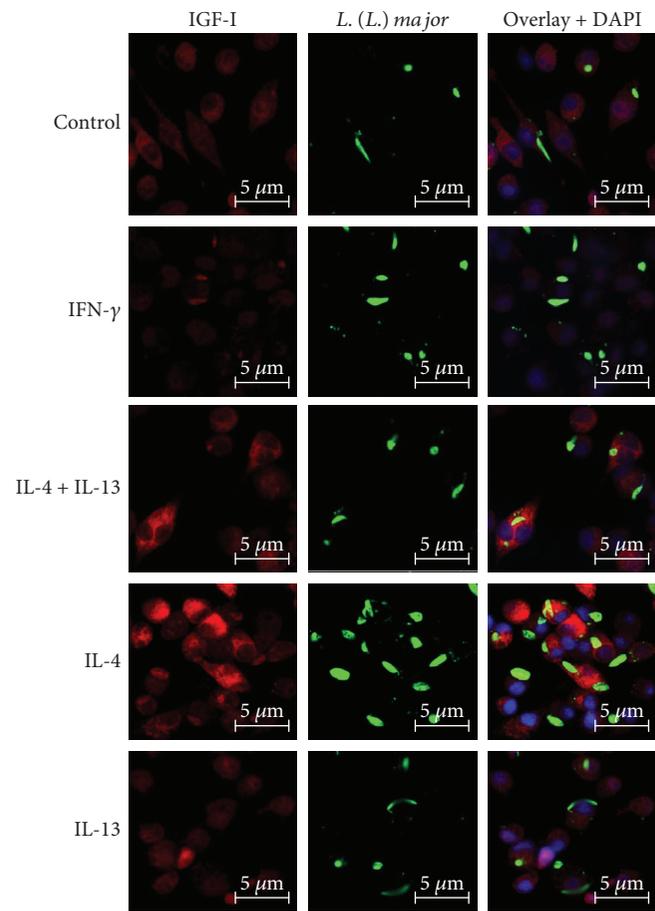
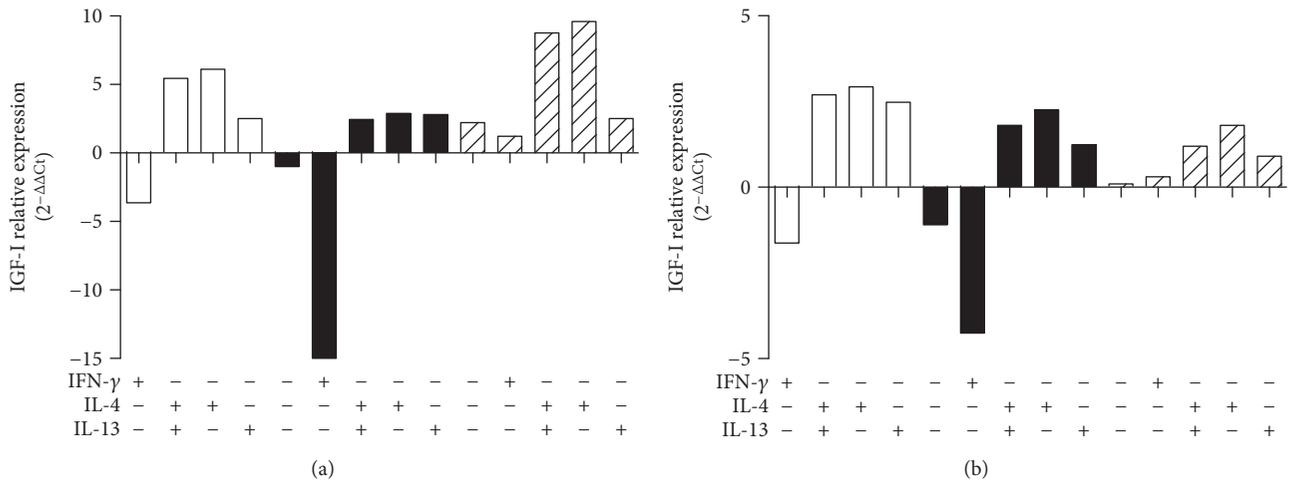


FIGURE 2: IGF-I expression in response to cytokine treatment. (a and b) Quantification of *Igf-I* mRNA in *L. major* promastigote- (black bars) or amastigote-infected (striped bars) or noninfected (white bars) RAW 264.7 cells (a) and BALB/c peritoneal macrophages (b) is shown. Cells were stimulated with IFN- γ (200 U/mL), IL-4 (2 ng/mL), and IL-13 (5 ng/mL) for 48 hours. One representative experiment from three independent assays is shown. (c) Detection of IGF-I expression using confocal microscopy of cells labeled with a 1 : 75 dilution of an anti-IGF-I antibody (using an Alexa Fluor 546-conjugated secondary antibody; red) and a 1 : 200 dilution of an anti-*Leishmania* antibody (using an Alexa Fluor 488-conjugated secondary antibody; green) in *L. major* promastigote-infected macrophages is shown. Nuclei were stained with DAPI (blue). Images were captured using a confocal Leica LSM510 microscope with a 63x oil immersion objective. The expressions are relative to the expression in untreated cells (the baseline).

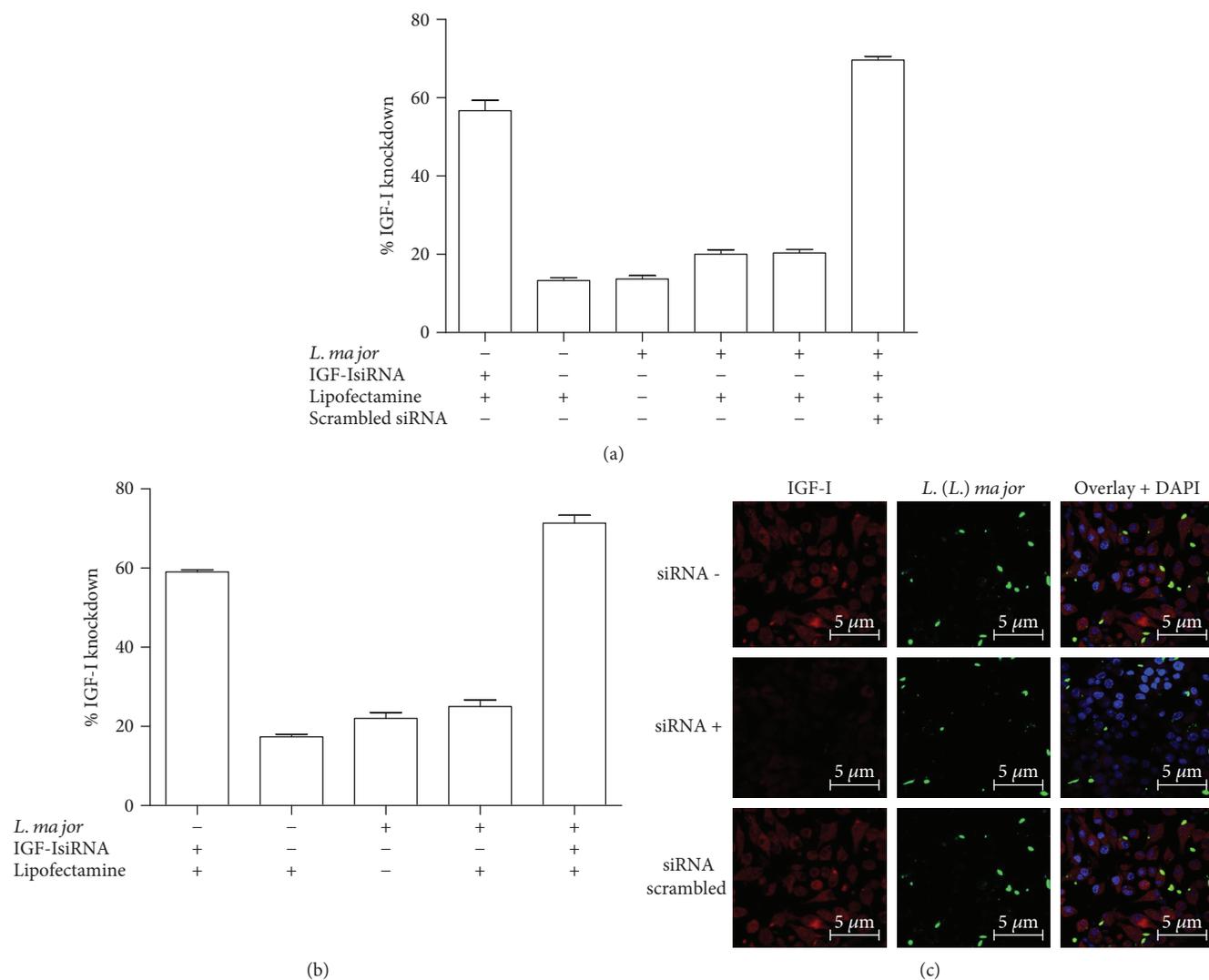


FIGURE 3: Expression of *Igf-I* mRNA upon IGF-I silencing with an siRNA. The percentage decrease in the amount of *Igf-I* mRNA in RAW 264.7 cells (a) or BALB/c peritoneal macrophages (b) infected with *L. major* promastigotes that were transfected with 150 μ M siRNA, scrambled siRNA, or Lipofectamine alone 6 h after infection is shown. One representative experiment from three independent assays is shown. (c) The detection of IGF-I expression in *L. major* promastigote-infected RAW 264.7 cells transfected with (siRNA+) or without the IGF-I siRNA (siRNA-) or with a scrambled siRNA using confocal microscopy of immunostaining with a 1:75 dilution of an anti-IGF-I antibody (using an Alexa Fluor 546-conjugated secondary antibody; red) and a 1:200 dilution of an anti-*Leishmania* antibody (using an Alexa Fluor 488-conjugated secondary antibody; green) is shown. Nuclei were stained with DAPI (blue). Images were captured using a confocal Leica LSM510 microscope with a 63x oil immersion objective.

When cells were treated with siRNA, all groups showed a significant decrease in both the *Arg1* and *Larg* mRNA amounts and arginase activity and an increase in the *Cat-2B* mRNA amount (Figure 5(c)).

When IGF-I was restored by adding rIGF-I to cells transfected with siRNA, we observed increases in both the *Larg* mRNA amount and arginase activity. No differences in the *Arg1* mRNA amount were observed in macrophages.

In another branch of the L-arginine metabolic pathway, we observed a decrease in the *Nos2* mRNA amount in all groups treated with rIGF-I compared with the respective control group. In the group that was not stimulated with cytokines, we observed an increase in the *Nos2* mRNA

amount after siRNA transfection. Upon the addition of Th2 cytokines, an alteration in NO production was not observed (Figures 5(e) and 5(f)). Similar results were obtained using amastigotes and BALB/c peritoneal macrophages (data not shown).

3.6. Evaluation of the Effects of siRNA and IL-4 on IGF-I Signaling Pathways. Because our results suggest that IGF-I is necessary for IL-4 to exert its effect on parasite growth in macrophages, we examined their intracellular signaling pathways. IGF-I and the cytokines IL-4 and IL-13 share common components in their signaling pathways. IGF-I triggers MAPK (ERK) and PI3K pathways [33, 34], and IL-4

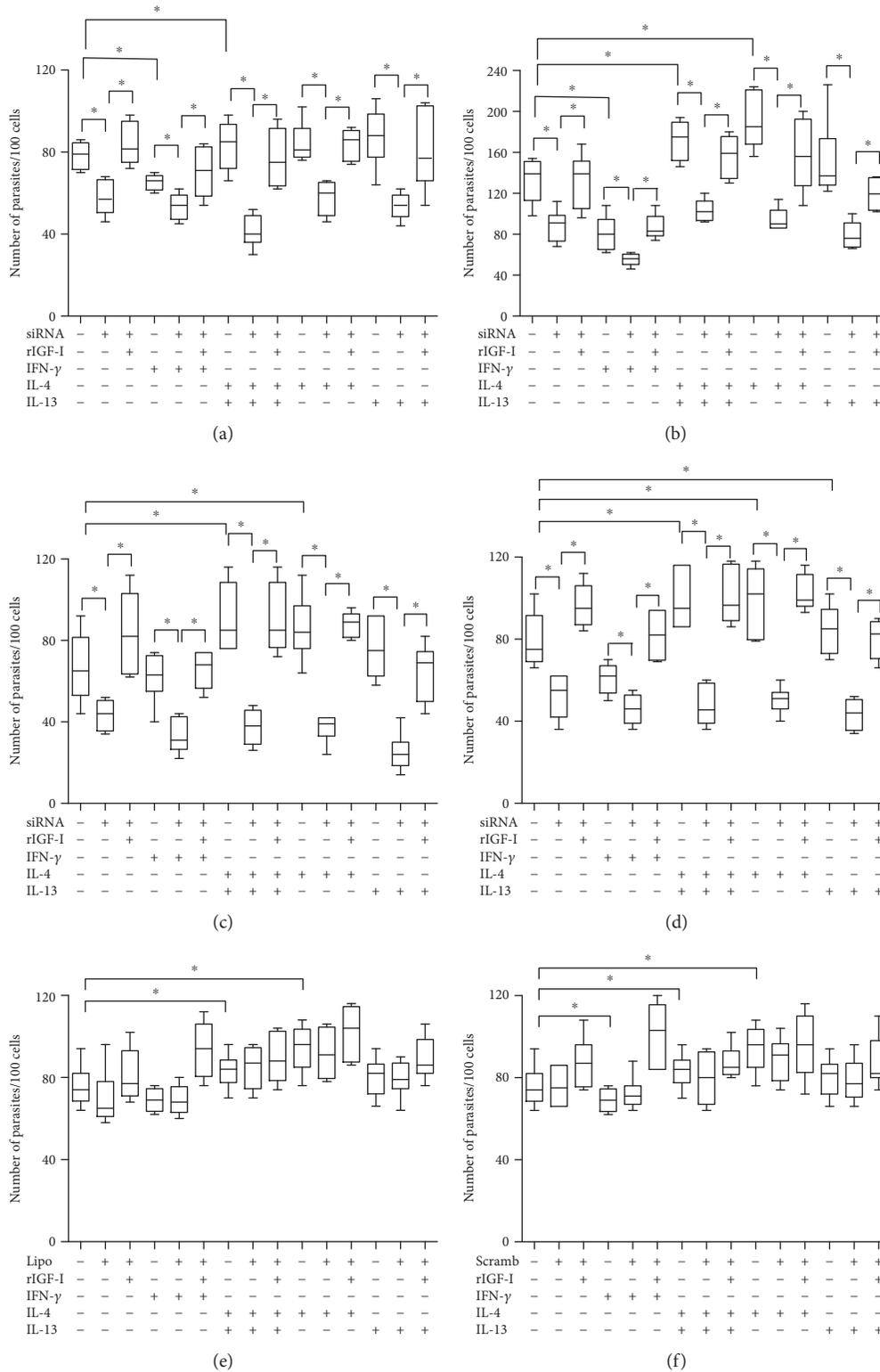


FIGURE 4: Parasitism in response to cytokine treatments and siRNA transfection. Parasitism (median number of parasites per 100 cells) in *L. major*-infected RAW 264.7 cells (a, b, e, and f) or BALB/c peritoneal macrophages (c and d) following transfection with IGF-I siRNA (a, b, c, and d), Lipofectamine alone (e), or scrambled siRNA (f) along with cytokine stimulation is shown. Promastigote- (a, c, e, and f) or amastigote-infected (b and d) cells transfected with or without siRNA or Lipofectamine were stimulated with IFN- γ (200 U/mL), IL-4 (2 ng/mL), IL-13 (5 ng/mL), and recombinant IGF-I (rIGF-I, 50 ng/mL) for 48 hours. One representative experiment from three independent assays is shown. * $P < 0.05$ (ANOVA and Tukey's tests).

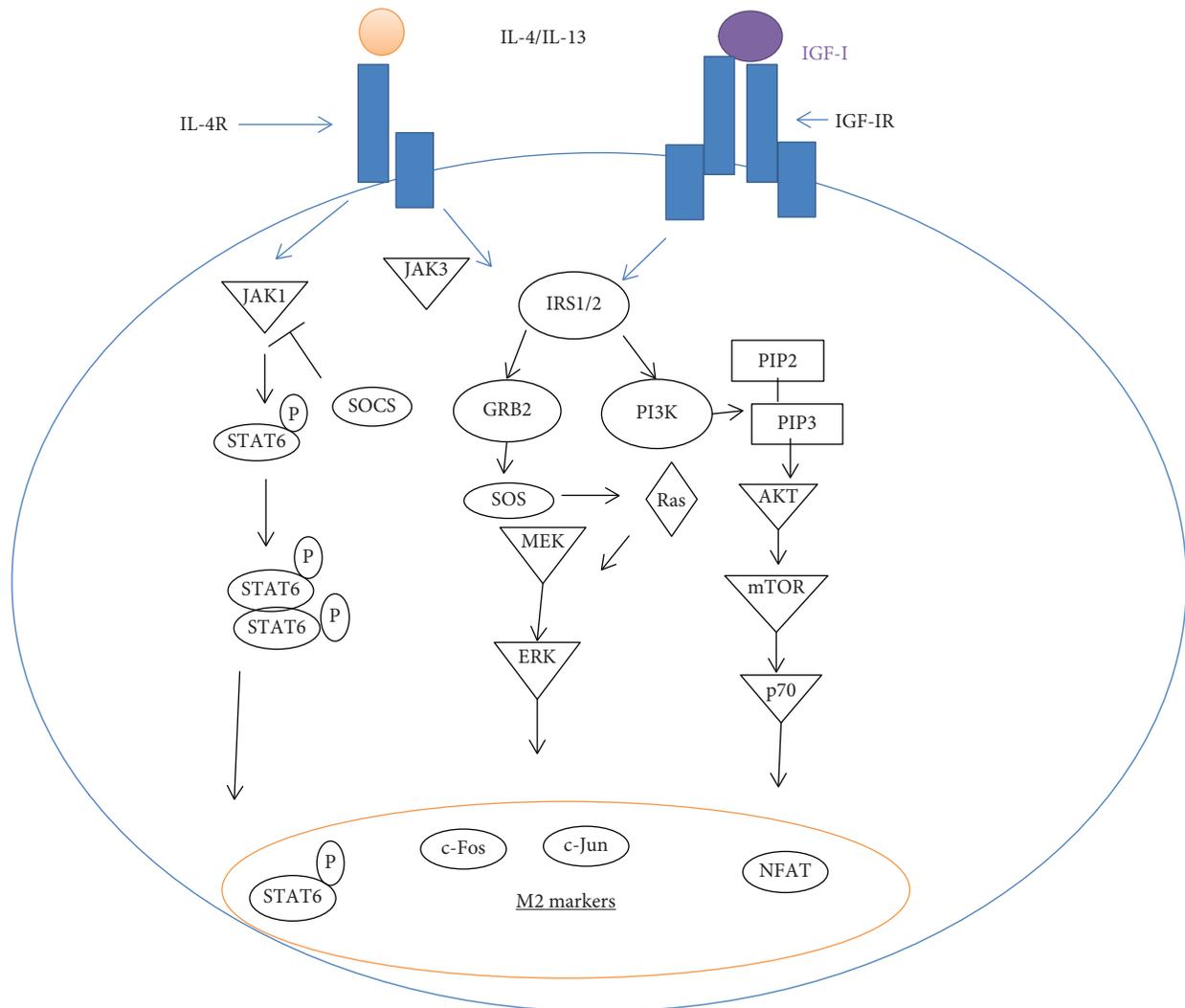


FIGURE 6: Scheme of the common components of the IGF-I and IL-4 signaling pathways.

Cells infected with *L. major* displayed a decrease in the levels of phospho-p44 (Figure 7(a)) and phospho-p38 (Figure 7(d)), but a difference in the phospho-AKT level was not observed (Figure 7(g)) compared with that in the noninfected RAW cells. We observed an increase in the levels of these phosphorylated proteins in all groups treated with rIGF-I compared with noninfected RAW cells. A similar increase was also observed with IL-4.

Upon silencing IGF-I expression using siRNA, all groups showed a decrease in the expression of all phosphoproteins. In IGF-I-silenced cells, Th2 cytokine stimulation did not restore the decreased expression of phospho-p44, phospho-p38, and phospho-AKT.

3.7. IGF-I Expression and the Effect of IGF-I on Lesion Development in *L. major*-Susceptible and -Resistant Mouse Strains. We initially evaluated the differences in the expression of IGF-I to determine whether the susceptibility of BALB/c mice and the resistance of C57BL/6 mice to *L. major* infection were related to IGF-I expression. The *Igf-I* mRNA

was detected in higher levels in BALB/c cells than in C57BL/6 cells ($P < 0.05$) (Figure 8(a)). Confocal microscopy indicated a correlation between the amount of *Igf-I* mRNA and IGF-I expression, confirming that the C57BL/6 peritoneal macrophages showed less IGF-I immunostaining than BALB/c cells did (Figure 8(b)).

Then, we analyzed the effect of rIGF-I on lesion development in *L. major*-infected BALB/c and C57BL/6 mice. Parasites were preincubated with 50 ng/mL IGF-I for five minutes and then washed and injected into the footpads of the mice. In control BALB/c mice, the lesions progressed continuously, but when the parasites were preincubated with IGF-I, we observed a significantly greater lesion volume than that observed in the control mice (Figure 8(c)). In control C57BL/6 mice, the lesions progressed for three weeks and then stabilized and tended to diminish, but animals infected with parasites that were preincubated with IGF-I displayed significantly greater lesions, which, interestingly, progressed continuously, similar to that in the BALB/c mice (Figure 8(d)).

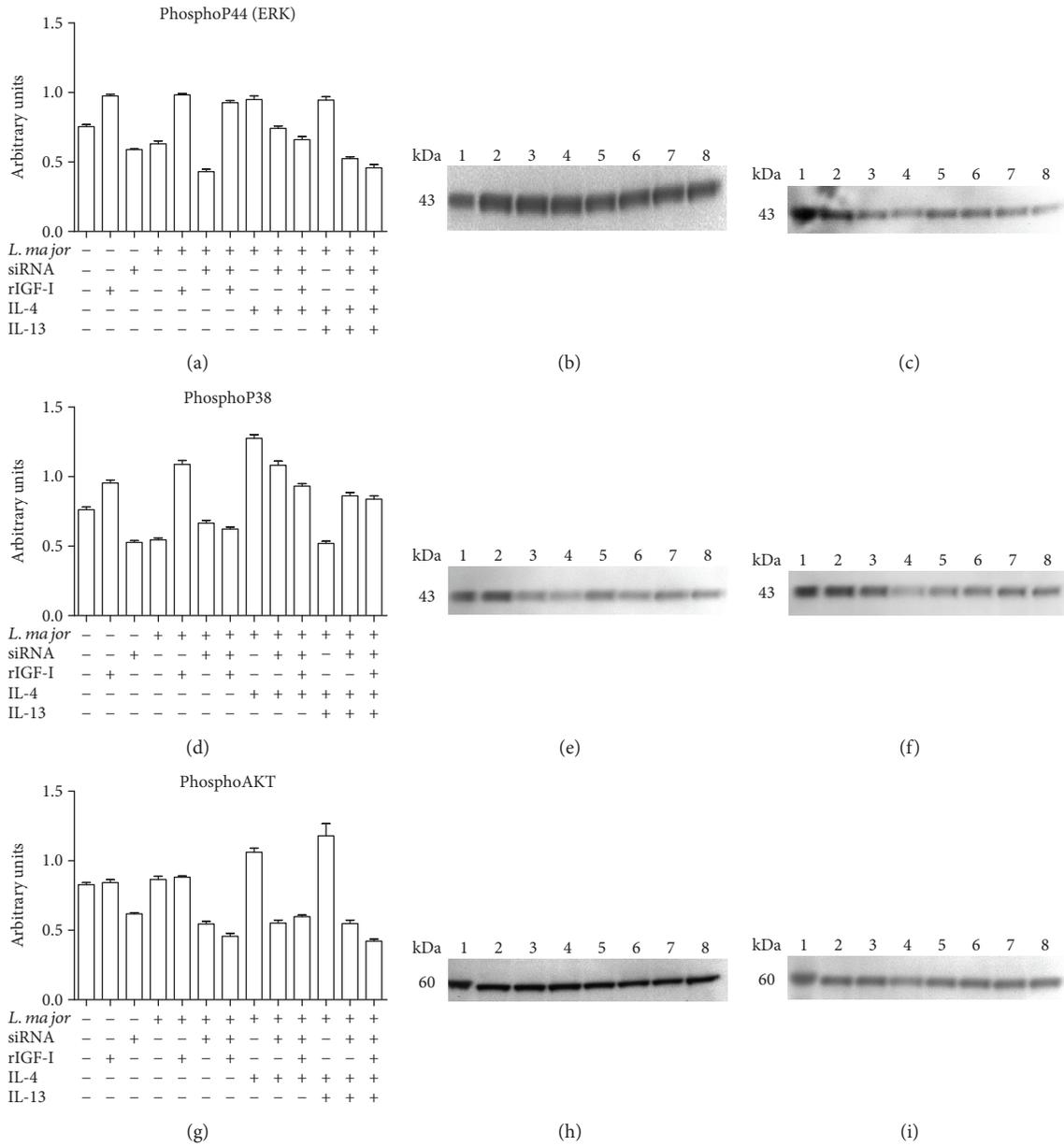


FIGURE 7: The effects of siRNA and IL-4 on components of the IGF-I signaling pathways: levels of phosphorylated p44 (ERK), p38 (MAPK), and AKT proteins. Promastigote-infected or noninfected cells transfected with or without IGF-I siRNA were stimulated for 30 minutes with IL-4 (2 ng/mL) and IL-13 (5 ng/mL). Cells were lysed, proteins were separated by 10% SDS-PAGE, and subsequently, Western blotting was performed using anti-phospho-p44 (a, b, and c), anti-phospho-p38 (d, e, and f), and anti-phospho-AKT (g, h, and i) antibodies. Protein bands corresponding to protein expression levels were subject to a densitometric analysis, and the data are expressed in arbitrary units (a, d, and g). A representative blot is shown. (b, e, h) The lanes represented the following: 1: control; 2: RAW; 3: RAW + rIGF; 4: RAW + siRNA; 5: RAW + Lm; 6: RAW + Lm + rIGF; 7: RAW + Lm + IL-4; and 8: RAW + Lm + IL-4 + IL-13. (c, f, i): 1: control; 2: RAW; 3: RAW + Lm + siRNA; 4: RAW + Lm + siRNA + rIGF; 5: RAW + Lm + siRNA + IL-4; 6: RAW + Lm + siRNA + IL-4 + rIGF; 7: RAW + Lm + siRNA + IL-4 + IL-13; and 8: RAW + Lm + siRNA + IL-4 + IL-13 + rIGF. See Materials and Methods for additional details.

4. Discussion

Due to the known roles of Th1 and Th2 cytokines in the resistance and susceptibility of certain inbred mouse strains to *L. major* infection and their effects on the expression of the hormone IGF-I, which has an important impact on *Leishmania* growth within host macrophages, we examined the effect of interference in the hormone IGF-I expression on

the adaptive immune response. We initially analyzed the effects of Th1 and Th2 cytokines on the amount of *Igf-I* mRNA and confirmed that IGF-I expression was decreased by IFN- γ and increased by IL-4 and IL-13, which was consistent with previous results [4, 6]. Furthermore, when we concomitantly analyzed IGF-I expression and the parasitism of *L. major* in RAW 264.7 cells or BALB/c peritoneal macrophages *in vitro*, we observed that the macrophages stimulated

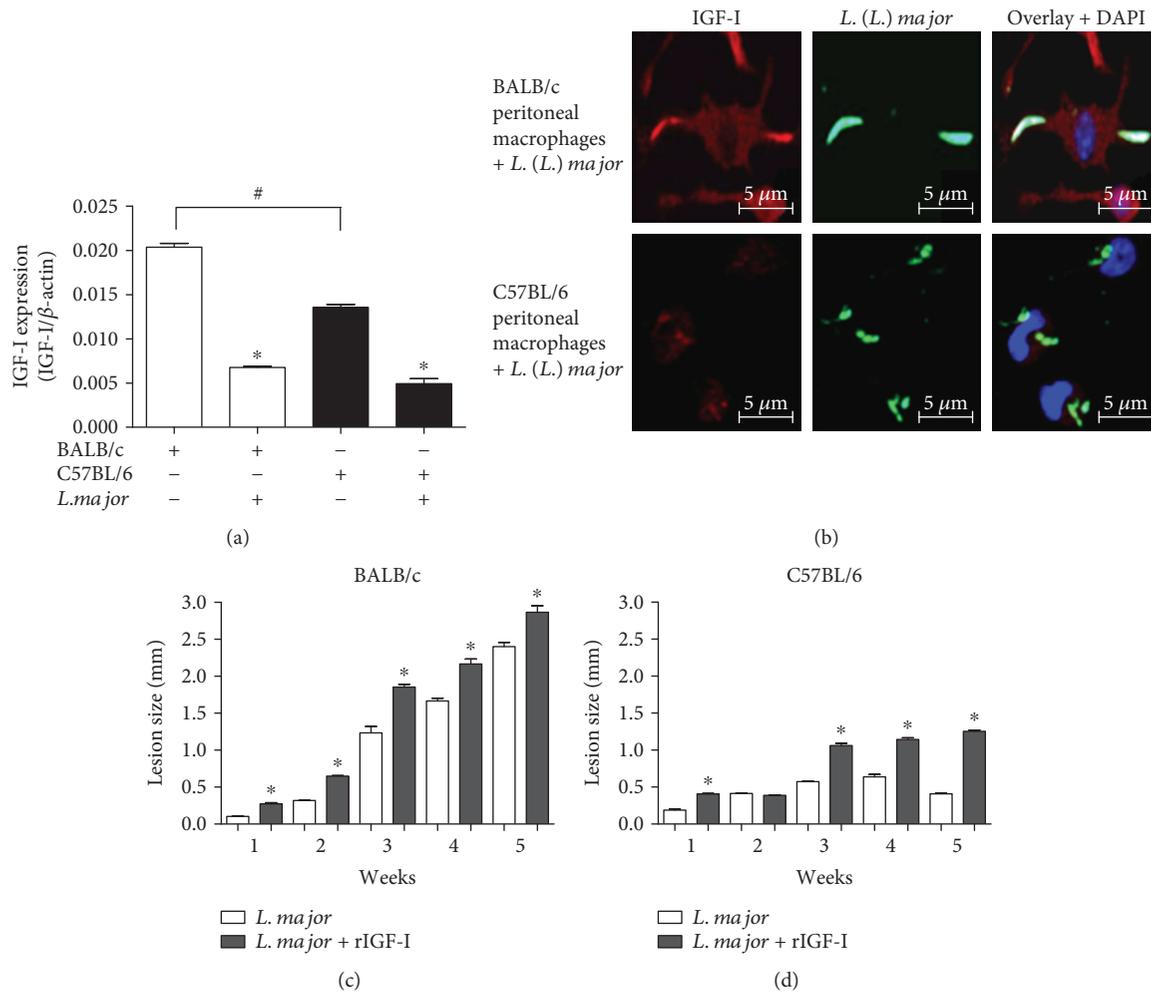


FIGURE 8: IGF-I expression and the effect of IGF-I on lesion development in *L. major*-susceptible and -resistant mouse strains. (a) The ratio of the *Igf-I* mRNA amount to β -actin mRNA amount in *L. major*-infected BALB/c (white bars) and C57BL/6 peritoneal macrophages (black bars) is shown. (b) Confocal microscopy was used to detect IGF-I expression via immunostaining with a 1:75 dilution of an anti-IGF-I antibody (using an Alexa Fluor 546-conjugated secondary antibody; red) and a 1:200 dilution of an anti-*Leishmania* antibody (using an Alexa Fluor 488-conjugated secondary antibody; green). DAPI (blue) was used to stain the nuclei. Images were captured using a confocal Leica LSM510 microscope with a 63x oil immersion objective. (c and d) Stationary-phase promastigotes (10^6) that were preincubated with or without recombinant IGF-I (50 ng/mL) for 5 min were injected into the footpads of BALB/c and C57BL/6 mice, and lesion development was measured for six weeks. One representative experiment from three independent assays is shown. * $P < 0.05$ (ANOVA and Tukey's tests) compared to the respective controls. # $P < 0.05$ (ANOVA and Tukey's tests) between BALB/c and C57BL/6.

with IFN- γ exhibited a reduction in the parasite load, accompanied by a parallel reduction in IGF-I expression and ARG1 activity and an increase in NO production. Furthermore, IL-4 and IL-13 stimulation increased parasitism, accompanied by a parallel increase in IGF-I expression and arginase activity and a reduction in NO production.

These data showing the parallel effects of those cytokines and the expression of IGF-I on parasitism compelled us to explore the interference/participation of this hormone in the actions of cytokines and other factors during *Leishmania* infection.

The idea of immune-endocrine cross talk is not new and has been described in studies examining the roles of prolactin [37], growth hormone (GH) [38, 39], IGF-I, and thyroid-stimulating hormone in the development, maintenance, and

function of the immune system, which in turn cause reciprocal changes in the endocrine system [5, 40].

IGF-I exhibits pleiotropic properties, including the ability to promote cellular proliferation, differentiation, nutrient transport, energy storage, gene transcription, protein synthesis, and activation of the immune response and inflammation [12, 41]. However, its specific role in the adaptive immune response is not known. Thus, we addressed this aspect in the present study using a knockdown strategy in RAW 264.7 and mouse peritoneal cells infected with *L. major* knowing that a significant amount of IGF-I colocalizes with *L. major* in the cytoplasm of *Leishmania*-infected RAW 264.7 cells.

Using an IGF-I siRNA, we silenced the *Igf-I* mRNA in macrophages and evaluated parasitism. We observed a

significant decrease in parasitism in the siRNA-transfected group compared with that in the control group without siRNA transfection in response to both promastigote and amastigote infections. This effect was reversed by the addition of rIGF-I, which induced an increase in the number of parasites, even when siRNA-mediated knockdown was maintained. This restoration observed upon the addition of recombinant IGF-I was likely induced by an increase in the levels of *Larg* mRNA and *Larg* activity, accompanied by a slight decrease in the *Nos-2* mRNA amount and NO production. Similar results were previously reported in which the addition of rIGF-I induced alternative activation of macrophages and arginase activation in *L. amazonensis*-infected macrophages [16, 17]. The present data definitively confirm the role of intrinsic IGF-I in intracellular parasite growth. Preliminary data further showed that the IGF-I siRNA decreased the parasite load in *Leishmania major*-infected BALB/c mouse footpad lesions (data not shown).

After observing such a clear-cut effect of IGF-I on parasite growth in macrophages, we proceeded to explore its role in infection development in *L. major*-infected macrophages stimulated with cytokines. After silencing *Igf-I* mRNA expression, the parasitism observed upon stimulation of the cells with cytokines did not follow the expected profile. IL-4 and IL-13 should have increased parasitism; however, they were completely ineffective when the *Igf-I* mRNA was silenced. Analyzing mRNA for components of L-arginine metabolism, we observed that the effect of IL-4 on infection progression was via the increase of *Arg1* and *Larg* mRNAs, while the effect of IL-13 on infection progression was only via the increase in *Larg* mRNA.

The effects of IL-4 and IL-13 were restored by the administration of rIGF-I to IGF-I-silenced cells in a mechanism dependent on *Leishmania* arginase production, but not by ARG1. In another study using *L. amazonensis*-infected macrophages, a novel L-arginine usage pathway independent of macrophage NOS2 and ARG1 activation was involved in the response, suggesting that *Leishmania* may have the ability to obtain access to the intracellular L-arginine pool while residing within the host macrophage [42, 43]. This evidence was confirmed in the present study, as we observed an increase in parasitism upon the addition of rIGF-I in silenced cells without changes in the amount of *Arg1* mRNA but an increase in the amount of *Larg* mRNA. Other studies have supported the importance of arginase production by the parasite since in vitro cultured *L. donovani* is capable of directly acquiring L-arginine from the medium and producing urea [44] or the deficiency in the infection and replication capabilities in *L. amazonensis* arginase knockout [45].

L-Arginine is supplied from the extracellular milieu by the cationic amino acid transporter 2 (CAT-2B), a member of the classical amino acid cationic transporter system y⁺ (SLC7) [42]. The observed increase in NOS2 expression may be related to an increase in CAT-2B expression since CAT-2B is required for the regulation of NOS2 activity that conversely may modulate CAT-2B expression through NO production [46–49].

The production of NO does not always follow the effect of the cytokines on parasitism, as the control of *L. major*

parasitic infections does not appear to be related to NO production but rather to the presence or absence of IGF-I. Based on these results, cytokines alone are not sufficient to induce or control parasite growth, and IGF-I plays a crucial role in this process. We postulate that IGF-I may be an effector element of IL-4, which to the best of our knowledge constitutes the first evidence of cross talk between this hormone and the adaptive immune system in *L. major* infection.

Immune-endocrine cross talk involving IGF-I has been observed by others to mainly involve inflammatory cytokines IL-1 and TNF- α , which may inhibit both the expression of IGF-I or IGF-IR and the IGF-I-induced tyrosine phosphorylation of IRS-1 and IRS-2. This is an effect that is mediated by receptor cross talk and leads to intracellularly mediated IGF resistance [5]. Thus, these findings fundamentally differ from the findings of the present study showing that IGF-I plays a fundamental role as an effector element of Th2 cytokines.

The interaction of the endocrine and immune systems is somewhat expected, as they share several ligands and receptors in their signaling pathways. By analyzing the signaling pathways of IL-4/IL-13, which are related to the susceptibility to infection, we noticed shared components with the IGF-I pathway.

The biological effects of IGF-I occur through its binding to its receptor (IGF-IR), which is present in several cell types and tissues, mainly in macrophages. IGF-I signaling consists of two main pathways, the PI3K/Akt and mitogen-activated protein kinase (Ras/MAPK/ERK) pathways, when IRS-1 associates with the GRB2/SOS complex. IGF-I can also bind to insulin receptor (IR) when some excess of free IGF-I is present in the system that could have occurred in the present study but with lower affinity. IGF-IR and IR are highly homologous tyrosine kinase receptors sharing many common steps, inducing IRS1/2 phosphorylation and also AKT and MAPK [34, 50, 51]. Thus, if some IGF-I binds to IR, the resulted signaling will be nearly the same generating similar biological effects.

IL-4 mediates its effects through two receptors: the type I IL-4 receptor (IL-4R α and IL-2R γ) and the type II receptor (IL-4R α and IL-13R α 1). Activation of these receptors results in STAT-6 phosphorylation that is necessary for the induction of the alternative macrophage pathway (M2). The ligation of the type I IL-4R activates JAK3 that participates in the activation of Akt, resulting in the induction of the M2 macrophage phenotype characterized by upregulation of molecules such as the mannose receptor, ARG1, and chitinase 3-like 3 [52]. IGF-I may also increase STAT-6 activity through IL-4, which is required to activate the expression of this cytokine [53].

In the present work, our analysis of the components of the IGF-I signaling pathway revealed increases in the amount of arginase mRNA, the phosphorylation of p44, p38, and Akt and parasitism in all groups treated either with rIGF-I or with IL-4. These results corroborated previous studies showing that IL-4 upregulates Akt activation and subsequently activates the alternative macrophage profile [54].

In the present study of *L. major* infection, we observed that all groups in which IGF-I expression was silenced using an siRNA, even IL-4-stimulated cells, showed decreases in

both macrophage and parasite arginase mRNA amounts and decreases in the levels of all evaluated phosphorylated proteins. A decrease in parasitism accompanied these results, reinforcing the importance of IGF-I in the signaling induced by IL-4. In the literature, a similar study using an anti-IGF-I antibody or PI3K inhibitor in bone marrow-derived macrophages showed that IGF-I inhibition attenuated the IL-4-induced increases in the mRNA amount of M2 markers, such as mannose receptor, *Arg1* mRNA and chitinase 3-like 3, as well as ARG1 protein expression, suggesting that IGF-I is required for IL-4-induced Akt phosphorylation and M2 activation [52]. Based on this evidence, we postulate that IGF-I is the element that actually activates the PI3K/Akt pathway, which IL-4 uses. In IFN- γ -treated cells, the application of the IGF-I siRNA strengthened the effect of decreasing the parasite load, and the addition of rIGF-I almost nullified this effect, returning it to levels similar to the control group. Reinforcing our finding, the inhibition of PI3K or treatment with an anti-IGF-I antibody exacerbates the effects of IFN- γ [52].

Our data are original in that they clearly show the interference of IGF-I on the IL-4 effect. In experimental visceral leishmaniasis, IGF-I increases the expression of arginase, while the deletion of IGF-IR leads to decreased arginase in a STAT-6-dependent mechanism and restriction of *L. donovani* growth [55]. These authors explored the role of extrinsic IGF-I but not of intrinsic IGF-I present within the cell, and they did not explore the interference of IGF-I on the IL-4 effect. Furthermore, it is known that the immune responses to *Leishmania* infection vary considerably according to the species of the parasite. In particular, the immune response to *L. donovani* and *L. infantum*, which are strains leading to visceral leishmaniasis, is quite different from the immune response established in the *L. major* model. In experimental visceral leishmaniasis, the role of IL-4 in the susceptibility to visceral disease is not clearly defined [55, 56]. Moreover, L-arginine metabolism of *L. donovani* is shown to be different from that of other species [57].

