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<td>Author(s)</td>
<td>Luo, W; Wang, CY; Jin, L</td>
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Baicalin Downregulates *Porphyromonas gingivalis*
Lipopolysaccharide-Upregulated IL-6 and IL-8 Expression in Human Oral Keratinocytes by Negative Regulation of TLR Signaling

Wei Luo¹, Cun-Yu Wang², Lijian Jin*¹

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Abstract

Periodontal (gum) disease is one of the main global oral health burdens and severe periodontal disease (periodontitis) is a leading cause of tooth loss in adults globally. It also increases the risk of cardiovascular disease and diabetes mellitus. *Porphyromonas gingivalis* lipopolysaccharide (LPS) is a key virulent attribute that significantly contributes to periodontal pathogenesis. Baicalin is a flavonoid from *Scutellaria radix*, an herb commonly used in traditional Chinese medicine for treating inflammatory diseases. The present study examined the modulatory effect of baicalin on *P. gingivalis* LPS-induced expression of IL-6 and IL-8 in human oral keratinocytes (HOKs). Cells were pre-treated with baicalin (0–80 μM) for 24 h, and subsequently treated with *P. gingivalis* LPS at 10 μg/ml with or without baicalin for 3 h. IL-6 and IL-8 transcripts and proteins were detected by real-time polymerase chain reaction and enzyme-linked immunosorbent assay, respectively. The expression of nuclear factor-κB (NF-κB), p38 mitogen-activated protein kinase (MAPK) and c-Jun N-terminal kinase (JNK) proteins was analyzed by western blot. A panel of genes related to toll-like receptor (TLR) signaling was examined by PCR array. We found that baicalin significantly downregulated *P. gingivalis* LPS-stimulated expression of IL-6 and IL-8, and inhibited *P. gingivalis* LPS-activated NF-κB, p38 MAPK and JNK. Furthermore, baicalin markedly downregulated *P. gingivalis* LPS-induced expression of genes associated with TLR signaling. In conclusion, the present study shows that baicalin may significantly downregulate *P. gingivalis* LPS-upregulated expression of IL-6 and IL-8 in HOKs via negative regulation of TLR signaling.


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Introduction

Periodontal disease is one of the main global oral health burdens and severe periodontal disease (periodontitis) is a major cause of tooth loss in adults globally [1]. Emerging evidence shows that it also increases the risk of some life-threatening diseases like cardiovascular disease and diabetes mellitus [2–4]. Periodontitis is characterized by bacteria-induced, uncontrolled inflammatory destruction of tooth-supporting tissues and alveolar bone in susceptible individuals [5]. *Porphyromonas gingivalis* is a major periodontal pathogen and its lipopolysaccharide (LPS) is one of the key virulent attributes that significantly contributes to periodontal pathogenesis [6,7]. It can stimulate the host to produce a variety of pro-inflammatory cytokines like IL-6 and IL-8, thereby involving in the initiation and progression of periodontal disease [8–10].

Toll-like receptors (TLRs) are a family of pattern recognition receptors (PRRs) that recognize microbial components and mediate the activation of host response [11]. Microbial LPS utilizes TLR4 to activate nuclear factor-κB (NF-κB), p38 mitogen-activated protein kinase (MAPK) and c-Jun N-terminal kinase (JNK), leading to the production of pro-inflammatory cytokines [11]. This process requires an initial recruitment of myeloid differentiation primary-response protein 88 (MyD88) to TLR4 [12–14]. In addition, there exists a TLR4-mediated MyD88-independent pathway that recruits toll/interleukin-1 receptor (TIR) domain-containing adaptor inducing interferon-β (TRIF) instead of recruitment of MyD88 to TLR4 in response to LPS, thereby activating the expression of interferon (IFN)-β and IFN-inducible genes like chemokine (C-X-C motif) ligand 10 (CXCL10) [15–18]. LPS is a TLR4 ligand and *P. gingivalis* LPS interacts with TLR4 to activate host response [19–21]. Nevertheless, it has been reported that *P. gingivalis* LPS could interact with TLR2 as well [22–24], due to the heterogeneity in lipid A structure of *P. gingivalis* LPS [8,25,26], and/or the contamination of LPS with some bioactive molecules like phosphorylated lipids and lipoproteins [27–29].

