

Porphyromonas gingivalis lipopolysaccharide lipid A heterogeneity differentially modulates the expression of IL-6 and IL-8 in human gingival fibroblasts

Herath TDK, Wang Y, Seneviratne CJ, Lu Q, Darveau RP, Wang CY, Jin L. Porphyromonas gingivalis lipopolysaccharide lipid A heterogeneity differentially modulates the expression of IL-6 and IL-8 in human gingival fibroblasts. J Clin Periodontol 2011; 38: 694–701. doi: 10.1111/j.1600-051X.2011.01741.x.

Abstract

Aim: *Porphyromonas gingivalis* lipopolysaccharide (LPS) displays a significant amount of structural heterogeneity, containing both tetra- (LPS_{1435/1449}) and penta-acylated (LPS₁₆₉₀) lipid A structures. This study investigated the effects of the two isoforms of *P. gingivalis* LPS on the expression of IL-6, IL-8 and TNF- α in human gingival fibroblasts (HGFs).

Materials and methods: HGFs were stimulated with *P. gingivalis* LPS_{1435/1449} and LPS₁₆₉₀ in both dose- $(1 \text{ ng}-10 \mu g/\text{ml})$ and time-dependent (2–48 h) experiments. Total RNA and protein were extracted and used for analysis of the IL-6, IL-8 and TNF- α transcripts as well as IL-6 and IL-8 proteins, by quantitative real-time polymerase chain reaction and enzyme-linked immunosorbent assay, respectively.

Results: *P. gingivalis* LPS₁₆₉₀ significantly up-regulated the mRNA and protein expression of IL-6 and IL-8, whereas *P. gingivalis* LPS_{1435/1449} did not induce significant host response. The expression levels of IL-6 and IL-8 up-regulated by *P. gingivalis* LPS₁₆₉₀ continuously increased with time course. In contrast, TNF- α transcript expression was up-regulated promptly by *P. gingivalis* LPS₁₆₉₀ after 2 h of stimulation and gradually declined afterwards.

Conclusions: This study suggests that *P. gingivalis* LPS heterogeneity may differentially modulate the pro-inflammatory cytokine expression in HGFs, which may contribute to periodontal pathogenesis.

Thanuja D. K. Herath¹, Yu Wang², Chaminda J. Seneviratne¹, Qian Lu¹, Richard P. Darveau³, Cun-Yu Wang⁴ and Lijian Jin¹

¹Faculty of Dentistry, The University of Hong Kong, Hong Kong SAR, China; ²Department of Pharmacology & Pharmacy, Faculty of Medicine, The University of Hong Kong, Hong Kong SAR, China; ³School of Dentistry, University of Washington, Seattle, WA, USA; ⁴School of Dentistry, University of California Los Angeles, Los Angeles, CA, USA

Key words: cytokines; human gingival fibroblasts; lipopolysaccharide; periodontal disease; *Porphyromonas gingivalis*

Accepted for publication 20 April 2011

Conflict of interest and source of funding statement

The authors declare that they have no conflict of interests.

This study was supported by the Hong Kong Research Grants Council (HKU766909M to LJJ). Periodontitis is characterized by inflammatory destruction of periodontal tissues due to uncontrolled, detrimental bacteria–host interactions in susceptible individuals (Darveau 2010). *Porphyromonas gingivalis* is an important periodontopathogen and its effects differ significantly from those elicited by other pathogens (Kebschull & Papapanou 2011, Wade 2011). *P. gingivalis* lipopolysaccharide (LPS) is one of the key virulent attributes, which is significantly involved in periodontal pathogenesis (Bainbridge & Darveau 2001, Lu et al. 2009). In general, bacterial LPS contains three major components including the outermost polysaccharide, core oligosaccharide regions and innermost lipid A structures (Dixon & Darveau 2005). Lipid A is biologically the most active part of LPS and it is a phosphorylated glucosamine disaccharide attached with multiple fatty acids. Its structure differs greatly among Gram-negative bacterial species depending on the differences in composition of attached fatty acids, number of phosphorylation sites and substituted groups attached to the phosphate residues (Dixon & Darveau 2005).

During periodontal disease process, P. gingivalis releases copious amount of outer membrane vesicles containing LPS that penetrate periodontal tissues and mediate an immuno-inflammatory response in the periodontal tissues (Darveau 2009). The exact nature and consequence of the host response to P. gingivalis LPS have been subjected to a debate, due to the conflicting results reported. Recently, it is revealed that P. gingivalis is able to generate heterogeneous LPS lipid A structures by changing the lipid A moiety through haemindependent modulation (Al-Qutub et al. 2006). Hence, P. gingivalis contains both tetra- (LPS_{1435/1449}) and penta-acylated (LPS₁₆₉₀) lipid A structures and generates opposing effects on innate immune responses, thereby playing a key role in modulating host immuno-inflammatory response (Darveau et al. 2004, Al-Outub et al. 2006, Reife et al. 2006).

Human gingival fibroblasts (HGFs) are the most abundant cell type in gingival tissues. They perpetually interact with microbes and their products, and the interplay between P. gingivalis and its LPS with HGFs plays a vital role in determining the healthy and diseased state of gingival tissues (Wang & Ohura 2002). Currently, it remains unknown how the heterogeneous lipid A structures of P. gingivalis LPS could affect host innate responses through modulation of the expression of pro-inflammatory cytokines in HGFs and the relevant clinical implications are largely unclear. This study investigated the modulatory effects of the two isoforms of P. gingivalis LPS_{1435/1449} and LPS₁₆₉₀ on the expression of IL-6, IL-8 and TNF- α in HGFs.