Regarding *Leishmania* infections in experimental models, we hypothesized that the profiles of mouse resistance and susceptibility to *L. major* infection are not only due to the effects of Th1 and Th2 cytokines, but that IGF-I may also play an important role in infection development due to constitutive differences in IGF-I expression. The BALB/c and C57BL/6 mouse strains did not exhibit similar expression profiles of IGF-I, with the latter displaying lower expression. Similarly, lower serum IGF-I levels have been detected in C57BL/6 mice compared to that in C3H/HeJ mice [29]. To address this issue, we analyzed the effect of IGF-I in vivo and found that lesion development in mice was increased when *L. major* promastigotes were preincubated with recombinant IGF-I and applied to susceptible and resistant mouse strains. The lesions in BALB/c mice increased in size and were progressive, but the profile of lesion development was more striking in C57BL/6 mice, as the lesions in mice injected with IGF-I-preincubated parasites not only increased in size but also became progressive, even in the late phase when the lesions in the control animals were diminishing. This resistant-to-susceptible profile reversion was not observed in certain previous studies [25, 28]. Although the lesions in

C57BL/6 mice increased progressively following treatment with rIGF-I, the lesion size was smaller than lesions in BALB/c mice. This difference might be due to the IL-4 production pattern in these mouse strains. IL-4 production is similar in the initial phase of infection in both susceptible and resistant mice; however, the production of this cytokine in resistant mice is transient [26]. Another study also showed a nonsustained IL-4 level. In resistant mice, treatment with rIL-4 at the beginning of the infection did not induce the susceptible profile due to the noncontinuous production of IL-4 during the infection [25]. Thus, the main characteristics and differences in terms of susceptibility and resistance observed in certain *L. major*-infected mouse strains may be due to cytokines to some extent, but the susceptibility essentially depends on the presence of IGF-I.

5. Conclusions

The present study provides new insights into the immunology of leishmaniasis, reinforcing the importance of IGF-I in *Leishmania* infection by revealing a significant immune-endocrine interaction in this context. Our data strongly suggest that IGF-I is an effector element of IL-4 actions, leading to M2 macrophage differentiation, involving the PI3K/Akt pathway during *L. major* infection.

Our findings raise questions about pathogenic processes in other diseases in which Th2 cytokines play an important role. In relation to the pathogenesis of leishmaniasis, a polymorphism in the IGF-I gene has been detected in the human population [58, 59]; thus, we speculate that individuals in endemic areas will be susceptible or resistant or will exhibit exacerbation or modulation of the pathogenic process, depending on the expression of basal IGF-I.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

This work was supported by grants from the Fundação de Amparo à Pesquisa do Estado de São Paulo (fellowships 2008/04106-0 to Luiza C. Reis and 2005/52271-1 to Fabricio Petitto-Assis), the Conselho Nacional de Desenvolvimento Científico e Tecnológico (Grant 484499/2006 and research fellowship to Hiro Goto), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior/SIU (Grant 001/2013 and fellowships 11613/13-0 to Luiza C. Reis and 11615/13-3 to Eduardo Milton Ramos-Sanchez), the Programa Nacional de Pós Doutorado (PNPD)/Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (fellowship 1476173 to Luiza C. Reis) and LIM 38 (Hospital das Clínicas, Faculdade de Medicina, Universidade de São Paulo). The authors acknowledge Ana Lúcia Garippo for providing

technical assistance with confocal microscopy, Celio Xavier da Costa dos Santos for providing initial assistance with the siRNA methodology, and Sandra Muxel for providing technical assistance with the arginase expression methodology.

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Research Article

Intrauterine Malnutrition Reduced Long Leptin Receptor Isoform Expression and Proinflammatory Cytokine Production in Male Rat Pulmonary Endothelial Cells Stimulated by Lipopolysaccharide

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Received 8 February 2018; Revised 8 May 2018; Accepted 27 May 2018; Published 9 July 2018

Academic Editor: Naïma Moustaid-Moussa

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Background/Aims. We have previously shown that low birth weight (LBW) rats exposed to intrauterine malnutrition have an impaired lung inflammatory response and reduced levels of inflammatory mediators; however, circulating leptin levels were not increased. We evaluated long leptin receptor isoform (Obrb) expression in lung endothelial cells from low birth weight rats and examined its role in the production of lipid mediators and cytokines. **Methods.** Lung endothelial cells were obtained from normal birth weight (NBW) rats or LBW rats subjected to intrauterine malnutrition. These cells were stimulated with leptin (10 ng/mL), LPS (lipopolysaccharide, 1 µg/mL), or leptin plus LPS. Six hours after stimulation, the production of inflammatory mediators (PGE₂, LTB₄, IL-1β, and IL-6) was evaluated using commercial ELISA kits, and Western blotting was performed to investigate p38MAPK, NF-κB, and Obrb expression. **Results.** Leptin increased IL-1β levels in only cells from the NBW group, whereas LPS increased PGE₂ and LTB₄ levels in cells from both groups; leptin addition potentiated lipid mediator production induced by LPS in the NBW group. LPS enhanced the production of IL-1β and IL-6 in only endothelial cells from NBW rats. Leptin receptor expression was decreased (63%) in endothelial cells from LBW rats. None of the stimuli increased NF-κB or p38 signaling pathway expression in cells from LBW rats. **Conclusion.** These results suggest that intrauterine malnutrition compromises leptin receptor expression and cytokine production in pulmonary endothelial cells stimulated by LPS; these effects seem to involve the NF-κB and p38MAPK signaling pathways.

1. Introduction

Leptin (derived from the Greek word “leptos,” meaning thin) is a nonglycosylated peptide hormone with a molecular weight of 16 kDa; in murine animals, leptin is encoded by the obese gene (Ob), which shows 84% homology with the human leptin gene [1]. Leptin, primarily synthesized by

adipocytes in white adipose tissue, is a pleiotropic molecule involved in promoting energy expenditure and satiety, as well as homeostasis, immunity, and reproductive neuroendocrine and neuroprotective functions [2–4]. These effects depend on binding to its receptor, long leptin receptor isoform (Obrb), a transmembrane protein with a cytoplasmic domain that activates signal transduction pathways,

including the Janus kinase-signal transducer and activator of transcription (JAK-STAT) and mitogen-activated protein kinase (MAPK) signaling pathways [5, 6].

In a recent review, Kaczyńska et al. demonstrated the involvement of leptin in pulmonary physiology by stimulating the lung ventilation process and in different respiratory diseases; in asthma, leptin increases airway hyperresponsiveness and induces eosinophil accumulation, and in obstructive sleep apnea syndrome, leptin appears to be involved in the apnea-hypopnea index and the incidence of hypercapnia episodes [7]. Other authors have demonstrated that leptin negatively regulates LPS-induced lung injury and modulates corticosterone and insulin levels [8].

Acute malnutrition is associated with reduced leptin levels and immunosuppression [9, 10], cytokine expression deregulation [11], and decreased leukotriene synthesis in alveolar macrophages [12]. In a previous study, we observed that rats with a normal birth weight had increased circulating leptin levels after allergic stimuli in the lung, whereas rats with a low birth weight did not have increased circulating leptin levels or leukotriene production in the lungs after allergic stimulation; these results suggest that leptin plays a role in the reduced inflammatory responses of these animals [13].

The endothelium plays an important role in maintaining vascular tone and laminar blood flow and in cellular and molecular events related to immune reactions and responses to tissue injury [14, 15]. In vitro models of endothelial cells from lung tissue are important tools for understanding the interactions between the endothelium and leukocyte trafficking [16]. In lung tissue, a variety of cells, including bronchial epithelial cells, alveolar type II pneumocytes, macrophages, and mast cells, has been shown to produce leptin [17–19]; in addition, the lungs are the peripheral tissues with the highest ObRb expression levels [17, 20], and numerous cell types, including airway smooth muscle cells [21], bronchial and pulmonary epithelial cells [19], and endothelial cells [22], display high leptin receptor levels.

Proinflammatory cytokines, such as tumor necrosis factor- α (TNF- α) and interleukin-1 β (IL-1 β), stimulate the endothelium to express adhesion molecules (selectins, vascular cell adhesion protein 1 (VCAM-1), platelet endothelial cell adhesion molecule 1 (PECAM-1), and intercellular adhesion molecule-1 (ICAM-1)) that mediate the rolling, adhesion, and migration of leukocytes through the vessels [23].

Low birth weight rats exposed to intrauterine malnutrition have an impaired lung inflammatory response that is associated with reduced leukotriene B₄ (LTB₄), leukotriene C₄ (LTC₄) [11], and interleukin-6 (IL-6) [24] levels in the lung tissue; in addition, circulating leptin levels are not increased. Based on this information, we proposed that leptin might play an important role in the reduced production of inflammatory mediators in these animals. Therefore, we investigated whether leptin can modulate the production of inflammatory mediators in LPS-stimulated primary cultured lung endothelial cells from low birth weight rats exposed to intrauterine malnutrition. We also evaluated the participation of the NF- κ B and p38MAPK signaling pathways in this process.

2. Materials and Methods

2.1. Animals. Animal care and research protocols were in accordance with the principles and guidelines adopted by the Brazilian College of Animal Experimentation (COBEA), and this project was approved by the Ethical Committee for the Animal Research of the Federal University of São Paulo (CEUA 1038/11). Seven male and twenty female Wistar rats from the CEDEME colony (Federal University of São Paulo) were used to obtain offspring. The rats were housed in a $22 \pm 1^\circ\text{C}$ environment at 60% humidity and were maintained on a 12 h light-dark cycle. The male offspring of dams that were nourished and malnourished during the entire gestational period were used at 12 weeks of age. We avoided using female rats because of the fluctuation in their hormone levels (estrogen/progesterone). Males and females have different catabolism, which can significantly alter the regulation and production of several hormones [25]. These differences could modulate the inflammatory response and influence our results.

2.2. Protocol for the Induction of Intrauterine Undernutrition. Timed mating was carried out in age-matched (12 to 16 weeks old) female and male Wistar rats. To assess the estrus stage of the females, vaginal smears were checked before the males were introduced. Day 1 of the pregnancy was determined as the day when spermatozoa were detected in the vaginal smear. After confirmation that mating occurred, the rats were housed individually in standard rat cages. The female rats were divided randomly into two groups: nourished ad libitum and undernourished. The nourished female rats were fed with a standard commercial rat diet (Nuvital, Nuvital Nutrientes S/A, PR, Brazil) containing protein (minimum 22%), carbohydrates (maximum 54%), fat (minimum 4.5%), cellulose (maximum 8%), minerals (maximum 10%), water (maximum 12.5%), and vitamins. The undernourished female rats were fed with the same diet at 50% of the nourished female rat intake; this rate was determined according to the amount of food consumed by the control group from day 1 of the pregnancy until day 23 (parturition). All rats were fed daily in the morning, and consumption was determined 24 h later. After parturition, the dams received food ad libitum; therefore, the pups differed in only prenatal dietary experience. In a previous study, we demonstrated that the litter size and male to female ratio did not differ between the offspring from malnourished and nourished rats [26]. To prevent variation in neonatal growth due to the availability of milk during suckling, the litter sizes were standardized to eight pups on day 1. We did not observe a significant difference in the lung weight/birth weight ratio between the normal birth weight (NBW = 0.00597) and low birth weight (LBW = 0.00588) groups.

2.3. Endothelial Cell Isolation and Culture. Cell cultures were established according to procedures previously described by Chen et al. [27]. Randomly selected male rats from different litters were euthanized at 12 weeks of age by an overdose of anesthesia (ketamine/xylazine); then, their lungs were excised, washed with phosphate-buffered saline (PBS), cut

into $1 \times 1 \times 1 \text{ mm}^3$ pieces, and placed in six-well (35 mm) dishes. The tissues were covered with Dulbecco's modified Eagle's medium (DMEM-low glucose) supplemented with fetal bovine serum (FBS, 20%) and gentamicin (40 mg/L), pH 7.4 and placed in a CO₂ incubator (Sheldon Mfg. Inc., USA) (37°C). Lung explants were discarded after 60 h, and the medium was changed every 2-3 days. The cells were grown to confluence and further propagated at a 1:4 ratio using trypsin (0.1%). The cells were maintained in culture until the fourth passage when all assays were performed.

2.4. Identification and Characterization of Endothelial Cells. Cells were seeded on sterile glass coverslips (13 mm) and fixed in paraformaldehyde (PFA, 4%) at room temperature for 30 min. The cells were permeabilized with Nonidet P40 (1%) and blocked with FBS (5%) in PBS for 30 min at 37°C. The samples were incubated overnight at 4°C with primary rabbit antibodies against von Willebrand factor (vWF) and *Ulex europaeus* lectin agglutinin I (UEA-1), which binds specifically to L-fucose residues on the endothelium (1:50 dilution). In all experiments, cellular staining was detected using bovine anti-rabbit IgG—Texas red-conjugated or goat antimouse IgG—FITC-conjugated secondary antibody at 1:100 dilution for 2 h at 37°C. Controls were obtained using coverslips incubated with only FBS, followed by secondary antibody. Cell nuclei were counterstained with 4,6-diamidino-2-phenylindole (DAPI) at 1:400 dilution for 5 min at 37°C. The coverslips were observed, and images were obtained by a fluorescence microscope (Axiovert 100M, Carl Zeiss SMT, Germany).

2.5. Inflammatory Stimulus (In Vitro). Cells were seeded in six-well dishes (500,000 cells/well), and semiconfluent cultures were incubated with DMEM supplemented with fetal bovine serum for 24 h in an incubator (37°C/5% CO₂). After 24 h, the cells were washed with ice-cold PBS; DMEM was added, and the cells were stimulated with LPS (1 µg/mL) [28–30] and/or leptin (10 ng/mL) [31, 32] for 6 h. Then, the cells were collected in cold PBS and centrifuged at 1500 rpm for 5 min at 4°C. For the negative control group, only DMEM was added to the cells. Finally, the cells and the supernatant from the cells were collected and stored in a freezer at –80°C for all subsequent analyses.

2.6. Quantification of Lipid Mediators in the Cell Supernatant. PGE₂ and LTB₄ concentrations were determined by using EIA kits (Cayman Chemical Co., MI, USA) according to the method of Pradelles et al. [33]. The sensitivity of the LTB₄ assay was 4.0 pg/mL, and that of the PGE₂ assay was 15 pg/mL. The CV% values were as follows: LTB₄: intra-assay < 8.37%, interassay < 24.41%; PGE₂: intra-assay < 3.7%, interassay < 20.9%.

2.7. ObRb Receptor, NF-κB p65, and Phospho-p38 MAPK Quantification by Western Blotting. Cells were stimulated with LPS (1 µg/mL) and/or leptin (10 ng/mL) for 6 h; then, they were collected in cold PBS and centrifuged at 1500 rpm for 5 min at 4°C. The cell pellet was suspended in lysis buffer (Tris-HCl 50 mmol/L, pH 7.4, NaCl 100 mmol/L, and NP40 0.5%) with a protease/phosphatase inhibitor

(Haloth TM, Thermo Scientific, USA). Protein concentrations were determined by a BCA protein assay kit (Thermo Scientific, USA). Equal amounts of protein (55 µg) were separated with 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). The proteins in the gel were transferred onto nitrocellulose membranes (0.45 µm) and blocked for 60 min with 5% (wt/vol) nonfat dry milk diluted in TTBS (Tris base 0.2 mmol/L, NaCl 1.4 mmol/L, and Tween 20 0.1%), pH 7.6. The membranes were incubated overnight with polyclonal antibodies against ObRb (sc-8325 (H-300) rabbit polyclonal IgG, Santa Cruz Biotechnology Inc., EUA), NF-κB p65 (number 3987, Cell Signaling; rabbit polyclonal IgG Tech, USA), or phospho-p38 MAPK (number 9215, Cell Signaling; rabbit polyclonal IgG Tech, USA) at 1:1000 dilutions. The blots were washed with TTBS (3 × 5 min) and incubated with a secondary horseradish peroxidase- (HRP-) conjugated goat anti-rabbit antibody (number 70745, Cell Signaling Tech, USA) at a 1:2000 dilution for 60 min at room temperature. ObRb receptor, NF-κB p65, and phospho-p38 MAPK expression was detected by chemiluminescence (GeneGnome System, Syngene, UK) and quantified by densitometry (Gene Tools Software, UK). β-Actin expression was used as an internal control (1:2000 dilution, number 4970, Cell Signaling).

2.8. Quantification of Cytokines in the Cell Supernatant. Milliplex® map Kit-Rat Cytokine chemokine magnetic bead panels (EMD Millipore Corporation, Darmstadt, Germany) were used to measure IL-1β, IL-6, and leptin levels in the cell supernatant. The kits were used according to the manufacturer's instructions (MAGPIX™, Luminex®, MiraiBio, Alameda, CA). The data were analyzed using xPONENT® software (MAGPIX, Luminex, MiraiBio, Alameda, CA). The standard curves ranged from 1.95 to 32,000 pg/mL. The lower limits of detection for each cytokine were as follows: IL-1β (2.0 pg/mL), IL-6 (0.6 pg/mL), and leptin (10 pg/mL). The CV% values were as follows: IL-1β: intra-assay < 15%, interassay < 20%; IL-6: intra-assay < 10%, interassay < 20%; and leptin: intra-assay < 20%, interassay < 25%.

2.9. Statistical Analysis. Statistical analyses were carried out using GraphPad Prism software (v.6; GraphPad Software, San Diego, CA, USA). The body weight gain is presented as the mean percentage, and the other results are presented as the means ± SEM. Statistical evaluations of the data were determined by two-way analysis of variance followed by the Tukey-Kramer multiple comparison test. Student's *t*-test was used when necessary. A *P* value lower than 0.05 was considered statistically significant.

3. Results

3.1. Characteristics of the Offspring. Litter size did not differ between the NBW and LBW groups, indicating that food restriction during the gestation period did not affect reproductive ability. These data agree with the results found by Landgraf et al. [26, 34]. The offspring from the undernourished dams throughout gestation had significantly lower birth weights than the nourished offspring (Figure 1(a)).

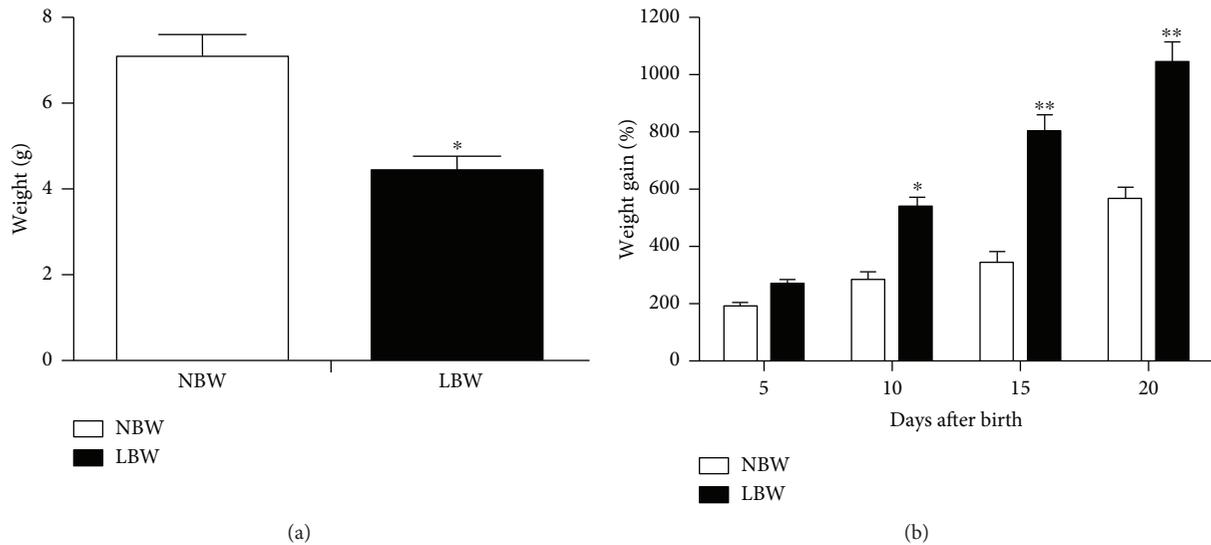


FIGURE 1: Offspring weight. (a) Offspring weight on the day of birth. The results are presented as the means \pm SEM of 12–15 animals/group, * $P < 0.05$ compared to the NBW group. (b) Mean percentage of weight gain from day 0 until day 20. The results are presented as the mean percentage of weight gain \pm SEM of 12–15 animals/group, * $P < 0.05$ and ** $P < 0.01$ compared to the NBW group.

After 10 days, the low birth weight (LBW) offspring had higher percentages of body weight gain than the normal birth weight offspring (NBW), and this difference remained until the twentieth day (Figure 1(b)).

3.2. Primary Cultured Endothelial Cells. Primary cultured endothelial cells obtained from the lung explants grew in a monolayer of polygonal cells, exhibited strong contact inhibition, and were characterized morphologically by a cobblestone appearance similar to that observed in a previous study [35]. Positive staining for UEA-1 (Figure 2(a)) and vWF (Figure 2(b)) was detected in more than 90% of the cells in culture.

3.3. Leptin Potentiated the LPS-Induced Secretion of Lipid Mediators in Only the Lung Endothelial Cell Supernatants from NBW Rats. Two-way ANOVA showed no significant interaction effect of intrauterine growth restriction and treatment on PGE_2 ($P = 0.26$) and LTB_4 secretion ($P = 0.86$), but there was a significant main effect for treatment ($P < 0.001$). A significant increase in LPS-induced PGE_2 and LTB_4 secretion in lung endothelial cells cultured from both NBW and LBW was observed. The addition of leptin potentiated the LPS-induced production of PGE_2 (86.33 ± 7.8 to 110.7 ± 2.1 ng/mL) and LTB_4 (460.8 ± 19.9 to 545.0 ± 25.5 pg/mL) in the supernatants of lung endothelial cells from NBW rats but not from LBW rats (Figures 3(a) and 3(b)).

3.4. LPS Induced Cytokine Secretion from Lung Endothelial Cells from Only NBW Rats. Lung endothelial cells from NBW rats showed increased IL-1 β and IL-6 production after LPS stimulation. The addition of leptin did not alter the production of these cytokines in cells from NBW rats (Figures 4(a) and 4(b)). Lung endothelial cells from LBW rats produced neither IL-1 β nor IL-6 leptin after stimulation.

A significant interaction effect of intrauterine growth restriction and treatment on IL-1 β ($P = 0.002$) and IL-6 ($P = 0.02$) production was confirmed by two-way ANOVA, indicating that these factors acted dependently. Moreover, the effects of intrauterine growth restriction ($P < 0.001$) and treatment ($P < 0.001$) on IL-1 β secretion were also significant. Although two-way ANOVA revealed a significant effect of intrauterine growth restriction on IL-6 production, no significant effect was observed for treatment ($P = 0.10$).

3.5. Leptin Secretion from Lung Endothelial Cells. We observed increases in leptin levels after treatment with only leptin and leptin plus LPS (Figure 5), and this effect was confirmed by two-way ANOVA, which indicated a significant effect of treatment on leptin levels ($P < 0.001$).

3.6. Lung Endothelial Cells from LBW Rats Showed Decreased *ObRb* Receptor Expression. In cells from NBW rats, both leptin and LPS enhanced *ObRb* expression, and LPS induced a significantly higher increase in *ObRb* expression than leptin; in addition, leptin did not potentiate the *ObRb* expression induced by LPS (Figure 6). *ObRb* receptor expression did not differ between the two groups under basal conditions, and the addition of leptin, LPS, or leptin plus LPS did not increase *ObRb* receptor expression in LBW rats (Figure 6).

3.7. Lung Endothelial Cells from LBW Rats Showed Decreased *p38* MAPK and *NF- κ B* Pathway Expression. We evaluated the *p38* MAPK and *NF- κ B* pathway expression in endothelial cells obtained from lung tissues. Both LPS and leptin administration increased the *NF- κ B* and *p38* pathway expression in cells from NBW rats (Figures 7(a) and 7(b)); in addition, leptin did not increase the *p38* MAPK and *NF- κ B* pathway expression induced by LPS. In cells from LBW rats, none of

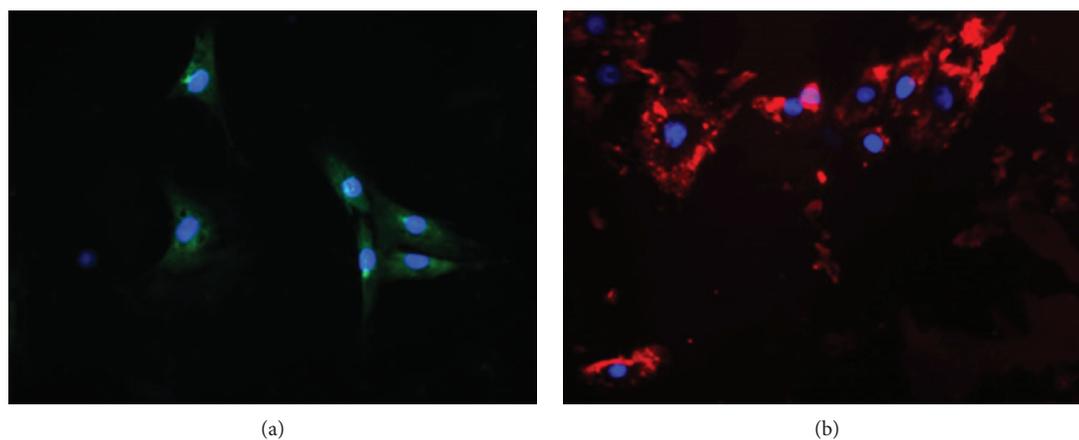


FIGURE 2: Immunostaining of specific endothelial cell markers. Staining for (a) *Ulex europaeus* lectin agglutinin I (UEA-1), green, and (b) von Willebrand factor (vWF), red. The nuclei were counterstained with DAPI solution for cellular localization. 400-fold increase.

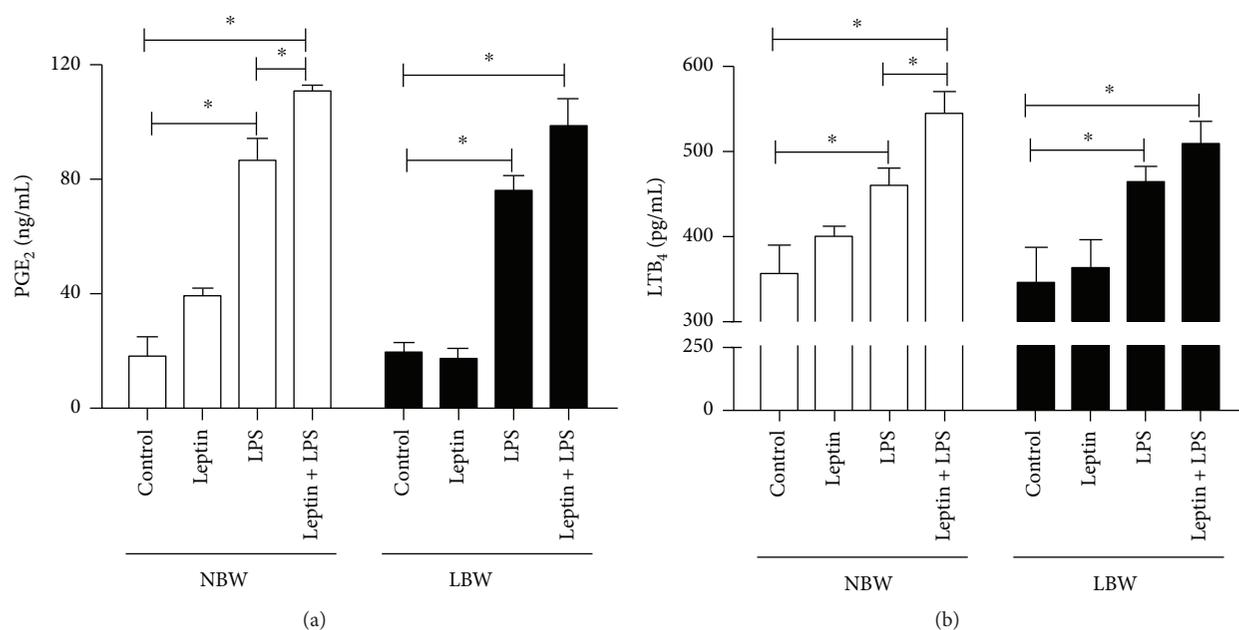


FIGURE 3: Effect of leptin on LPS-induced PGE₂ and LTB₄ secretion into the supernatants of pulmonary endothelial cells. PGE₂ and LTB₄ were measured in the supernatants of pulmonary endothelial cells using an EIA kit 6 h after stimulus with LPS and/or leptin. Cells were obtained from 8 male Wistar rats selected randomly from 6 different litters per group. The results are presented as the means \pm SEM, * $P < 0.05$.

the stimuli mediated changes in the p38 MAPK and NF- κ B pathways (Figures 7(a) and 7(b)).

4. Discussion

In the present study, we demonstrated that lung endothelial cells from intrauterine undernourished rats with a low birth weight had deficient IL-1 β and IL-6 production after inflammatory stimuli. This deficiency could be associated with the lack of ObRb receptor expression.

Maternal prenatal undernutrition could result in important alterations in offspring development [36, 37]. Consistent with previous studies, we observed that the offspring of prenatally undernourished mothers presented with a 30% reduction in birth weight, followed by accelerated growth

characterized by rapid weight gain [22]. Frisncho [38] suggested that this phenomenon might be a compensatory mechanism associated with reduced fat oxidation and increased carbohydrate metabolism.

In this study, we used a technique described by Chen et al. [27] and Loiola et al. [35]; lung endothelial cells derived from lung tissue explants were grown in FBS- (fetal bovine serum-) enriched medium, and no substances that could damage the structure and function of the pulmonary endothelial cells were added. Here, the lung endothelial cells were characterized using selective markers for these cells, namely, ULEX, which binds specifically to endothelial cell-specific glycoproteins and glycolipids [39], and the von Willebrand factor, which is a glycoprotein produced exclusively by endothelial cells and platelets [40].

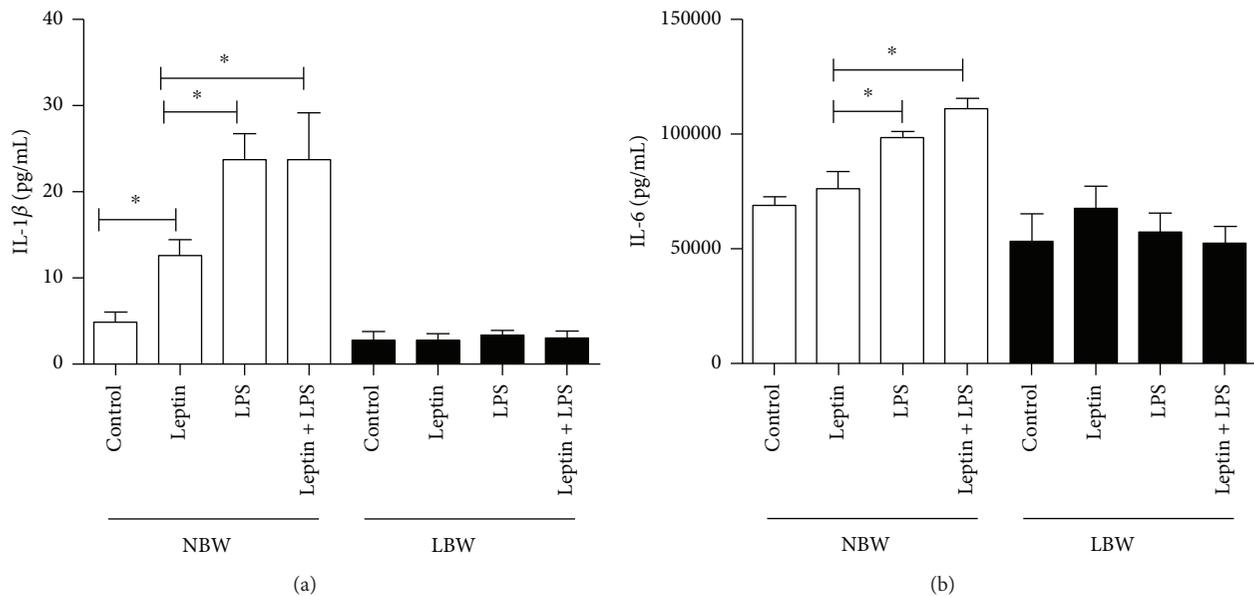


FIGURE 4: Effect of leptin on LPS-induced cytokine secretion into the supernatants of pulmonary endothelial cells. (a) Interleukin-1 β (IL-1 β) and (b) interleukin-6 (IL-6) were quantified in the supernatants of pulmonary endothelial cells 6 h after stimulus with LPS and/or leptin by multiplex assays as described in Materials and Methods. Cells were obtained from 8 male Wistar rats selected randomly from 6 different litters per group. The results are presented as the means \pm SEM, * $P < 0.05$.

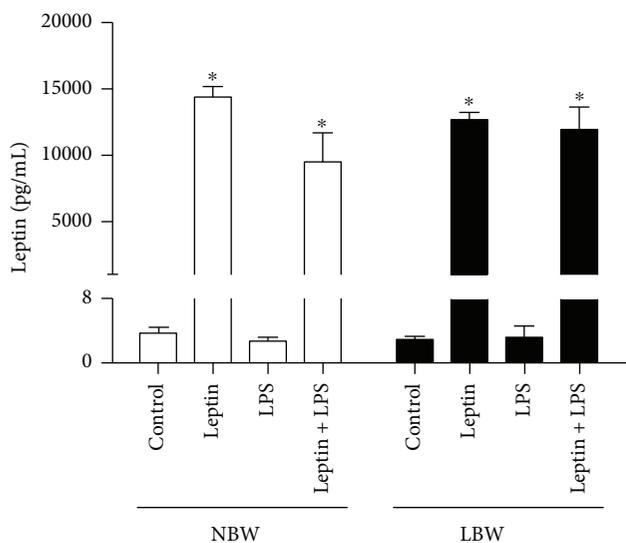


FIGURE 5: Effect of leptin on LPS-induced leptin secretion into the supernatants of pulmonary endothelial cells. Leptin was quantified in the supernatants of pulmonary endothelial cells 6 h after stimulus with LPS and/or leptin by multiplex assays as described in Materials and Methods. Cells were obtained from 8 male Wistar rats selected randomly from 6 different litters per group. The results are presented as the means \pm SEM, * $P < 0.05$.

Leptin is an adipocyte-derived protein encoded by the *ob* gene; although its plasma levels are directly correlated with body fat mass, this protein can be synthesized to a lesser extent by other tissues, such as brown adipose tissue, placenta [41], liver, stomach, intestine [42], hypothalamus, pituitary [43], skeletal muscle [44], and immune cells [45]. Leptin can

modulate not only the endocrine system but also homeostasis, hematopoiesis, energy metabolism, innate and adaptive immune responses, and endothelial cell activation [31, 46].

Lipopolysaccharide (LPS), also termed endotoxin, is the major component of the outer membrane of Gram-negative bacteria [47]. It is considered a potent inducer of inflammation, and it directly activates the vascular endothelium, leading to the production of cytokines and inflammatory mediators and the expression of adhesion molecules, which contribute to diapedesis [48]. In the present study, LPS induced the production of lipid mediators and cytokines in endothelial cells from NBW rats, thus confirming the data from previous studies.

According to Rola-Pleszczynski and Stankova [49], two classes of soluble mediators act as important agents in the orchestration of the inflammatory response: lipid mediators and cytokines, which are synthesized from phagocytes and parenchymal cells. A loop involving eicosanoids and cytokine production has been previously demonstrated [49, 50]. The release of PGE₂ and LTB₄ augments the response to a variety of inflammatory stimuli, such as IL-1, IL-6, and TNF- α ; on the other hand, leukotrienes could also modulate the release of these cytokines. However, in studying eicosanoid metabolism in porcine endothelial cells, Bustus et al. [51] demonstrated that the addition of anti-IL-1 β antibodies did not alter cyclooxygenase-2 (COX-2) expression in stimulated endothelial cells, indicating that IL-1 β was not responsible for the increases in COX-2 and PGE₂ in that system. Our data demonstrated that the LPS stimulation of endothelial cells from LBW rats increased PGE₂ and LTB₄ but not IL-1 β levels, indicating that the production of lipid mediators was not dependent on IL-1 β in our model; these results contrast those observed by Bustus et al. [51].

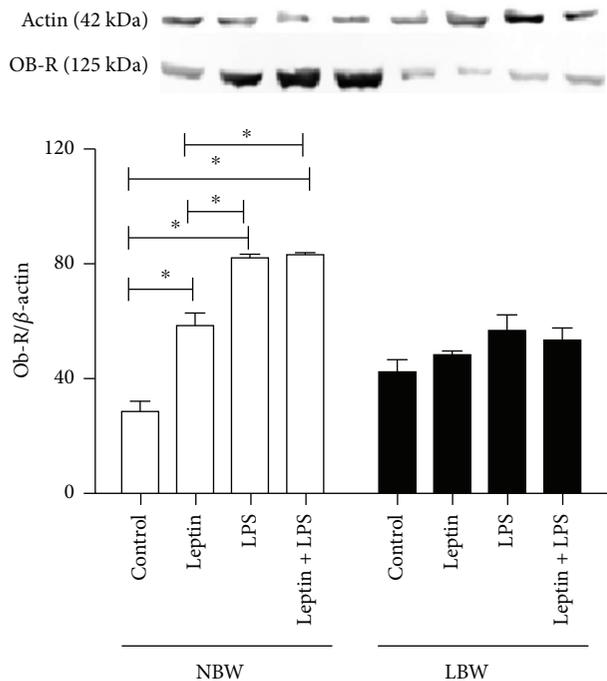


FIGURE 6: Effect of leptin on LPS-induced Ob-R expression in pulmonary endothelial cells. Endothelial cells were harvested 6 h after stimulus with LPS and/or leptin to quantify the expression levels of Ob-R using Western blotting. The graphs represent the band intensities determined by densitometric analyses and normalized to the total amount of β -actin present in each lane. Cells were obtained from 8 male Wistar rats selected randomly from 6 different litters per group. The results are presented as the means \pm SEM, * $P < 0.05$.

The production of IL-1 β during cell injury, infection, or inflammation occurs primarily in monocytes and macrophages, in addition to nonimmune cells, such as fibroblasts and endothelial cells [52]. In the present study, we found an important interaction effect of treatment with LPS and leptin and intrauterine growth restriction (and consequently low birth weight) on cytokine secretion. Leptin significantly increased IL-1 β production and potentiated IL-1 β production induced by LPS in cells from NBW rats, but the same effects were not observed in endothelial cells from LBW rats; regardless of the stimulus, IL-1 β production remained at basal levels and did not change. Studies concerning the role of leptin in the production of inflammatory mediators are conflicting. It has been suggested that leptin has anti-inflammatory effects and that the administration of high doses of leptin could result in neutrophil inhibition in the lungs of rats with acute lung injury induced by acute pancreatitis [53]. Recently, we demonstrated that leptin down-regulates LPS-induced acute lung injury by modulating corticosterone and insulin levels [8]. However, it has already been shown that leptin potentiates the effects of LPS on proliferation, monocyte activation, and proinflammatory cytokine production *in vitro* [54–56]. IL-1 β and IL-6 stimulate the expression of adhesion molecules on the vascular endothelium and contribute to leukocyte migration [57]. It has already been demonstrated that LBW rats have reduced

expression levels of adhesion molecules, such as L-selectin, P-selectin, and ICAM-1; these reductions can attenuate leukocyte migration [26]. Based on these data, we suggest that the failure of endothelial cells from LBW rats to produce IL-1 β and IL-6 after LPS stimulation could be an important factor associated with reduced adhesion molecule expression and the consequently decreased leukocyte migration.

In endothelial cells, leptin receptor activation is associated with oxidative stress, chemokine and cytokine production, and adhesion molecule expression [57]. Mice lacking leptin receptors (db/db) are obese and present with a series of dysfunctions, such as hyperinsulinemia, increased cortisol levels, and impaired immune function [58, 59]. Leptin acts on target cells through interacting with its receptor, Ob-R, which is widely expressed in different parts of the body [60]. The expression of short (ObRa) and long (ObRb) leptin receptors has already been demonstrated in bronchial and alveolar epithelial cells in the lung [19, 61]. The ability of the short leptin isoform to activate the JAK signaling pathway is low, and it cannot activate the STAT pathway at all [62]. In addition, it has been demonstrated in adipocyte culture that the activating effects of leptin on the STAT3 and MAPK pathways are exerted through its long receptor [63]. Another study demonstrated that pulmonary macrophages express high levels of the long form leptin receptor; this isoform is the only one capable of inducing STAT3 signaling and is one of the main targets of leptin action in the lung [64]. Our results demonstrated that lung endothelial cells could not produce leptin after LPS stimulation. Both leptin and LPS additions significantly increased the expression of ObRb in endothelial cells from NBW rats, unlike what was observed in cells from LBW rats. Considering these data, we suggest that the reduced Ob-R response to the inflammatory stimuli might compromise the production of cytokines and lipid mediators in endothelial cells from LBW rats.

LPS can initiate several intracellular signaling events, such as stimulating pathways to activate NF- κ B and p38 MAPK, inducing cytokine expression [65, 66], and reducing proinflammatory cytokine expression, including IL-1 β and TNF- α , to decrease NF- κ B and p38 MAPK pathway activation [67]. In addition, HUVEC exposure to leptin upregulates ObRb receptor expression and enhances NF- κ B activation and proinflammatory cytokine secretion [68]. Our data agree well with the literature data because we demonstrated that LPS and leptin-treated endothelial cells from NBW rats presented with increased proinflammatory cytokine expression and NF- κ B and p38 MAPK activation. In endothelial cells from LBW rats, increases in proinflammatory cytokine expression and NF- κ B and p38 MAPK activation were not observed, even after stimulation with LPS and/or leptin, suggesting that these pathways may be compromised in these animals and thus contribute to the decreased inflammatory response observed in our previous results [8, 13, 26].