Recently, host modulatory therapy (HMT) has been proposed as a promising adjunct to conventional periodontal treatment [30,31]. Some examples of HMT in treatment of periodontitis include subantimicrobial dose of doxycycline, lipoxins and resolvins.
sterilization. Working solutions were made with fresh oral
baicalin was dissolved in pure dimethyl sulfoxide (DMSO) (Sigma), and
Kong Jockey Club Institute of Chinese Medicine, Hong Kong. It
seeded at 5000 cells/cm² with the oral keratinocyte medium
atmosphere of 5% CO₂ and 95% air. The medium was changed
(Sciencell). The incubation condition was set at 37
m
P. gingivalis
downregulated
baicalin may inhibit IL-1
and collagens in rat models of periodontitis [37,38]. Furthermore,
in human periodontal ligament cells, and reduces the loss of bone
and collagens in rat models of periodontitis [37,38].

Materials and Methods

Preparation of P. gingivalis LPS and Baicalin

Lyophilized LPS from P. gingivalis with type II fimA (strain code
TDC60) was kindly provided by Prof. Y. Abiko (Nihon University,
Japan). The LPS was prepared using the hot phenol water method
[40,41]. It was reconstituted in Dulbecco’s phosphate-buffered saline (DPBS) to a concentration of 1.0 mg/ml, followed by
filtration through a 0.2 m cellulose acetate membrane filter
(Milipore, MA, USA). Baicalin powder (solvant extracted with a
purity >95% as tested by HPLC) was obtained from the Hong
Kong Jockey Club Institute of Chinese Medicine, Hong Kong. It
was dissolved in pure dimethyl sulfoxide (DMSO) (Sigma), and
then diluted in DPBS to 1.0 mM and finally filtered for
sterilization. Working solutions were made with fresh oral
keratinocyte medium on the experiment day.

Total RNA Extraction and cDNA Synthesis

Total RNA was extracted using the RNasy mini kit (Qiagen,
CA, USA). Briefly, cells were lysed with the buffer RLT, and the
lysat was applied to an RNasy Mini spin column. After several
rounds of washes using the buffer RW1 and RPE, total RNA was
bound to the column and other cell components were efficiently
washed away. At the end, total RNA was eluted in RNase-free
water. To avoid the contamination of genomic DNA, on-column
DNase digestion was performed during RNA purification. The
concentration of purified RNA was quantified by measuring its
260 nm UV absorbance on a NanoDrop spectrophotometer
(Thermo, MA, USA). The integrity of purified RNA was evaluated
by checking the ratio of 28 S rRNA and 18 S rRNA bands on an
agarose gel. cDNA was synthesized using the Quantitect Reverse
Transcription Kit (Qiagen). In brief, 1.0 µg of total RNA was pre-
incubated with the gDNA Wipout Buffer at 42°C for 2 min to remove any residual genomic DNA. The mixture was then
incubated with the QuantiScript Reverse Transcripase, Quanti-
script RT Buffer and RT Primer Mix at 42°C for 30 min, followed
by a termination step at 95°C for 5 min.

Real-time Polymerase Chain Reaction (PCR)

Each real-time PCR reaction mix contained 10.0 µl of the
QuantFast SYBR green master mix (Qiagen), 1.0 µl of cDNA
template (5.0 ng), 1.0 µl of forward primer (10 µM), 1.0 µl of reverse primer (10 µM) and 7.0 µl of ultra-pure water. The
reaction condition was set as follows: an initial activation at 95°C
for 5 min, followed by 40 cycles at 95°C for 10 s and 60°C for
50 s. The primer sequences were: for IL-6, 5’-AATCAT-
CACATGCTCTTTTGGAAG (forward), 5’-
GCATTGGTGTGGTGTTGCTGCA (reverse); and for IL-8, 5’-GA-
CATACCTCAGACCTTTCCACC (forward), 5’-AACATGTCTC-
CAGAACCCTCTG (reverse); for β-actin (ACTB), 5’-
TTGGCAATGAGCGGTTTT (forward), 5’-AGTGAAGGG-
TAGTTCTGTTGGAAT (reverse). All the primers were designed
to amplify a region that lasts 100–250 base pairs long and contains
at least one intron. They had passed our in-house amplification
efficiency and specificity tests prior to usage. To check for
non-specific primer binding or co-amplification of residual genomic
DNA, the melting curve was analyzed after each running. To
detect foreign DNA contamination, a no-template control which
contained all the reagents except the cDNA template was included
in each running. Raw fluorescence data were analyzed by an Excel
workbook called DART-PCR which automatically calculates
threshold cycles, relative quantification values and amplification
efficiencies [12].