In a previous study, our group demonstrated that LBW rats, despite normal basal leptin levels, did not have increased leptin levels after an inflammatory stimulus, and this inability to upregulate leptin levels was accompanied by an attenuated inflammatory response [13]. Here, the deficiency in ObRb expression likely reflects the ability of endothelial cells to

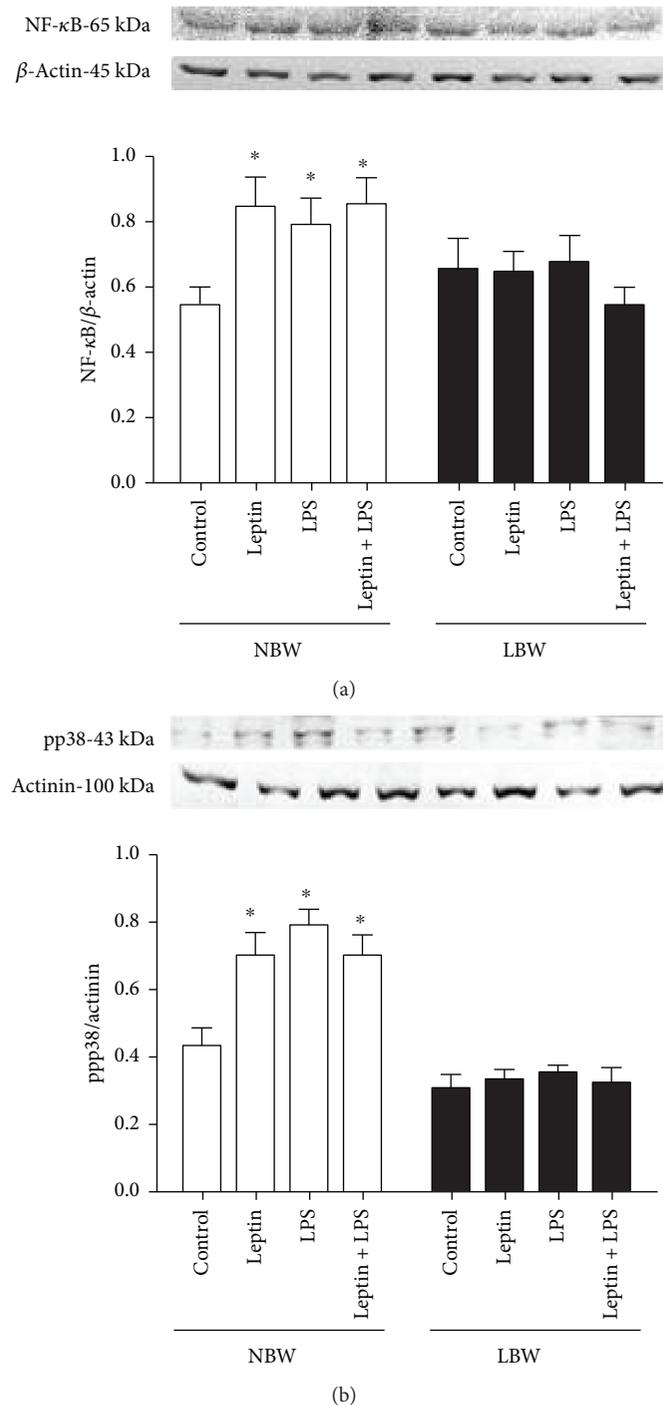


FIGURE 7: Involvement of the p38 kinase and NF- κ B pathways in the regulation of Ob-R expression on LPS-induced Ob-R expression in pulmonary endothelial cells. Endothelial cells were harvested 6 h after stimulus with LPS and/or leptin to quantify the activation of the p38 MAPK and NF- κ B pathways using Western blotting. The graphs represent the band intensities determined by densitometric analyses and normalized to the total amount of β -actin (NF- κ B) and β -actinin (pp38) present in each lane. Cells were obtained from 8 male Wistar rats selected randomly from 5 different litters per group. The results are presented as the means \pm SEM, * P < 0.05.

adequately respond to LPS and leptin itself and contributes to the decreased production of inflammatory mediators.

Therefore, we suggest that the low birth weight induced by intrauterine malnutrition could induce molecular changes to the physiological responses of pulmonary endothelial cells

to compromise the expression of ObRb and reduce the expression of inflammatory mediators and cytokines; our data also indicate the participation of the NF- κ B and p38 MAPK pathways in this process. These events could contribute to the attenuation of the inflammatory response observed

in intrauterine malnourished rats with a low birth weight. Taken together, these data indicate a key role of leptin in the reduced inflammatory response of LBW rats.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Disclosure

Some of the data presented in this article were included in a poster presentation at the 39th ESPEN (The European Society for Clinical Nutrition and Metabolism), The Hague, Netherlands, 2017 [69].

Conflicts of Interest

The authors confirm that there are no conflicts of interest.

Authors' Contributions

Maristella A. Landgraf and Richardt G. Landgraf contributed equally to this work.

Acknowledgments

This work was financially supported by grants from the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and the Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) (2010/01404-0, 2012/51104-8, 2014/18760-4, and 2017/02042-3).

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Research Article

Protective Effect of Sex Hormone-Binding Globulin against Metabolic Syndrome: *In Vitro* Evidence Showing Anti-Inflammatory and Lipolytic Effects on Adipocytes and Macrophages

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Received 20 February 2018; Revised 14 May 2018; Accepted 16 May 2018; Published 25 June 2018

Academic Editor: Joilson O. Martins

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Sex hormone-binding globulin (SHBG) is a serum protein released mainly by the liver, and a low serum level correlates with a risk for metabolic syndrome including diabetes, obesity, and cardiovascular events. However, the underlying molecular mechanism(s) linking SHBG and metabolic syndrome remains unknown. In this study, using adipocytes and macrophages, we focused on the *in vitro* effects of SHBG on inflammation as well as lipid metabolism. Incubation with 20 nM SHBG markedly suppressed lipopolysaccharide- (LPS-) induced inflammatory cytokines, such as MCP-1, TNF α , and IL-6 in adipocytes and macrophages, along with phosphorylations of JNK and ERK. Anti-inflammatory effects were also observed in 3T3-L1 adipocytes cocultured with LPS-stimulated macrophages. In addition, SHBG treatment for 18 hrs or longer significantly induced the lipid degradation of differentiated 3T3-L1 cells, with alterations in its corresponding gene and protein levels. Notably, these effects of SHBG were not altered by coaddition of large amounts of testosterone or estradiol. In conclusion, SHBG suppresses inflammation and lipid accumulation in macrophages and adipocytes, which might be among the mechanisms underlying the protective effect of SHBG, that is, its actions which reduce the incidence of metabolic syndrome.

1. Introduction

SHBG is a 40–50 kDa protein mainly synthesized in the liver and secreted into the bloodstream. This protein is comprised

of two laminin G-like (LG) domains [1], and the molecular weights of serum SHBG proteins are partially dependent on their glycosylation status [2]. The conventional roles of SHBG involve transporting sex hormones and the regulation

of hormone dynamics [3]. Numerous studies have confirmed the relationship between the serum SHBG concentration and metabolic syndrome. Low SHBG concentrations correlate with higher levels of serum inflammatory markers [4, 5]. Relatively low levels of SHBG are also a risk factor for obesity, metabolic syndrome, and diabetes [6–10]. Thus, the serum SHBG concentration has been regarded as a biomarker for metabolic syndrome.

On the other hand, interestingly, db/db mice overexpressing human SHBG reportedly show resistance to the development of obesity and hepatosteatosis [11, 12]. In addition, a single nucleotide polymorphism related to an elevated plasma SHBG concentration reportedly correlates with a reduced risk of diabetes [13]. The hormone-like effect of SHBG has also been demonstrated in experiments using prostatic cells [14, 15], MCF-7 breast cancer cells [16], cytotrophoblasts [17], proximal tubule epithelial cells [18, 19], and hepatocytes [12]. The results of these previous studies led us to speculate that the serum SHBG level is not only simply a consequence of altered metabolic conditions but also exerts favorable effects protecting against the development of metabolic disorders.

In this study, using adipocytes and macrophages, we focused on the *in vitro* effects of SHBG in inflammation as well as lipid metabolism, since lipid accumulation and inflammation are both necessary for the development of metabolic syndrome. Herein, we present evidence of the favorable actions of SHBG in adipocytes and macrophages.

2. Materials and Methods

2.1. Chemicals and Reagents. SHBG protein was purchased from two companies, Abcam (ab151275) and Fitzgerald Industries (30-AS40). According to the explanations provided by these manufacturers, SHBG protein was purified from human sera, and its purity exceeded 90%. While we confirmed the effects of SHBG from these two companies to be the same, the data presented herein were those obtained with the SHBG from Abcam. In addition, we measured the amounts of testosterone and estradiol contaminating the SHBG protein, since no information was given regarding this issue in the materials provided by the manufacturers. Sex hormones were measured using the ELISA kits for testosterone and estradiol (Cayman) according to the manufacturer's instructions. Diethyl ether was added to the SHBG protein samples and mixed thoroughly with a vortex. The upper ether layer was collected using a pasteur pipette and transferred into a clean tube. This extraction procedure was repeated four times. After evaporating the combined ether extracts, the samples were dissolved in the buffer and subjected to analysis with the ELISA kits.

Lipopolysaccharide (LPS) (from *Escherichia coli* 0111:B4) was purchased from Sigma. Recombinant murine TNF α was purchased from Genzyme (3410T). Anti- β -actin antibody (sc-1616), anti-CCAAT/enhancer binding protein α (CEBP α) antibody (sc-61), and horseradish peroxidase- (HRP-) labeled anti-goat IgG antibody (sc-2020) were from Santa Cruz Biotechnology. Anti-TNF α antibody (#11948), anti-stress-activated c-Jun amino-terminal kinase (JNK)1/2 antibody

(#9252), anti-phospho-extracellular signal-related kinase (ERK)1/2 (Thr202/Tyr204) antibody (#9101), anti-ERK1/2 antibody (#9102), anti-adipose triglyceride lipase (ATGL) antibody (#2439), HRP-labeled anti-rabbit (#7074), and anti-mouse IgG antibody (#7076) were all from Cell Signaling Technology. Anti-phospho-JNK1/2 (Thr183/Tyr185) antibody was obtained from BD Biosciences (#562480).

2.2. 3T3-L1 Cell Culture and Differentiation. 3T3-L1 cells were differentiated as previously described [20, 21] with some modifications. Briefly, 3T3-L1 cells were cultured in Dulbecco's Modified Eagle's medium (DMEM) (Wako) containing 10% donor calf serum (Invitrogen) in a 5–10% CO₂ incubator. For the experiments, cells were spread onto collagen type I coated plates (Iwaki) and induced to differentiate with DMEM containing 10% fetal calf serum (FCS) (Biowest), 0.5 mM 3-isobutyl-1-methylxanthine (Sigma), 4 μ g/ml dexamethasone (Sigma), and 167 nM insulin (Sigma). Two days later, the media were replaced with DMEM containing 10% FCS and 167 nM insulin. After another two days, the media were replaced with DMEM containing 10% FCS and the media were then changed every other day. Penicillin-streptomycin (Invitrogen) was added to all media at a 0.5% concentration.

For experiments on mature 3T3-L1 cells, we used cells that had been differentiating for more than 6 days [22]. Mature adipocytes were treated with SHBG proteins in phenol red-free DMEM (Wako) containing 0.2% fatty acid-free bovine serum albumin (BSA) (Wako). The concentration of BSA was much higher than that of SHBG protein. We used phenol red-free media to eliminate estrogen-like effects of phenol red [23].

For experiments evaluating inflammatory cytokine levels in adipocytes, 3T3-L1 cells were pretreated overnight with 20 nM SHBG, followed by stimulation with 1 ng/ml LPS or 1 ng/ml TNF α for 12–24 hrs. In some experiments, 1 or 20 μ M testosterone (T) (Wako, 208-08341) or 17 β -estradiol (E₂) (Sigma, E8875) was coadded with 0–20 nM of SHBG protein. Considering the amounts and the reported association constants of T and E₂ with SHBG ($1.6 \times 10^9 \text{ M}^{-1}$ and $6.8 \times 10^8 \text{ M}^{-1}$, resp. [24]), it was assumed that more than 99% of SHBG would form a complex with T or E₂.

2.3. Quantitative Reverse-Transcription Polymerase Chain Reaction (qRT-PCR). Total RNA was extracted using the RNeasy Mini Kit (Qiagen). Reverse transcription was performed using Transcriptor Universal cDNA Master (Roche) followed by RT-PCR employing LightCycler 480 SYBR Green I Master (Roche). Sequences of the primers used in this study are listed in Table 1. The 36B4 mRNA level served as the internal control.

2.4. Preparation of Mouse Peritoneal Macrophages. The isolation protocol was reported previously [39, 40] and achieved a final cell population comprised of more than 90% macrophages. We employed this protocol, with a slight modification. Peritoneal macrophages were collected from C57BL/6N mice. RPMI 1640 media without phenol red (Gibco) was used, and the cells were incubated at 37°C in a

TABLE 1: Primer sequences used for this study.

Gene	Forward primer (5' → 3')	Reverse primer (5' → 3')	Reference
<i>36B4</i>	GCTCCAAGCAGATGCAGCA	CCGGATGTGAGGCAGCAG	[25]
<i>Mcp-1</i>	AGGTCCCTGTCATGCTTCTG	TCTGGACCCATTCTTCTTG	[26]
<i>Tnfa</i>	GAAGTGGCAGAAGAGGCACT	AGGGTCTGGGCCATAGAAGT	[26]
<i>Il-6</i>	TCGTGGAAATGAGAAAAGAGTTG	AGTGCATCATCGTTGTCATACA	[27]
<i>Cebpa</i>	TGAGCCGTGAACTGGACACG	CAGCCTAGAGATCCAGCGAC	[28]
<i>Pparg</i>	TCTTCCATCACGGAGAGGTC	GATGCACTGCCTATGAGCAC	[28]
<i>Srebp1</i>	AAGCAAATCACTGAAGGACCTGG	AAAGACAAGGGGCTACTCTGGGAG	[29]
<i>Fas</i>	ATCCTGGAACGAGAACACGATCT	AGAGACGTGTCACTCCTGGACTT	[30]
<i>Acs1l</i>	GACGACCTCAAGGTGCTTCA	ACCCAGGCTCGACTGTATCT	—
<i>Pepck</i>	CTAACTTGGCCATGATGAACC	CTTCACTGAGGTGCCAGGAG	[31]
<i>Pgc1b</i>	GCTCTGACGCTCTGAAGGAC	CACCGAAGTGAGGTGCTTATG	[30]
<i>Hsl</i>	CAGTGCCTATTCAGGGACAGAG	CACTCCTGCGCATAGACTCC	—
<i>Mgl</i>	AGGCGAACTCCACAGAATGTT	AGCCAGCTCATATAACGGC	—
<i>Acrp30</i>	GCTCCTGCTTTGGTCCCTCCAC	GCCCTTCAGCTCCTGTCATTCC	[32]
<i>Glut4</i>	CAGCTCTCAGGCATCAAT	TCTACTAAGAGCACCGAG	[33]
<i>Fabp4</i>	TGGGAACCTGGAAGCTTGTC	CTTTCCTTGTGGCAAAGCCC	—
<i>Atgl</i>	AACACCAGCATCCAGTTCAA	GGTTCAGTAGGCCATTCTCTC	[34]
<i>Ucp2</i>	CTACAAGACCATTGCACGAGAGG	AGTGCTCATAGGTGACAAACAT	[35]
<i>Agt</i>	AGGTTGGCGCTGAAGGATAC	GATGTATACGCGGTCCCCAG	[36]
<i>Pgc1a</i>	GCCCGGTACAGTGAGTGTTT	CTGGGCCGTTTAGTCTTCTCT	[30]
<i>Cebpb</i>	CAAGCTGAGCGACGAGTACA	AGCTGCTCCACCTTCTTCTG	[37]
<i>Ppara</i>	CGGGAAAGACCAGCAACAAC	TGGCAGCAGTGGAAGAATCG	[30]
<i>Chrebp</i>	GATGGTGCGAACAGCTCTTCT	CTGGGCTGTGTCATGGTGAA	[30]
<i>Ucp1</i>	GATGGTGAACCCGACAACCTT	CTGAAACTCCGGCTGAGAAG	[38]
<i>Cpt1a</i>	GACTCCGCTCGCTCATTC	ACCAGTGATGATGCCATTCTTG	—

5% CO₂ incubator. Macrophages were collected by injection of 5 ml of RPMI 1640 media containing 10% FCS intraperitoneally under diethyl ether anesthesia and then left on ice until centrifugation. After centrifugation at 1500 rpm for 2 minutes at room temperature, the supernatant was removed, and hemolysis buffer (BD PharmLyse) was added to remove the red blood cells. After 2 minutes, we centrifuged the samples at 1500 rpm for 2 minutes at room temperature and the supernatant was removed. Cells were seeded at a density of 1.5×10^6 cells/well in a 12-well plate in RPMI 1640 media containing 10% FCS. Two hours later, the cells were gently washed twice with RPMI 1640 media to remove nonadherent cells and the medium was then replaced with RPMI 1640 containing 0.2% fatty acid-free BSA for the experiments. For experiments evaluating inflammatory cytokine levels in macrophages, cells were pretreated with 20 nM SHBG overnight, followed by 1 ng/ml LPS for 0–8 hrs.

2.5. Immunoblotting Analysis. The cells were solubilized with Laemmli buffer (0.2 M Tris-HCl, 4% SDS, 10% glycerol, 5% 2-mercaptoethanol, and 0.1% bromophenol blue) containing 100 mM dithiothreitol. Equal amounts of protein from whole cell lysates were resolved by SDS-PAGE. Then, the proteins were transferred to Immobilon (Millipore), blocked with 1% BSA (Intergen), reacted with the primary antibodies and subsequently with the HRP-labeled secondary antibodies.

Chemiluminescence was detected using an ImageQuant LAS 4000 mini (Fuji Film).

2.6. Coculture System of 3T3-L1 Adipocytes and Murine Macrophages. The 3T3-L1 adipocytes and murine macrophages were cocultured in a transwell system (Corning, Acton, MA) with a 0.4 μ m porous membrane to separate the upper and lower chambers. Mouse peritoneal macrophages were harvested and seeded at a density of 1.5×10^6 cells/well in the upper chamber, while differentiated 3T3-L1 cells were in the lower chamber. Both macrophages and differentiated 3T3-L1 cells were washed with RPMI 1640 medium, and the culture medium was then replaced with RPMI 1640 containing 0.2% fatty acid-free BSA for the experiments. SHBG at the 20 nM concentration was added to both the upper and the lower chambers, and coculture was then started. After incubation overnight, 100 pg/ml LPS was added and the cells were collected 12 hrs later.

2.7. Lipid Staining. Differentiated 3T3-L1 cells were treated with 0–100 nM SHBG protein in serum-free media and incubated for 3 days, followed by Oil Red O staining or Nile Red staining.

Oil Red O (Sigma) was dissolved in isopropanol to assure that the concentration would be 0.3%. This stock solution was mixed with distilled water (3 : 2), followed by incubation

for 30 minutes, and filtered with 0.45 μm before use. The cells were washed twice with PBS and fixed with 10% neutral buffered formalin for 10 minutes. After the cells were washed twice with PBS, Oil Red O working solution was added followed by another 10-minute incubation and then washed with PBS. Images were taken using a light microscope FSX100 (Olympus).

Nile Red (AdipoRed, Lonza) becomes fluorescent when it is partitioned in a hydrophobic environment and shows selective fluorescence for intracellular lipid droplets [41]. The staining protocol was carried out according to the manufacturer's instructions. Fluorescence with excitation at 485 nm and emission at 535 nm was measured using ARVO MX-fla (PerkinElmer).

2.8. Measurement of Glycerol in the Culture Medium. Differentiated 3T3-L1 cells were treated with 20 nM SHBG protein for 18 or 35 hrs. Glycerol concentrations in culture media were measured employing a Glycerol Assay Kit (Sigma). With this kit, the glycerol concentration is determined by a coupled enzyme assay involving glycerol kinase and glycerol phosphate oxidase, resulting in a colorimetric product.

2.9. cAMP Measurement. Differentiated 3T3-L1 cells were treated with 20 nM SHBG protein or 10 μM isoproterenol for 1 or 18 hrs. Intracellular cAMP concentrations were measured using a cAMP EIA kit (Cayman). This assay is based on the competition between free cAMP and a cAMP tracer. Measurements were carried out according to the manufacturer's instructions. Stimulation with isoproterenol (Sigma) was used to confirm the production of cAMP.

2.10. Data Analysis. All data are presented as the means \pm standard deviation (S.D.). The differences between two groups were evaluated by *t*-test. $p < 0.05$ was considered to indicate a statistically significant difference.

3. Results

3.1. SHBG Suppressed LPS- or TNF α -Induced Inflammatory Cytokine Levels in Mouse Peritoneal Macrophages and Differentiated 3T3-L1 Cells. First of all, we measured the concentrations of testosterone and 17 β -estradiol contaminating the SHBG protein purchased from Abcam, to exclude the possibility of its functions being attributable to these sex hormones. The results obtained with the ELISA assay kits revealed that Abcam's SHBG protein contained molar ratios of 1 : 5600 and 1 : 10000 for testosterone and estradiol, respectively, to SHBG. Therefore, it is unlikely that the contaminant testosterone and 17 β -estradiol contributed to the results obtained using Abcam's SHBG protein in this study.

Murine macrophages were stimulated with or without 1 ng/ml LPS for 8 hrs, and the effects of 20 nM SHBG were examined. While LPS markedly raised mRNA levels of monocyte chemoattractant protein-1 (MCP-1), TNF α , and IL-6, SHBG suppressed them under both basal and LPS-stimulated conditions in the approximate range of 50–90% (Figure 1(a)).

Next, the effects of SHBG on the signal transductions leading to inflammatory cytokine levels were investigated.

Maximal phosphorylations of JNK1/2 and ERK1/2 occurred at 30 min after the addition of 1 ng/ml LPS, while the intracellular TNF α content peaked around 2 hrs. In the presence of 20 nM SHBG, LPS-induced phosphorylations of JNK1/2 and ERK1/2 as well as TNF α production were reduced. The band intensity of TNF α normalized by β -actin at 2 hrs, phosphorylation of JNK normalized by JNK at 1 hr, and phosphorylation of ERK normalized by ERK at 1 hr were significantly decreased (Figure 1(b)).

Similarly, the effects of SHBG on MCP-1 and IL-6 levels in 3T3-L1 adipocytes were investigated, by stimulating these cells with LPS or TNF α and comparing the results to those in adipocytes without stimulation. It was revealed that 20 nM SHBG markedly suppressed LPS-induced MCP-1 and IL-6 mRNA upregulations as well as TNF α -induced MCP-1 levels (Figure 1(c)). These results indicate that SHBG exerts anti-inflammatory effects directly on macrophages and adipocytes.

3.2. Inflammatory Cytokine Levels Were Also Suppressed in the Coculture System of Peritoneal Macrophages and 3T3-L1 Adipocytes. We cocultured 3T3-L1 adipocytes and murine macrophages using a transwell system. Then, LPS was added, and the resulting cytokine levels in both 3T3-L1 adipocytes and macrophages were compared between the presence and the absence of 20 nM SHBG. In this experiment, SHBG exerted inhibitory effects on basal cytokine levels in 3T3-L1 adipocytes. Notably, the addition of 20 nM SHBG markedly suppressed LPS-induced MCP-1 and IL-6 levels in 3T3-L1 adipocytes (Figure 2(a)), as well as MCP-1, TNF α , and IL-6 levels in murine macrophages (Figure 2(b)). Although the optimal medium for 3T3-L1 cells is DMEM, coculturing in RPMI did not apparently impair the functions of 3T3-L1 cells.

3.3. SHBG Reduced the Lipid Accumulation in 3T3-L1 Adipocytes. Differentiated 3T3-L1 cells were treated with SHBG proteins at the indicated concentrations in serum-free media and incubated for 3 days and followed by Oil Red O staining (Figure 3(a)). It was revealed that SHBG protein reduced lipid accumulation in 3T3-L1 adipocytes in a concentration-dependent manner. Glycerol concentrations in the culture media were increased in the presence of 20 nM SHBG for 18 or 35 hrs (Figure 3(b)), which suggests lipolysis to be enhanced by SHBG. It was found that SHBG did not alter the intracellular cAMP concentration, in contrast to the marked cAMP increase induced by isoproterenol (Figure 3(c)). Interestingly, treatment with 20 nM SHBG proteins for 3 days markedly reduced CEBP α and increased ATGL proteins (Figure 3(d)).

3.4. SHBG Altered the mRNA Levels Related to Lipid Metabolism in Differentiated 3T3-L1 Adipocytes. Differentiated 3T3-L1 cells were treated with 20 nM SHBG protein for 18 hrs, and mRNA levels were measured by RT-PCR. Importantly, mRNA levels of CEBP α , peroxisome proliferator-activated receptor γ (PPAR γ), and sterol regulatory element-binding protein 1 (SREBP1), gene encoding key transcriptional factors for adipogenic differentiation

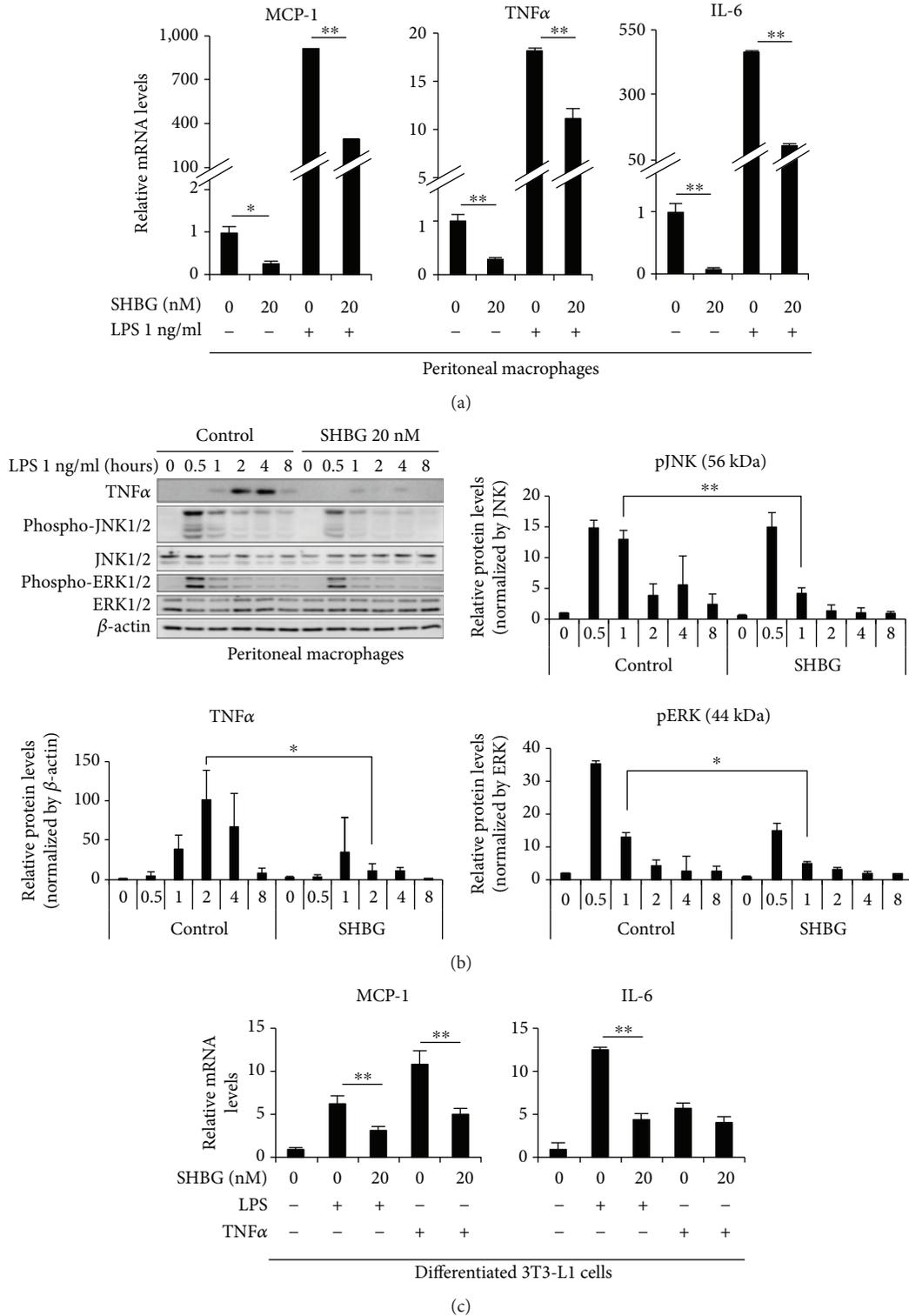


FIGURE 1: SHBG inhibits inflammatory cytokine levels in peritoneal macrophages and differentiated 3T3-L1 cells. (a) Peritoneal macrophages from C57BL/6 mice were treated with SHBG overnight, followed by 1 ng/ml LPS stimulation for 8 hrs. mRNA levels of inflammatory cytokines were measured by RT-PCR. Student's *t*-test was performed. Data are the means \pm S.D. ($n = 4$, $*p < 0.05$, $**p < 0.01$). (b) Peritoneal macrophages from C57BL/6 mice were treated with SHBG protein overnight, followed by 1 ng/ml LPS stimulation for the indicated times. Inflammatory signaling was evaluated by Western blotting. Each band was quantified using ImageJ. Relative intensities are shown. Data are the means \pm S.D. ($n = 3$, $*p < 0.05$, $**p < 0.01$). (c) Differentiated 3T3-L1 cells were treated with SHBG proteins overnight, followed by 1 ng/ml LPS or 1 ng/ml TNF α stimulation for 24 hrs. mRNA levels of MCP-1 and IL-6 were measured by RT-PCR. Student's *t*-test was performed. Data are the means \pm S.D. ($n = 3$, $**p < 0.01$).

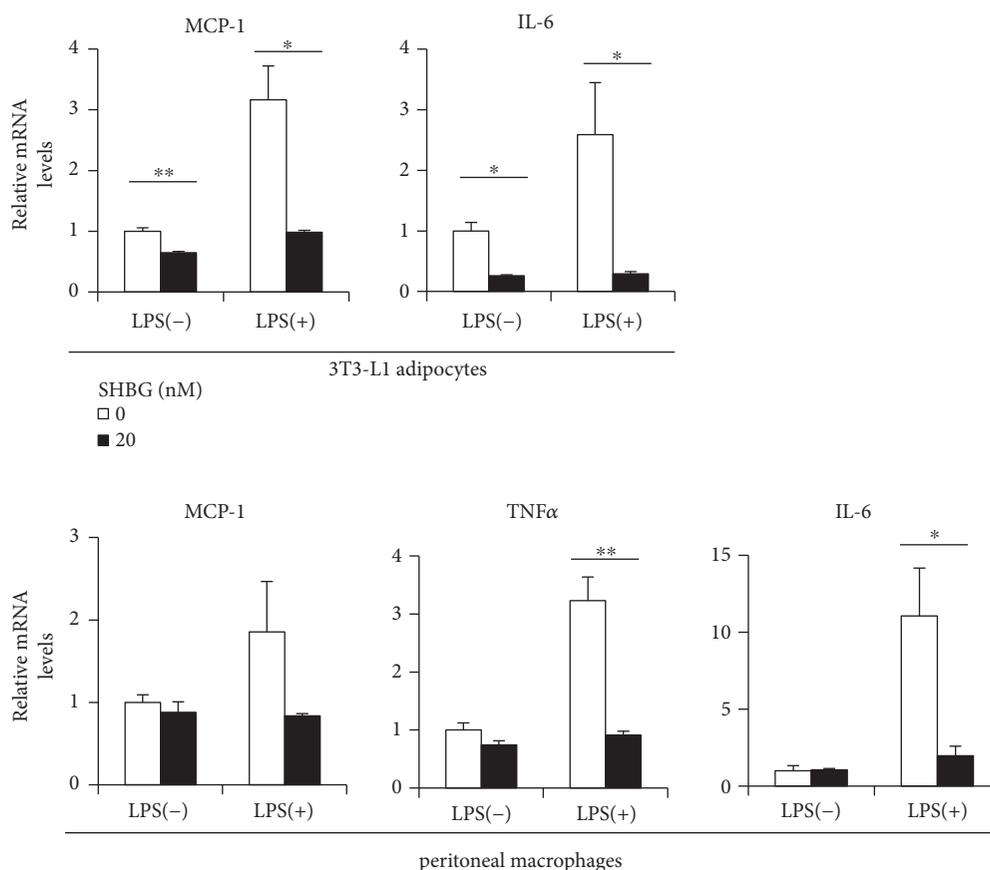


FIGURE 2: SHBG inhibits inflammatory cytokine levels in 3T3-L1 cells cocultured with peritoneal macrophages. Differentiated 3T3-L1 cells and peritoneal macrophages from C57BL/6 were cocultured using a transwell system overnight, in culture media with or without SHBG protein. Thereafter, we added 100 pg/ml LPS to the culture media and cells were collected 12 hrs later. mRNA levels of inflammatory cytokines in each cell were measured by RT-PCR. Student's *t*-test was performed. Data are the means \pm S.D. ($n = 3$, * $p < 0.05$, ** $p < 0.01$).

and triglyceride synthesis, are significantly downregulated by 18 hrs of incubation with 20 nM SHBG. The genes downregulated by SHBG included fatty acid synthase (FAS), acyl-CoA synthetase 1 (ACSL1), phosphoenolpyruvate carboxykinase (PEPCK), PPAR γ co-activator-1 β (PGC1 β), hormone-sensitive lipase (HSL), monoacylglycerol lipase (MGL), adipocyte complement-related protein of 30 kDa (ACRP30), glucose transporter type 4 (GLUT4), and fatty acid binding protein 4 (FABP4), while ATGL, uncoupling protein-2 (UCP2), and angiotensinogen (AGT) were all upregulated. PGC1 α , CEBP β , PPAR α , carbohydrate response element binding protein (ChREBP), UCP1, and carnitine palmitoyl-transferase 1A (CPT1A) were not significantly changed. Taken together, these observations raise the possibility that SHBG induces dedifferentiation via downregulation of its key transcription factors and lipid metabolism genes (Figure 4).

3.5. Coincubations with an Excess of Testosterone or 17 β -Estradiol Did Not Affect the Function of SHBG. Differentiated 3T3-L1 cells were treated with 20 nM SHBG in the presence or absence of 1 μ M testosterone or 17 β -estradiol overnight and then stimulated with 1 ng/ml LPS for 12 hrs. The suppressive effects of SHBG on MCP-1 and IL-6

levels were unaffected by testosterone or 17 β -estradiol (Figure 5(a)). Similarly, no significant effect of testosterone or 17 β -estradiol on the reduced lipid content by SHBG was observed in 3T3-L1 adipocytes (Figure 5(b)).

4. Discussion

In the present study, it was clearly demonstrated that SHBG exhibits anti-inflammatory effects involving macrophages and adipocytes, as evidenced by suppressed mRNA levels for inflammatory cytokines such as MCP-1, TNF α , and IL-6. MCP-1, which is known to be highly expressed in adipocytes, is related to the induction of chronic inflammation [42]. Chronic inflammation in adipose tissues is reportedly exacerbated by LPS from the intestinal tract accompanied by obesity or high-fat diets [43–45]. In addition, it is very likely that SHBG enhances lipolysis or induces dedifferentiation of mature adipocytes, based on the effects on a series of mRNA level data. Under conditions of obesity, macrophages reportedly infiltrate adipose tissue, and interactions between macrophages and adipocytes occur via a paracrine mechanism [46], which exacerbates the metabolic syndrome phenotype. Our experiments

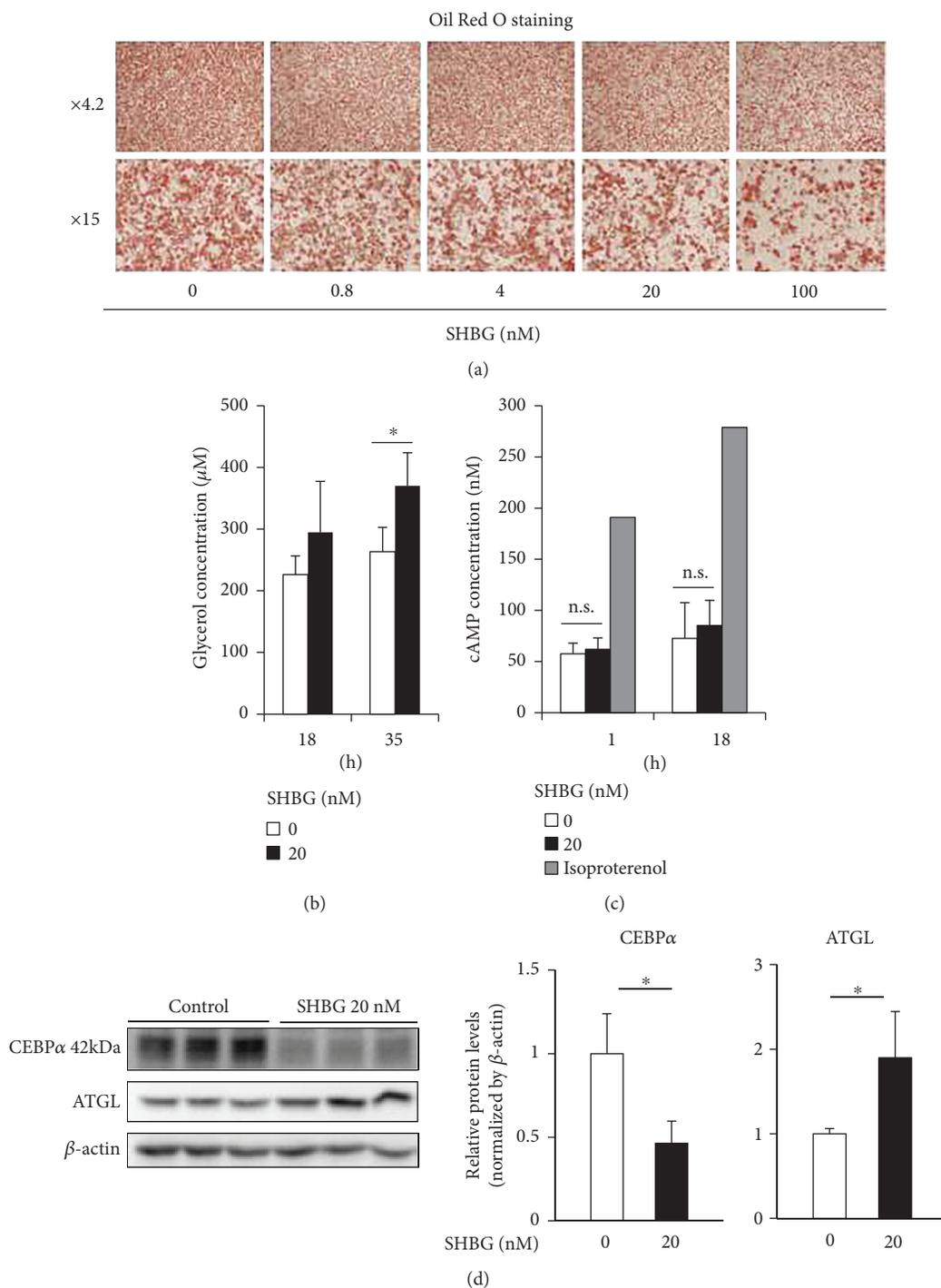


FIGURE 3: SHBG reduces lipid contents of differentiated 3T3-L1 cells with alterations in corresponding protein levels. (a) Differentiated 3T3-L1 cells were treated with SHBG proteins at the indicated concentrations in serum-free media and incubated for 3 days. Oil Red O staining was performed. Representative fluorescent microscopy images are shown. (b) Differentiated 3T3-L1 cells were treated with 20 nM SHBG proteins for 18 or 35 hrs. Glycerol concentrations in culture media were measured by ELISA. Student's *t*-test was performed. Data are the means ± S.D. ($n = 3$, $*p < 0.05$). (c) Differentiated 3T3-L1 cells were treated with 20 nM SHBG proteins or 10 µM isoproterenol for 1 or 18 hrs. Intracellular cAMP concentrations were measured. Student's *t*-test was performed. Data are the means ± S.D. (SHBG 0 and 20 nM: $n = 4$). (d) Differentiated 3T3-L1 cells were treated with 20 nM SHBG proteins for 3 days. Protein levels of CEBPα and ATGL were evaluated by Western blotting. Each band was quantified using ImageJ. Relative intensities normalized by β-actin are shown. Data are means ± S.D. ($n = 3$, $*p < 0.05$).

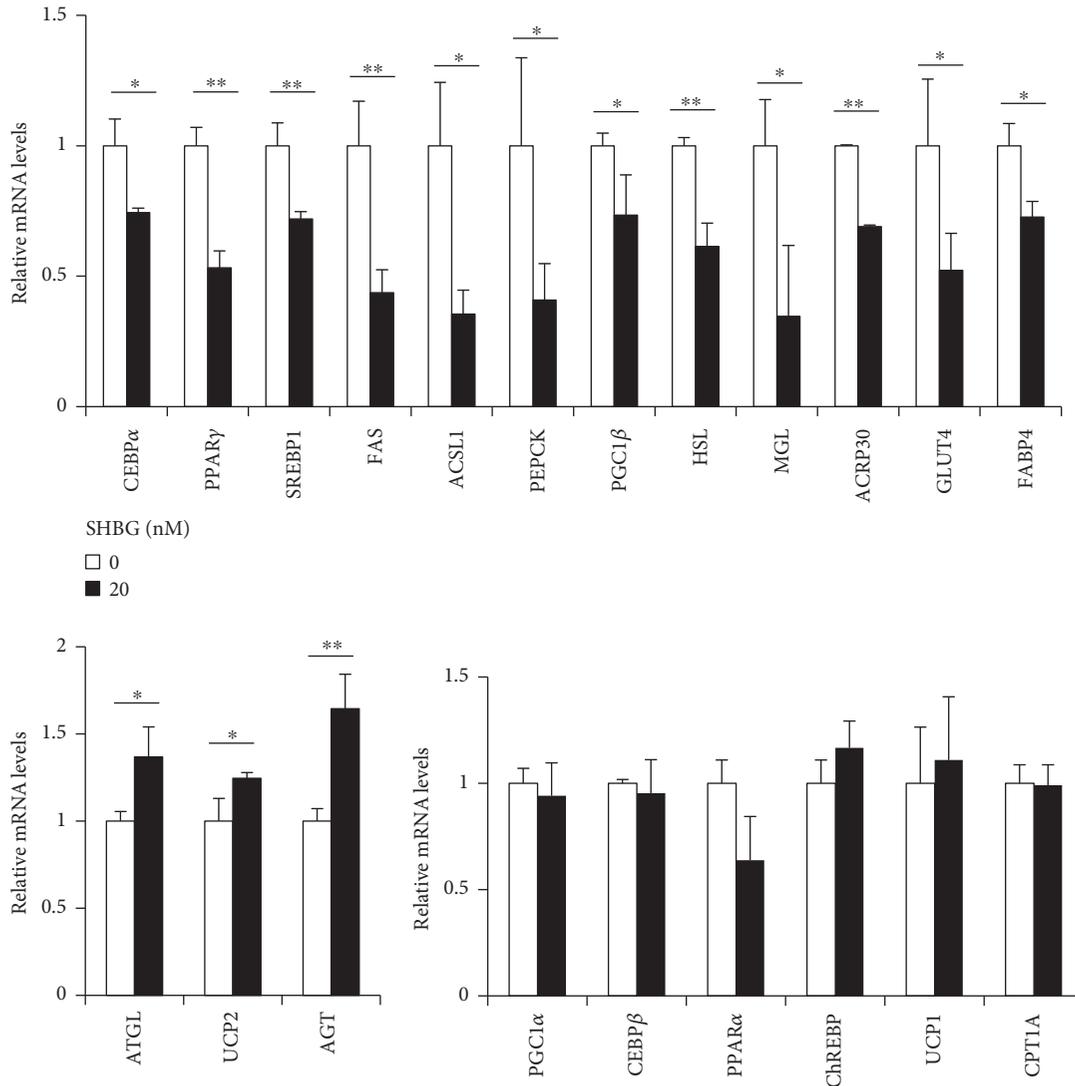


FIGURE 4: SHBG alters some of the mRNA levels related to lipid metabolism in differentiated 3T3-L1 cells. Differentiated 3T3-L1 cells were treated with 20 nM SHBG proteins for 18 hrs. mRNA levels were measured by RT-PCR. Relative levels normalized by the 36B4 level are shown. Student's *t*-test was performed. Data are the means \pm S.D. ($n = 3$, * $p < 0.05$, ** $p < 0.01$).

using a coculture system yielded results supporting the anti-inflammatory effects of SHBG.