Enzyme-linked Immunosorbent Assay (ELISA)

ELISA kits (R&D, MN, USA) were used to quantitatively
determine the concentrations of IL-6 and IL-8 in culture
supernatants. In brief, protein samples were pipetted into a
microplate pre-coated with anti-IL-6 or anti-IL-8 antibodies and
incubated at room temperature (RT) for 2 h. The plate was then
washed three times with washing buffer to remove unbound
samples. Subsequently, enzyme-linked polyclonal anti-IL-6 or
anti-IL-8 antibodies were added and incubated at RT for 1 h.
Following another three washes, a substrate solution was added
and incubated at RT for 20 min. A blue color was then developed
in direct proportion to the amount of the target cytokine in each
well. Lastly, a stop solution was added to stop the color reaction.
The absorbance was measured at 450 nm by a microplate reader
(PerkinElmer, MA, USA).

Protein Extraction

Cytoplasmic and nuclear proteins were extracted using the NE-
PER Nuclear and Cytoplasmic Extraction kit (Thermo). Two
reagents, the Cytoplasmic Extraction Reagents I and II, were
added to cell pellets to lyse cells. The cytoplasmic proteins released
were collected by centrifugation. The remaining intact nuclei were
lysed with the Nuclear Extraction Reagent and the nuclear
proteins released were collected by centrifugation. The concen-
trations of fractionated proteins were measured by the BCA
protein assay kit (Thermo).

Western Blot

Protein samples were separated on 10% SDS-polyacrylamide
gels by electrophoresis and subsequently transferred to polyvinyl-
idenefluoride membranes (Roche, IN, USA) by using the Mini-
PROTEAN tetra electrophoresis system and Mini Trans-Blot transfer system (Bio-rad, CA, USA). Afterwards, the membranes were incubated with the Protein-Free T20 (TBS) Blocking Buffer (Thermo) at RT for 1 h and then probed with the primary antibodies (1:2000) at 4°C overnight with gentle agitation. On the next day, the membranes were washed and incubated with horseradish peroxidase (HRP)-conjugated secondary antibodies at RT for 1 h. They were then washed again and incubated with the SuperSignal West Pico Chemiluminescent Substrate (Thermo) for 5 min. The signals of antigen-antibody complexes were developed on X-ray films. The density of the developed bands was quantified by the ImageJ software. The rabbit monoclonal antibodies (mAbs) against human IkBα, phospho-IkBα (serine32), phospho-p38 MAPK (Thr180/Tyr182), phospho-JNK (Thr183/Tyr185) and α-tubulin were obtained from Cellsignaling (MA, USA). HRP-conjugated goat polyclonal antibodies against rabbit IgG were obtained from Thermo.

NF-κB p65 Transcription Factor Assay

A NF-κB p65 Transcription Factor Kit (Thermo) was used to measure the level of p65 transcription factor in nuclear protein samples. It contains a 96-well plate pre-coated with a biotinylated consensus DNA sequence which only binds p65. Briefly, nuclear protein samples were added to each well with binding buffer and incubated at RT for 1 h. The plate was then washed and incubated with primary anti-p65 antibody at RT for 1 h.

Figure 1. Baicalin significantly downregulates P. gingivalis LPS-upregulated IL-6 expression. A. Baicalin (BI) at 40 μM and 80 μM significantly downregulated P. gingivalis (P.g.) LPS-upregulated IL-6 mRNA expression. B. Baicalin at 10 μM, 20 μM, 40 μM, and 80 μM markedly downregulated P.g. LPS-upregulated IL-6 protein expression. Cells treated with culture media alone served as the blank control group, and those treated with P.g. LPS (10 μg/ml) alone represented the positive control group. Cells treated with 0.08% DMSO and P.g. LPS at 10 μg/ml served as the vehicle control group. Data of three independent experiments were depicted as relative fold change as compared with the blank control group (set as 1) (A), or presented as protein concentration (B). *p<0.05 and **p<0.01 as compared with the positive control group (P.g. LPS).