It should be noted that the SHBG concentration used in this study is physiological. The median serum SHBG concentration is 20.8 nM in young adult men, increasing to 44.5 nM with aging [47]. Women have serum SHBG concentrations several times higher than those in men, reaching approximately 100 nM [47, 48]. Thus, the 20 nM mainly used in our experiments is the approximate normal lower limit. Thus, it may be reasonable to regard SHBG as contributing to protection from metabolic syndrome accompanying inflammation and obesity.

Assuming the presence of a specific receptor for SHBG, signal transduction from the SHBG receptor reportedly suppresses the phosphorylations of JNK and ERK, possibly inhibiting the activation of transcriptional factors such as AP-1 [49, 50]. AP-1 regulates MCP-1, a key chemokine for monocyte/macrophage migration and infiltration [51].

Lipolytic actions of SHBG were observed to be accompanied by changes in various mRNA and protein levels. Key transcription factors such as CEBP α , PPAR γ , and SREBP1 controlling adipogenesis and lipogenesis were suppressed by SHBG. SHBG might influence the metabolic processes in adipocytes by modulating nutrient usage or hormonal cascades including growth factor signaling. There are many other documented mechanisms of action of SHBG. The increased intracellular cAMP levels in several cells [14, 16, 17] suggest the involvement of G protein and adenylate cyclase, though neither of these responses was observed in our present experiments. SHBG protein itself might not exert activity inducing signaling cascades. For example, SHBG reportedly competes with osteocalcin-induced signaling by binding to GPRC6A [52]. Such chronic and low-grade inhibition or modulation of other protein receptor-mediated processes might be important. Although SHBG is certainly a trace protein in serum, the local concentrations in tissues can be high,

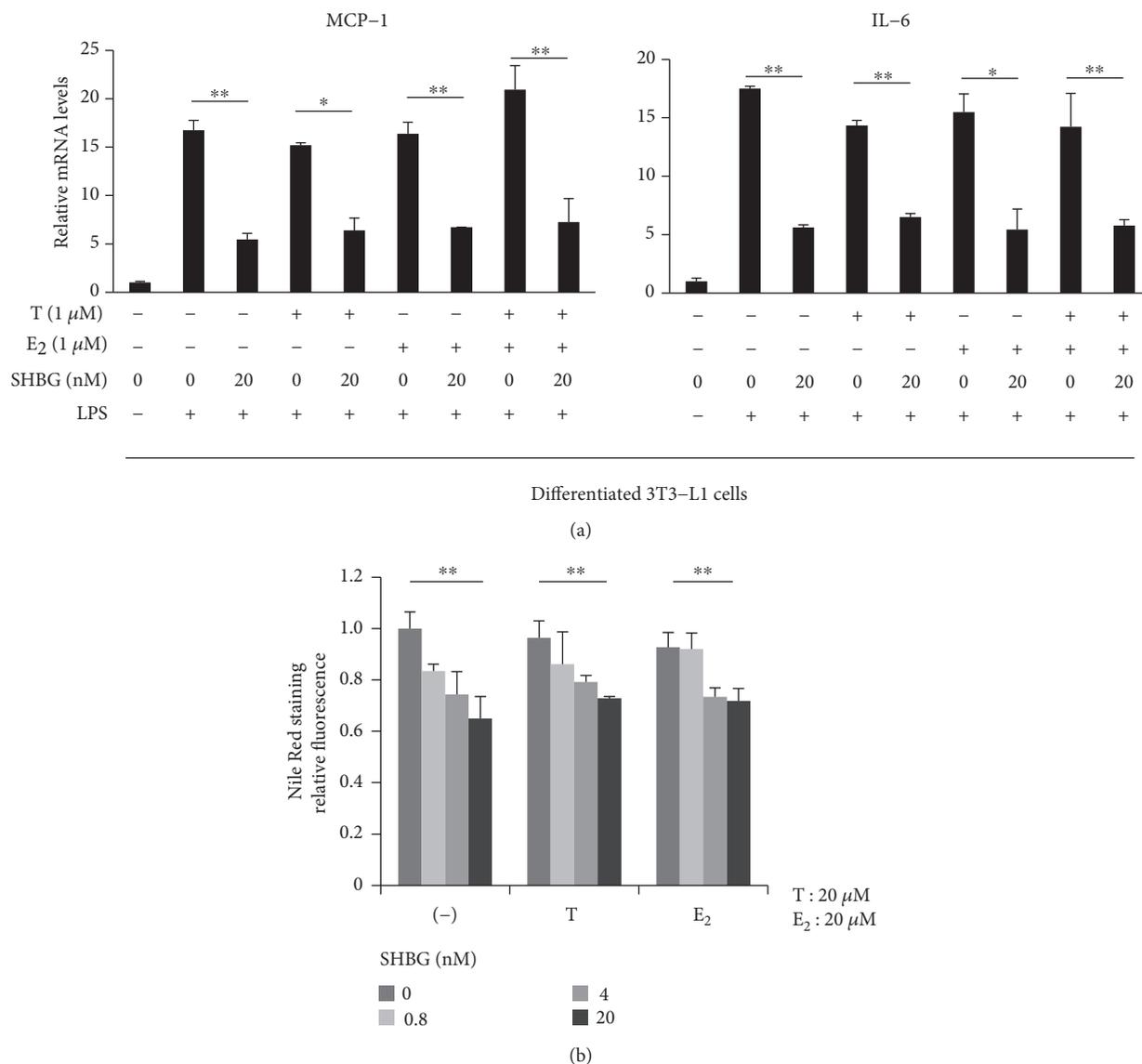


FIGURE 5: Coincubation with testosterone or 17 β -estradiol did not affect the function of SHBG. (a) Differentiated 3T3-L1 cells were treated with SHBG protein in the presence or absence of 1 μ M testosterone (T) or 17 β -estradiol (E₂) overnight, followed by stimulation with 1 ng/ml LPS for 12 hrs. mRNA levels of MCP-1 and IL-6 were measured by RT-PCR. Student’s *t*-test was performed. Mean \pm S.D. (*n* = 3, **p* < 0.05, ***p* < 0.01). (b) Differentiated 3T3-L1 cells were treated with SHBG protein at concentrations ranging from 0–20 nM in serum-free media containing 20 μ M of testosterone (T) or 17 β -estradiol (E₂). Three days later, Nile Red staining was performed and fluorescence was quantified. The Jonckheere test was performed. Mean \pm S.D. (*n* = 4, ***p* < 0.01).

considering the finding that the fibulin family sequesters SHBG and possibly controls access of some molecules to target cells [53, 54]. Furthermore, the internalization of SHBG and actions within cells, reportedly enhancing or inhibiting sex hormone actions [15, 18, 19], might be physiologically meaningful. The modes of SHBG action might differ depending on the targeted cell or phenotype, although the relevant SHBG receptor(s) has not yet been identified. Further investigations are necessary to unravel these mechanisms.

SHBG exists as a complex with sex hormones to some degree in sera. In human sera, the proportion of unbound SHBG to total SHBG is 50% in men and 80% in women [55]. Considering the reported association constants [24], the coincubations with an excess of testosterone or 17 β -

estradiol in our experiments were postulated to have saturated the binding sites of SHBG proteins. One limitation of this study is that we could not determine precisely the proportions of SHBG protein coupled and uncoupled with sex steroids when excess amounts of sex hormones were added. However, considering that very small amounts of sex steroids were present as contaminants of Abcam’s SHBG protein and that the addition of excess amounts of sex steroids did not affect the actions of SHBG, it is reasonable to regard SHBG as exerting anti-inflammatory and lipolytic actions regardless of whether or not it is coupled with sex hormones.

It is possible that the actions of SHBG observed herein might be modified by residual steroids in cells, which had

proliferated in serum-containing media before the experiments. Sex hormones exert effects on certain cell types via SHBG and the putative SHBG receptor complex, as previously reported [56, 57].

In rodents, the *Shbg* gene is not expressed in the liver postnatally. The role of SHBG in rodents might be limited during the fetal period. However, our findings suggest that human SHBG protein exerts activity on adipocytes and macrophages derived from mice. These findings are concordant with the report that human SHBG-Tg mice with the db/db background are resistant to the development of obesity [11]. Effects of human SHBG protein on human adipocytes or macrophages warrant further examinations.

SHBG concentration changes have previously been considered to result from metabolic abnormalities including inflammation [58] and hepatic lipogenesis [59]. Thus, SHBG may be regarded as a good biomarker for metabolic syndrome. However, our results also raise the possibility that SHBG suppresses chronic inflammation, in good agreement with several previous studies employing SHBG transgenic mice, and also exerts direct effects on numerous cell types, as mentioned in the Introduction.

5. Conclusions

In conclusion, at a physiological concentration, SHBG suppresses inflammation and lipid accumulation in macrophages and adipocytes, which may be among the mechanisms underlying the protective effect of SHBG which acts to suppress the development of metabolic syndrome.

Conflicts of Interest

The authors have no conflicts of interest to declare regarding the publication of this paper.

Acknowledgments

The authors thank Natsuko Horikawa-Shirai, Kiyoko Shimazaki, Masako Fujita, and Yuriko Muta-Fukuda for their technical assistance. This study was supported by the Institute for Adult Diseases Asahi Life Foundation grant for medical research and JSPS KAKENHI (Grant no. JP17K16158).

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Research Article

GLP-1 Analogue Liraglutide Enhances SP-A Expression in LPS-Induced Acute Lung Injury through the TTF-1 Signaling Pathway

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Received 16 December 2017; Revised 1 March 2018; Accepted 28 March 2018; Published 22 May 2018

Academic Editor: Joilson O. Martins

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The reduction of pulmonary surfactant (PS) is essential for decreased pulmonary compliance and edema in acute lung injury (ALI). Thyroid transcription factor-1 (TTF-1) plays a major role in the regulation of surfactant protein-A (SP-A), the most abundant protein component of PS. Simultaneously, the glucagon-like peptide-1 (GLP-1) analogue can enhance SP-A expression in the lung. However, the underlying mechanism is still unknown. The purpose of this study was to explore whether liraglutide, a GLP-1 analogue, upregulates SP-A expression through the TTF-1 signaling pathway in ALI. In vivo, a murine model of ALI was induced by lipopolysaccharide (LPS). Pulmonary inflammation, edema, insulin level, ultrastructural changes in type II alveolar epithelial (ATII) cells, and SP-A and TTF-1 expression were analyzed. In vitro, rat ATII cells were obtained. SP-A and TTF-1 expression in cells was measured. ShRNA-TTF-1 transfection was performed to knock down TTF-1 expression. Our data showed that LPS-induced lung injury and increase in insulin level, and LPS-induced reduction of SP-A and TTF-1 expression in both the lung and cells, were significantly compromised by liraglutide. Furthermore, we also found that these effects of liraglutide were markedly blunted by shRNA-TTF-1. Taken together, our findings suggest that liraglutide enhances SP-A expression in ATII cells and attenuates pulmonary inflammation in LPS-induced ALI, most likely through the TTF-1 signaling pathway.

1. Introduction

Pulmonary surfactant (PS), a complex of various lipids and proteins lining the alveolar surface, is synthesized by type II

alveolar epithelial (ATII) cells [1, 2]. Its principle function is to maintain pulmonary compliance and pulmonary fluid balance, to prevent the lung from collapsing at the end of expiration, and to regulate the size of alveoli [1, 2].

Meanwhile, PS also plays a role in pulmonary immune defenses [3].

Acute lung injury (ALI)/acute respiratory distress syndrome (ARDS) is one of most common fatal diseases with an extremely high morbidity rate in critically ill patients [4]. Alveolar epithelial and endothelial cells are the major injury targets of ALI/ARDS [5, 6]. It is well known that reduction of PS is essential for decreased pulmonary compliance and pulmonary edema in ALI/ARDS [7, 8]. Surfactant protein-A (SP-A), a hydrophilic collectin, is the most abundant protein component of PS [9]. The main function of SP-A is to facilitate tubular myelin formation; however, it also plays an active role in defense against pathogens and immunological regulation in the lung [3, 9–11]. Simultaneously, several studies have shown that thyroid transcription factor-1 (TTF-1), also known as Nkx2.1, contributed substantially to the regulation of SP-A expression in ATII cells [12–14]. Chen et al. found that hypoxia-induced reduction of SP-A expression was attenuated by leptin through promoting TTF-1 translation in rat ATII cells [13].

Glucagon like peptide-1 (GLP-1), a peptide hormone synthesized and secreted by the L-cells in guts, is essential for glycometabolism and lipid metabolism. Recently, the GLP-1 receptor (GLP-1R), a transmembrane G-protein coupled receptor, has been found in a variety of tissues outside of the pancreas, such as the lung, heart, blood vessels, and kidney [15–17]. Viby et al. showed that GLP-1R was widely expressed in the airway and alveolar epithelium, in both mice and humans [16]. Romani-Pérez et al. reported that liraglutide, a GLP-1 analogue, upregulated SP-A expression in the fetal lung and promoted lung development in newborn rats [17]. However, the underlying mechanism remains unclear. In addition, some studies also confirmed that GLP-1 possessed a potent anti-inflammatory property in different inflammatory conditions [15, 18–20]. Our recent study also showed that ovalbumin- (OVA-) induced airway inflammation and mucus hypersecretion were significantly suppressed by liraglutide in a murine model of asthma [15].

Therefore, the purpose of the current study was to explore whether GLP-1 analogue liraglutide upregulates SP-A expression in ATII cells and attenuates inflammation in LPS-induced ALI and to elucidate its underlying mechanism.

2. Methods and Materials

2.1. Animals. All procedures involving animals were approved by the Animal Experimental Ethics Committee of West China Medical School of Sichuan University. The current study was performed according to the recommendations in the Guide for the Care and Use of Laboratory Animals. All surgeries were performed using sodium pentobarbital anesthesia, and all efforts were made to minimize suffering. Six-eight-week-old male BALB/c mice (18–22 g) and male Sprague-Dawley (SD) rats (200–220 g) were maintained under specific pathogen-free conditions in the animal center facilities of our University. The mice and rats were kept in a temperature-controlled room (12 h dark/light cycles) and offered ad libitum access to food and water.

Animals underwent an acclimatization period of at least 1 week before study.

2.2. Knockdown of TTF-1 by shRNA in Mice. To silence the expression of TTF-1 in the lung, a recombinant lentiviral vector for TTF-1 (shRNA-TTF-1, sc-36757-V, Santa Cruz Biotechnology, CA, USA) was used. Lentivirus-expressing nontargeting sequences (sc-108080; Santa Cruz Biotechnology, CA, USA) were used as the negative control (shRNA-scramble). In brief, thirty male BALB/c mice were divided into 3 groups—control, shRNA-scramble, and shRNA-TTF-1 groups—with 10 mice in each group. After anesthesia, shRNA-TTF-1 lentiviral vector (40 μ L) for the shRNA-TTF-1 group or negative control lentivirus (40 μ L) for the shRNA-scramble group was given by intratracheal injection. The mice in the control group were then administered sterile saline. Three days after transfection, the left lower lung was resected. Histology changes were observed by HE staining. The efficiency of shRNA transfection was measured by qPCR and Western blot analysis.

2.3. Murine Model of LPS-Induced ALI. Fifty male BALB/c mice were randomly and evenly divided into 5 groups: control, liraglutide (Lira), LPS, LPS+Lira, and LPS+Lira+shRNA-TTF-1 groups, with 10 mice in each group. ALI was induced by intratracheal injection of LPS (*Escherichia coli*; serotype O111:B4; Sigma-Aldrich, St. Louis, MO, USA) [6, 21]. In brief, mice were anesthetized with 30 mg/kg of pentobarbital sodium, followed by intratracheal injection of 10 μ g of LPS in 50 μ L sterile saline with a 3-gauge needle. ShRNA-TTF-1 (40 μ L) was also given by intratracheal injection 3 days before LPS stimulation. The mice in the control group were administered sterile saline instead. According to our previous studies, liraglutide (2 mg/kg in 200 μ L sterile saline, Novo Nordisk A/S, Novo Alle, DK-2880 Bagsvaerd, Denmark) was given by intraperitoneal injection, 20 min after LPS injection [15, 22]. In 3 days, liraglutide was given every 12 h (7 times in total).

2.4. Bronchoalveolar Lavage Fluid (BALF) and Cell Counting. Seventy-two hours later, mice were sacrificed under anesthesia by pentobarbital (50 mg/kg i.p.). BALF was collected by cannulating the upper part of the trachea, by lavage 3 times with 1.0 mL phosphate-buffered saline (pH 7.2) [23]. The fluid recovery rate was about 90%. The sediment cells were stained with Diff-Quik (International Reagents Corp., Japan) for cytospin preparations. The number of total cells, neutrophils, macrophages, and lymphocytes was then counted double-blindly with a hemocytometer.

2.5. TNF- α , IL-6, and IL-1 β in BALF. As described before, the BALF supernatant was collected and stored at -80°C before performing the cytokine assay [6, 21]. TNF- α , IL-6, and IL-1 β expression levels in BALF were measured by ELISA (R&D Systems, USA).

2.6. Myeloperoxidase (MPO) Activity Assay. Seventy-two hours after LPS injection, mice were sacrificed and their lungs were collected. According to our previous studies,

MPO activity was detected. Results are expressed as units of MPO activity per gram of lung tissue [6, 21].

2.7. Lung Wet/Dry Weight Ratio. Seventy-two hours after LPS injection, mice were sacrificed and their lungs were collected. The severity of pulmonary edema was assessed by the wet-to-dry ratio (W/D) [6, 21]. The left lower lung was weighed and then dehydrated at 60°C for 72 h in an oven.

2.8. H&E Staining and Lung Injury Score. Seventy-two hours after LPS injection, mice were sacrificed and their lungs were collected. The right lower lung of each mouse was fixed in 10% formalin, embedded in paraffin, cut into 5 μ m sections, and stained with H&E to observe the pathological alterations in the lung tissues. According to our previous studies, the lung injury score was measured by a blinded pathologist with a 0- to 4-point scale according to combined assessments of inflammatory cell infiltration in the airspace or vessel wall, alveolar congestion, hemorrhage, alveolar wall thickness, and hyaline membrane formation [6, 21]. Five microscope fields from each histological section were taken and scored. The final score of each sample was the average of 5 scores. Briefly, a score of 0 represented no damage, 1 represented mild damage, 2 represented moderate damage, 3 represented severe damage, and 4 represented very severe histological changes.

2.9. Immunohistochemistry. Seventy-two hours after LPS injection, mice were sacrificed and their lungs were collected. SP-A expression in the lung was determined by immunohistochemistry. Briefly, tissue sections (right lower lung) were deparaffinated and rehydrated. Samples were treated with Target Retrieval (Dako, Glostrup, Denmark) at 95°C, blocked at room temperature with Protein Block Serum-Free (Dako, Glostrup, Denmark), and incubated with anti-SP-A antibody (1:400; sc-7699, Santa Cruz Biotechnology, Santa Cruz, CA, USA). After washing, sections were incubated with biotin-conjugated anti-rabbit immunoglobulin G (IgG) for 30 min at room temperature. The biotinylated reagents were detected with ABC complex HRP (Dako, Glostrup, Denmark).

2.10. Transmission Electron Microscopy (TEM). Seventy-two hours after LPS injection, mice were sacrificed and their lungs were collected. TEM was performed to observe the ultrastructural changes in pulmonary epithelial cells and to identify rat ATII cells [21, 24]. Lamellar bodies, the principal storage site of pulmonary surfactant, are the specific organelle and the feature of ATII cells. In brief, the fresh left upper lung tissues and isolated cells were obtained for observation. Images were taken with an electron microscope (H-600IV, Hitachi, Tokyo, Japan).

2.11. Fasting Serum Insulin. Blood was taken from the tail vein without anesthesia, 72 h after LPS injection and 6 h after the last feeding, before sacrifice. The procedure was done in the afternoon. According to the instructions of the manufacturer, the fasting serum insulin level was analyzed using an ELISA kit (ALPCO Diagnostics).

2.12. Rat ATII Cell Isolation and Characterization. Rat ATII cells were isolated from male pathogen-free SD rats (200–220 g) as described previously [25]. In brief, the lungs were perfused via the pulmonary artery to remove the blood. The lung was digested with intratracheally instilled 3 U/mL elastase (Sangon Biotech, Shanghai, China) three times at 37°C for 40 minutes. Due to Fc γ receptors (Fc γ R), the receptor of IgG, only expressed on non-ATII cells in the lung, rat IgG can be used to remove non-ATII cells in the lung. In our study, ATII cells were purified by differential adhesion to IgG-pretreated dishes (Boster Biological Technology, Wuhan, China). More than 95% of the cells obtained were viable, which was assessed by trypan blue exclusion assay. Cells were resuspended in DMEM supplemented with FBS (10%), penicillin (100 U/mL), and streptomycin (100 μ g/mL). Cells were then used in experiments after a 24 h culture period. TEM was used to identify the ATII cells, as mentioned above.

2.13. Cell Transfection with shRNA. According to our previous study, ATII cells were transfected at 70% confluence with shRNA-TTF-1 (336312, Qiagen, Valencia, CA) or shRNA-scrambled (sc-108060, Santa Cruz Biotechnology, CA, USA) [26]. Twenty-four hours after transfection, ATII cells were used for further experiments. Meanwhile, total and nuclear proteins and mRNA were extracted from cells and kept at –80°C for qPCR and Western blot. Then, knockdown of TTF-1 expression was analyzed by qPCR and Western blot. β -Actin was used as an internal control.

2.14. Cell Intervention. ShRNA-TTF-1-transfected and non-transfected ATII cells were pretreated with liraglutide (100 nM) for 4 h and then stimulated with LPS (100 ng/mL) for 4 h [21, 26, 27]. Then, total and nuclear proteins and mRNA were extracted from cells and kept at –80°C for qPCR and Western blot. MTT assay (Promega, Madison, WI) was used to assess cell viability at 0 h and 4 h after interventions.

2.15. Quantitative PCR. The mRNA expression of SP-A and TTF-1 was detected by qPCR [15, 22]. β -Actin was used as an internal reference. Briefly, mice were sacrificed and their lungs were collected. The right upper lung tissues were kept at –80°C. Then, total RNA of lung tissues and rat ATII cells were isolated by TRIzol reagent. PrimeScript[®] RT reagent kit with gDNA eraser (Takara Bio Inc., Otsu, Japan) was used for reverse transcription. PCR was then performed with iQ[™]5 Multicolor Real-Time PCR Detection System (Bio-Rad Laboratories Inc., USA) and a SYBR Green PCR kit (Takara Bio Inc., Otsu, Japan) in a final volume of 20 μ L, containing 1.6 μ L cDNA template, forward and backward primers (0.8 μ L each), 10 μ L SYBR[®] Premix Ex Taq[™] II, and 6.8 μ L dH₂O. The primers and TaqMan probes were designed using Primer Premier (PREMIER Biosoft International, Canada). The premier sequences were as follows. mTTF-1: (forward) 5'-AACAGC GGCCATGCAG CAGC AC-3' and (reverse) 5'-CCATG TTCTTGC TCACGTCC-3'; mSP-A: (forward) 5'-TCGGA GGCAGACA TCCACA-3' and (reverse) 5'-GCCAGCA ACAACAGTC AAGAAG AG-3'; m β -actin: (forward) 5'-GATTA CTGCTCTGG CT CCTAGC-3' and (reverse) 5'-ACTCAT CGTACTCC TGC

TTGCT-3'; rTTF-1: (forward) 5'-AAATT TGGGGGT CT TTCTGG-3' and (reverse) 5'-AGAGT GCATCCA CAGG GAAG-3'; rSP-A: (forward) 5'-AGCCTG CAGGTCTG TATGTGGA-3' and (reverse) 5'-TTGCAC TTGATACCA GCGACAAC-3'; and r β -actin: (forward) 5'-ATCATGTT TGAGACCT TCAACA-3' and (reverse) 5'-CATCTC TT GCTCGA AGTCCA-3'. Changes in the expression of target genes were calculated using the $2^{-\Delta\Delta Ct}$ method, $\Delta\Delta Ct = (Ct_{\text{target}} - Ct_{\beta\text{-actin}})_{\text{sample}} - (Ct_{\text{target}} - Ct_{\beta\text{-actin}})_{\text{control}}$.

2.16. Western Blot. Western blot was performed to evaluate the protein expression [21, 28]. Briefly, 72 hours after LPS injection, mice were sacrificed and their lungs were collected. The lung tissues were kept at -80°C . Protein lysates from the left upper lung tissues and rat ATII cells were subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis and then transferred to nitrocellulose membranes. Antibodies against mSP-A, mTTF-1, rSP-A, rTTF-1, m β -actin, and r β -actin were purchased from Santa Cruz Biotechnology (Santa Cruz, CA, USA). The relative protein levels of mSP-A, rSP-A, mTTF-1, and rTTF-1 were normalized to that of β -actin.

2.17. Statistical Analysis. Statistical analyses were performed with SPSS software, version 17.0 (SPSS Inc., Chicago, IL, USA). All data were presented as mean \pm standard error of mean (SEM). One-way analysis of variance (ANOVA) with Student-Newman-Keuls (SNK) test was performed. $P < 0.05$ was considered to be statistically significant.

3. Results

3.1. TTF-1 Expression Was Inhibited after Transfection of the Lung with shRNA-TTF-1. After 3 days of transfection, no pathological alterations were observed in the control, shRNA-scrambled, shRNA-TTF-1 groups (Figure 1(a)). However, TTF-1 expression was largely inhibited by shRNA-TTF-1 in the lung (Figures 1(b) and 1(c)).

3.2. Liraglutide Attenuated Pulmonary Inflammation and Pulmonary Edema in LPS-Induced ALI. After 72 h of LPS injection, severe and typical pulmonary pathological alterations were observed, including severe and extensive inflammatory cell infiltration, interstitial and intra-alveolar edema and patchy hemorrhage, interalveolar septal thickening, and hyaline membrane formation with some alveoli collapsed (Figure 2(a)). As shown in Figure 2(c), the W/D ratio was significantly increased after 72 h of LPS injection. Figure 2(d) demonstrates that MPO activity was significantly enhanced by LPS injection. However, LPS-induced lung injury, W/D ratio, and MPO activity were all notably suppressed by liraglutide (Figure 2). Furthermore, these effects of liraglutide were substantially blunted by shRNA-TTF-1. No pathological changes were observed in the control and Lira groups (Figure 2(a)).

3.3. Liraglutide Reduced Inflammatory Cell Counts and Inflammatory Mediators in BALF. As shown in Figure 3,

the number of total cells, neutrophils, and macrophages and the levels of TNF- α , IL-6, and IL-1 β in BALF were notably increased after 72 h of LPS injection. Meanwhile, our data also demonstrated that the increase in the number of total cells, neutrophils, and macrophages and increased levels of TNF- α , IL-6, and IL-1 β in BALF, induced by LPS, were remarkably reduced by liraglutide. These effects of liraglutide were substantially blocked by shRNA-TTF-1. No difference in the number of lymphocytes in BALF was found among all groups (Figure 3(a)).

3.4. Liraglutide Alleviated Pathological Alterations in ATII Cell Ultrastructure in LPS-Induced ALI. After 72 h of LPS injection, significant ultrastructural pathological alterations were observed in ATII cells. These features included cell swelling with a cytoplasm of low electronic density, unclear cell structure, mitochondrial edema with dilated mitochondrial cristae, chromatin margination, and reduced and indistinct cell surface microvilli, along with decreased and vacuolated lamellar bodies (Figure 4). Meanwhile, as shown in Figure 4, these ultrastructural alterations were alleviated by liraglutide. However, shRNA-TTF-1 notably abolished this effect of liraglutide. No ultrastructural pathological change was observed in the control and Lira groups.

3.5. Liraglutide Enhanced SP-A Expression by Increasing TTF-1 in LPS-Induced ALI. As shown in Figures 5(b) and 5(c), the expression of SP-A was substantially decreased after 72 h of LPS injection, and liraglutide significantly enhanced SP-A expression in the lung after LPS injection. In addition, SP-A expression in the ATII cells was reduced after LPS administration (Figure 5(a)). Subsequently, as shown in Figure 6, LPS-induced suppression of TTF-1 expression was markedly alleviated by liraglutide. Furthermore, our data also demonstrated that these effects of liraglutide were largely abrogated by shRNA-TTF-1.

3.6. Liraglutide Reduced Serum Insulin Level in LPS-Induced ALI. Fasting serum insulin level (72 h after LPS injection, 6 h after last feeding) was measured. Fasting serum insulin level was markedly increased after 72 h of LPS injection. Meanwhile, as shown in Figure 7, the increased level of fasting serum insulin induced by LPS was significantly reduced by liraglutide. This effect of liraglutide was substantially blocked by shRNA-TTF-1. No difference in the level of serum insulin was found among the control, Lira, and shRNA-TTF-1 groups.

3.7. Identification of Rat ATII Cells and Evaluation of Cell Viability. Isolation primary rat ATII cells were confirmed by TEM. Lamellar bodies, the characteristic organelles of ATII cells, were observed in our isolated cells (Figure 8(a)). To evaluate the cell viability of rat ATII cells, MTT assay was performed. As shown in Figure 8(b), no significant difference in cell viability was found between different groups after 4 h of intervention.

3.8. The Expression of TTF-1 Was Inhibited after shRNA-TTF-1 Transfection in Rat ATII Cells. QPCR and Western blot were performed to analyze the mRNA and protein

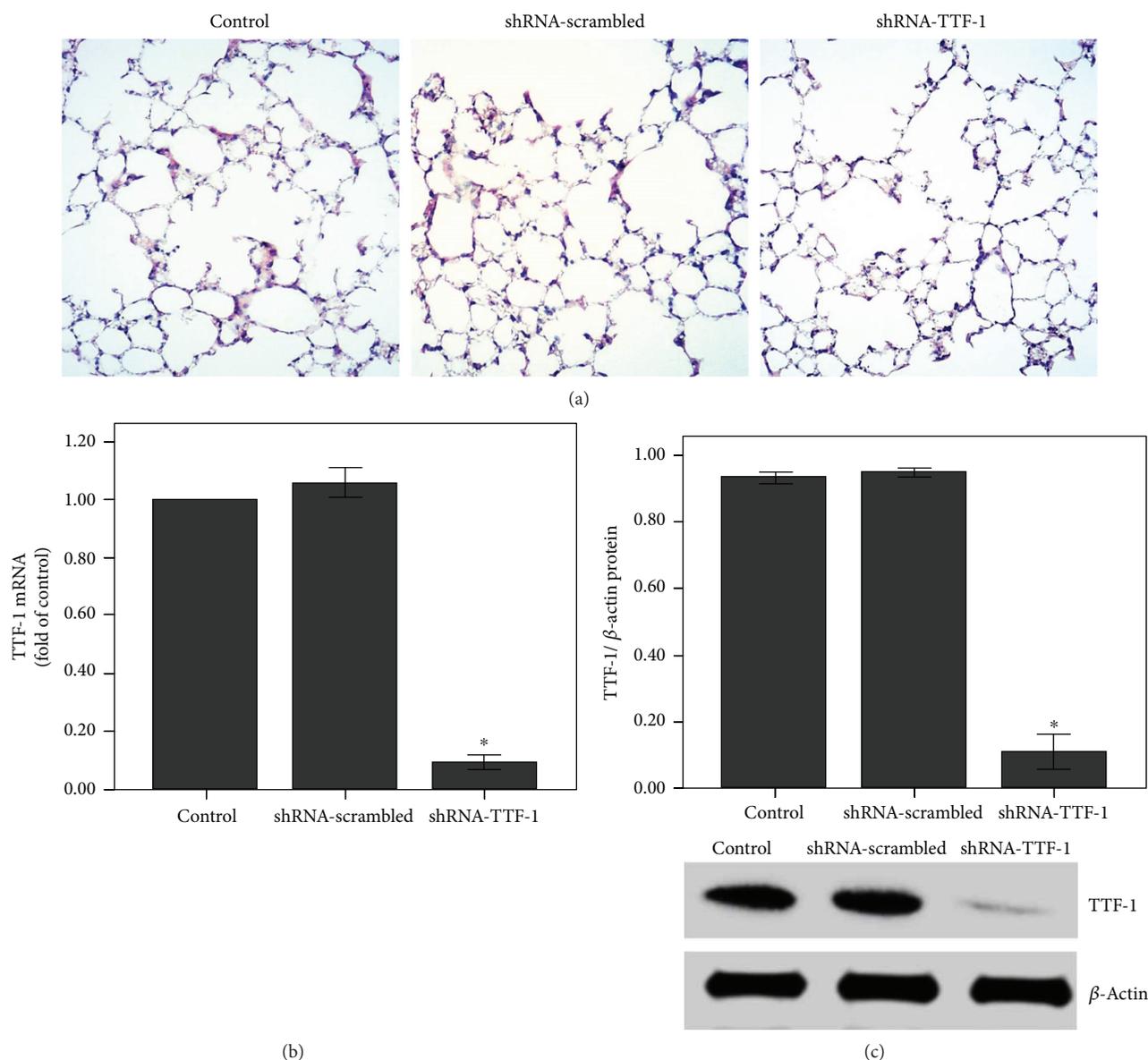


FIGURE 1: The expression of TTF-1 was inhibited after shRNA-TTF-1 transfection in the lung. Mice were transfected with shRNA-TTF-1 or shRNA-scrambled by intratracheal injection. Seventy-two hours after transfection, the expression of TTF-1 was measured. (a) After 72 h of transfection, mice were sacrificed and their right lower lungs were fixed. The tissue sections were then stained with H&E. The figure demonstrates a representative view ($\times 200$) from each group. (b) QPCR was used to analyze the mRNA expression of TTF-1. (c) Western blot was performed to evaluate the protein expression of TTF-1. Each bar represents the mean \pm SEM of 10 mice. * $P < 0.05$ compared with control.

expression of TTF-1 in rat ATII cells. After 24 h of transfection, TTF-1 expression was markedly inhibited by shRNA-TTF-1 in rat ATII cells (Figure 9).

3.9. Liraglutide Promoted SP-A Expression by Increasing TTF-1 in Rat ATII Cells. As shown in Figures 10(a) and 10(b), the expression of SP-A was notably reduced after 4 h of LPS stimulation. Liraglutide remarkably enhanced SP-A expression in ATII cells after LPS stimulation. Subsequently, LPS-induced suppression of TTF-1 expression was also notably abolished by liraglutide in ATII cells (Figures 10(c) and 10(d)). Furthermore, our data also demonstrated that these effects of liraglutide were substantially abrogated by shRNA-TTF-1.

4. Discussion

In the current study, our results showed that LPS-induced pulmonary inflammation, pulmonary edema, increase in insulin level and alveolar cell injuries, and LPS-induced reduction of SP-A expression were markedly compromised by GLP-1 analogue liraglutide both in vivo and in vitro. Furthermore, our data also indicated that this SP-A-enhancing property of liraglutide was most likely mediated via the TTF-1 signaling pathway.

ALI/ARDS, characterized by damage to the alveolar-capillary barrier, is induced by self-amplified and uncontrolled lung inflammation [4]. Although substantial progress has

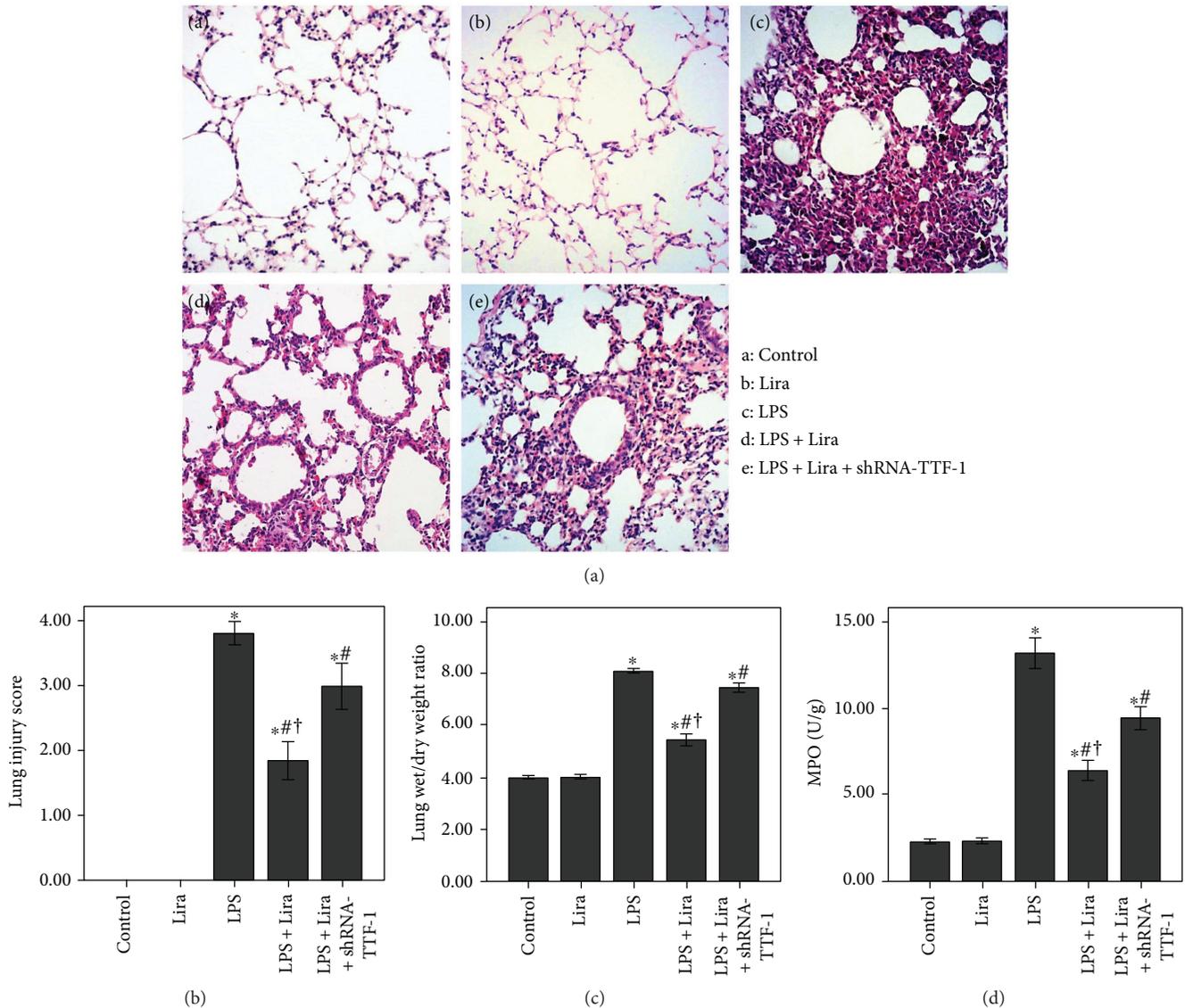


FIGURE 2: Liraglutide attenuated pulmonary inflammation and pulmonary edema in LPS-induced ALI. (a) After 72 h of intervention, mice were sacrificed and their right lower lungs were fixed. The tissue sections were then stained with H&E. The figure demonstrates a representative view ($\times 200$) from each group. (b) Severity of lung injury was measured by the lung injury scoring system. (c) The left lower lungs were obtained to evaluate the W/D ratio of the lung tissues. (d) MPO activity was measured to evaluate the accumulation and activation of neutrophils in the lung tissues. Each bar represents the mean \pm SEM of 10 mice. * $P < 0.05$ compared with control. # $P < 0.05$ compared with LPS. † $P < 0.05$ compared with LPS+Lira+shRNA-TTF-1.

been made in the understanding of ALI/ARDS, effective treatments are still limited in clinical practice.

GLP-1 is mainly synthesized and secreted by intestinal L-cells [18]. GLP-1 analogues, including liraglutide and exenatide, have been successfully used in type 2 diabetes mellitus treatment. Several recent studies have confirmed that GLP-1R is also expressed in many extrapancreatic tissues, including endothelial cells, airway and alveolar epithelial cells, macrophages, gastrointestinal tract, myocardium, and kidney [15–17]. A previous study revealed the protective role of liraglutide in a murine model of obstructive lung disease [16]. Moreover, our previous investigation also showed that OVA-induced airway inflammation and mucus

hypersecretion were markedly inhibited by liraglutide in mice [15]. Meanwhile, our other study demonstrated that bleomycin-induced pulmonary inflammation and fibrosis were notably attenuated by liraglutide in mice [22]. After 72 h of LPS injection, severe and typical pathological changes in the lungs were observed (Figure 2(a)). Our results showed that these typical pathological alterations and enhanced lung injury scores were both significantly improved by liraglutide (Figures 2(a) and 2(b)). Meanwhile, according to previous studies, MPO activity is a marker of accumulation and activation of neutrophils in inflammatory processes [6, 21]. Our findings demonstrated that LPS-induced increase in MPO activity in the lung was largely inhibited by liraglutide

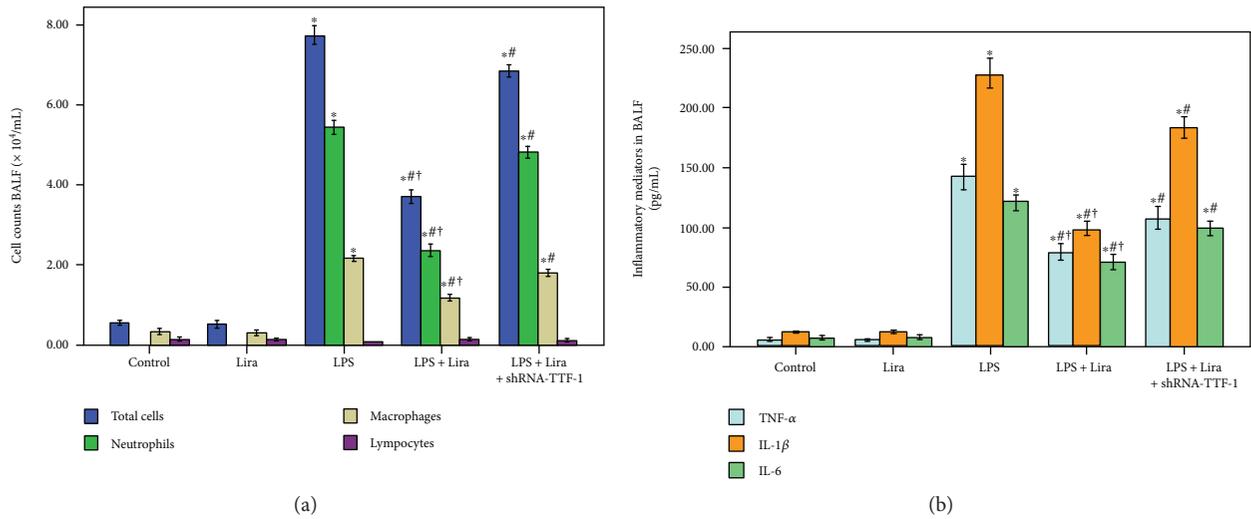


FIGURE 3: Liraglutide reduced inflammatory cell counts and inflammatory mediators in BALF. (a) Cells in BALF were collected, and cytospin preparations were made. The number of total cells, neutrophils, macrophages, and lymphocytes in BALF were assessed. (b) TNF- α , IL-6, and IL-1 β levels in BALF were detected by ELISA. Each bar represents the mean \pm SEM of 10 mice. * $P < 0.05$ compared with control. # $P < 0.05$ compared with LPS. † $P < 0.05$ compared with LPS+Lira+shRNA-TTF-1.

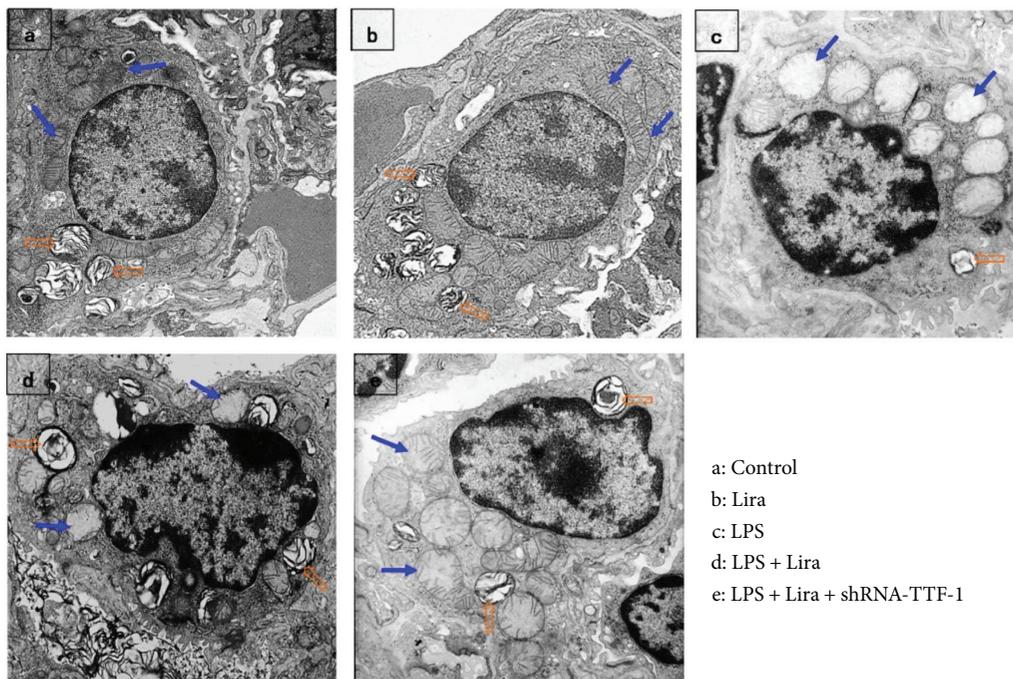


FIGURE 4: Liraglutide alleviated pathological alterations in ATII cell ultrastructure in LPS-induced ALI. After mice were sacrificed, the left upper lung tissues were taken and observed by TEM. The figure demonstrates a representative view ($\times 6000$) from each group. Mitochondrion, blue arrow; lamellar body, orange open arrow.

(Figure 2(d)). At the initial stage of infection-induced acute inflammation, pathogen-associated molecular patterns (PAMPs), including LPS and CpG DNA, are recognized and interacted by inflammatory cells with pattern recognition receptors (PPRs), such as mannose receptor (MR) and toll-like receptors (TLRs) [29, 30]. Following this, a wide range of inflammatory mediators, including TNF- α , IL-6, and IL-1 β , are released [29, 30]. In our study, we found that LPS-

induced increase in the number of total cells, neutrophils, and macrophages and LPS-induced increase in TNF- α , IL-6, and IL-1 β levels in BALF were remarkably compromised by liraglutide (Figure 3). Additionally, noncardiogenic pulmonary edema is another major pathological feature of ARDS, a major cause of the failure of oxygenation [31]. Our data showed that LPS-induced increase in the W/D ratio was markedly reduced by liraglutide (Figure 2(c)).

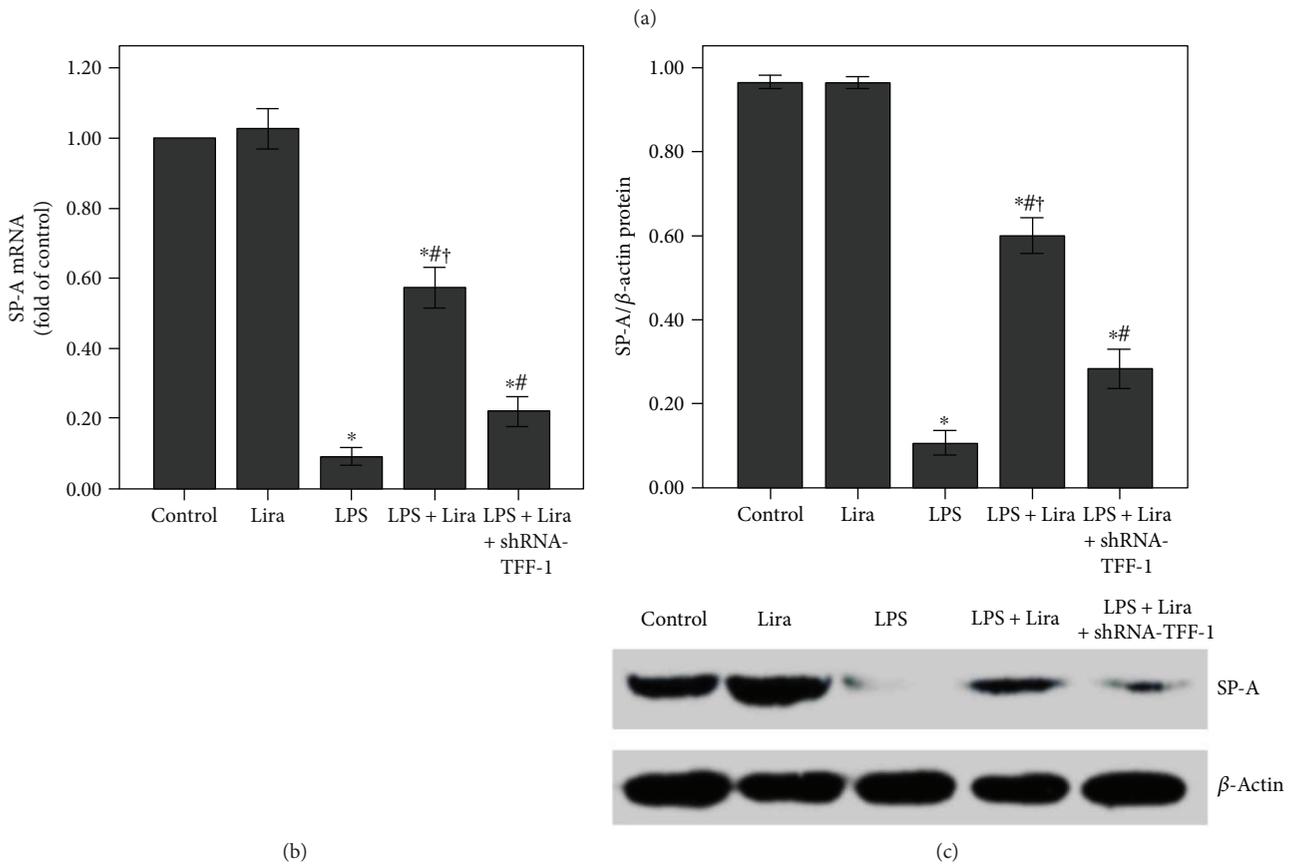
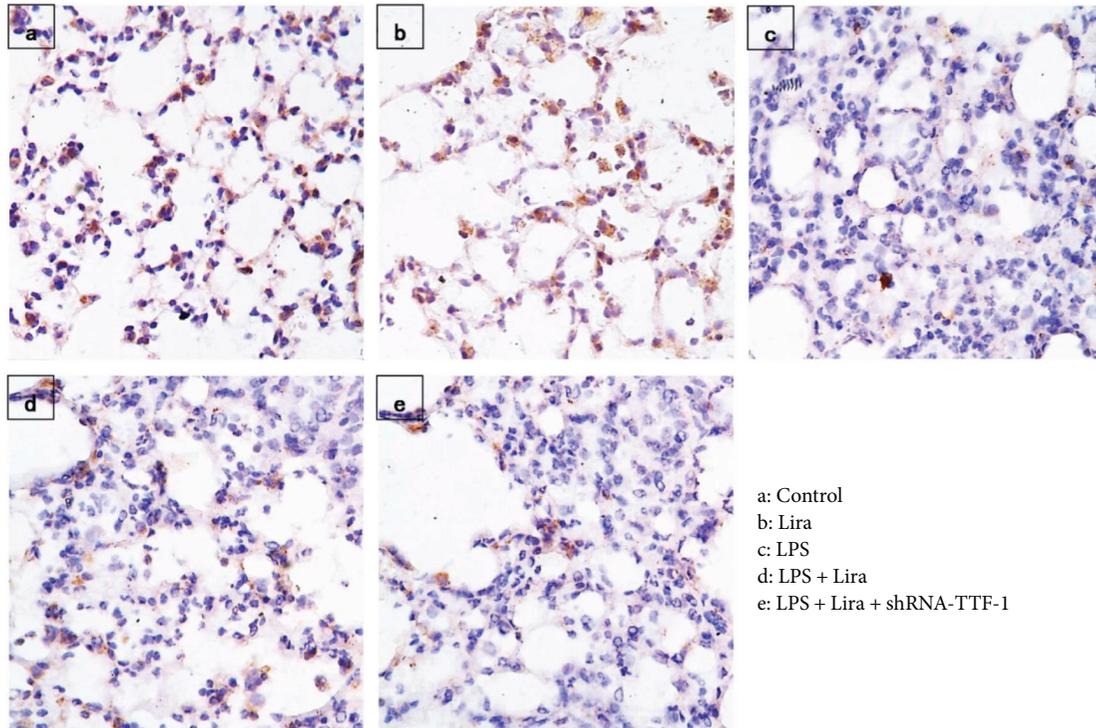


FIGURE 5: Liraglutide enhanced SP-A expression in LPS-induced ALI. (a) After 72 h of interventions, mice were sacrificed and their right lower lungs were fixed. Immunohistochemistry was then performed to observe SP-A expression in the lung. (b) QPCR was used to analyze the mRNA expression of SP-A. (c) Western blot was performed to evaluate the protein expression of SP-A. Each bar represents the mean ± SEM of 10 mice. * $P < 0.05$ compared with control. # $P < 0.05$ compared with LPS. † $P < 0.05$ compared with LPS+ Lira+ shRNA-TTF-1.

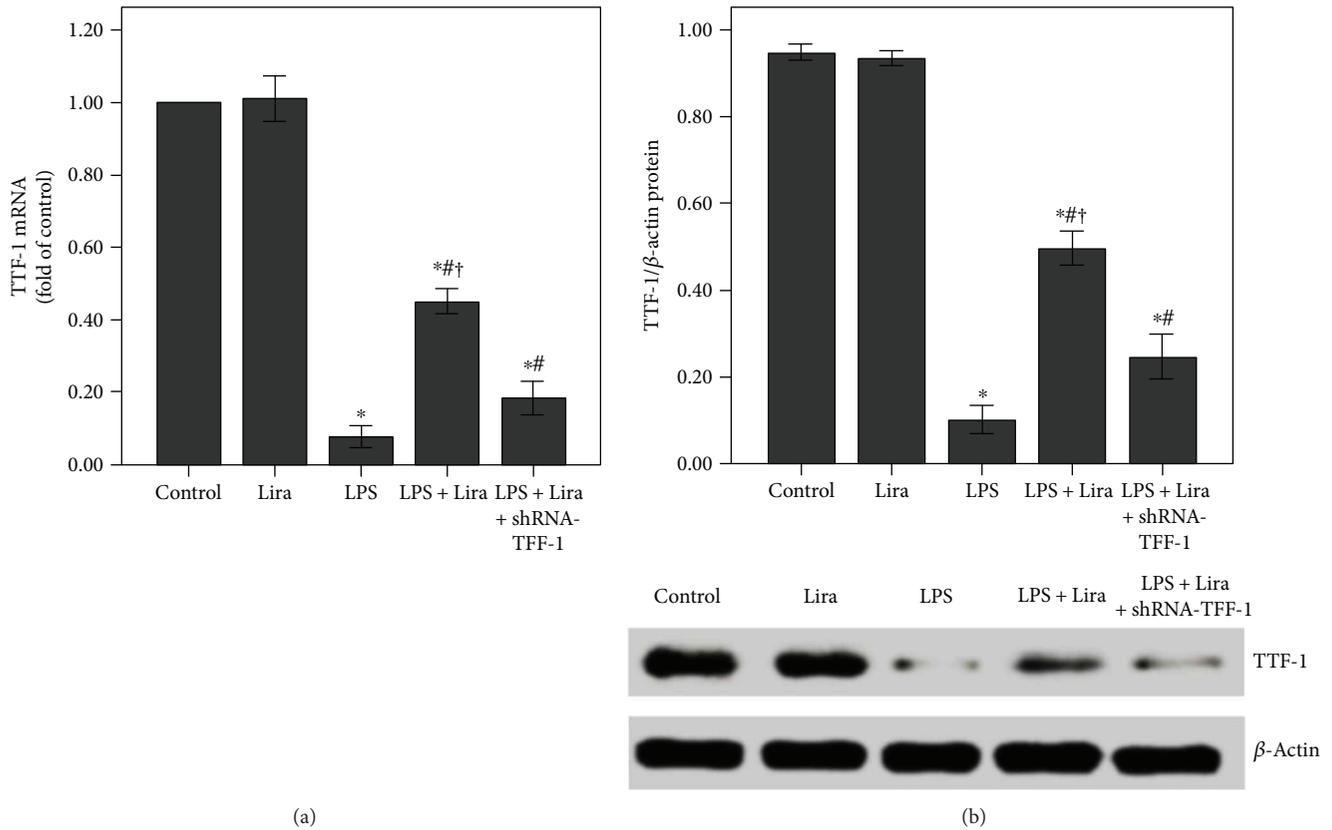


FIGURE 6: Liraglutide increased the expression of TTF-1 in LPS-induced ALI. (a) QPCR was used to analyze the mRNA expression of TTF-1. (b) Western blot was performed to evaluate the protein expression of TTF-1. Each bar represents the mean \pm SEM of 10 mice. * $P < 0.05$ compared with control. # $P < 0.05$ compared with LPS. † $P < 0.05$ compared with LPS+Lira+shRNA-TTF-1.

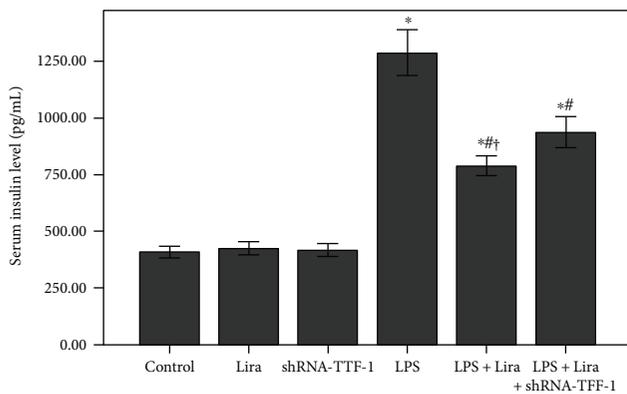


FIGURE 7: Liraglutide reduced the serum insulin level in LPS-induced ALI. Fasting serum insulin level (72 h after LPS injection and 6 h after last feeding) was detected by ELISA. Each bar represents the mean \pm SEM of 10 mice. * $P < 0.05$ compared with control. # $P < 0.05$ compared with LPS. † $P < 0.05$ compared with LPS+Lira+shRNA-TTF-1.

Therefore, these findings indicated that LPS-induced pulmonary inflammation, injury, and edema were substantially attenuated by liraglutide in mice.

GLP-1 is a key regulator of insulin secretion. It has been found that the effect of GLP-1 in promoting pancreatic β cell insulin secretion was dependent on blood glucose

concentration [32]. Fransson et al. showed that liraglutide did not influence serum insulin level in nondisease mice; however, corticosterone-induced hyperinsulinemia was alleviated by liraglutide [33]. It is well known that insulin tolerance is impaired in severe conditions, such as ARDS, severe sepsis, and severe burn. Inflammation plays a critical role in insulin intolerance in these conditions. Landgraf et al. found that LPS-induced insulin tolerance impairment was alleviated by leptin, resulting from its anti-inflammatory effect, in mice [34]. In the current study, our data showed that LPS-increased fasting serum insulin was suppressed by liraglutide (Figure 7). Our data also demonstrated that fasting serum insulin level was not influenced by liraglutide in nondisease mice. This result indicates that LPS-increased insulin level was remarkably suppressed by liraglutide in mice, possibly stemming from its anti-inflammatory effect.

PS is a complex of various lipids (90%) and proteins (10%), mainly synthesized by ATI cells [35, 36]. PS is responsible for increasing pulmonary compliance, preventing the lung from collapsing at the end of expiration, maintaining fluid balance in the lung, regulating the size of alveoli, and modulating the lung's innate immune system [3, 35, 36]. Lamellar bodies, the main sites for the synthesis and metabolism of surfactants, are the specialized organelles of ATI cells [1, 36]. Simultaneously, it is well known that mitochondria, the powerhouse of the cell, is the most sensitive and vulnerable organelle, responding to injury and

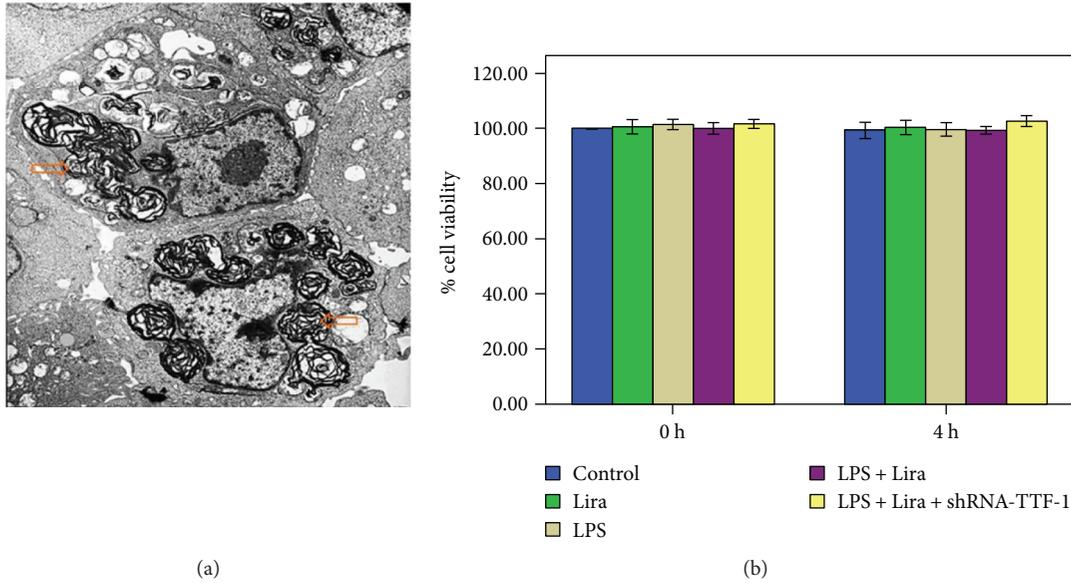


FIGURE 8: Identification of rat ATII cells and evaluation of cell viability. (a) Isolated and cultivated rat ATII cells were identified by TEM. The figure demonstrates a representative view ($\times 6000$). Lamellar body, orange open arrow. (b) MTT assay was performed to evaluate rat ATII cell viabilities. Quantitative data were presented as mean \pm SEM ($n = 5$). * $P < 0.05$ compared with control.

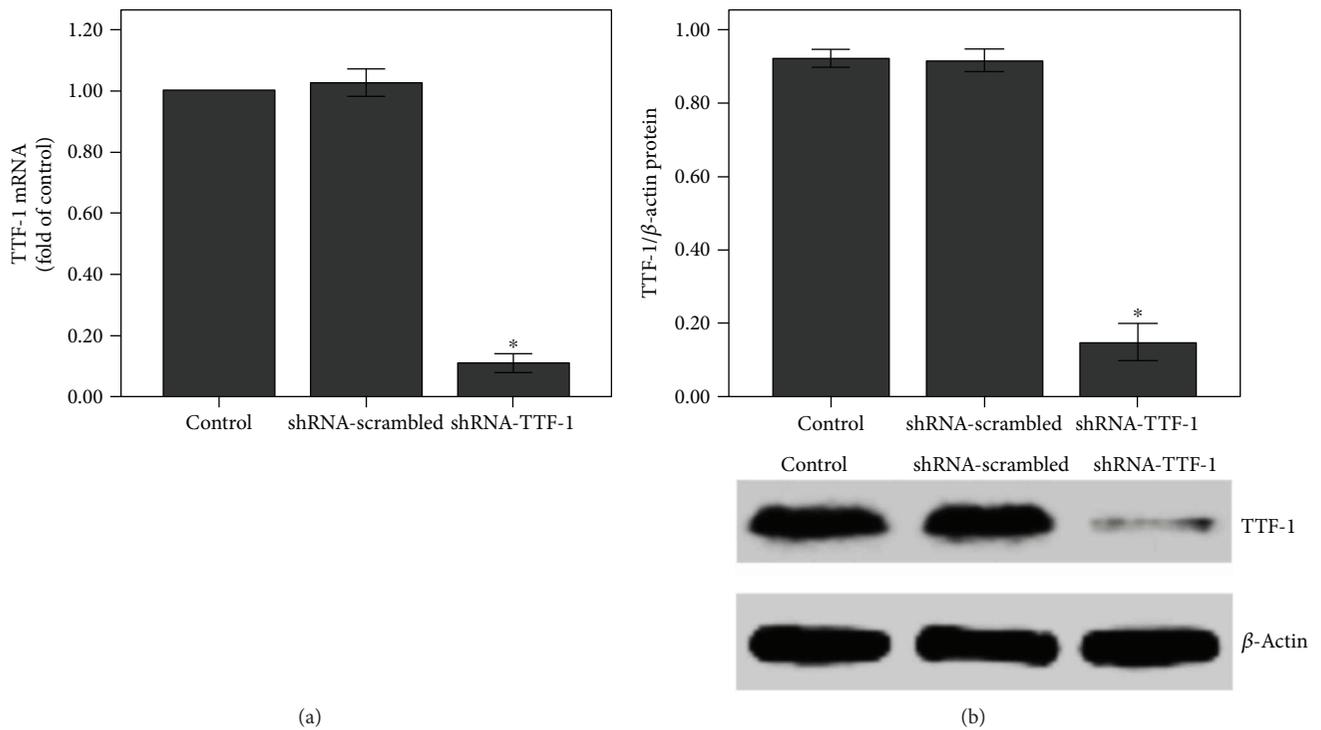


FIGURE 9: The expression of TTF-1 was inhibited after shRNA-TTF-1 transfection in rat ATII cells. Rat ATII cells were transfected with shRNA-TTF-1 or shRNA-scrambled. Twenty-four hours after transfection, the expression of TTF-1 was measured. (a) QPCR was used to analyze the mRNA expression of TTF-1. (b) Western blot was performed to analyze the protein expression of TTF-1. Quantitative data were presented as mean \pm SEM ($n = 5$). * $P < 0.05$ compared with control.

hypoxia. Even slight injury can cause mitochondrial dysfunction and structure changes which usually is the first and most common finding after cell damage. ATII cell is the major injury target of ARDS [21]. Some investigations have shown that the degree of functional impairment and structural

abnormality of lamellar bodies and mitochondria were correlated with the severity of ALI [21, 37, 38]. Our data also showed that LPS-induced ultrastructural alterations, particularly lamellar bodies and mitochondria, in ATII cells were notably attenuated by liraglutide in mice (Figure 4). Thus,

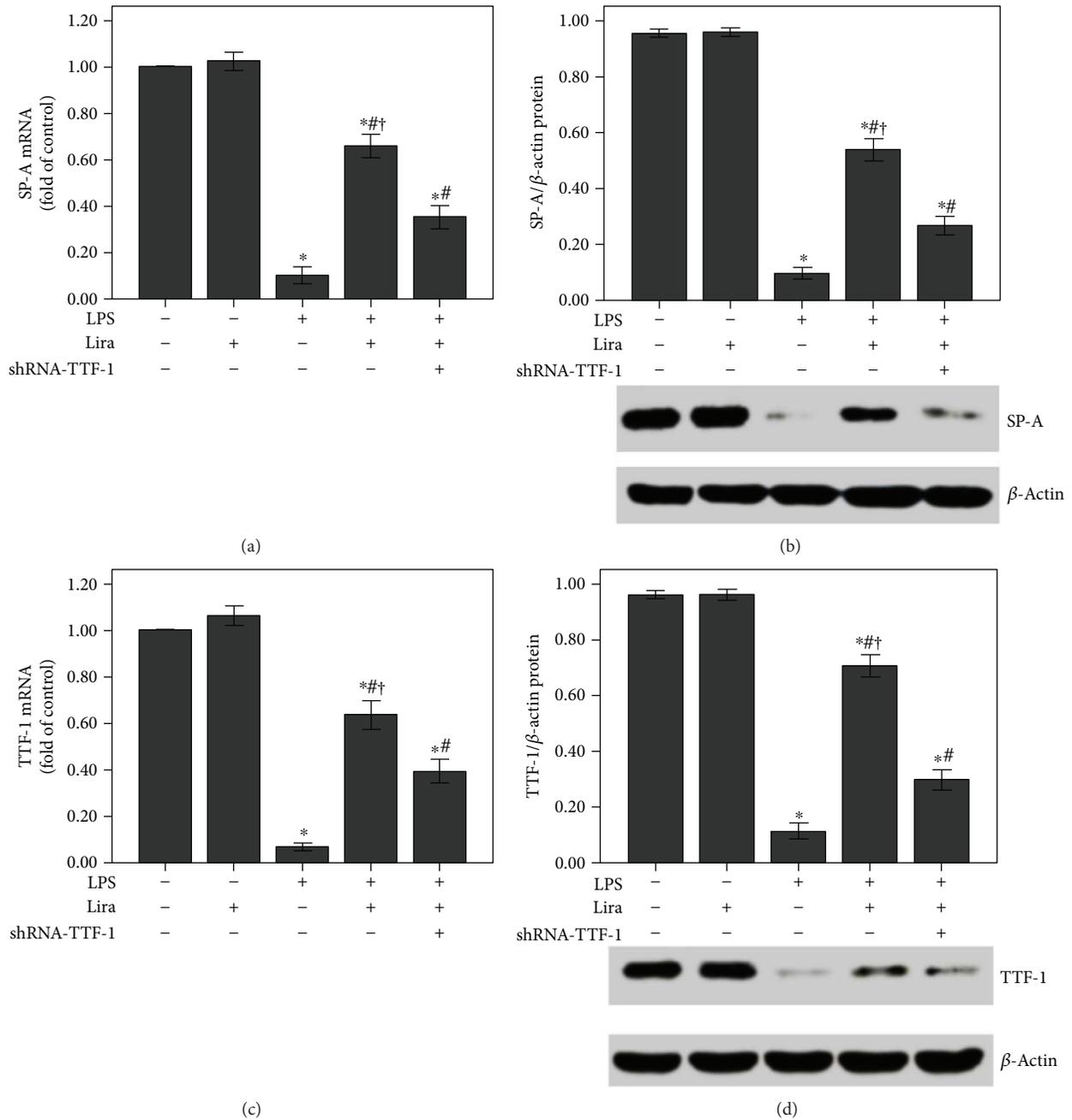


FIGURE 10: Liraglutide increased the expression of SP-A and TTF-1 in rat ATII cells. ShRNA-TTF-1-transfected and nontransfected ATII cells were pretreated with liraglutide (100 nM) for 4 h and then stimulated with LPS (100 ng/mL) for 4 h. (a and c) QPCR was used to analyze the mRNA expression of SP-A and TTF-1. (b and d) Western blot was performed to analyze the protein expression of SP-A and TTF-1. Quantitative data were presented as mean \pm SEM ($n = 5$). * $P < 0.05$ compared with control. # $P < 0.05$ compared with LPS. † $P < 0.05$ compared with LPS+Lira+shRNA-TTF-1.

this result suggested the protective role of liraglutide in LPS-induced ATII cell injury.

SP-A is the most abundant protein component of PS [1, 39]. SP-A plays an indispensable role in tubular myelin formation and recycling of PS [35]. Tubular myelin, the precursor of a monomolecular surfactant form, is an ultrathin film lining the surface of the alveolus [35]. Moreover, a number of studies have reported that SP-A is essential for innate

immunity in the lung [3, 10, 39]. Many previous studies have shown that SP-A expression is significantly reduced in ALI/ARDS [40, 41]. It is well known that reduction of PS is essential for decreased pulmonary compliance and edema in ALI/ARDS. There is broad evidence that the expressions of SP-A and other PS components were reduced after ATII injury in ALI [21, 42–45]. Then, in the current study, our results also indicate that the reduction of SP-A expression

in the lung was correlated with the severity of lamellar body damage and ATII cell injury in ALI (Figures 4 and 5). Therefore, we presumed that upregulation of SP-A might benefit in treating ARDS. Simultaneously, GLP-1 played a critical role in regulation of SP-A and lung development. Previously, it was found that SP-A expression was upregulated and the lung size was increased by liraglutide in fetal and neonatal rats [17]. Furthermore, another study also showed that streptozotocin-induced reduction of SP-A expression was prevented by liraglutide through the TTF-1 signaling pathway in a rat model of diabetes [46]. In the current study, our data demonstrated that LPS-induced downregulation of SP-A expression could be abolished by liraglutide (Figure 5).

TTF-1 is considered to be a central regulator of SP-A transcription in ATII cells [12, 13]. Meanwhile, it is reported that TTF-1 also played a role in LPS and other inflammatory stimulator-induced ATII cell injuries [42, 45]. Das et al. figured out that TNF- α could directly inhibit TTF-1 expression by binding the TTF-1 proximal promoter in H441 and primary alveolar type II cells [42]. TNF- α , one of the most critical inflammatory mediators, has been implicated in the pathogenesis of ARDS and inhibits surfactant protein levels [21, 45]. The TTF-1-binding element (TBE) has been identified in the promoter region of SP-A [12]. Chen et al. revealed that SP-A expression in rat ATII cells could be upregulated by leptin via the TTF-1 signaling pathway under hypoxic conditions [13]. In the current study, our data indicated that liraglutide upregulated SP-A expression through the TTF-1 signaling pathway in LPS-induced ALI (Figures 6 and 10).

SP-A is essential for modulating lung inflammation [3, 39]. Some studies have determined the anti-inflammatory role of SP-A in different conditions [10, 11]. Du et al. found that pneumonia severity and intestinal injury were notably attenuated by SP-A in a murine model of *Staphylococcus aureus* pneumonia [47]. Minutti et al. demonstrated that SP-A attenuated IFN- γ /LPS-induced alveolar macrophage activation [48]. Another study also reported that TTF-1 played a role in the regulation of pulmonary inflammation [49]. In the current study, our data revealed that the effects of liraglutide on LPS-induced pulmonary inflammation, pulmonary edema, increase in insulin level, and ATII cell injury were significantly blunted by shRNA-TTF-1. Thus, this result suggested that the effects of liraglutide were induced by increasing TTF-1 expression. Nevertheless, the underlying mechanism of how liraglutide regulates TTF-1 expression in ATII cells in ALI is still unclear. However, several studies, including our previous study, found that the cAMP/PKA signal pathway was essential for the bioactivity of GLP-1 in different conditions [15, 18]. Steven et al. demonstrated that GLP-1 receptor activation in platelets by linagliptin and liraglutide attenuated LPS-induced microvascular thrombosis, systemic inflammation, vascular dysfunction, and end organ damage by a cAMP/PKA-dependent mechanism [18]. Therefore, we highly supposed that the cAMP/PKA signal pathway would play a critical role in liraglutide-induced TTF-1 expression in ATII cells in ALI. Meanwhile, we also supposed that one or more intermediate molecules probably were involved in this process. Thus, we presume that

liraglutide-induced TTF-1 expression in ALI is indirect. And this is an important area that requires further research.

Additionally, it is reported that haploinsufficient mutations in *TTF-1* are associated with pulmonary disease in infants and with variable inhibitory effects on the expression of SPs in human [50, 51]. However, in our current study, shRNA-TTF-1 was given 3 days before LPS injection. The time period was too short to cause significant pulmonary histological changes. As shown in Figure 1, after 3 days of transfection, no pathological alterations were observed in the control, shRNA-scrambled, and shRNA-TTF-1 groups of mice. Meanwhile, in the current study, TTF-1 knockdown via shRNA is not sufficient to completely abrogate TTF-1 expression in ATII cells. TTF-1 conditional knockout mice should be used to further confirm this mechanism. Interestingly, we also noticed that liraglutide alone could not promote SP-A expression both in vivo and in vitro (Figures 5 and 10). This result can probably be attributed to the complex SP-A metabolic balance. The molecular mechanisms responsible for SP-A metabolic balance in ATII cells should be investigated.

For the safety and tolerance of liraglutide, a comparable high dosage of liraglutide (2 mg/kg) was given to mice in the current study [15, 22]. It is reported that body weight and food intake reduction are the major side effects of GLP-1 analogues in both human and animals [52, 53]. Then, we also observed that the food intake of mice with liraglutide administration was suppressed in our study. And the role of energy and food consumption in the pathogenesis of ALI needs to be elucidated in the future.

Taken together, our results indicated that liraglutide upregulated SP-A expression in ATII cells and attenuated pulmonary inflammation, pulmonary edema, and increase in insulin level in LPS-induced ALI, most likely through the TTF-1 signaling pathway, suggesting that liraglutide may be considered an effective drug for the potential treatment of ARDS in the future.

Conflicts of Interest

The authors have no conflicts of interest to disclose.

Acknowledgments

This study was supported by the National Natural Science Foundation of China (81230001, 81470236, and 81670038), China Postdoctoral Science Foundation (2014M552369), Natural Science Foundation of Guangdong Province (201707010282), Scientific Research Project of Guangzhou (2017A030310286), Medical Scientific Research Foundation of Sichuan Province (150123), Medical Science Foundation for Yong Innovative Project of Sichuan Province (Q15002), and Science and Technology Planning Project of Guangdong Province (2014A020212627 and 2016A020215099).

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Review Article

Diabetes Mellitus and Liver Surgery: The Effect of Diabetes on Oxidative Stress and Inflammation

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Received 22 October 2017; Revised 2 April 2018; Accepted 11 April 2018; Published 8 May 2018

Academic Editor: Fumio Tsuji

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Diabetes mellitus (DM) is a metabolic disorder characterized by hyperglycaemia and high morbidity worldwide. The detrimental effects of hyperglycaemia include an increase in the oxidative stress (OS) response and an enhanced inflammatory response. DM compromises the ability of the liver to regenerate and is particularly associated with poor prognosis after ischaemia-reperfusion (I/R) injury. Considering the growing need for knowledge of the impact of DM on the liver following a surgical procedure, this review aims to present recent publications addressing the effects of DM (hyperglycaemia) on OS and the inflammatory process, which play an essential role in I/R injury and impaired hepatic regeneration after liver surgery.

1. Introduction

To extirpate a macroscopic lesion or accomplish a transplant, the blood flow to the liver must be interrupted to avoid the haemorrhagic process. Despite the safety of surgical procedures that involve the interruption of blood flow to the liver (ischaemia), this interruption contributes to tissue damage, which is potentiated by the restoration of blood flow (reperfusion). This phenomenon, known as ischaemia-reperfusion (I/R) injury [1, 2], is associated with inflammation and oxidative stress (OS) [3].

Diabetes mellitus (DM) is a metabolic disorder resulting from deficient insulin secretion and/or insulin action, leading to hyperglycaemia (high blood glucose) [4], which causes oxidative damage and activates inflammatory signalling cascades [5], in addition to acting as a damaging agent exacerbating the pathological conditions of DM [6, 7]. Considering the growing need for knowledge about the impact of DM on livers undergoing a surgical procedure, the present review aims to present recent data concerning the effects of DM (hyperglycaemia) on OS and the inflammatory process.

2. Oxidative Stress

Under normal conditions, the hepatic production of prooxidants, such as reactive oxygen species (ROS), is counterbalanced by antioxidants. An imbalance in favour of prooxidants corresponds to OS, and the direct action of ROS on cell viability and function is directly related to the occurrence of several pathological processes in the liver [8]. OS plays an essential role in liver surgery [9], and diabetes is generally followed by increased free radical production [10–13] or reduced antioxidant protection [14, 15]. To better understand the effect of DM (hyperglycaemia) on OS, this section will describe research findings that help clarify the association of DM with liver surgery.

2.1. Diabetes Mellitus and Ischaemia-Reperfusion Injury. Hydrogen peroxide (H_2O_2), a mild and relatively stable oxidant that is formed in tissues exposed to I/R, has been considered a representative ROS for evaluating the response of cells to OS [16]. Although H_2O_2 is not a free radical, its accumulation may promote the formation of more toxic species, such as hydroxyl radicals ($\bullet OH$), through

the Fenton reaction [17]. H_2O_2 can cause permanent growth arrest [18, 19] and apoptosis [20–22] in a number of cell types. Nuclear (8-hydroxy-2'-deoxyguanosine) 8-OHdG formation indicates the presence of OS in nuclei [23]. The liver is a major organ affected by ROS [24] and is susceptible to the effects of OS induced by hyperglycaemia, causing liver injury [25–27]. Zhang et al. [28] found that serum H_2O_2 and nuclear 8-OHdG levels were higher in streptozotocin (STZ-) induced diabetic rats subjected to I/R compared with the diabetic control group. ROS induce lipid peroxidation, which causes membrane injury, in addition to changes in ion permeability, enzyme activity, and, ultimately, cell death. Malondialdehyde (MDA), an indicator of oxidative injury produced via lipid peroxidation [29], is significantly enhanced in STZ-induced diabetic rats compared with normal rats and increases after I/R [28, 30] (Figure 1).

Apoptosis and necrosis can occur after I/R. An intense injury leads to initial necrotic killing, whereas late apoptosis may follow moderate injury [31]. STZ-induced diabetic rats exposed to an ischaemic period present significantly increased hepatocyte degeneration, sinusoidal dilatation, nuclear pyknosis, and cellular necrosis compared with the diabetes sham group [30]. In spite of this experimental difference, Behrends et al. [32] reported that necrosis is the preferential form of cell death in the liver of hyperglycemic rats (due to intraperitoneal injection of 25% glucose) subjected to I/R. The authors [32] noted that this increased injury may be associated with the inhibition of heat shock proteins (HSPs), which is only possible through the association of hyperglycaemia and I/R. The hyperglycaemia alone was not enough for HSP32 and HSP70 downregulation. HSPs are considered to be an indispensable protective agent against I/R injury because they are able to protect the liver from OS [33] (Figure 1).