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Following another round of washing, secondary HRP-conjugated antibodies were added to the plate and incubated at RT for 1 h. Lastly, a chemiluminescent substrate solution was added to the wells. The signal image was captured with a CCD camera and the signal intensity was measured by a multiplate reader.

PCR Array
A panel of 89 genes associated with TLR signal transduction was investigated simultaneously using the RT² Profiler™ PCR Arrays (SAbiosciences, MD, USA). RNA samples were firstly reverse transcribed into cDNA templates by the RT² First Strand Kit (SAbiosciences). The diluted cDNA templates were subsequently mixed with the RT² qPCR Master Mix (SAbiosciences) and H₂O. 25 μl of the mixture were loaded into each well of the array plate which contained pre-coated specific primers. The real-time PCR was performed as follows: an initial incubation at 95°C for 10 min, then 40 cycles at 95°C for 15 s and 60°C for 1 min. Data analysis was undertaken by using the SAbiosciences web-based PCR array data analysis software.

Statistical Analysis
All experiments were repeated three times. The data were presented as mean±SD and the statistical significance was evaluated by one way ANOVA using the SPSS 16.0 software. A p-value<0.05 was considered statistically significant.

Figure 2. Baicalin significantly downregulates *P. gingivalis* LPS-upregulated IL-8 expression. A. Baicalin (BI) at 80 μM significantly downregulated *P. gingivalis* (*P.g.*) LPS-upregulated IL-8 mRNA expression. B. Baicalin at 80 μM significantly downregulated *P.g.* LPS-upregulated IL-8 protein expression. Cells treated with culture media alone served as the blank control group, and those treated with *P.g.* LPS (10 μg/ml) alone represented the positive control group. Cells treated with 0.08% DMSO and *P.g.* LPS at 10 μg/ml served as the vehicle control group. Data of three independent experiments were depicted as relative fold change as compared to the blank control group (set as 1) (A), or presented as protein concentration (B). *p<0.01 as compared with the positive control group (*P.g.* LPS).

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Results

Baicalin Downregulated *P. gingivalis* LPS-upregulated Expression of IL-6 and IL-8

HOKs were pre-treated with baicalin (0–80 \text{mM}) for 24 h, and subsequently treated with fresh media containing *P. gingivalis* LPS (10 \text{mM}) with or without baicalin (0–80 \text{mM}) for 3 h. The culture supernatants and total RNA were collected for ELISA and real-time PCR analyses, respectively. We discovered that baicalin at 40 \text{mM} and 80 \text{mM} significantly suppressed *P. gingivalis* LPS (10 \text{mM}) expression (Fig. 1A). Baicalin at 80 \text{mM} also significantly suppressed *P. gingivalis* LPS upregulated IL-6 mRNA expression (Fig. 1B). As baicalin at 80 \text{mM} contained 0.08% DMSO, the observed downregulation could have been partially caused by DMSO. To exclude this possibility, a vehicle control group was set up by treating cells firstly with 0.08% DMSO for 24 h, and then with *P. gingivalis* LPS (10 \text{mM}) and 0.08% DMSO for 3 h. No DMSO-mediated inhibition on IL-6 or IL-8 expression was found (Figs. 1 and 2).

Baicalin Displayed Inhibitory Effect on *P. gingivalis* LPS-induced Activation of NF-\(\kappa\)B, p38 MAPK and JNK

In resting cells, inactive NF-\(\kappa\)B (p65/p50) is retained in the cytoplasm by an inhibitory protein called IkB\(\alpha\) [43]. Upon stimulation, IkB\(\alpha\) is ubiquitinated and degraded by 26 S proteasome, resulting in the translocation of NF-\(\kappa\)B to the nucleus where it binds to the target genes and initiates gene transcription [43]. As NF-\(\kappa\)B plays a central role in *P. gingivalis* LPS-mediated cell response and the expression of IL-6 and IL-8 is dependent on NF-\(\kappa\)B signaling [44], we were interested to exam whether baikalin could have any inhibitory effects on *P. gingivalis* LPS-induced activation of NF-\(\kappa\)B, p38 MAPK and JNK.