Cell adaptation to OS is a consequence of the upregulation of distinct cytoprotective genes responsible for buffering the antioxidant capacity of the cell [34]. Under physiological conditions, an antioxidant defence system protects the body against the harmful effects of free radicals [35]. Diabetic livers are vulnerable to attack by oxygen free radicals because they present overall antioxidant depression [14]. Release of ROS and the concurrent consumption of endogenous antioxidants and cell death (apoptosis or necrosis) occur during hepatic I/R [36]. After I/R, nuclear factor (erythroid-derived 2)-like-2 factor (Nrf2), a transcription factor that mediates the expression of many endogenous antioxidants plays an important role in opposing hepatic injury [37]. Zhang et al. [28] reported that, after I/R injury, hepatocytes pretreated with high glucose (25 mM) exhibited a reduction in the antioxidant ability of the Nrf2 pathway and a substantial increase in nuclear factor kappa B (NF- κ B) translocation; however, NF- κ B activation was already enhanced in these hepatocytes before I/R injury. Interestingly, NF- κ B, a transcription factor that reacts to redox signals, may directly repress Nrf2 signalling at the transcriptional level [38, 39]. Zhang et al. [28] postulated that high glucose-induced ROS overproduction could initiate the inhibitory interaction between NF- κ B and Nrf2 (Figure 1). However, the precise mechanisms involved in the NF- κ B and Nrf2

interaction under hyperglycaemic conditions require further elucidation.

Under normal conditions, the body presents a potent antioxidant system that is responsible for protecting it from the harmful effects of ROS [40]. Endogenous antioxidant enzymes attenuate I/R injury in the liver [36]. In both type 1 and type 2 DM, antioxidant defence enzymes are deficient, and there is an increase in oxidative damage [41]. High levels of ROS such as superoxide (O_2^-) are found in diabetes and especially during I/R injury [42]. Cem Sezen et al. [30] showed that there is an increase in glutathione s-transferase (GST) in STZ-induced diabetic mice post-I/R with respect to diabetic rats. Between these two groups, there was no difference in the level of superoxide dismutase (SOD); however, compared with the sham group (nondiabetic), there was a marked decrease in SOD levels. The orchestrated actions of several antioxidants in mammalian cells are essential for efficiently detoxifying free radicals. Therefore, any impairment in this pathway will influence the activities of other enzymes [43, 44]. Reduction in the activity of SOD will result in an increased level of O_2^- [45]. GST is known to be an early and sensitive marker of liver injury and has been shown to increase after liver ischaemia/reperfusion [46]. This increased activity of GST could be explained as a compensatory mechanism to protect the organism against injury [47]. These findings are not only in accord with the diverse signalling pathways related to postoperative liver injury associated with DM (Figure 1) but also indicate the importance of the determination of increased ROS production and its characteristic consequences in post-ischaemic tissues, permitting the identification of interventions that stimulates ROS detoxification, and consequently protect against reperfusion injury [16], mainly in a diabetic context (Figure 1).

2.2. Diabetes Mellitus and Liver Regeneration. An increase in lipid peroxidation was found to be important for a normal proliferative process to occur in the liver remnant after partial hepatectomy (PH) [48, 49]. Francés et al. [50] reported that OS is increased by hyperglycaemia and is juxtaposed with the effect of PH in STZ-induced diabetic rats. Postoperative recovery depends on the regenerative capacity of the residual liver. The liver presents altered intracellular signalling pathways in type 1 DM specimens [51–53] and a consequent deficient regenerative response [54]. STZ-induced diabetic rats were found to present an increase in \bullet OH production, which could result in DNA damage [55, 56] (Figure 1). Hyperglycaemia in STZ-induced diabetic rats leads to an increase in hepatic ROS production and is further enhanced after PH. STZ-induced diabetic rats subjected to PH present a decrease in the level of proliferating cell nuclear antigen (PCNA) and a significant decrease in cyclin D1 levels, suggesting that few hepatocytes are capable of entering the cell cycle [50].

Hyperglycaemia enhances \bullet OH radical levels and consequent Bax protein induction. After PH, STZ-induced diabetic rats were found to present an increase in proapoptotic events (Bax/Bcl-xL ratio, caspase-3 activity, and cytosolic cytochrome c) compared with the diabetic group

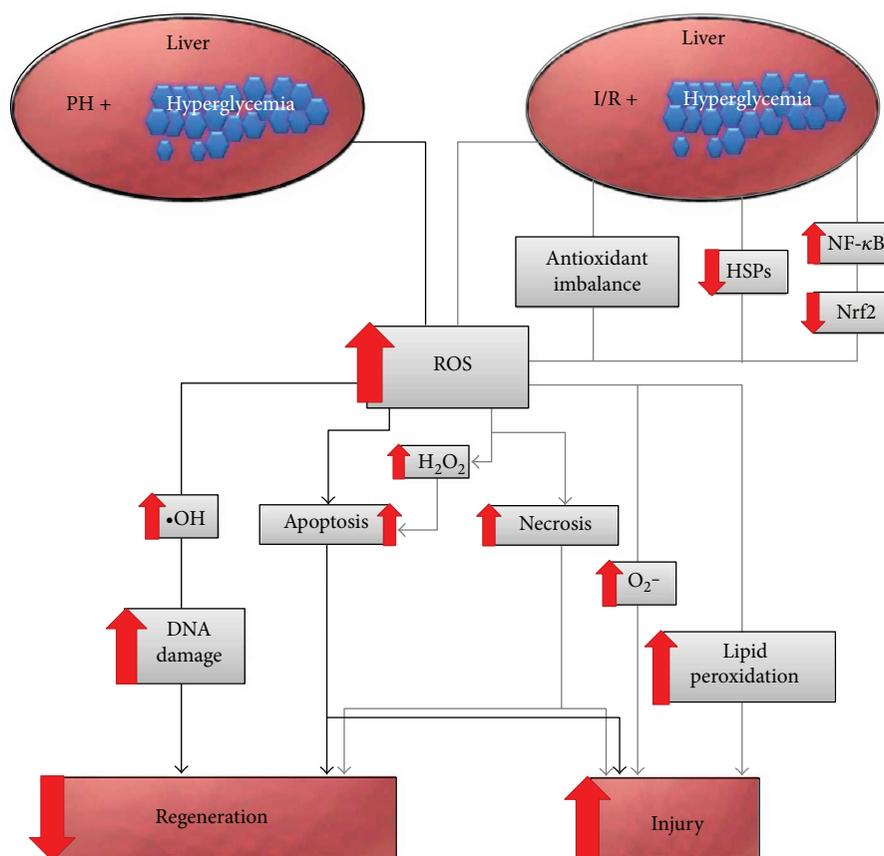


FIGURE 1: Mechanisms of OS in the promotion of liver damage and impaired regeneration after liver surgery in association with DM. The illustration shows the molecular events subsequent to the surgical procedure performed on the diabetic liver, which leads to a significant increase of ROS, inducing liver injury and regeneration. PH, partial hepatectomy; I/R, ischaemia-reperfusion; O₂^{•-}, superoxide anion; HSP, heat shock protein; NF-κB, nuclear factor kappa B; Nrf2, nuclear factor (erythroid-derived 2)-like-2 factor; H₂O₂, hydrogen peroxide; •OH, hydroxyl radical.

[50] (Figure 1). The diversity of the results of different studies [30, 32, 50, 55] shows that the association of hyperglycaemia with different surgical modalities leads to differences in the type of cell death. It is imperative to identify the effects of diabetes on cell death after more complex surgical procedures leading to pronounced liver injury, such as liver transplantation and PH under I/R.

3. Inflammation

Hepatic inflammation is a complex process that is initiated in response to stressful conditions to protect hepatocytes from injury. However, overly intense inflammatory responses are followed by massive hepatocyte loss, causing irreversible parenchymal damage [57]. Liver damage is a serious complication in DM [58]. Surgical procedures induce acute inflammation, which is characterized by the production and release of various chemical mediators, including cytokines [59]. In the next section, the effects of DM (hyperglycaemia) on the hepatic inflammatory process after a surgical procedure will be discussed.

3.1. Diabetes Mellitus and Ischaemia-Reperfusion Injury. The pathophysiology of hepatic I/R injury is not only related to

the direct cell impairment caused by ischaemic insult but also results from the restoration of blood flow, which triggers the proinflammatory environment. Diabetic patients present a variety of deficient immune cell functions [60, 61], and diabetic animals exhibit abnormalities in the course of the inflammatory response, with a consequent decrease in the number of leukocytes in inflammatory injuries [62, 63], the airway inflammatory response to antigen challenge [64, 65], mast cell degranulation [66, 67], superoxide generation, and tumour necrosis factor- (TNF-) α release by leukocytes upon exposure to lipopolysaccharides [68]. The difficulty in arriving at any consistent conclusion is due to the conflicting views regarding the impact of hyperglycaemia on inflammatory responses between different reports. Since clinical observations have revealed that the association between hyperglycaemia and immune alterations could increase the risk for rejection in transplantation, the substantial inflammatory response associated with I/R injury appears to be mediated by an exaggerated adhesion of leukocytes to the endothelium [69, 70].

The hyperinflammatory phenotype associated with DM may induce a liver immune response against I/R, which could favour an increase in parenchymal damage [71]. In the initial phase of liver injury, different events trigger a complex

inflammatory pathway that leads to hepatic accumulation of neutrophils [72]. Through the release of oxidants and proteases, hepatocytes are directly damaged by recruited neutrophils, which are involved in by the later phase of liver injury induced by I/R [73]. In the livers of hyperglycaemic rats subjected to I/R, Behrends et al. [32] observed an increase in neutrophil infiltration (Figure 2). Interestingly, in association with microvascular dysfunction in response to I/R, neutrophil infiltration is exacerbated in DM, suggesting that DM predisposes tissues to the detrimental consequences of I/R, which is a deleterious process that is broadly mediated by neutrophils [69].

The immune system responds to liver injury and/or stress through the activation of resident Kupffer cells (KCs), which release proinflammatory cytokines and other factors [74]. A prominent feature of liver injury is an increase in the hepatic macrophage population [75]. Considering cellular and molecular mechanisms, Yue et al. [71] showed that I/R stimulates the release of advanced glycation end products (AGE) into the blood of STZ-induced diabetic mice and that KCs express higher levels of the receptor for AGE (RAGE). The authors [71] proposed that RAGE may exhibit different functions in a cell type-specific manner. In normal mice, RAGE regulates hepatocyte proliferation during the restoration phase of I/R, whereas in diabetic mice, RAGE activates the hepatic immune system. These findings support the hypothesis that DM may be a factor involved in the course and evolution of I/R injury after liver surgery.

Activated KCs respond with a classic inflammatory reaction and consequent production of proinflammatory cytokines [76–80]. At 6 hours after reperfusion, TNF- α and interleukin- (IL-) 6 levels were found to be increased, while the IL-10 level was decreased on STZ-induced diabetic mice [71, 81] (Figure 2), whereas in control mice, KCs not only presented increases in TNF- α and IL-6 but also an increase in IL-10 [81]. The activation of IL-10 during a proinflammatory response may represent an important agent in the regulation of intensive inflammation in a stressful situation. These findings not only illustrate the defensive role of KCs during liver I/R injury in opposing the hyperinflammatory response through IL-10 expression but also show that hyperglycemic mice subjected to I/R present a significant decrease in IL-10 secretion, by KCs, which is related to uncontrolled inflammation and robust hepatic I/R injury [81].

Several studies suggest that endoplasmic reticulum stress and CHOP signalling could be upregulated by RAGE signalling [82–85]. After 6 hours of reperfusion, C/EBP homologous protein (CHOP) levels in KCs were found to be stimulated by I/R and were further increased in STZ-induced hyperglycemic mice. In hyperglycemic KCs, overactivation of CHOP is related to the inhibition of STAT3 and STAT6 activation. The signal transducers and activators of transcription (STATs) regulate the polarization of macrophages [86], and diabetic mice present M2 KC phenotype inhibition, which results in increased inflammation under hepatic I/R when the rodents exhibit interruption of IL-10-secreting M2 differentiation [81]. Additionally, mice that are only subjected to ischaemia show development of M2-

type macrophages, which protect livers from I/R via an IL-10-dependent mechanism [87] (Figure 2).

In the pathogenesis of DM, activated innate immunity and inflammation are important factors. Type 2 DM involves inflammatory elements [88, 89], and type 1 DM is regarded as an inflammatory process [90]. NF- κ B is a transcription factor that is activated in the diabetic liver [91–93] and is involved in events that lead to inflammation [94]. NF- κ B regulates the expression of many inflammatory cytokines, including monocyte chemoattractant protein-1 (MCP-1), IL-6, and TNF- α [95, 96], which are proinflammatory cytokines that may activate neutrophils and KCs [97]. Zhang et al. [28] showed that after 6 hours of reperfusion, the levels of these hepatic cytokines were significantly higher in STZ-induced diabetic rats and further increased after the ischaemic period. These results suggested that NF- κ B might also be involved in hepatic I/R in diabetic rats (Figure 2). The investigation of NF- κ B activation in diabetic livers subjected to surgical procedures should be extended to cell death. Between NF- κ B and TNF- α , there is an autocrine-reinforcing loop [98, 99]. The hepatic increase of TNF- α in STZ-induced diabetic rats leads to pronounced upregulation of the NF- κ B pathway [100], and NF- κ B activation induced by hyperglycaemia mediates cell apoptosis [101, 102].

Several inflammatory cytokines (e.g., TNF- α) and arachidonic acid metabolites (prostaglandins and thromboxanes) are involved in liver injury induced by I/R. Cyclooxygenase (COX) regulates the production of prostanoids [103], and inhibition of COX-2 protects against hepatic I/R injury [104, 105], which suggests that COX-2 is associated with organ injury and contributes to hepatic microvascular and hepatocellular injuries through TNF- α production [103]. Hepatocyte apoptosis stimulated by TNF is associated with c-Jun N-terminal kinase (JNK) activation [106]. Conversely, Francés et al. [107] showed that STZ-induced diabetic COX-2 transgenic mice presented a substantial decrease in apoptosis and that COX-2 overexpression could prevent the increase in JNK activity stimulated by high glucose. The authors [107] also showed that the increased expression of COX-2 in diabetic COX-2 transgenic mice induces an increase of phosphoinositide 3-kinase (PI3K) activity compared with diabetic wild-type mice, in addition to favouring the activation of Akt and producing an antiapoptotic signal [107]. These studies call attention not only to the contradictory roles of diabetes in orchestrating hepatocyte activity but also to the necessity of clearly understanding the consequences of diabetes for cell death after liver surgery (Figure 2).

3.2. Diabetes Mellitus and Liver Regeneration. In a model of type 2 DM (ob/ob murine), liver regeneration was found to be impaired after 70% PH, which resulted in 90% mortality [108]. The regenerative ability of the liver is compromised in type 1 diabetic rats subjected to PH [51, 52, 109]. In patients subjected to a major hepatectomy, DM tends to induce postoperative liver failure [110]. Considering the mechanisms of regeneration failure, diabetic and obese KK-Ay mice exhibit abnormal responses after PH [111] and present excessive induction of hepatic TNF- α

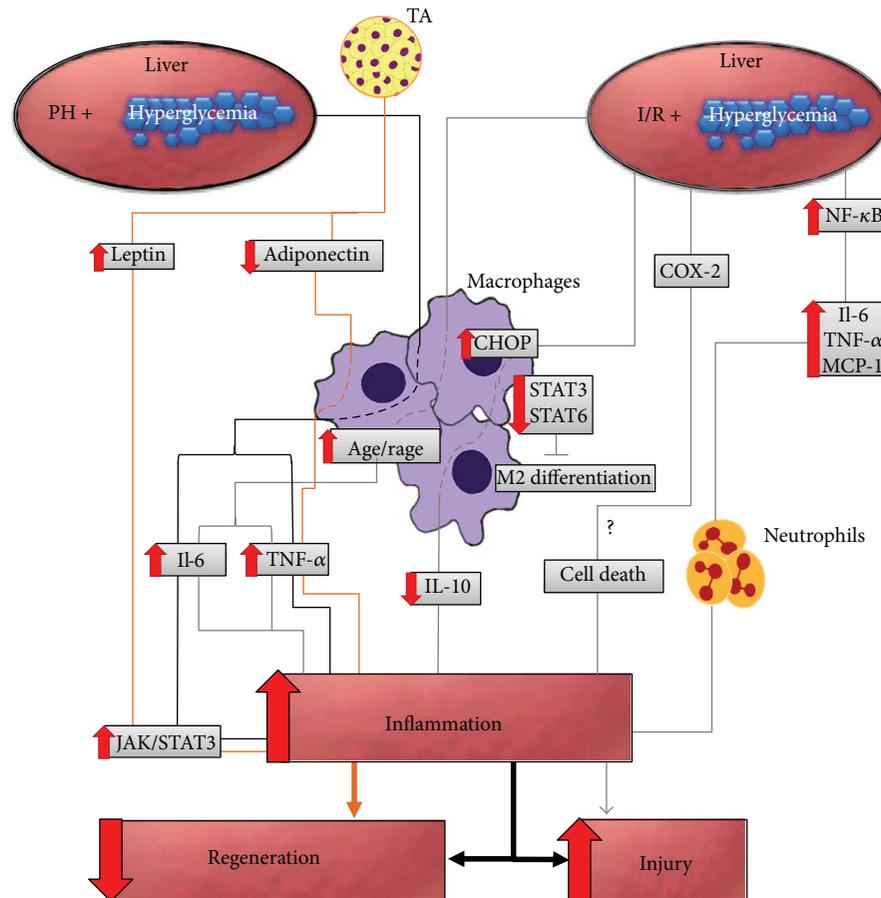


FIGURE 2: Inflammatory mechanisms underlying the promotion of liver damage and impaired regeneration after liver surgery in association with DM. The illustration shows the molecular events subsequent to the surgical procedure performed on the diabetic liver, inducing the participation of inflammatory cells and consequent cytokine production, leading to liver injury and regeneration. TA, adipose tissue; AGE, advanced glycation end products; RAGE, receptor for AGE; IL-6, interleukin-6; IL-10, interleukin-10; TNF- α , tumour necrosis factor- α ; MCP-1, monocyte chemoattractant protein-1; JAK, Janus kinase; STAT3, signal transducer and activator of transcription 3; CHOP, C/EBP homologous protein; NF- κ B, nuclear factor kappa B; COX-2, cyclooxygenase-2; PH, partial hepatectomy; I/R, ischaemia-reperfusion.

expression. Although TNF- α is important for the initiation of normal hepatic regeneration [112, 113], excess induction of TNF- α in KCs might interfere with the regenerative process [111] (Figure 2).

Adipose tissue is involved in a number of biological functions, including inflammation, and acts as an endocrine organ through the secretion of several biologically active substances known as “adipokines” [114]. During liver regeneration, systemic adipose stores are required as a source of various adipokines, such as adiponectin, which is an essential signal for liver regeneration [115]. Aoyama et al. [111] showed that the serum adiponectin level was significantly reduced in KK-Ay mice before PH and tended to decrease gradually after PH. Adiponectin has been found to inhibit the lipopolysaccharide-dependent activation of macrophages [116, 117]. The significant hypoadiponectinemia presented by KK-Ay mice could be related to the fact that the KCs of these animals are more susceptible to certain stimuli; moreover, the hypoadiponectinemia caused by this susceptibility could be further associated with the increased production of TNF- α by KCs, which may interfere with regenerative

responses [111] (Figure 2). Adiponectin mediates anti-inflammatory effects. However, since this role for adiponectin was found to depend on surgical conditions, the function of adiponectin in the inflammatory process is a controversial issue [118]. While injurious effects of adiponectin on steatotic livers subjected to warm ischaemia (60 minutes) were identified by Massip-Salcedo et al. [119], the beneficial (anti-inflammatory) effects of adiponectin on small fatty grafts subjected to cold ischaemia (40 minutes) were observed by Man et al. [120]. Although these findings were obtained in steatotic livers, these results suggest opportunities for investigation of the effect of adiponectin on diabetic livers subjected to different surgical procedures.

IL-6 is a protein synthesized by fibroblasts, monocytes, macrophages, T cells, and endothelial cells [121] that plays an important role in hepatic regeneration [122, 123]. Adipokines exhibit proinflammatory or anti-inflammatory activities [124], and leptin presents proinflammatory properties [125, 126]. IL-6 and leptin function in the Janus kinase-(JAK-) STAT3 signalling pathway [111]. KK-Ay mice present a substantial increase in the levels of IL-6 and leptin

following PH [111]. Despite the important role of the JAK-STAT pathway in hepatic protection against different hepatic injuries [127, 128] and the evidence that IL-6, leptin, and the JAK-STAT signalling pathway are essential to liver regeneration [129–132], Aoyama et al. [111] showed that the role of the JAK-STAT pathway in hepatic regeneration seems to be complex and dependent on the intensity of the stimulus, showing that hyperphosphorylation of STAT3 favours poor hepatic regeneration as a result of direct downregulation of cyclin D1 expression (Figure 2).

4. Diabetes Mellitus in Clinical Situations

There is an absence of clinical studies elucidating signalling pathways related to liver damage and impaired regeneration in diabetic patients undergoing surgery. Nevertheless, it is indispensable to discuss and generate hypotheses about this issue, which is quite controversial because some studies have shown that DM patients present a poorer prognosis after hepatic surgery in comparison with non-DM patients, whereas others show no difference [133].

Focusing on the issues addressed in this review (OS and inflammation), Li et al. [133] and Shields et al. [134] described the typical change in microcirculation that occurs in diabetic patients after liver surgery. The ischaemic period and liver perfusion recovery are important factors related to hepatocellular damage because microcirculatory collapse is followed by a pronounced reduction of tissue oxygenation [135], which might result in degeneration and necrosis of hepatocytes and consequent liver dysfunction [136]. Experimental models of I/R injury have offered evidence that insufficient hepatic microcirculatory perfusion, inflammatory cell activation, and consequent generation of ROS, cytokines, and chemokines can be considered essential in I/R syndrome [137]. Although the authors [133, 134] did not report the relationship between diabetic liver failure after liver surgery and microcirculation collapse, we take this opportunity to raise this question for the development of future studies.

The alterations of hepatic haemodynamics are also related to hepatic steatosis, and a decrease in portal vein haemodynamics is observed in patients with a fatty liver disease [138, 139]. Moreover, experimental animals with steatosis present decreased parenchymal microcirculation [140]. Hepatic steatosis has long been reported in type 1 [141] and type 2 DM [142]. Steatosis is common in diabetic patients (36% incidence) [143], and increased steatosis raises the sensibility of the liver parenchyma to I/R injury [144]. In steatotic livers, the parenchymal regeneration ability is impaired, particularly after a surgical procedure [115], which may partially explain the incapacity of some diabetic patients to resist liver surgery. The high mortality observed in diabetic patients is absent in nondiabetic patients with steatosis [143]. In hepatocytes, increased accumulation of fatty acids induces OS arising from mitochondria, peroxisomes, or microsomes. ROS and lipid peroxidation products can influence KCs and stimulate NF- κ B activation, which in turn stimulates the production of TNF- α and several proinflammatory cytokines, such as IL-6 [143], which are presented in this

review as factors involved in decreased regeneration and increased liver damage.

5. Conclusion

The purpose of this review was to discuss the literature addressing the damaging effect of DM on liver recovery after a surgical procedure and, especially, to highlight the need to expand knowledge of this issue to benefit patients with DM subjected to surgical procedures, which are increasing in clinical practice. Extensive work is still necessary to assess the differences between the diabetic and nondiabetic liver after a surgical procedure. Exploring this subject will enable the development of new treatments that will improve the success of diabetic liver recovery after surgery.

Conflicts of Interest

The authors declare that they have no conflicts of interest. The authors declare that there is no conflict of interest that would prejudice the impartiality of this scientific work.

Acknowledgments

The authors apologize to the many researchers whose work they have not been able to discuss in this limited review. The authors are supported by Grants 2016/24992-0 and 2017/11540-7 from the São Paulo Research Foundation (FAPESP), Grant 301617/2016-3 from the National Council of Technological and Scientific Development (CNPq, PQ-1D), and the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

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Review Article

Wound Healing and Omega-6 Fatty Acids: From Inflammation to Repair

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Received 4 December 2017; Accepted 8 March 2018; Published 12 April 2018

Academic Editor: Naïma Moustaid-Moussa

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Wound healing is an evolutionarily conserved process that is essential for species survival. Wound healing involves a series of biochemical and cellular events that are tightly controlled, divided into 3 concomitant and overlapping phases: inflammation, proliferation, and remodelling. Poor wound healing or a chronic wound represents a silent epidemic that affects billions of people worldwide. Considering the involvement of immune cells in its resolution, recent studies are focused on investigating the roles of immune nutrients such as amino acids, minerals, and fatty acids on wound healing. Among the fatty acids, much attention has been given to omega-6 (ω -6) fatty acids since they can modulate cell migration and proliferation, phagocytic capacity, and production of inflammatory mediators. The present review summarizes current knowledge about the role of ω -6 fatty acids in the wound healing context.

1. Wound Healing: A Vital Process

Wound healing occurs after a chemical, physical, or biological insult results in epithelial barrier disruption. This process involves activation of platelets, neutrophils, macrophages, endothelial cells, keratinocytes, and fibroblasts; moreover, the production and release of protein mediators (growth factors and cytokines) released by these cell types and lipid mediators (prostaglandins, leukotrienes, thromboxanes, and lipoxins) are needed to coordinate the tissue repair and to reestablish tissue homeostasis [1, 2].

The process is divided into 3 concomitant and overlapping phases: inflammation, proliferation, and remodelling (Figure 1).

After a tissue lesion, the disruption in vasculature blocks the oxygen and nutrient supply to the injured area, leading to a hypoxic condition that induces the production of reactive oxygen species (ROS) and reactive nitrogen species (RNS) [3–5], initiating a coagulation cascade. Blood elements such as platelets, erythrocytes, and fibrin form a framework for the recruitment of immune cells [6, 7]. Platelets produce

platelet-derived growth factor (PDGF), transforming growth factor- β (TGF- β), and epidermal growth factor (EGF) that induce migration and activation of immune cells [8].

The extracellular matrix (ECM), which is composed of fibronectin, fibrinogen, fibrin, thrombospondin, and vitronectin, fills the tissue defect and enables migration of different cell types required for the healing process [9].

Inflammation is the body's natural and essential defence mechanism responsible for combating antigens, restoring homeostasis, and repairing tissue damage [10, 11]. The inflammatory response consists of a variety of events triggered by immune cells, which involves influx of leukocytes to the injured area and production of pro- and anti-inflammatory mediators [12].

Neutrophils are the predominant cells in the first hours after the tissue injury, and they respond to proinflammatory cytokines, such as interleukin-1 β (IL-1 β), tumor necrosis factor alpha (TNF- α), and interferon gamma (IFN- γ) at the lesion site, phagocytizing microorganisms and cellular debris [10, 13]. For microorganism destruction, the degranulation process occurs, releasing granule enzymes such as defensins,

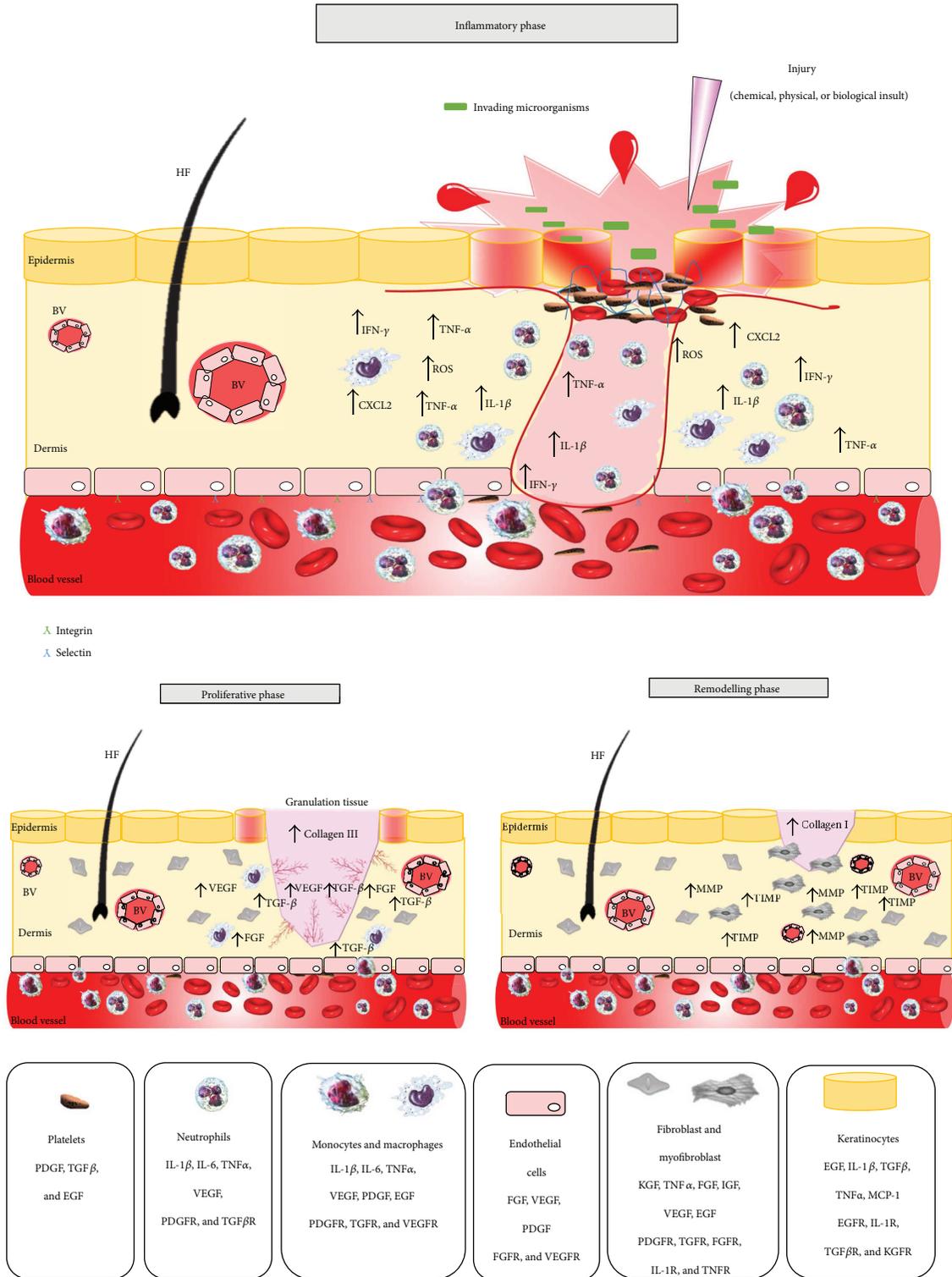


FIGURE 1: Wound healing process. The illustration shows the inflammatory, proliferative, and remodelling phases of wound healing. Early stages of wound healing include coagulation and activation of inflammatory cells. The proliferative stage involves proliferation of fibroblasts and angiogenesis. The remodelling phase includes restoration of the barrier and contraction of the wound by myofibroblasts. The process is orchestrated by immune cells and growth factors and cytokines and chemokines (listed below) [8]. HF = hair follicle; BV = blood vessels; TNF = tumor necrosis factor; IL-1beta = interleucina 1beta; IL-6 = interleucina 6; ROS = reactive oxygen species; CXCL2 = chemokine (C-X-C motif) ligand 2; IFN-gamma = interferon-gamma; VEGF = vascular endothelial growth factor; TGF-beta = transforming growth factor beta; FGF = fibroblast growth factor; KGF = keratinocyte growth factor; MCP1 = monocyte chemoattractant protein-1; IGF = insulin growth factor; TIMPs = tissue inhibitors of metalloproteinases; MMPs = matrix metalloproteinases; PDGF = platelet-derived growth factor; EGF = epithelial growth factor.

cathelicidins, elastase, myeloperoxidase (MPO), lactoferrins, and cathepsins inside the phagosome. In addition to their microbicidal activities, these molecules also act in the chemoattraction of macrophages to the lesion site. They also amplify the production of cytokines and chemokines, such as chemokine C-X-C motif ligand-2 (CXCL2) that will attract macrophages to the wound area. Neutrophils produce IL-1 β , TNF- α , and vascular endothelial growth factor (VEGF) and express PDGF and TGF- β receptors [8]. These cytokines also induce the expression of adhesion molecules on the endothelial cell surface that will interact with selectins and integrins expressed in macrophages, facilitating the rolling, attachment, and transmigration of these cells to injured areas [13–15].

Macrophages are phagocytes that have PDGF, TGF- β , and VEGF receptors, and thus, they migrate in response to mediators produced by platelets and neutrophils in the injured tissue [8].

After 72 hours, macrophages are the predominant cells at the wound site, and they release growth factors (VEGF, PDGF, and EGF) and cytokines (IL-1 β , IL-6, and TNF- α) that promote the migration of other cells such as fibroblasts and endothelial cells [10, 16]. They also produce prostaglandins that activate endothelial cells and act as potent vasodilators, affecting the permeability of microblood vessels [17].

The lack of control in the amplitude and time to resolve inflammation is one of the factors that most influence the genesis of chronic inflammatory diseases, such as cardiovascular diseases, diabetes, cancer, asthma, dementia, and Alzheimer's disease [11, 12, 18], as well as chronic wounds.

The proliferative stage begins within the first 48 hours and can unfold up to the 14th day after a tissue injury [17]. This phase is characterized by angiogenesis and fibroplasia, restoring the blood vessels and forming the granulation tissue [10].

Angiogenesis is the formation of new blood vessels from preexisting vessels and it is initiated by growth factors such as VEGF, PDGF, and fibroblast growth factor (FGF) [10, 19]. Fibroplasia is the formation of granulation tissue, and its main characteristic is proliferation of fibroblasts in response to PDGF, TGF- β , FGF, IL-1, and TNF α . At this time, the production of collagen occurs, and there is a release of growth factors such as keratinocyte growth factor (KGF), TNF- α , FGF, insulin growth factor (IGF), VEGF, and EGF [8, 16]. Then, the provisional matrix initially formed is replaced by granulation tissue composed of fibroblasts, granulocytes, macrophages, and blood vessels in complex with collagen bundles that form the basis for cell adhesion and migration, growth, and differentiation [10, 19].

The remodelling phase occurs approximately from the 21st day after injury and can last for years. During this period, there is intense production and digestion of collagen as well as the substitution of collagen III for collagen I. These events are aimed at maintaining the fibres in the same direction as in unwounded tissue to reestablish its functions and mechanical forces [20].

Matrix metalloproteinases (MMPs) are zinc-dependent endopeptidases that degrade ECM components (collagens),

and their gene expression is regulated at the transcriptional level by cytokines and growth factors as well as by their natural inhibitors, tissue inhibitors of metalloproteinases (TIMPs) [21].

In all of the processes cited above, it is important to emphasize that exogenous and endogenous factors can modulate such events and influence the healing process. More specifically, systemic disorders, such as diabetes, immunosuppression, and venous stasis as well as those resulting from external agents, such as the use of corticotherapy and smoking, can hinder the early closure of the wound.

Chronic wounds are defined as wounds with a full thickness in depth and a slow healing tendency. The time an open wound needs to remain to define chronicity is still not well established, ranging from 4 weeks to more than 3 months [22]. Including diabetic foot ulcers, venous leg ulcers, and pressure ulcers, they represent a silent epidemic that affects a large fraction of the world population, becoming a public health problem [23, 24].

Complications of chronic wounds include infection that can lead to lower extremity amputations and impacts on health and life quality of patients because they cause pain and suffering, loss of function, loss of productivity, depression, distress and anxiety, social isolation, prolonged hospital stays, and chronic morbidity or even death [25].

Moreover, the treatment of chronic wounds causes economic expenditures by the individual and the healthcare system, and therefore, they are a matter of political interest [26]. In the USA, for example, chronic wounds affect 6.5 million patients, with nearly US\$ 50 billion spent on treatment of chronic wounds and complications related to them per year [22, 25].

In developed countries, 1 to 2% of the population will experience a chronic wound throughout their lives [22] due to population ageing and increases in noncommunicable diseases such as obesity, diabetes, and cancer [27, 28].

Animal and human studies have shown that in the elderly population (age over 60 years), there is an increase in the number of cases of poor wound healing and chronic wounds due to delayed T-cell infiltration, decreased chemokine production, and reduced macrophage phagocytic capacity, in addition to delayed reepithelization, collagen synthesis, and angiogenesis [28].

Alterations of the peripheral nervous system with decreased protective sensation and foot deformities enhance the risk of chronic skin ulcerations on the lower extremities of diabetic subjects, mainly on the foot, that affect 15% of diabetic patients [29], and five-year postamputation, the mortality rate is 50–59% [30].

Chronic inflammation, insufficient angiogenic response, production of ROS greater than antioxidant capacity, collagen accumulation, dysfunction of migration and proliferation of fibroblast and keratinocytes, and an imbalance between the accumulation and degradation of ECM are some of the mechanisms responsible for poor healing in diabetic patients [1, 28].

These scenarios show the necessity for studies that investigate possible therapies that accelerate tissue repair, reducing the susceptibility to infections [31].

2. Omega-6 Fatty Acids: From Inflammation to Regeneration

For decades, nutritional supplementation was mainly used to avoid nutritional deficiency. However, currently it is being recognized that adequate levels of essential nutrients can prevent as well as treat some disturbances [32].

Fatty acids are carboxylic acids formed by hydrogen and carbon atoms [33]. Based on the presence of double bonds, fatty acids are classified as saturated (no double bonds) or unsaturated (with double bonds). Among the unsaturated fatty acids, there is also a classification that takes into account the number of unsaturations: monounsaturated fatty acids (MUFAs) present with one double bond on acyls (the main food source is olive oil) and polyunsaturated fatty acids (PUFAs) contain two or more double bonds [33].

PUFAs are classified by the position of the first double bond counting from the methyl terminal. Then, when the first double bond is at the 6th carbon atom from the methyl terminal, PUFAs are called omega-6, ω -6, or n-6. They include linoleic acid (LA, C18:2 ω -6), an essential fatty acid because it cannot be synthesized by the human body. LA can be “stretched” and desaturated into other ω -6 fatty acids, such as γ -linolenic (GLA, 18:3 ω -6) and the arachidonic acid (AA, 20:4 ω -6). Moreover, biohydration of linoleic acid by bacteria (anaerobic bacteria such as *Butyrivibrio fibrisolvens*) in the gut of animals and the action of Δ 9 desaturation of 18:1 *trans*-11 in animal tissue can generate conjugated linoleic acid (CLA) [34].

Fatty acids alter skin structural and immunological status since they constitute the stratum corneum, and they can alter the permeability of the skin. They also interfere with maturation and differentiation of the stratum corneum and inhibit production of proinflammatory eicosanoids, reactive species (ROS and RNS), and cytokines, thus influencing the inflammatory response and possibly wound healing [35–38].

The objective of this study was to review the scientific literature on the relationship between omega-6 fatty acids (linoleic, conjugated linolenic, gamma-linolenic, and arachidonic acid) and the wound healing process.

2.1. Linoleic Acid. Linoleic acid (LA, 18:2 ω -6, *cis*-9, 12-octadecadienoic acid) is the PUFA most commonly consumed in the human diet, being mainly found in safflower, corn, and sunflower oils, present in medium quantities in soy, sesame, and almond oils, and in smaller quantities in canola, olive, coconut, and palm oils [39].

2.1.1. Effects of LA on Tissue Repair. In developing countries, creams with linoleic acid are used to treat wounds. One of the first studies in this area described that topical application of a solution containing 1.6 g of essential fatty acid (mainly linoleic acid) prevented pressure ulcers in hospitalized patients [40]. This improvement was related to better hydration and elasticity. In this study, the control group received a solution with 1.6 g of mineral oil, which is a liquid paraffin. Although frequently used in baby creams to maintain hydration, in the present study, only 22% of the patients in the control group presented a hydrated skin. On the other hand, 98%

of the patients treated with a linoleic solution showed a hydrated skin. These results indicate that maintenance of hydration is a mechanism by which linoleic acid improves wound healing.

In 2008, Magalhães et al. [41] did not observe any effects of topical application of medium chain triglycerides (caprylic, capric, caproic, and lauric acids), linoleic acid, soy lecithin, or a vitamin A and E mixture on wound healing in rats. The main problem with this protocol is the composition of the mixture tested and the control used, since the control group received a 0.9% NaCl solution without antioxidant vitamins or fatty acids.

Other studies described positive effects of oils rich in linoleic acid such as lucuma nut oil (LNO) and pumpkin oil on wound healing [42, 43]. The major constituents of LNO are LA (38.9%), oleic acid (27.9%), and palmitic and stearic acids (18.6 and 8.9%, resp.). Rojo et al. [42] used two different models to prove the beneficial effects of LNO: the zebrafish (*Danio rerio*) model and a CD-1 murine model. At first, LNO (20–100 μ g/mL) was added to a zebrafish larva plate after a tail primordial cut. Through fluorescence microscopy and image analysis of fluorescent endothelial cells from zebrafish, it was observed that LNO accelerated the regeneration. This prohealing effect was attributed to increases in angiogenesis. However, the authors evaluated the number of fluorescent endothelial cells and not the number of new vessels formed. Angiogenesis is a complex process that involves release of proangiogenic factors, such as VEGF, PDGF, and FGF, as well as proteolytic degradation of basement membrane, and the migration, proliferation, and organization of endothelial cells in a tube form [44]. Angiogenesis is a crucial step for proper wound healing since it reestablishes the oxygen and nutrient supply.

LNO was also tested in a CD-1 murine model. For this, a wound was induced in the back region of mice and topically treated with 200, 500, or 100 μ g of LNO daily. Corroborating the results with zebrafish, LNO (500 and 1000 μ g) also induced a more rapid wound closure in CD-1 mice. The authors hypothesize that this effect could be related to the anti-inflammatory actions of the fatty acids present in the LNO [42]; however, they did not show any results that could support this hypothesis.

Linoleic acid has been thought to be behind the effects of pumpkin oil on wound healing. Pumpkin oil is constituted, mainly by LA (50%), oleic acid (25%), and palmitic acid (15%) [43]. This high content of LA was correlated with improvement in wound closure, since it shortened bleeding time, suggesting a stabilization of fibrin and consequent migration of fibroblast; it augmented hydroxyproline content, possibly due to fibroblast activation; and it reduced the number of infiltrating macrophages in wound tissue 11 days after lesion induction. Altogether, these results indicate that topical treatment with pumpkin oil accelerates tissue repair, mainly due to the effects of LA [43].

Considering these results with LA-rich oils, some groups have tested the effects of pure LA on wound healing. The use of isolated fatty acids ensures that the observed effects are not due to minor oil compounds or a combination of fatty acids.

In this context, it was also reported that there were beneficial effects of pure LA topically applied into wounds. BALB/c mice treated with pure LA (30 μ M) for 20 days exhibited accelerated tissue repair 48 hours after wound induction [45]. This result was related to increased production of nitric oxide (NO). NO is a free radical derived from L-arginine oxidation through the nitric oxide synthase (NOS) activity. After an inflammatory insult, inducible nitric oxide synthase (iNOS) is expressed in immune cells and produces a large amount of NO that will generate other free radicals, expanding the inflammatory response [46]. NO plays important roles such as activation of macrophages and fibroblasts, induction of collagen synthesis, and the proliferation of keratinocytes during wound healing, thus accelerating reepithelization [47].

However, in Wistar rats, topical treatment with pure LA did not alter the wound area, although there was an increase in wet wound weight (oedema) and in neutrophil numbers, indicating a positive effect on the migratory response during the inflammatory phase [48].

Another approach used to investigate LA effects on wound healing is oral supplementation.

Wistar rats orally supplemented with pure LA (0.22 g per kg body weight) by gavage during the 5 days prior to wound induction had an increased inflammatory response 1 hour (initial stage of inflammation) after skin injury. This proinflammatory effect was characterized by an increase in inflammatory cell influx into the wound site due to elevations in hydrogen peroxide (H_2O_2) production and chemokine release. On the other hand, 24 hours later, LA reduced the activation of nuclear transcription factor (NF- κ B) and then diminished the production of proinflammatory cytokines such as IL-1 β and IL-6. At the same time, there was an elevation in AP-1 (activator protein-1) activation. AP-1 is a transcription factor that induces the expression of genes related to proliferation of keratinocytes and fibroblasts, which are two important cells involved in the proliferative phase of wound healing. Therefore, LA accelerated the inflammatory phase of wound healing, allowing the next phase (proliferation) to start early and accelerating wound healing over a period of 7 days [49].

More recently, the same protocol was tested in diabetic Wistar rats; the results showed that LA positively modulates tissue repair not only by accelerating the inflammatory phase but also by inducing angiogenesis. During the proliferative phase (7 days), it was observed that LA increased the number of vessels in the wound tissue, which was related to an elevation in VEGF concentration and ANGPT-2 (angiopoietin-2) expression [38]. VEGF and ANGPT-2 are proangiogenic factors essential for new vessel formation. VEGF induces ANGPT-2 expression, which primes endothelial cells to respond to inflammatory cytokines, thereby augmenting the migration and proliferation of endothelial cells [50].

Taken together, these studies demonstrate that linoleic acid can improve wound healing due to its mechanical properties and by modulating the cellular response, increasing the migration and functions of inflammatory and endothelial cells as well as inducing angiogenesis at the wound site.

2.1.2. Mechanisms of Action of LA. The mechanisms described so far to explain the effects of LA on wound healing involve inflammatory responses of neutrophils and macrophages.

Neutrophils are the first cell type recruited to the inflammatory site, being determinants for the healing process [51]. To analyse the effects of LA on neutrophil migration, an air pouch was induced into the dorsal region of Wistar rats treated with LA (100 μ M), and 4 hours later, the exudate was collected and the cells were counted. LA increased neutrophil influx to the pouches [48], corroborating the results described in wound tissue. This effect on migration can be explained by the induction of adhesion molecules such as L-selectin on neutrophil surfaces [52]. Neutrophil recruitment is a highly regulated process that involves at least four steps: rolling, activation, adhesion, and transmigration. Through the intravital microscopy assay, it was observed that LA also elevated leukocyte-endothelium interactions (rolling and adhesion) [52].

Once in the injured site, neutrophils produce cytokines, chemokines, ROS, and other molecules to expand the inflammatory response. Measuring intra or extracellular ROS production, Hatanaka et al. [53] demonstrated that LA increased anion superoxide and H_2O_2 in a dose-dependent manner. The authors tested 5 different techniques (luminol- and lucigenin-amplified chemiluminescence, cytochrome c, hydroethidine, and phenol red reduction) and described that LA interfered with luminol and cytochrome c reactions, jeopardizing the ROS results [53]. In the wound healing context, ROS production is the first event that occurs after tissue disruption due to hypoxia [54]. Low concentrations of H_2O_2 are important to support wound healing [55] since ROS not only disinfects the injured area but also acts as signalling messengers regulating gene expression [56] and cellular function such as migration [57] and cytokine production [58].

Inflammation control is crucial to tissue repair, since chronic inflammation can worsen the wound. In this sense, LA has also shown a beneficial effect since it increases the release of proinflammatory mediators in the initial inflammation phase (1–4 hours) and reduces them in the resolution phase (18–48 hours) [52].

Another important cell type that is involved in inflammatory responses is the macrophage. As observed with neutrophils, LA reduced the production of IL-1 β , IL-6, and VEGF in the absence of LPS, although it accelerated IL-1 β release and decreased IL-10 synthesis when cells were stimulated with LPS. However, LA did not affect ROS production (superoxide anion, hydrogen peroxide, and NO) as well as the lipid mediators, prostaglandin E_2 (PGE $_2$), leukotriene B_4 (LTB $_4$), and 15(S)-hydroxyeicosatetraenoic acid (15[2]-HETE) [59]. Lipid mediators are a class of inflammatory molecules derived from the metabolism of arachidonic [60], eicosapentaenoic (EPA), or docosahexaenoic (DHA) acids. Classes 2 and 4 are derived from AA and exhibit more proinflammatory effects, increasing migration, production of cytokines, and ROS. On the other hand, classes 3 and 5 are derived from EPA and DHA and are related to anti-inflammatory effects. More recently, a new class of lipid mediators derived from omega-3 fatty acids (EPA and DHA) were described, the maresins, resolvins, and

protectins that exert proresolution effects, resolving inflammation [61]. During the inflammatory response, it is important that there is a shift between proinflammatory molecules to proresolution to limit the damage induced by exacerbated inflammation.

During the proliferation and remodelling phases, fibroblasts, endothelial cells, and keratinocytes play important roles in producing growth factors that orchestrate the reconstruction of vessels and induce wound contraction [62]. In this context, Rojo et al. [42] described a promigratory effect of LNO (60 $\mu\text{g}/\text{mL}$) on human fibroblasts, which was related to an increase in vinculin expression. Vinculin is a focal adhesion protein essential for fibroblasts-ECM interactions [63] involved in wound contraction.

One important aspect not fully clarified is if LA must be metabolized to exert its effects on cellular functions or if it acts as an effector molecule. To answer this question, some studies have described G-protein coupled receptors (GPCR or GPR) as responsible for fatty acid effects [64, 65]. GPR is a class of seven transmembrane receptors involved in a broad spectrum of cellular responses [64]. Among GPR, GPR40 has been described as a sensor for LA, oleic acid (OA), CLA, and other long chain fatty acids [65, 66]. In HaCaT cells (keratinocyte cell line), once activated, it reduced the production of cytokines (CCL-5 and CCL17) and suppressed allergic inflammation in skin [67], and then, it could be involved in the effects of LA on wound healing. These results indicate that LA can modulate immune response by acting as an effector molecule. However, considering the importance of LA to cellular membranes, it is possible that the results observed are due to its metabolization as well. More studies are needed to clarify this point.

In conclusion, it has been shown that LA-rich oil or pure LA modulates cellular functions such as migration, production of ROS, cytokines, and chemokines, expression of adhesion molecules, and interaction with ECM. These alterations seem to be related to improvements in tissue repair.

2.2. Conjugated Linoleic Acid (CLA). The presence of conjugated linoleic acid (CLA) was first reported in 1930 [68], but only in the 1980s was CLA described as a bioactive dietary constituent, and the interest in CLA's effects has increased due its anticarcinogenic properties and reduction of adipose tissue mass observed in mice [69].

CLA comprises a mix of positional and geometric isomers of linoleic acid with a single pair of conjugated double bonds. CLA is formed during LA biohydration by bacteria in the gut of ruminant animals, and thus, the main natural sources of CLA are ruminant meats (beef and lamb) and dairy products (milk and cheese) [69, 70].

At least 28 CLA isomers are known, but the *cis*-9, *trans*-11 (c9, t11) is the most abundant form of CLA in nature, and nutritional supplements are a mixture of c9, t11 and *trans*-10, *cis*-12 (t10, c12) CLA [71, 72]. Initially, it was thought that the effects of CLA were global, and the results were due to interactions between its two main isomers: c9, t11 and t10, c12. However, later evidence suggested that the physiological effects of CLA may be different between the isomers, animal species (rats and mice), and cell types [73].

The last decade has seen a plethora of claims, supported by animal and cell lineage models, that dietary CLA intake is associated with potential health benefits [70]. These include reduction in fat deposition, protection from atherosclerosis and cancer, and enhanced immunity [69, 74].

Although preclinical data suggest benefits of CLA supplementation, clinical findings in humans have yet to show evidence of a positive effect, and even the findings in animals are still controversial [73].

Some studies revealed that CLA can induce adverse effects such as fatty liver, insulin resistance, and lipodystrophy [75]. Thus, it is recommended that ingestion of a balanced diet with natural sources of CLA be followed.

2.2.1. Effects of CLA on Tissue Repair. Mice fed a diet supplemented with 0.5% or 1% CLA (38% c9, t11 CLA; 39% t10, c12 CLA; 3% c9, c11 CLA; and 1% t9, t11 CLA) for 2 weeks presented a reduction in wound area (1% CLA) that was related to an increase in antioxidant defences [76]. ROS are essential to protect the organism against invading bacteria and other microorganisms; moreover, they are important to intracellular signalling. However, excessive production of ROS or impaired detoxification of these molecules causes oxidative stress [54]. To understand the prohealing effect, the authors measured malondialdehyde (MDA) content in the liver, a marker of lipid peroxidation, and the expression of antioxidant enzymes at the wound site. Mice supplemented with CLA had a reduced MDA content and increased CuZn superoxide dismutase (SOD) and MnSOD protein expression, showing an antioxidant effect of this fatty acid, which can explain its benefit on wound healing. At the same time, they described a reduction of phosphorylated inhibitor kappa B alpha ($\text{pI}\kappa\text{B}\alpha$) protein expression at the end of the inflammatory phase of wound healing [76]. In the cytoplasm, NF- κB is found complexed with $\text{I}\kappa\text{B}$. Once phosphorylated, $\text{I}\kappa\text{B}$ releases NF- κB that translocates to the nucleus and induces the expression of genes related to inflammatory responses [77]. Therefore, the reduction in $\text{pI}\kappa\text{B}\alpha$ indicates that NF- κB is in the cytoplasm, and the expression of proinflammatory genes is reduced. To show this, the expression of cyclooxygenase-2 (COX-2) and HO-1 was evaluated. CLA reduced the protein expression of these inflammatory genes, confirming its inhibitory effect on NF- κB activation [76].

In the carcinogenic context, topical application of CLA to hairless mouse skin also reduced COX-2 expression due to inhibition of NF- κB activation in the skin [78]. To elucidate the CLA effects on the NF- κB pathway, it was described that this fatty acid downregulated the catalytic activity of $\text{I}\kappa\text{B}$ kinase ($\text{IKK}\alpha/\beta$), mitogen-activated protein kinase (p38 MAPK), and protein kinase B (Akt) [78]. We suggest Zhang et al. [77] for a comprehensive review of the NF- κB signalling pathway.

2.2.2. Mechanisms of Action of CLA. The mechanisms by which CLA modulates immune function are not completely elucidated, but they include regulation of prostaglandin and cytokine production, since it has been observed that CLA reduces COX-2 expression and modulates NF- κB activation [76, 78, 79].

Peripheral blood mononuclear cells (PBMC) treated with t10, c12 CLA (100 μ M) for 24 hours diminished TNF- α production. This effect seems to be isomer-specific since treatment with c9, t11 CLA (100 μ M) or LA (100 μ M) had no effect on TNF- α concentration [80].

Cho et al. [81] suggested that t10, c12 CLA has a priming effect on polymorphonuclear (PMN) and mononuclear cells isolated from dogs. PMN or mononuclear cells directly treated with CLA did not alter TNF- α production. Thus, they took this preconditioned medium and added it to a new cell culture. This preconditioned medium increased TNF- α concentrations and augmented the oxidative burst activity and phagocytic capacity of PMN and mononuclear cells [81]. When the recombinant anti-TNF- α antibody was added to this preconditioned medium, the effects were abolished, suggesting that the effects of CLA are mediated by TNF- α released from PBMC.

Taken together, these results showed that dietary administration of CLA can improve wound healing due to antioxidant and anti-inflammatory effects in the later inflammatory phase of tissue repair.

2.3. Gamma Linolenic Acid (GLA). Gamma-linolenic acid (GLA, 18:3 ω -6) is an omega-6 fatty acid formed through LA metabolization, due to delta-6-desaturase action [82]. It is found in plant seed oils, such as borage, black current seed, and primrose oil [83]. The most common form of GLA consumption is through oral supplementation with GLA-rich oil capsules, mainly from evening primrose oil (EPO) [84].

GLA has been investigated in chronic inflammatory diseases such as rheumatoid arthritis [83, 85, 86], atopic dermatitis, acne vulgaris, and psoriasis [87–89] due to its anti-inflammatory effects. GLA can be converted into dihomo- γ -linoleic acid (DGLA), which is metabolized into prostaglandin E1 (PGE1) or 15-hydroxyeicosatrienoic acid (15-HETrE) [82, 89]. These eicosanoids have anti-inflammatory and immunoregulatory effects [85].

2.3.1. Effects of GLA on Tissue Repair. GLA ingestion was also used to treat patients with acne vulgaris [88]. In this study, 45 patients received 2 capsules of borage oil (400 mg of GLA) for 10 weeks, and acne lesion number and severity were assessed as well as inflammation by histological analysis. The GLA group had a reduction in the lesion number and severity, which could be associated with a reduction in inflammation and interleukin-8 (IL-8) staining demonstrated by histologic analysis [88]. Although the authors speculate that two mechanisms (modulation of inflammation and improvement of skin quality) could explain their results, no other analyses were made of their samples. Therefore, it is not possible to affirm how GLA had beneficial effects on acnes vulgaris.

Ingestion of GLA-rich oil capsules was also related to clinical improvement of atopic dermatitis (AD) [89]. The clinical effect was positively correlated with plasma GLA and DGLA concentrations after 4 weeks of capsule consumption.

2.3.2. Mechanisms of Action of GLA. Considering the relevance of macrophages in inflammatory processes such as

arthritis and wound healing, it is of great value to investigate the effects of GLA on their functions.

In the RAW 264.7 macrophage cell line, GLA concentrations (100 to 200 μ M) reduced the expression of inducible nitric oxide synthase (iNOS) and consequently the NO concentration [90]. GLA also inhibited the expression of COX-2 and prointerleukin-1, suggesting a reduction in inflammatory responses. To explain these results, the authors evaluated the expression of proteins involved in the NF- κ B pathway. GLA diminished I κ B phosphorylation and degradation, blocking the transmigration of NF- κ B to the nucleus, which was confirmed by the reduction in nuclear p65 protein expression. Altogether, these results explain the reduced activation of NF- κ B in GLA-treated macrophages [90].

More studies are necessary to prove the beneficial effects of GLA on wound healing.

2.4. Arachidonic Acid. Arachidonic acid (AA, 20:4 ω -6) is the second most abundant fatty acid in injured tissue after a tissue lesion [91]. Once released from membrane phospholipids by phospholipase A₂, AA is metabolized by cyclooxygenases and lipoxygenases and produces the eicosanoids [92].

Eicosanoids are a wide variety of 20-carbon bioactive lipid products that include prostaglandins (PGs) and thromboxanes (TXs) of series 2 and leukotrienes (LTs) of series 4, lipoxins (LXs), hydroxyeicosatetraenoic acids (HETEs), and epoxyeicosatrienoic acids (EETs) [93] that modulate inflammatory responses. They are highly potent, short-lived molecules that act locally and have been strongly associated with a variety of physiological and pathological processes including cancer, inflammatory diseases, and wound healing [92]. In the wound healing process, the effects of AA are associated mainly with the production of eicosanoids, because they are abundant in the wound bed [94].

The AA metabolites are predominantly proinflammatory because they stimulate the chemotaxis of inflammatory cells, increase the activity of elastase that degrades extracellular proteins, and impair the formation and remodelling of healing tissue [94].

2.4.1. Effects of AA on Tissue Repair. Considering that AA generates eicosanoids and that these molecules modulate tissue repair, an AA-enriched diet was tested in an intestinal ischaemia-injured model [95]. The diets were enriched with 0.5 or 5% of AA and administered over 10 days to pigs. After this period, blockage of the mesenteric blood vessels induced an ischaemic ileum injury, and the protective and reparative effects of AA administration were analysed. It was observed there was a protective effect of AA (5%) since the percentage of denuded villus area was reduced in relationship to the control. At the same time, the AA group presented an improvement in recovery since these animals showed a reduction in mucosal-to-serosal flux of ³H-mannitol and ¹⁴C-inulin when compared with the control group (0% of AA), suggesting that the epithelial barrier is more preserved in the AA group [95]. Although AA-enriched diet (5%) does not alter COX-2 mRNA expression, it was observed that there was an increase in PGE₂ concentration after ischaemic injury [95]. This effect

TABLE 1: Effects of linoleic (LA) fatty acid.

Fatty acid	Condition	Study model	Treatment time	Dose/concentration	Molecules associated	Effect in tissue repair	Reference
	Wound healing	Diabetic Wistar rats	18 days	0.22 g/Kg bw (oral administration)	Increased VEGF and ANGPT-2	Accelerated the inflammatory phase and angiogenesis	[38]
	Pressure ulcers	Healthy humans	21 days	1.6 g EFA with LA extracted from sunflower oil (topical application)	NA	Increased hydration and elasticity.	[40]
	Wound healing	Healthy rats	12 days	0.14 g solution with TGs, LA, vitamins A and E, and soy lecithin (topical application)	NA	No effects	[41]
	Wound healing	Zebrafish	48 hours	10–100 μ g/mL of lucuma nut oil	NA	Improved regeneration (100 μ g/mL)	[42]
	Wound healing	CD-1 mice	11 days	200, 500, or 1000 μ g of lucuma nut oil (topical application)	NA	Improved wound healing and formation of new blood vessels (500 and 1000 μ g)	[42]
	Wound healing	Healthy rats	11 days	0.52 μ L/mm ² of pumpkin oil (topical application)	Increased hydroxyproline content	Accelerated wound closure and bleeding time, improved fibrin stabilization, and increased migration of fibroblasts, and reduced infiltration of macrophages	[43]
LA	Wound healing	Healthy BALB/c mice	20 days	30 μ M of pure LA (topical application)	Increased NO production	Accelerated tissue repair	[45]
	Wound healing	Healthy Wistar rats	24 hours	300 μ L of pure LA (topical application)	Increased total protein and DNA contents and elevated VEGF- α and IL-1	No effect on wound area	[48]
	Wound healing	Healthy Wistar rats	5 days	0.22 g/Kg bw of pure LA (oral administration)	Increased H ₂ O ₂ and AP-1 and reduced NF- κ B, IL-1 β , and IL-6	Accelerated the inflammatory phase	[49]
	Neutrophil functions	Intraperitoneal neutrophils from healthy Wistar rats	10 days	0.11, 0.22, and 0.44 g/kg of bw (oral administration)	Increased L-selectin, IL-1 β , and CINC-2 α β	Increased leukocyte-endothelium interactions	[52]
	Neutrophil functions	Intraperitoneal neutrophils from healthy Wistar rats	20 minutes	0, 10, 25, 50, 100, and 200 μ M (<i>in vitro</i>)	Increased O ₂ ⁻ and H ₂ O ₂ (50 μ M)	Increased ROS	[53]
	Macrophage functions	Macrophages from healthy Wistar rats	10 days	0.22 g/Kg bw (oral administration)	Reduced IL-6, VEGF, and IL-10	Modulated cytokine production by macrophages	[59]

Essential fatty acids (EFA); triglycerides (TGs); nitric oxide (NO); deoxyribonucleic acid (DNA); vascular endothelial growth factor (VEGF); interleukin-1 β (IL-1 β); body weight (bw); hydrogen peroxide (H₂O₂); activator protein-1 (AP-1); nuclear transcription factor (NF- κ B); interleukin-6 (IL-6); angiotensin-2 (ANGPT-2); cytokine-induced neutrophil chemoattractant-2 (CINC-2 α β); reactive oxygen species (ROS); lipopolysaccharides (LPS); interleukin-10 (IL-10); not analysed (NA).

TABLE 2: Effects of conjugated linoleic acid (CLA).

Fatty acid	Condition	Study model	Treatment time	Dose/concentration	Molecules associated	Effect in tissue repair	Reference
	Wound healing	Healthy mice	2 weeks	0.5 or 1% of CLA (diet)	Increased CuZnSOD, and MnSOD and reduced pI κ B α , COX-2, HO-1, and MDA	Increased the antioxidant defences and reduced the wound area (1%)	[76]
CLA	Hairless skin	Mice	6 hours	0.25 or 1 mg (topical application)	Reduced NF- κ B, COX-2, IKK α / β , MAPK, and Akt	Antitumor (1 mg)	[78]
	Inflammatory diseases	Bovine PBMC	24 hours	100 μ M (<i>in vitro</i>)	Decreased TNF- α	Additional studies are needed	[80]
	Inflammatory diseases	Blood phagocytes isolated from dogs	24 hours	10 μ M (<i>in vitro</i>)	Increased TNF- α	Increased oxidative burst activity and phagocytic capacity	[81]

CuZn superoxide dismutase (CuZnSOD); Mn superoxide dismutase (MnSOD); cyclooxygenase-2 (COX-2); malondialdehyde (MDA); nuclear transcription factor (NF- κ B); I κ B kinase (IKK α / β); mitogen-activated protein kinase (MAPK); protein kinase B (Akt); tumor necrosis factor α (TNF- α); peripheral blood mononuclear cells (PBMC); not analysed (NA).

TABLE 3: Effects of gamma linolenic (GLA) fatty acid.

Fatty acid	Condition	Study model	Treatment time	Dose/concentration	Molecules associated	Effect in tissue repair	Reference
GLA	Acne vulgaris	Healthy humans	10 weeks	400 mg (oral administration)	Reduced IL-8	Reduced lesion number, severity, and inflammation	[88]
	Atopic dermatitis (AD)	Humans	12 weeks	320 or 480 mg (oral administration)	NA	Improvement of clinical signs of AD	[89]
	Macrophage functions	RAW 264.7 macrophages		100 to 200 μ M (<i>in vitro</i>)	Reduced iNOS, NO, COX-2, pro-IL-1, pI κ B, and NF- κ B	Decreased inflammation	[90]

Interleukin-8 (IL-8); inducible nitric oxide synthase (iNOS); oxide nitric (NO); cyclooxygenase-2 (COX-2); prointerleukin-1 (pro-IL-1); nuclear transcription factor (NF- κ B); not analysed (NA)

TABLE 4: Effects of arachidonic (AA) fatty acid.

Fatty acid	Condition	Study model	Treatment time	Dose/concentration	Molecules associated	Effect in tissue repair	Reference
AA	Wound healing	hUCB-MSC	24 hours	5 or 10 μM (<i>in vitro</i>)	Increased mTOR ^{ser2481} , Akt ^{ser407} , PKC ζ , and MMPs	Increased cell migration and angiogenesis (10 μM)	[91]
	Intestinal ischemic injury	Pigs	10 days	0.5 or 5% of AA (diet)	Increased PGE ₂	Preservation of epithelial barrier (5%)	[95]
	IBD	Rats	8 weeks	0, 5, 35, or 240 mg/Kg of bw (oral administration)	Increased COX-2, LTB ₄ , TXB ₂ , and MPO	Increased inflammation and macrophage infiltration	[98]
	Angiogenesis	Porcine endothelial cells	24 hours	0, 20, 50, 60, and 80 μM (<i>in vitro</i>)	NA	Increased cell spreading (20 μM) and reduced cell spreading (80 μM)	[101]

Prostaglandin E2 (PGE₂); inflammatory bowel disease (IBD); body weight (bw); cicloxygenase-2 (COX-2); leukotriene B₄ (LTB₄); thromboxane (TXB₂); myeloperoxidase (MPO); human umbilical cord blood-derived mesenchymal stem cell (hUCB-MSC); mammalian target of rapamycin complex 1 phosphorylation (mTOR^{ser2481}); protein kinase B (Akt^{ser407}); phosphorylates protein kinase C ζ (PKC ζ); matrix metalloproteinases (MMPs); not analysed (NA).

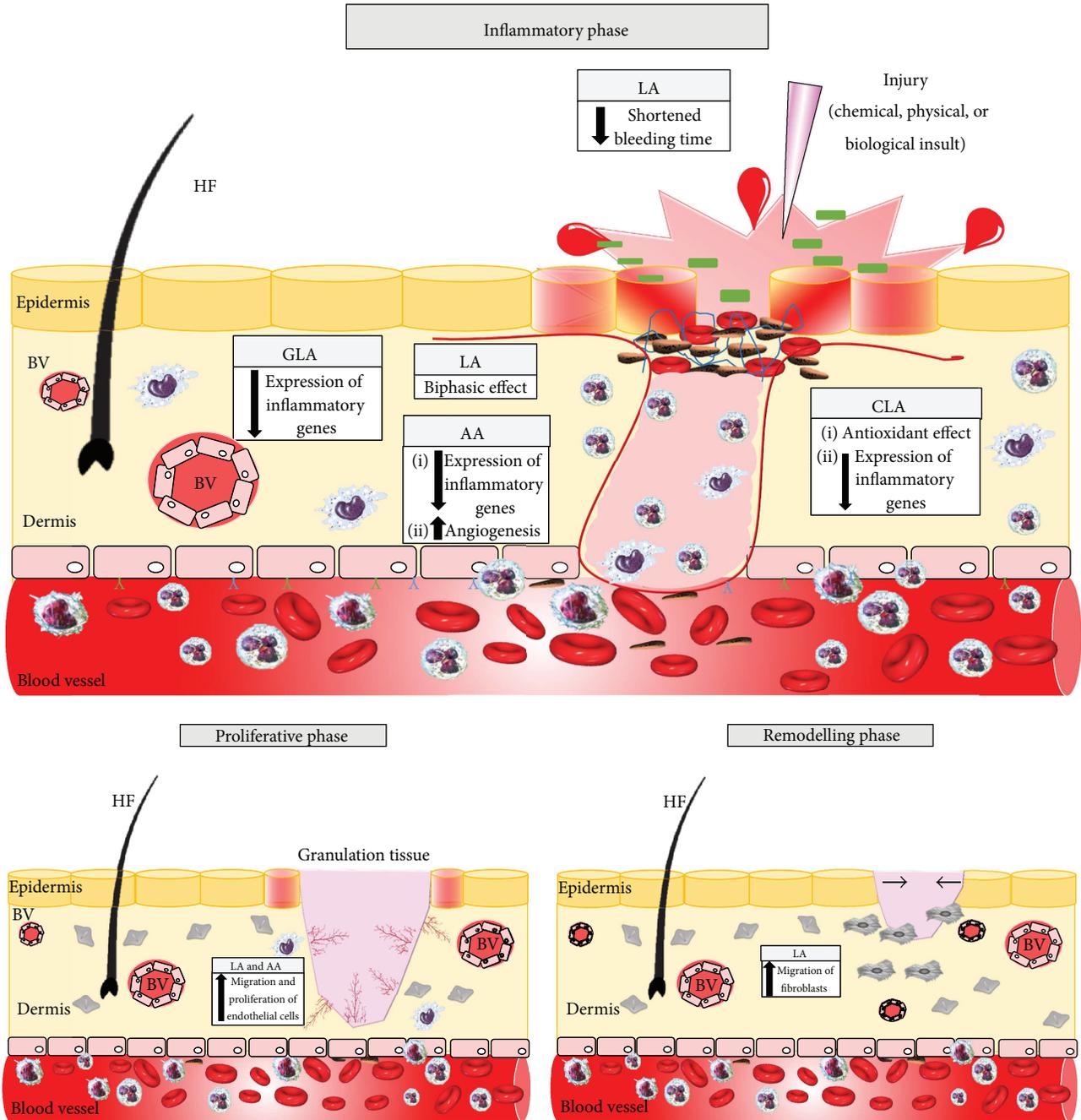


FIGURE 2: Effects of linoleic acid (LA), conjugated linoleic acid (CLA), gamma linolenic acid (GLA), and arachidonic acid on wound healing phases.

was abolished when animals received indomethacin, a nonselective COX inhibitor. PGE₂ has been described to be a protective factor that stimulates the recovery of gut injury [96]. One of the mechanisms involved is the induction of angiogenesis due to an increase in VEGF content [97].

In the dextran sodium sulphate-induced inflammatory bowel disease (IBD) model, oral administration of AA (240 mg/kg of body weight) for 8 weeks aggravated inflammation since it increased COX-2, LTB₄, and TXB₂ concentrations in colonic tissue. AA also elevated myeloperoxidase

(MPO) activity and macrophage infiltration, which reinforces its proinflammatory effect [98].

Epoxyicosatrienoic acids (EETs) are metabolites produced from AA due to cytochrome P450 (CYP450) activity, predominantly in the endothelium. EETs can stimulate angiogenesis and organ or tissue regeneration [21, 99]. Local application of 11,12- or 14,15-EETs (10 μM/methylcellulose discs) accelerated wound healing due to the increase in MMP2 and MMP7 and reduction in TIMP-1 and TNF-α during the proliferative phase of wound healing

(12 days). These results indicate that EETs favoured extracellular matrix degradation and endothelial cell migration, two important steps in the angiogenesis process [21]. These positive effects were also confirmed in transgenic animals that exhibit high or low EET. In this model, the wound healing was accelerated in high EET animals due to vascularization [100].

To better explain the roles of lipid mediators during impaired wound healing, a lipidomic approach was carried out in transgenic animals (LIGHT^{-/-}) that exhibited an exacerbated inflammatory response characterized by high levels of oxidative stress and cytokines and imbalance between production and degradation of ECM [99]. These animals had increased concentrations of 11-, 12-, and 15-hydroxyeicosatetraenoic acid, leukotrienes (LTD₄ and LTE), prostaglandins (PGE₂ and PGF₂), thromboxane (TXA₂/TXB₂), and prostacyclins in early stages (1 day) of wound healing. These results were associated with enhanced coagulation and infiltration of neutrophils in LIGHT^{-/-} when compared with wild type mice [99].

The factors that lead to colitis, ischemia-reperfusion damage, and skin wound are physiologically different as well as the responses observed in these conditions. Although a general inflammatory response is usually observed, which is characterized by recruitment and activation of inflammatory cells, production of cytokines and growth factors as well as the repair of the damaged tissue, there are specificities inherent to each tissue that can change the effect of determined fatty acid.

2.4.2. Mechanisms of Action of AA. In agreement with the *in vivo* studies, AA induced endothelial cell adhesion *in vitro*. Once again, this modulatory effect presented a biphasic pattern as also observed with other fatty acids, such as LA. In the first phase, the positive effect on cell spreading was independent of AA concentration. However, in the later phase, there was an inverse correlation between AA concentration and spreading [101]. Low AA concentrations (20 μM) increased cell spreading, and high AA concentrations (80 μM) reduced it. This effect could be associated with the metabolites generated from AA oxidation. At a low concentration, AA is totally metabolized, and the products can induce cell adhesion. On the other hand, at high concentrations, the reaction is saturated in AA, and the enzymes involved are not sufficient to metabolize all AA available. Then, there is a reduction in AA metabolites and consequently a reduction in cell spreading [101]. AA also randomizes the migration of endothelial cells. This action is related to the loss of direction during migration due to the presence of AA and seems to be inversely correlated with AA concentration [101].

Some of these AA effects, observed in endothelial cells, were also described in human umbilical cord blood-derived mesenchymal stem cells (hUCB-MSCs), and once again, AA concentration was inversely related with the migratory response. The mechanism behind this effect seems to involve GPR40 [91], a membrane receptor for fatty acids [102].

In a very detailed study, Oh et al. [91] demonstrated that AA binds to GPR40 and then induces mammalian

target of rapamycin complex 1 (mTORC2) phosphorylation (mTOR^{ser2481}) that activates Akt^{ser407}, which phosphorylates protein kinase Cζ (PKCζ). pPKCζ activates p38, through Sp1 phosphorylation, and increases the expression of matrix metalloproteinases (MMPs). MMP degrades fibronectin, an extracellular matrix component, promoting the migration of hUCB-MSCs.

Altogether, the studies demonstrate that AA and its metabolites promote wound healing due to induction of cell migration and angiogenesis. However, these positive effects are closely related with the concentrations used.

3. Summary

Wound healing is an evolutionarily conserved process essential for species' survival. An investigation of factors that improve wound healing is of crucial interest. Experimental and clinical studies indicate that LA improves wound healing due to its biphasic effects on the inflammatory phase of tissue repair (Table 1). CLA seems to have antioxidant and anti-inflammatory effects on the later inflammatory phase of tissue repair, favouring the beginning of the proliferative phase (Table 2). Although less studied, GLA presented positive effects controlling inflammation (Table 3). Studies investigating the effects of AA demonstrated that AA and its metabolites promoted wound healing due to induction of cell migration and angiogenesis (Table 4).

In general, omega-6 fatty acids positively modulate all phases of wound healing, but more studies are necessary to clarify the mechanisms involved (Figure 2).

Clinical studies are essential to establish the strategies of fatty acid administration (topically or orally), the optimal concentrations, and their safety.

Conflicts of Interest

None of the authors have any conflict of interest or anything to disclose.

Authors' Contributions

All authors did the literature search. Jéssica R. Silva and Beatriz Burger wrote the manuscript and contributed equally to this paper. Hosana G. Rodrigues also wrote the manuscript and critically revised the manuscript. All authors read and approved the final manuscript.

Funding

This research was supported by the Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP 2013/06810-4).

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Research Article

Rooming-in Reduces Salivary Cortisol Level of Newborn

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Received 23 November 2017; Revised 9 January 2018; Accepted 15 January 2018; Published 8 March 2018

Academic Editor: Francisco Rios

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Background. Rooming-in practice improves breastfeeding and reduces newborn stress reactivity. When this modality is not available, partial rooming-in after birth can be considered. Salivary cortisol levels (SCLs) are considered reliable biomarkers to indicate stress. **Objective.** To test the hypothesis that rooming-in duration impacts neonatal stress response in hospitalized newborns. **Design/methods.** Forty term newborns, enrolled in the Neonatology and Obstetrics Nursing, C.G. Ruesch, Naples, Italy, were divided, according to the mother's choice, into the study (SG; $n = 20$) and control (CG; $n = 20$) groups if they received full (24 hs) or partial (14 hs) rooming-in care, respectively. Saliva samples were collected from all babies between 7:00 a.m. and 8:00 a.m. of the 3rd day of life by using oral swab. Salivary cortisol levels were measured using an enzyme immunoassay kit (Salimetrics LLC, PA, USA). **Results.** A statistically significant difference in the SCLs between SG and CG was found (median: 258 ng/dl versus 488.5 ng/dl; $p = 0.048$). **Conclusions.** Data support the practice of full rooming-in care compared with partial rooming-in. The rooming-in duration clearly reduces SCLs and likely neonatal stress. These lower SCLs may have long-term positive effects reducing the risk of metabolic syndrome, high blood pressure, and cognitive and behavioural changes.

1. Introduction

According to clinical managements, newborns are often exposed to painful and stressful situations. The concept of infant pain and effects of pain exposure during hospitalization of infants has progressed greatly in the past 25 years [1]. Grunau et al. and Miller and Ferriero investigated whether neonatal procedural pain/stress impacts the developing brain, discovering that greater exposure to procedural pain-related stress was associated with reduced development of white matter and subcortical gray matter [2, 3]. Therefore, the knowledge of socioemotional stress reactivity during the early period of neonatal life is crucial to understand the brain neurodevelopmental trajectory [4]. When the infant faces up to a stressful situation, the developing hypothalamic-pituitary-adrenal axis is activated: the hypothalamus secretes the corticotropin-releasing hormone, which starts the release of adrenocorticotrophic hormone by

the pituitary gland. This hormone induces, in the adrenal gland cortex, the secretion of glucocorticoids as cortisol, considered a stress indicator hormone since its plasma levels will be high as a result of the psychological and physical stress response [5]. Long-term side effects of high concentration of cortisol can result in insulin resistance, hyperlipidaemia, immunologic deficiencies, and destructive changes in the hippocampus [6]. Salivary cortisol has been reported as a useful biomarker of psychological stress and related mental or physical diseases [7]. Since Francis et al. in 1987 [8] showed a correlation between infants' plasma and saliva cortisol, only few studies investigated salivary cortisol levels (SCL) due to the complexity of methodology measurement. Morelius et al. published an easy method to collect and analyse cortisol concentration in small amount of saliva [9]. Some studies performed with this method detected patterns of high hormonal stress response to heel lance for infants aged between 34 and 41 weeks of gestation [10]. Infants aged

under three months showed increased cortisol levels from baseline in response to painful interventions (e.g., heel lance and inoculation) as well as routine handling interventions (e.g., physical examination, diaper changing, and removal from bath) [11]. Conversely, mother-infant proximity and interactions reduce infants' and mothers' stress during the early postpartum period. Rooming-in practice allows mothers and babies to stay together in the same room during the hospitalization time. Separate care consists in keeping the baby in the hospital nursery and bringing him to the mother only for breastfeeding. These two different approaches may influence mother-infant interaction and neonatal stress response [12].

We tested the hypothesis that full-time rooming-in (for 24 hs) is better than partial rooming-in (for 14 hs) to reduce neonatal stress response in hospitalized newborns.

2. Materials and Methods

2.1. Enrollment and Group Composition Participants. The study was carried out from January to September 2016, in Neonatology and Obstetrics Nursing, C.G. Ruesch, and Gynaecology and Obstetrics of the Villa Cinzia Hospital in Naples, Italy. Healthy newborns from families that were Italians for more than 3 generations were consecutively recruited while written informed consent was obtained from the families. Eligibility criteria for newborns included patients with gestational age > 37 weeks, 3 days of life, body weight > 2500 gr. Exclusion criteria were patients who underwent painful, stressful procedures, patients born from smoking mothers, mothers with maternal diabetes, placenta abruption, chronic pathologies or using drugs/alcohol during pregnancy, or infants with foetal growth restriction, foetal malformations, chromosomopathy, metabolic disorders, or clinical signs of maternal or foetal infection. Newborns' mothers were <35 years old and primiparous. They had a body mass index between 19 and 24. Infants were divided according to the mother's choice, into the study (SG; $n = 20$) and control (CG; $n = 20$) groups if they received rooming-in care for 24 hs or 14 hs (7:00 a.m.–9:00 p.m.), respectively. The control group (CG) was enrolled from January to June 2016 in Villa Cinzia Hospital and assisted in rooming-in care for 14 hours (7:00 a.m.–9:00 p.m.) as required by the mother. The study group (SG) was enrolled from June to September 2016 in Neonatology and Obstetrics Nursing, C.G. Ruesch, and treated with rooming-in care for 24 hours.

All babies received the same clinical management, the only difference was the rooming-in length. Both hospitals had 20 beds for newborns. Parents could observe clinical bedside round and hold meetings with physicians in the places for rooming-in at 9:00 a.m. in both hospitals. If necessary, families could hold meetings with paediatric nurses every 3 hours. Newborns were not subjected to painful procedures in the first 3 days of life, and during this period, parents could change the diaper, medicate the umbilicus, and breast-feed their children in both hospitals; only the wrapping was performed by paediatric nurses. The environment of the childbirth centres was strictly controlled; the temperature did not have to rise above 25°C, while the luminosity was

set at 2000 lux and the noises did not get over 45 dB. The detection of the stress level of the newborns was performed by sampling saliva from 7:00 a.m. to 8:00 a.m. on the 3rd day of life by a paediatric nurse, who was the same throughout the study, to exclude interoperator sampling collecting bias. An oral swab was positioned in the oral cavity for 60–90 sec. to obtain 200–1000 microl. of saliva. The oral swabs were stored in a test tube (stored at a temperature < 20°C) and brought, after two weeks, to the analytical laboratory.

2.2. Instruments. During hospital stay of the newborns, one of the authors, aware of the study, recorded clinical features (nationality, parents' residence, gestational age, body weight at birth, days of life in a database (Excel 2007)).

Paediatric nurses who were on duty measured the body weight of the newborns with a seca 354 baby scale. The oral swabs used for this study were SalivaBio Infant's Swab (Salimetrics) while the test tubes were SalivaBio Storage Tube (Salimetrics). The correct collection of the salivary sample considered that patients did not have to eat 60 min before the sampling, the documentation of the oral injury, and vigorous physical activity, as well as, 10 min before the sampling, the cleaning of the oral mucosa with water to remove food leftovers. The cortisol levels in salivary samples were quantified with the Salimetrics Salivary Cortisol Enzyme Immunoassay Kit (Salimetrics LLC, 101 Innovation Boulevard, Suite 302, State College, PA 16803). The method is based on a competitive immunoassay. Cortisol levels were measured in duplicate. Cortisol in standards and samples compete with cortisol conjugated to horseradish peroxidase for the antibody binding sites on a microtiter plate. Bound cortisol enzyme conjugate is measured by the reaction of the horseradish peroxidase enzyme to the substrate tetramethylbenzidine (TMB). The optical density is read on a standard plate reader at 450 nm. In brief, the thawed salivary samples were vortexed and centrifuge at 1500 \times g for 15 minutes to remove mucins ad debris. 25 μ l of samples and standard solution with concentration ranging from 0.012 to 3 μ g/dl were mixed in a pipette into the plate wells. After, 200 μ l of enzyme conjugate cortisol diluted 1 : 1600 in assay diluent was added to all the wells. After an incubation of 1 hour at room temperature, the plate was washed four times with washing buffer. The enzymatic reaction was started by adding 200 μ l of TMB Substrate Solution. Mixed on a plate rotator for 5 minutes at 500 rpm and incubated in the dark at room temperature for an additional 25 minutes. The reaction was stopped by adding 50 μ l of stop solution and rapidly read at 450 nm with a plate reader. The cortisol levels were determinate by interpolating the optical density on the standard curve obtained with 4-parameter nonlinear regression curve fit. The intra-assay coefficient of variation was 4% at 2.07 μ g/dl, and the interassay coefficient of variation was 3% at 1.99 μ g/dl. The analytical sensitivity was 0.007 μ g/dl.