Figure 3. Baicalin inhibits *P. gingivalis* LPS-induced activation of NF-\(\kappa\)B, p38 MAPK and JNK. A. The representative western blot experiment was performed by pooling cytoplasmic protein extracts equally from three independent experiments. 25 \text{ug} aliquots were loaded into each lane. The membrane was firstly probed with the rabbit anti-phospho-IkB\(\alpha\) mAbs (1:2000), and sequentially stripped and re-probed with rabbit anti-IkB\(\alpha\) mAbs (1:2000), and rabbit anti-IkB\(\alpha\) mAbs (1:4000). B. The densitometry analysis of the signals. Cells treated with culture media alone served as the blank control group, and those treated with *P. gingivalis* (P.g.) LPS (10 \text{ug/ml}) alone represented the positive control group. Cells treated with P.g. LPS at 10 \text{ug/ml} and 0.08% DMSO served as the vehicle control group. Data of three independent experiments were depicted as relative fold change as compared with the blank control group (set as 1). For the p-IkB\(\alpha\) protein, the positive control group (LPS) was set as 1 since the signals of the blank control group at 15 min and 30 min were undetectable. *p<0.05 and **p<0.01 as compared with the respective positive control group (LPS) at each time point. B: baikalin.
doi:10.1371/journal.pone.0051008.g003

Baicalin Downregulates IL-6 and IL-8 in HOKs

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activated NF-κB. Cells were pre-treated with baicalin (80 μM) for 24 h, and thereafter treated with fresh media containing P. gingivalis LPS (10 μg/ml) with or without baicalin (80 μM) for 15, 30, and 60 min. A vehicle control group was set up by treating cells firstly with 0.08% DMSO for 24 h, and then with P. gingivalis LPS (10 μg/ml) and 0.08% DMSO for 15, 30, and 60 min. As shown in Fig. 3, baicalin significantly inhibited to different extents P. gingivalis LPS-induced phosphorylation of IκBα, p38 MAPK and JNK which act as the downstream of TLR2/4 signaling pathways [45].

Baicalin Suppressed P. gingivalis LPS-induced Nuclear Translocation of p65

The effect of baicalin on P. gingivalis LPS-induced nuclear translocation of p65 was examined by using a p65 transcription factor kit. Cells were pre-treated with baicalin (80 μM) for 24 h, and then treated with fresh media containing P. gingivalis LPS (10 μg/ml) with or without baicalin (80 μM) for 15, 30, and 60 min. Compared with P. gingivalis LPS-treated samples, baicalin succeeded to suppress the amount of translocated p65 in the nuclear protein extracts at 60 min (Fig. 4).

Baicalin Modulated P. gingivalis LPS-induced Expression of Genes Associated with TLR Signaling

Lastly, a PCR array assay was undertaken to profile the expression of genes associated with TLR signaling. Cells were pre-treated with baicalin (80 μM) or culture media for 24 h, and then treated with fresh media containing P. gingivalis LPS (10 μg/ml) with or without baicalin (80 μM) for 3 h. The total RNA was purified and reverse transcribed into cDNA templates. The templates used in PCR array were pooled equally from three independent experiments. Compared with the P. gingivalis LPS-treated cells, the expression of CCL2, CSF2, CSF3, CXCL10, IL-8, V-fos FBJ murine osteosarcoma viral oncogene homolog (FOS) and interferon, beta 1, fibroblast (IFNB1) was significantly downregulated over two folds in baicalin/P. gingivalis LPS treated samples.
Table 1. The fold change in the expression of genes in baicalin/P. gingivalis LPS-treated cells (test) with reference to the P. gingivalis LPS-treated cells (control).

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<th>Wells</th>
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The genes downregulated over four folds are highlighted in bold, and those up or downregulated two to four folds are highlighted in italics.

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cells (Table 1). Notably, CCL2, CSF3 and CXCL10 were markedly downregulated over four folds. On the other hand, other genes including cluster of differentiation 80 (CD80), interleukin-1 receptor-associated kinase 1 (IRAK1), jun proto-oncogene (JUN), TLR6, Ubiquitin-conjugating enzyme E2 variant 1 (UBE2N1), sterile α and TIR motif–containing 1 (SARM1), single Ig IL-1-related receptor (SIGIRR), TIR domain containing adaptor protein (TIRAP) and TLR1 were significantly upregulated over two folds in baicalin/LPS-treated cells (Table 1).

Discussion

Periodontal disease results essentially from the consequence of a disrupted immuno-inflammatory homeostasis of bacteria-host interactions [5]. In susceptible individuals, when host response fails to limit and resolve early infection timely, cytokine expression may become dysregulated and destructive to tissues [46,47]. As IL-6 is a stimulator of bone resorption and IL-8 is a potent neutrophil chemoattractant and activator [48,49], prolonged and excessive production of these pro-inflammatory cytokines could contribute to periodontal tissue damage. Our present study shows that baicalin could significantly downregulate P. gingivalis LPS-upregulated production of IL-6 and IL-8 in HOKs. This observation goes in line with the concept of host modulatory therapy, suggesting that baicalin could potentially be used for modulation of host response in treatment of periodontal disease.

The present study also reveals that baicalin may inhibit P. gingivalis LPS-induced activation of NF-kB, p38 MAPK and JNK. Due to their involvements in a variety of human diseases, NF-kB, p38 MAPK and JNK have become therapeutic targets and several NF-kB inhibitors have been discovered, such as salinade [50], IKK inhibitor [51,52] and resveratrol [53]. It has been shown that SD828, a p38 MAPK antagonist, could suppress LPS-induced alveolar bone loss in periodontitis rats [54], and JNK inhibitors like CEP-1347 and AS601245 exhibit protective effects on neurons [55,56]. In the present study, the exact mechanism of baicalin-induced inhibition of P. gingivalis LPS-upregulated expression of IL-6 and IL-8 in HOKs remains to be further elucidated. While it could be speculated that the inhibition observed could have been exerted directly on IKK, p38 MAPK and JNK; or on the upstream kinases such as transforming-growth-factor-β-activated kinase 1 (TAK1) (kinase of IKK and p38/JNK MAPK) [57–59], interleukin-1 receptor-associated kinase 1 (IRAK1) (kinase of TIR1), or IRAK4 (kinase of IRAK1) [60–62].

According to the PCR array results, CCL2 [63], CSF3 [64,65] and CXCL10 [66] were greatly downregulated over four folds by baicalin treatment. The transcription of CCL2 and CSF3 is regulated by NF-kB [67,68]. In response to LPS, CXCL10 is induced in a TLR4-mediated MyD88-independent pathway [15,69,70]. The exact reasons that baicalin could downregulate both LPS-induced MyD88-dependent and MyD88-independent genes remain unclear. The possible mechanisms are as follows: i) baicalin might enable to interfere with the binding of P. gingivalis LPS to TLR4; ii) it could inhibit multiple downstream kinases of TLR4 signaling, such as IKK, TAK1 and TANK-binding kinase 1 (TBK1) (kinase of IRF3) [71]; iii) as the optimal transcription of CXCL10 requires a coordinated binding of activated IRF3 and NF-kB to the promoter region [15,69], baicalin-mediated inhibition of NF-kB could have interfered with the expression of CXCL10. Further study is warranted to clarify these points.

Over the last three decades, the growing knowledge of periodontal pathogenesis has appreciated the crucial role of host response in the initiation and development of periodontal disease. Recently, TLR signaling has become an attractive target of host response in the initiation and development of periodontal disease.
modulation therapy due to its central role in activating immunoinflammatory response in the development of periodontitis [72].

To date, a number of negative regulatory strategies for over-activated TLR signaling have been proposed, such as natural/synthetic antagonists [73,74], BB-loop peptides [75], miRNA [76] and kinase inhibitors [77]. Here we report for the first time that baikalin can significantly downregulate *P. gingivalis* LPS-upregulated IL-6 and IL-8 expression in HOKs, through negative regulation of TLR signaling. Based on these findings, baikalin may potentially serve as a host response modulator in the control of periodontal disease by negative regulation of TLR signaling. Further clinical study is warranted to investigate the effectiveness of baikalin as a potential adjunct in treatment of patients with inflammatory diseases like periodontal disease.

**Acknowledgments**

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**Author Contributions**

Conceived and designed the experiments: LJJ WL CYW. Performed the experiments: WL LJJ CYW. Contributed reagents/materials/analysis tools: LJJ CYW. Wrote the paper: WL LJJ.


58. Baicalin Downregulates IL-6 and IL-8 in HOKs