2.3. Statistical Analysis. Analyses of the differences in clinical outcomes were performed by a statistician who was aware of the study aims using IBM SPSS Statistics for Windows, Version 20.0 (Armonk, NY: IBM Corp.). Data with a normal

TABLE 1: Clinical characteristics of study population.

	Control group ($n = 20$)	Study group ($n = 20$)
	Partial rooming-in practice (14 hs)	Full rooming-in practice (24 hs)
Nationality	Italian	Italian
Parents' residence	Campania	Campania
Type of delivery	Elective caesarean section	Elective caesarean section
Maternal age (yrs)	32 ± 2	33 ± 1.5
Maternal BMI	22 ± 2	20 ± 1
Parity	0	0
Gestational age (wks)	38.31 ± 0.63	38.89 ± 1
Birth weight (g)	3072 ± 406	3294.5 ± 357
Days of life at the time of sampling	3	3
Salivary cortisol levels (ng/dl)	727.4 ± 797.18	323 ± 231.8

Data are expressed as mean \pm SD. BMI: body mass index.

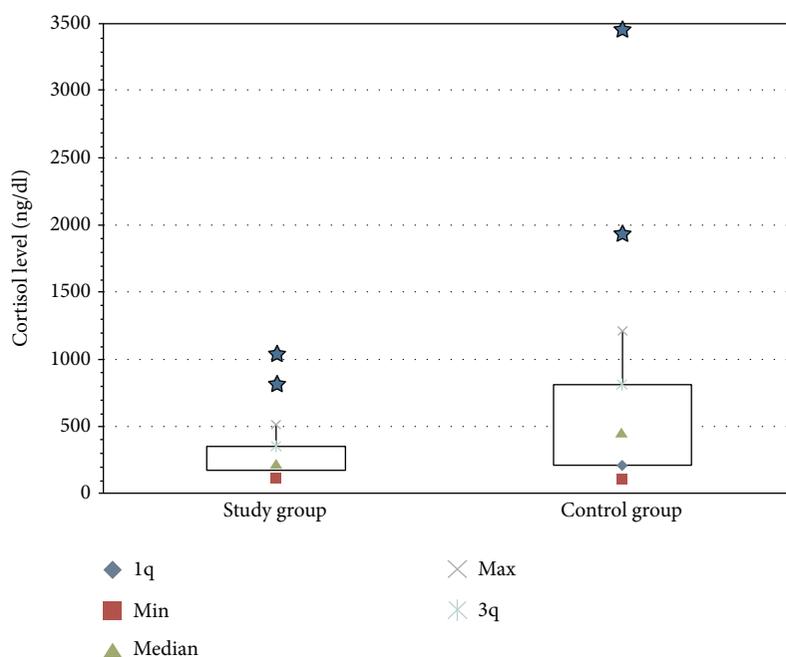


FIGURE 1: Salivary cortisol levels in the study group and the control group.

distribution were analysed using the Kolmogorov–Smirnov test. Homogeneity of data groups was assessed using an unpaired t -test while the different SCLs between the two groups were analysed by Mann–Whitney U test.

3. Results

A total of 20 newborns as control group and 20 newborns as study group were recruited. Preliminary data analysis validated the homogeneity of the samples. As showed in Table 1, all newborns and their families were Italian and resided in Campania. There was no difference between the case and study groups for the following parameters: body weight at birth, gestational age, and type of delivery. The sampling of saliva obtained on the 3rd day of life revealed

that SCLs were lower in the study group than in the control group (Table 1).

There was a statistically significant difference in the SCLs ($p = 0.048$) between the study group (median: 258 ng/dl) and the control group (median: 488.5 ng/dl) (Figure 1).

4. Discussion

Keeping the mother and infant together (rooming-in) or separating them after birth are both traditional practices seen in many cultures. Mother–infant proximity during after birth may influence neonatal stress response: this time, shortly after birth represents a sensitive or critical period for programming future physiology and behaviour [13, 14]. According to mammalian neuroscience, rooming-in practice allows the intimate contact that evokes neurobehaviours ensuring

fulfilment of basic biological needs [15]. Als suggested that the neurodevelopmental subsystem interaction between the neonate's internal functioning, the environment, and caregivers was the foundation of the neonatal developmental process: if a lack of equilibrium occurs within one subsystem, all other subsystems are affected [16]. Recently, rooming-in has been encouraged also for its benefits both for infants at risk of neonatal abstinence syndrome [17] and for implementation of the duration of breastfeeding [12]. The present paper aims to assess if the presence of the family, using different modalities of rooming-in care, reduces recovery stress by measuring SCLs in hospitalized newborns.

Usually, the procedures practiced are continuous rooming in (for 24 hs), which seems to be preferable, or partial. In literature are no evidence-based reports on which of these two practices is the best. Our work has the purpose to light up this lack of information about these procedures, to minimize pain, and to identify which interventions in hospital reduce stress in infants and to prioritize this intervention in everyday care.

Stress can be defined as a reaction to any real or perceived threat that leads to a disorder in the dynamic equilibrium between the organism and its environment [18, 19]. Newborns are often living and developing in an environment that can be stressful in many ways, starting from the time of birth. An organism's capacity to respond to stressors and maintain homeostasis is regulated by the hypothalamic-pituitary-adrenal (HPA) axis through the cortisol production. Since the beginning of the second trimester, the HPA axis functions and organizes in response to the environment [20]. Different life events, including trauma events, have been shown to influence the HPA, that is, cortisol secretion; therefore, cortisol is considered a major biomarker of stress, also among infants [21]. Recently, it has been showed that prenatal exposure to maternal stress could affect the subsequent cortisol reactivity of the infant [22]. Consequently, we excluded from our study all infants born from a nonphysiological pregnancy or from mothers with chronic pathologies or using drugs/smoke/alcohol. As Taylor et al. affirmed, also the mode of delivery could influence neonatal stress response: they found a lower cortisol reactivity during a procedure among infants delivered by caesarean section compared to those vaginally born [23]. Relying on this, we considered appropriate selecting only newborns born from a caesarean section, to exclude another source of external stress.

Secretion of the cortisol is essential for lung maturation at birth; hence, there is a corresponding increase in cortisol levels with increasing gestational age [21, 24]. Our population consists of full-term newborns, to equalize basal levels of cortisol in all our neonates.

Recently, some authors presented cortisol reference intervals for infants during the first twelve months of life, but only one month after birth, full-term healthy infants develop a circadian rhythm of salivary cortisol with increasing morning levels and corresponding decreasing evening levels [25]. The detection of the stress level in newborns was performed during the morning, in all patients at the same time. There are no cortisol reference

values during the first hours of life; thus, it has been possible to establish which of the practice between continuous and partial rooming-in was less stressful only by comparing the cortisol levels between the two groups. Since 1987, cortisol in saliva has been used as a valid method to assess adrenocortical activity in newborns and their response to stressful stimuli [8]: it is an easy and painless method to collect cortisol samples, to analyse neonatal stress. Nowadays, it is possible to collect enough saliva without disturbing the infant, for instance, during sensitive situations, such as mother-infant interaction [6].

In this pilot study, performed in a limited number of newborns, we observed a statistically significant difference between the SG and CG groups in SCLs that strongly suggested that full-time rooming-in is a better practice than partial rooming care in reducing neonatal stress response.

Our data strongly support the practice of rooming-in for 24 hours compared with partial rooming-in. We hypothesize that lower SCLs may have long-term positive effects in reducing the risk of metabolic syndrome, high blood pressure, and cognitive and behavioural changes. The results of this study pave the way for longer RCTs to confirm these preliminary results. Moreover, long-term follow-up studies are needed to verify the long-term effects on brain neurodevelopment.

Disclosure

The paper was represented as a poster in Conference: PAS San Francisco 2017.

Conflicts of Interest

The authors declare that there is no conflict of interests regarding the publication of this article.

Acknowledgments

The authors thank EURAIBI (Europe Against Infant Brain Injury) foundation for its partial grants.

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Research Article

Neutrophils Release Metalloproteinases during Adhesion in the Presence of Insulin, but Cathepsin G in the Presence of Glucagon

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Received 27 October 2017; Accepted 19 December 2017; Published 14 February 2018

Academic Editor: Joilson O. Martins

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In patients with reperfusion after ischemia and early development of diabetes, neutrophils can attach to blood vessel walls and release their aggressive bactericide agents, which damage the vascular walls. Insulin and 17 β -estradiol (E2) relieve the vascular complications observed in metabolic disorders. In contrast, glucagon plays an essential role in the pathophysiology of diabetes. We studied the effect of hormones on neutrophil secretion during adhesion to fibronectin. Amino acid analysis revealed that proteins secreted by neutrophils are characterized by a stable amino acid profile enriched with glutamate, leucine, lysine, and arginine. The total amount of secreted proteins defined as the sum of detected amino acids was increased in the presence of insulin and reduced in the presence of glucagon. E2 did not affect the amount of protein secretion. Proteome analysis showed that in the presence of insulin and E2, neutrophils secreted metalloproteinases MMP-9 and MMP-8 playing a key role in modulation of the extracellular matrix. In contrast, glucagon induced the secretion of cathepsin G, a key bactericide protease of neutrophils. Cathepsin G can promote the development of vascular complications because of its proinflammatory activity and ability to stimulate neutrophil adhesion via the proteolysis of surface receptors.

1. Introduction

Neutrophils, or polymorphonuclear leukocytes, play an important role in host defense against bacterial or fungal pathogens due to their ability to penetrate into infected tissue and phagocytose and kill microbes. To kill microbes, bactericide agents that are localized in the neutrophil secretory granules are released into the formed phagosomes and outwards [1]. Bactericides, being released outside, cause the destruction of surrounding host tissues and the development of inflammation.

Neutrophils can release their bactericides to the outside also in the absence of infection. In patients with certain

metabolic disorders, neutrophils that normally roll in the bloodstream can attach to the walls of the blood vessels and secrete their aggressive products. Adherence of neutrophils to endothelial cells is an early and requisite event in ischemia/reperfusion-induced inflammatory injury [2, 3]. The authors of many modern studies consider the integrin-dependent adhesion of neutrophils and associated secretion of neutrophil bactericidal agents to be the cause of the early stages of retinopathy [4–6] or nephropathy [7, 8] in patients with diabetes.

Insulin produced by β -cells of the pancreatic Langerhans islets plays a key role in maintaining vascular health. Clinical evidence indicates that intensive insulin therapy protects the

endothelium in cardiovascular diseases, during critical illness [9, 10], and reduces major cardiovascular events in diabetics [11]. In particular, insulin attenuates neutrophil accumulation in myocardial ischemia/reperfusion rabbit hearts and inhibits neutrophil adhesion to cultured endothelial cells subjected to simulated ischemia/reperfusion [12].

Glucagon produced by α -cells of the Langerhans islets is a physiological antagonist of insulin. In healthy patients, production of glucagon is inhibited by insulin at a high level of glucose in the blood. In patients with diabetes, an oral glucose load induced a paradoxical rise in glucagon secretion. Absolute or relative hyperglucagonaemia has been recognized for years in all experimental or clinical forms of diabetes [13]. Glucagon seems to play an essential role in the pathophysiology of diabetes. Knockout of the glucagon receptor or administration of a monoclonal specific glucagon receptor antibody makes insulin-deficient type 1 diabetic rodents thrive without insulin [14–16]. However, the mode of glucagon action remains to be elucidated. Despite the active search, a glucagon antagonist, which can be effective in treating diabetes, has not yet been found. In the treatment of type 2 diabetes, there are largely used drugs that act, in part, by inhibiting the secretion or action of glucagon, such as glucagon-like peptide-1 (GLP-1) and GLP-1 receptor agonists, dipeptidyl peptidase-4 inhibitors (DPP-4), and metformin [17–19]. Inhibition of glucagon secretion and stimulation of insulin release equally contribute to a decrease in glucose with respect to the action of GLP-1 [17].

The action of GLP-1 is transient, since the peptide is rapidly inactivated by DPP-4. DPP-4 inhibitors are used to prolong the action of GLP-1. Metformin has a glucose-lowering effect, inhibiting hepatic gluconeogenesis and counteracting the action of glucagon [19]. GLP-1 receptor agonists, DPP-4 inhibitors, and metformin have beneficial effects on cardiovascular complications in patients with type 2 diabetes, as well as in patients with reperfusion after ischemia [20–22]. Prevention of vascular adhesion of monocytes contributes to the cardiovascular protective effect of GLP-1 analogs [23, 24]. Metformin also could reduce vascular complication of diabetes by decreasing leukocyte oxidative stress and undermining adhesion molecule levels and leukocyte-endothelium interactions [25].

Female hormones play an important role in maintaining vascular health, as evidenced by an increase in the incidence of cardiovascular disease in women after menopause [26]. Pretreatment with estrogen prior to myocardial ischemia and reperfusion causes a decrease in neutrophil infiltration into the irreversibly injured myocardium [27]. Traditionally, estrogen acts via classical nuclear estrogen receptors. In addition to this “genomic” signalling pathway, a “rapid, nonnuclear” signalling pathway mediated by cell membrane-associated estrogen receptors also has been recognized. This nonnuclear signalling appears to be critical for the protective effects of estrogen in the cardiovascular system [28–30].

In this work, we studied the effect of insulin, glucagon, and 17β -estradiol (E2) on secretion of human neutrophils upon adhesion to fibronectin. We used scanning electron microscopy to study the morphology of the attached

neutrophils, as well as amino acid analysis and mass spectrometry to study the amount and composition of secreted proteins.

2. Material and Methods

2.1. Materials. Ficoll-Paque for neutrophil isolation was obtained from Pharmacia (Uppsala, Sweden). Fibronectin was from Calbiochem (La Jolla, USA). Bicarbonate-free Hank's solution, Ca^+ -free Dulbecco PBS, insulin, glucagon, and 17β -estradiol were purchased from Sigma. Trypsin was from Promega, and Coomassie Brilliant Blue G-250 was from Serva.

2.2. Neutrophil Isolation. Neutrophils were isolated from the blood of healthy volunteers, who did not take any medication for 2 weeks, using experimental procedures approved by the Ethics Committee of A. N. Belozersky Institute. Erythrocytes were precipitated with 3% dextran T-500 at room temperature. Neutrophils were isolated from the plasma by centrifugation via Ficoll-Paque (density 1.077 g/mL). The remaining red blood cells were eliminated by hypotonic lysis. After washing, neutrophils (purity 96–97%, viability 98–99%) were stored before the experiment in Dulbecco's PBS containing 1 mg/mL glucose (without CaCl_2).

2.3. Adhesion of Neutrophils to Fibronectin-Coated Cover Slips. For scanning electron microscopy (SEM), neutrophils were plated onto fibronectin-coated glass coverslips. The coverslips were coated with fibronectin for 2 hours by incubation in Hank's solution containing 5 $\mu\text{g}/\text{mL}$ of fibronectin at room temperature and washed with buffer. Neutrophils adhered to the fibronectin-coated coverslips (3×10^6 cells in 2 mL per well) for a 20 min incubation in Hank's solution containing 10 mM HEPES (pH 7.35) at 37°C. Insulin, glucagon, or 17β -estradiol (0.1 μM) was added to the cells before plating. After that, the cells were fixed for SEM.

2.4. Sampling of the Extracellular Medium to Determine the Amino Acid and Protein Composition of Neutrophil Secretion. Six-well culture plates were coated with fibronectin for 2 hours of incubation in Hank's solution containing 5 $\mu\text{g}/\text{mL}$ fibronectin at room temperature and washed. Neutrophils adhered to the protein-coated wells (3×10^6 cells in 1.3 mL per well) in Hank's solution containing 10 mM HEPES (pH 7.35) for 20 minutes at 37°C. Insulin (0.1 μM), glucagon (0.1 μM), or 17β -estradiol (0.1 μM) was added to the cells prior to plating. After the incubation, the extracellular medium was sampled from the control and hormone-treated cells. Aliquots were collected from six similar wells and combined. Inhibitors of metalloproteinase, serine and cysteine proteinases, and myeloperoxidase (EDTA, 5 mM; PMSF, 200 μM ; E64, 10 μM ; and sodium azide, 0.025%, resp.) were immediately added to the samples. Unattached neutrophils were removed by centrifugation at 2000g.

2.5. Extraction, Concentration, and Hydrolysis of Proteins. Proteins from the collected EM samples were extracted with an equal volume of a chloroform-methanol mixture (2:1, v/v). The mixture was vortexed for 1–2 minutes and

stirred in a shaker at 4°C for 30 minutes. The chloroform and methanol phases were then separated by centrifugation at 11,000g for 20 minutes, and the solvents were evaporated. The chloroform phase contained almost all of the proteins detected. The water-methanol fractions contained trace amounts of protein. Concentrated extracts of chloroform phases were subjected to electrophoresis. For amino acid analysis, the same extracts were prehydrolysed, as described by Tsugita and Scheffler [31].

2.6. Quantitative Determination of Amino Acids with Ninhydrin. The amino acid profile of protein hydrolysates was determined by an L-8800 amino acid analyser (Hitachi, Tokyo, Japan) with an electronic heating bath and two single-channel colorimeters according to the manufacturer's user manual (Hitachi High-Technologies Corporation, Japan, 1998). The protein hydrolysates were separated on a 2622SC-PF ion-exchange column (Hitachi Ltd., P/N 855-4507, 4, 6 × 60 mm) by a step gradient of four Li-citrate buffers at a flow rate of 0.35 mL/min and a thermostating column at 30–70°C. Postcolumn derivatization (136°C, flow rate 0.35 mL/min) was performed using a mix of equal volumes of ninhydrin buffer R2 and ninhydrin solution R1 (Wako Pure Chemical Industries, P/N 298-69601). Colored products were detected by measuring the absorbance at 570 nm for all amino acids except proline and at 440 nm for proline. Data were processed using MultiChrom for Windows software (Ampersand Ltd., Moscow, Russia).

The total amount of proteins released by control cells was defined as the sum of detected amino acids (Table 1). Insulin and glucagon are protein hormones with a molecular mass of 5800 and 3482, respectively. When used at 0.1 μM, they contribute 0.58 or 0.35 μg of protein per millilitre. Bearing in mind that the total volume of each sample is 7.8 mL (1.3 mL × 6), we subtracted 4.5 or 2.7 μg, respectively, from the total amount of proteins secreted by insulin- or glucagon-treated cells.

2.7. Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis. Protein separation was performed using one-dimensional sodium dodecyl sulfate electrophoresis on a 15% polyacrylamide gel under nonreducing conditions in the Mini-PROTEAN 3 Cell (Bio-Rad) [32]. Prior to electrophoresis, aliquots of the preparations were boiled for 3 minutes in lysis buffer (Tris-HCl 30 mM, pH 6.8; SDS 1%; urea 3 M; glycerin 10%; bromophenol blue 0.02%). Gels were stained with Coomassie Brilliant Blue G-250 0.22% (Serva).

2.8. Mass Spectrometry Identification of Proteins and Preparation of Samples. A MALDI-time of flight (ToF)-ToF mass spectrometer (Ultraflex II Bruker, Germany) equipped with a neodymium-doped (Nd) laser was used for matrix-assisted laser desorption ionization mass spectrometry (MALDI-MS) and tandem mass spectrometry (MS/MS) analysis of proteins. Proteins separated by electrophoresis were subjected to trypsin hydrolysis directly in the gel. To this end, after electrophoresis, 1 × 1 mm slices of gel were cut from each Coomassie-stained protein band. Gel pieces were washed twice with 100 μL acetonitrile 40% in

TABLE 1: Effect of hormones on the amount of protein secreted by neutrophils in adhesion to fibronectin.

Treatment	Average amount of secreted proteins, μg/18 × 10 ⁶ cells
Control	64.6 ± 1.8
E2	62.5 ± 3.2
Insulin	76.1 ± 2.0*
Glucagon	50.0 ± 1.9*

Proteins were extracted from extracellular medium samples collected from neutrophils that were attached to fibronectin during a 20 min incubation in the presence of 0.1 μM E2, insulin, or glucagon. After acid hydrolysis, the protein hydrolysates were subjected to amino acid analysis. The amount of secreted proteins was determined as the sum of the amounts of the detected amino acids. **p* < 0.05 when compared to the control value.

NH₄HCO₃ 100 mM (pH 7.5) for 30 min at 37°C, dehydrated with 100 μL acetonitrile, and air-dried. Then, they were incubated with 4 μL modified trypsin 12 μg/mL (Promega) in NH₄HCO₃ 50 mM for 6 h at 37°C. The resulting peptides were recovered through incubation with 6 μL trifluoroacetic acid solution 0.5% in acetonitrile 10% for 30 min. For mass spectrometric analysis, sample aliquots (1 μL) were mixed on a steel target with 0.3 μL 2,5-dihydroxybenzoic acid (20 mg/mL in acetonitrile 20% and trifluoroacetic acid 0.5%) and air-dried at room temperature. The [MH]⁺ molecular ions were measured in reflector mode; the accuracy of mass peak measurement was within 0.005%. Identification of proteins was carried out by a peptide fingerprint search using Mascot software (<http://www.matrixscience.com>) through the Unipro+ (SwissPro+) mammalian protein database with the indicated accuracy. The search allowed for possible oxidation of methionine by environmental oxygen and modification of cysteine with acrylamide, and where a score was >71, protein matches were considered significant (*p* < 0.05).

2.9. Scanning Electron Microscopy Technique. Neutrophils that were attached to fibronectin were fixed in 2.5% glutaraldehyde in Hanks buffer, which did not contain Ca²⁺ or Mg²⁺ ions, but contained inhibitors of metalloproteinases and serine proteases (5 mM EDTA and 0.5 mM PMSF, resp.) and 10 mM HEPES at pH 7.3. The cells were additionally fixed with 1% solution of osmium tetroxide in 0.1 M sodium cacodylate containing 0.1 M sucrose at pH 7.3. The samples were then dehydrated in an acetone series (10–100%) and dried at a critical point with liquid CO₂ as the transition liquid in the Balzers apparatus. The samples were sputter-coated with gold/palladium and observed at 15 kV using a Camscan S-2 scanning electron microscope.

3. Results and Discussion

3.1. Effect of Insulin, E2, and Glucagon on the Morphology of Human Neutrophils Attached to a Fibronectin-Coated Substrate. The adhesion of resting neutrophils (control neutrophils) to a glass or polystyrene itself leads to cell activation [33]. We studied the secretion of neutrophils in the process of adhesion to substrates coated with fibronectin, the extracellular matrix protein, since neutrophils exhibit

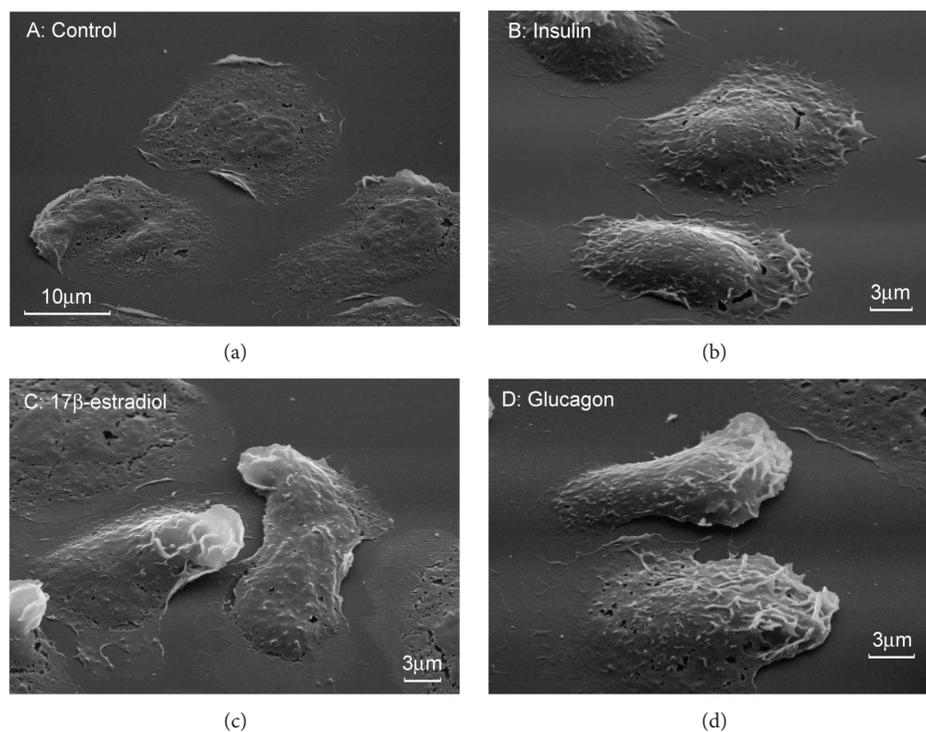


FIGURE 1: Effect of hormones on the morphology of human neutrophils attached to fibronectin. Scanning electron microscopy images of neutrophils that were attached to fibronectin for 20 min in control conditions (a) or in the presence of $0.1 \mu\text{M}$ insulin (b), $0.1 \mu\text{M}$ E2 (c), or $0.1 \mu\text{M}$ glucagon (d). Pictures represent typical images observed in two independent experiments.

only a priming activation when adhered to fibronectin. We compared the morphology of neutrophils that were attached to fibronectin-coated substrata in the presence $0.1 \mu\text{M}$ of insulin, glucagon, or E2. Scanning electron microscopy showed that the control cells and insulin-, glucagon-, or E2-treated cells were attached and spread on fibronectin-coated substrates (Figures 1(a)–1(d)). At the concentration used in the experiment, the hormones contribute only minor features to the morphology of the cells.

3.2. Effect of Insulin, Glucagon, and E2 on the Amount and Amino Acid Composition of Proteins Released by Neutrophils in Adhesion to Fibronectin. Neutrophils secrete their products via a variety of the mechanisms, including fusion of secretory granules with the plasma membrane [34] and shedding of membrane vesicles (ectosomes) from the plasma membrane [35–39]. Secreted proteins enter the extracellular medium as separate molecules or as part of membrane structures. To analyse all secreted proteins, we extracted proteins from the extracellular medium using a chloroform-methanol mixture. Earlier, we were convinced that practically all proteins are in the chloroform fraction [40]. After evaporation of the solvent, the proteins in the chloroform fraction were separated by electrophoresis or subjected to acid hydrolysis and subsequent amino acid analysis.

We used amino acid analysis to determine the total amount of protein secreted by neutrophils during adhesion to fibronectin under various conditions. After acid hydrolysis, the quantitative content of the individual amino acids

in the protein hydrolysate was determined using an amino acid analyser (Figure 2).

In the process of acid hydrolysis, tryptophan was destroyed, and glutamine and asparagine were converted into glutamic and aspartic acid, respectively. Therefore, tryptophan is absent from the histogram, and the columns corresponding to glutamic acid and aspartic acid represent the sum of asparagine and aspartic acid or glutamine and glutamic acid, respectively. Amino acid analysis revealed a stable amino acid profile of proteins released by neutrophils that were attached to fibronectin under control conditions. The protein hydrolysate was enriched with serine, glutamate/glutamine, leucine, lysine, and arginine (Figure 2(a)). Summarizing the number of all detected amino acids, we determined the total amount of protein secreted by the cells under different experimental conditions (Table 1). The amount of secreted proteins increased by 18% in the presence of insulin but reduced in the presence of glucagon. The female hormone E2 had little effect on the amount of protein secreted by neutrophils.

A comparison of the percentage of individual amino acids in hydrolysates of proteins showed that the amino acid profile of protein secretion was generally retained for neutrophils that were attached to fibronectin in the presence of insulin, E2, or glucagon (Figure 2(b)). The amino acid profile of secretion products can serve as a type of “fingerprint” of human neutrophil secretion.

3.3. Effect of E2 on the Protein Composition of Neutrophil Secretion in Adhesion to Fibronectin. To determine which

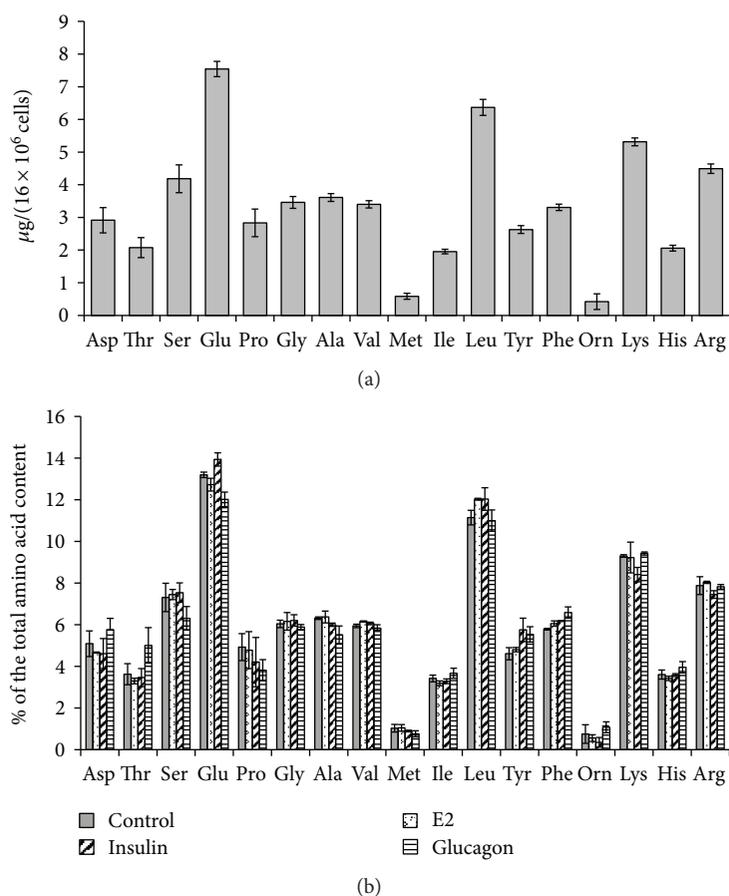


FIGURE 2: Effect of hormones on the amino acid composition of proteins secreted by neutrophils in adhesion to fibronectin. Human neutrophils were attached to a substrate coated with fibronectin for 20 min under control conditions or in the presence of 0.1 μ M E2, insulin, or glucagon. The proteins were extracted from the extracellular medium, concentrated, and after acid hydrolysis subjected to amino acid analysis. (a) The amount of detected amino acids in the hydrolysate of proteins secreted by control neutrophils (mean \pm SEM) is presented. (b) Comparison of the percentage of individual amino acids in hydrolysates of proteins secreted by neutrophils under control conditions and in the presence of hormones. Amino acid profiles were obtained by summing the results of three independent experiments.

proteins are secreted by neutrophils under the action of hormones, protein extracts of extracellular media after removal of chloroform were separated by electrophoresis (Figure 3). Identification of proteins represented by separate bands in the gel was carried out by mass spectrometry after trypsin hydrolysis directly in the gel (Table 2).

Previously, we have shown that control neutrophils during 20 min of adhesion to fibronectin secreted lactoferrin (LF), neutrophil gelatinase-associated lipocalin (NGAL), lysozyme, and myeloperoxidase (MPO), as well as albumin and cytosolic S100A8 and S100A9 proteins [40, 41]. Neutrophils contain secretory granules of four types [1]. The composition of granules of different types largely overlaps [42]. Nevertheless, LF and NGAL are considered components of the secondary granules, MPO is contained mainly in the primary granules, and albumin belongs to secretory vesicles.

When neutrophils adhere to fibronectin in the presence of E2, they release the same proteins as the control cells (LF, albumin, NGAL, S100A8, and S100A9) and, in addition, metalloproteinase 9 (MMP-9) (Figure 3(a), Table 2). MMP-9 is localized presumably in the tertiary or gelatinase granules

of neutrophils [43]. Metalloproteinases are involved in the adhesion and migration of neutrophils because of their ability to modulate the extracellular matrix and remove the barriers of the basement membranes [44]. The balance between MMPs and their tissue inhibitors (TIMPs) tightly regulates physiological and pathological processes characterized by the degradation and accumulation of the extracellular matrix [45]. We assume that the ability of E2 to initiate the secretion of MMP-9 in adherent neutrophils can alter the result of the interaction of neutrophils with the walls of the blood vessel and contribute to the protective effect of E2 in metabolic diseases.

3.4. Effect of Insulin on the Protein Composition of Neutrophil Secretion in Adhesion to Fibronectin. Neutrophils that adhered to fibronectin in the presence of insulin secreted the same proteins as the control cells and, in addition, MMP-9 and matrix metalloproteinase 8 (MMP-8) (Figure 3(b); Table 2). MMP-8, or neutrophil collagenase, is involved in degradation of all structural components of extracellular matrix and plays a crucial role in many physiological processes including inflammatory and cardiovascular

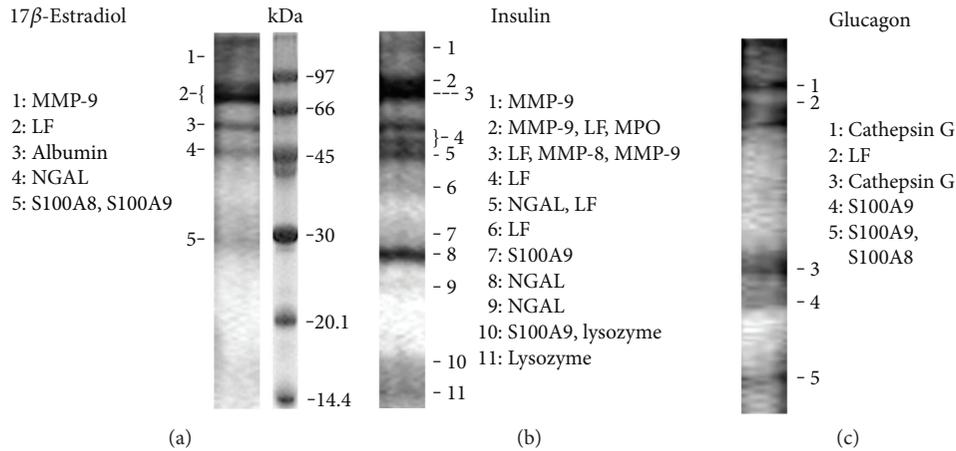


FIGURE 3: SDS-PAGE separation of proteins secreted by neutrophils upon adhesion to fibronectin in the presence of hormones. Human neutrophils were attached to fibronectin-coated substrata for 20 min in the presence of $0.1 \mu\text{M}$ E2 (a), $0.1 \mu\text{M}$ insulin (b), or $0.1 \mu\text{M}$ glucagon (c). Samples of extracellular medium were collected, and proteins were extracted and subjected to 15% SDS-PAGE. Pictures represent typical protein profiles observed in the three independent experiments for each hormone.

TABLE 2: List of proteins secreted by neutrophils in adherence to fibronectin in the presence of hormones.

	Protein name				Peptides matched/total	Coverage, %	MOWSE score
	Control	Insulin	E2	Glucagon			
MMP-9_HUMAN		MMP-9	+		18/85	25	240
MMP-8_HUMAN		MMP-8			15/85	31	240
CATG_HUMAN				Cath. G	15/77	40	75
PERM_HUMAN	+	MPO			17/85	21	119
TRFL_HUMAN	+	LF	+	+	29/85	43	240
ALBU_HUMAN	+		Albumin		15/28	24	130
NGAL_HUMAN	+	NGAL	+		7/15	42	105
LYSC_HUMAN	+	Lysozyme*	+			31	98
S10A9_HUMAN	+	S100-A9	+	+	9/19	48	147
S10A8_HUMAN	+		S100-A8	+	5/30	44	84

Neutrophils were attached to fibronectin for 20 minutes under control conditions (marked +), or in the presence of $0.1 \mu\text{M}$ insulin, $0.1 \mu\text{M}$ E2, or $0.1 \mu\text{g}$ glucagon. Mass spectrometric analysis data were taken from experiments with insulin. Analogous proteins that were identified in control experiments or in experiments with E2 or glucagon are marked (+). Mass spectrometric data for cathepsin G are taken from experiments with glucagon, and those for albumin and S100A8 from experiments with E2. Proteins were separated by SDS-PAGE and identified by mass spectrometric analysis. *Protein was identified by MSMS analysis. Proteins identified in two or three analogous experiments were included in the list.

disorders [46]. Since many inflammatory processes are accompanied by increased levels of MMP-8, it is assumed that the enzyme contributes to the development of inflammation. However, modern research refutes this view. The emergence of MMP-8-deficient mice resulted in the publication of a number of studies demonstrating an anti-inflammatory role of MMP-8 during lipopolysaccharide- (LPS-) mediated acute lung injury [47, 48] or allergen-induced airway inflammation [49].

Another characteristic feature of insulin-stimulated secretion was the presence of NGAL (neutrophil gelatinase-associated lipocalin) in several electrophoretic bands (Figure 3(b), bands 5, 8, 9) corresponding to monomeric (24 kDa) or homodimeric (46 kDa) forms of the protein [50]. In secretion from control [40] or E2-treated cells (Figure 3(a), band 4), NGAL was represented by minor bands corresponding to its homodimer form. These data

indicating that, in the presence of insulin, neutrophils secrete an increased amount of NGAL are consistent with previously published work demonstrating that hyperinsulinaemic induction in humans significantly increases circulating levels of lipocalin-2. Additionally, in omental adipose tissue explants, insulin caused a significant dose-dependent increase in lipocalin-2 protein production and secretion into conditioned media [51].

A characteristic feature of NGAL is the ability to form complexes with MMP-9 after these components are in the extracellular environment. According to some researchers, the complex with NGAL supports allosteric activation of MMP-9 [52]. From another point of view, the formation of complex with NGAL protects MMP-9 from degradation by TIMPs, thereby maintaining the activity of the enzyme [44, 53, 54]. In any case, insulin initiates the secretion of MMP-9 in neutrophils and, at the same time, increases

the release of lipocalin, which helps maintain the activity of MMP-9.

3.5. Effect of Glucagon on the Protein Composition of Neutrophil Secretion in Adhesion to Fibronectin. The main components of the secretion of neutrophils adherent to fibronectin in the presence of glucagon were the cathepsin G, LF, and S100A9 proteins (Figure 3(c), Table 2). Cathepsin G is one of the three serine proteases (along with proteinase-3 and elastase) that are contained in primary (azurophil) granules of neutrophils and involved in clearance of internalized pathogens, proteolytic modification of chemokines and cytokines, and shedding of cell surface receptors [55]. Cathepsin G deficiency in gene-targeted mice increases susceptibility to *Staphylococcus aureus* and fungal infections indicating the key role of the enzyme in neutrophil antimicrobial activity [56, 57].

The glucagon-induced neutrophil secretion is also enriched in LF. Recent data show that LF can serve as an allosteric enhancer of the proteolytic activity of cathepsin G [58]. LF potently increases the activity of cathepsin G at pH 7.4 and to an even higher extent at pH 5, as well as in granulocyte-derived supernatant. Furthermore, LF might induce a conformational change of cathepsin G resulting in advanced substrate selectivity. LF and cathepsin G appear to act synergistically during secretion by granulocytes augmenting the process associated with host defense. We suggest similar synergistic interactions may occur in blood vessels between cathepsin G and LF that are secreted by glucagon-treated neutrophils attached to the vessel walls in patients with metabolic disorders.

Cathepsin G secreted by neutrophils can damage the vascular walls via promotion of inflammation or disruption of the neutrophil surface receptors. Cathepsin G, for example, is able to cleave leukosialin (CD43), the predominant cell surface sialoprotein of leukocytes, and releases its extracellular domain [59]. The shedding of highly negatively charged membrane sialoglycoprotein CD43 is commonly thought to enhance neutrophil adhesion. Thus, glucagon-induced cathepsin G secretion, in turn, may further potentiate the adhesion of neutrophils and the corresponding damage to blood vessels [60, 61].

3.6. Conclusions. Our in vitro experiments revealed that insulin and E2 stimulated secretion of MMP-9 and MMP-8 by human neutrophils during adhesion to fibronectin-covered substrata. In contrast, glucagon stimulated secretion of cathepsin G. We assume that hormones can affect the state of blood vessels in diabetes and metabolic disorders, regulating the adhesion of neutrophils to the walls of blood vessels and their corresponding secretion. Extracellular matrix proteins play a crucial role in the process of cell adhesion. Insulin and E2 can alter the adhesion of neutrophils initiating the secretion of metalloproteinase, which modifies extracellular matrix proteins. Glucagon can contribute to the development of metabolic vascular disorders by initiating the secretion of cathepsin G, the key enzyme of the bactericide activity of neutrophils. Cathepsin G may promote inflammation and

stimulate further neutrophil adhesion via proteolysis of cell surface receptors.

Abbreviations

SEM:	Scanning electron microscopy
MPO:	Myeloperoxidase
Lf:	Lactoferrin
NGAL:	Neutrophil gelatinase-associated lipocalin
S100A8, S100A9:	The S100 calcium-binding proteins, known also as calgranulins A and B or myeloid-related proteins MRP8 and MRP14
MMP-9:	Matrix metalloproteinase 9 or gelatinase B, 92 kD
MMP-8:	Matrix metalloproteinase 8
TIMPs:	Tissue inhibitors of metalloproteinases
E2:	17 β -Estradiol
SDS-PAGE:	Sodium dodecyl sulfate polyacrylamide gel electrophoresis.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

The work was supported by a grant from the Russian Foundation of Basic Research 16-04-670-a.

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