Materials and Methods Culture of HGFs

Primary HGFs were commercially obtained (ScienCell Research Laboratories, Carlsbad, CA, USA). The cells were continuously subcultured for over 10 passages and those in third to fourth passages were determined appropriate for the experiments without any signs of senescence. The cells suspended at 10^5 cell/ml were seeded on six-well-plates and grown until confluent at 37° C with 5% CO₂ in a culture medium for fibroblasts, consisting of basal medium with 2% foetal bovine serum containing penicillin/streptomycin (0.01% w/v) and fibroblast growth supplement (Di Domenico et al. 2003, Poggi et al. 2003).

LPS preparation and stimulation

P. gingivalis LPS was provided by one of the co-authors (R. P. D.). It was isolated from P. gingivalis ATCC 33277 and prepared by the cold MgCl₂-ethanol procedure as described previously (Darveau et al. 2004, Al-Qutub et al. 2006). It was further purified with < 0.1% of protein contamination. The fatty acids composition was analysed by gas chromatographic-mass spectroscopy. Separate extractions of P. gingivalis LPS_{1435/1449} and LPS₁₆₉₀ were then produced and analysed by the matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Escherichia coli LPS (JM 83-wild type strain) was provided by R. P. D. as well.

In the dose-dependent assay, HGFs were treated with various concentrations of P. gingivalis LPS1435/1449 and LPS1690 as well as E. coli LPS as a positive control at the concentrations of 1 ng/ml, 10 ng/ml, 100 ng/ml, 1 μ g/ml and 10 μ g/ ml for 24 h. Three wells containing only the culture medium served as the negative controls. Upon the results of dosedependent assay, 1 µg/ml of P. gingivalis LPS or E. coli LPS was selected as the optimal dose for the subsequent time-dependent assay. HGFs were then incubated with $1 \mu g/ml$ of *P. gingivalis* LPS or E. coli LPS and harvested at 2, 12, 24 and 48 h. HGFs treated with culture medium alone served as the negative controls.

The culture media were collected and centrifuged at 4° C to remove any contaminated cell debris, and stored at – 70° C for assay of protein levels. The attached cells were then washed with PBS and collected for extraction of total RNA and protein, respectively.

cDNA synthesis and quantitative real-time polymerase chain reaction analysis (Q-RT-PCR)

Total RNA was extracted from the homogenized HGFs using RNeasy

Mini Kit (Qiagen, Hilden, Germany) following the manufacturer's instructions. cDNA was synthesized by reverse transcriptase-PCR at 43°C for 90 min. in a 20 μ l of reaction mixture containing $1 \mu g$ of total RNA, $1 \mu l$ (200 U) of SuperScript[™] First-Strand Synthesis System (Invitrogen Corp., Carlsbad, CA, USA), $0.5 \mu g$ of oligo dT-primer, first-strand buffer, 10 mM DTT and 1 mM dNTPs. A control reaction was performed without reverse transcriptase for all isolates to verify the absence of genomic DNA contamination. O-RT-PCR was performed by using the StepOne Real-Time PCR System (Applied Biosystems, Foster City, CA, USA) in three separate experiments. Amplification reactions were undertaken in $20 \,\mu$ l of reaction mixture containing $10 \,\mu$ l of Power SYBR[®] Green PCR Master Mix (Applied Biosystems), $1 \mu l$ of cDNA template and 1 μ l of each pair of primers for the targeting cytokine genes (Sigma, St. Louis, MO, USA). Real-time primer pairs were designed using ABI software to amplify a sequence containing two or more exons whenever possible, with the amplification efficiencies over 90%. The specific sequences for each pair of primers are listed in Table 1. β -actin was amplified as an internal control. The Q-RT-PCR reaction conditions were set at 95°C for 10 min. followed by 40 cycles at 95°C for 15 s and 60°C for 60 s. The results were analysed using the comparative cycle threshold (Ct) method as described previously (Lu et al. 2009). The expression level of each gene was normalized to a β -actin (Δ Ct) and the fold changes for each gene were calculated by comparing the test and control samples from the $\Delta\Delta$ Ct values.

Protein extraction and enzyme-linked immunosorbent assay (ELISA)

Total protein from the homogenized HGFs was extracted using CelLytic[™] MT-mammalian cell lysis extraction reagent (Sigma). The protein concentrations in both of the cell-bound fraction and culture media were measured, respectively, by a protein assay following the manufacturer's instruction (Bio-Rad Laboratories, Hercules, CA, USA). The levels of IL-6 and IL-8 were determined by ELISA with a minimal detectable concentration of 0.70 and 10 pg/ml. respectively. The absorbance values were determined by a microplate reader (Victor, Vienna, VA, USA) at an optical absorbance of 450 nm. The final concentration was determined with reference to a standard curve.

Statistical analysis

All experiments were repeated in three assays for Q-RT-PCR and two assays for ELISA. The results were presented as mean \pm SD. The statistical significance of differences between the data sets from the dose-dependent assay was evaluated by student *t*-test, one-way analysis of variance (ANOVA) and post hoc testing using both the Bonferroni and LSD methods. Additionally, the repeated measures of ANOVA were used to determine the differences between the data sets from the time-dependent assay. A *p*-value with <0.05 was considered statistically significant. All statistical

analysis was performed using a software program (SPSS 14.0, SPSS Inc, Chicago, IL, USA).

Results

Dose-dependent assay

The expression of IL-6 and IL-8 in HGFs was differentially regulated by *P. gingivalis* LPS₁₆₉₀ and LPS_{1435/1449}. *P. gingivalis* LPS₁₆₉₀ significantly induced the expression of IL-6 and IL-8 in a dose-dependent manner both at transcriptomic (Fig. 1a and b) and protein levels (Fig. 2a and c). In contrast, *P. gingivalis* LPS_{1435/1449} did not induce the expression of these cytokines. Compared with *P. gingivalis* LPS₁₆₉₀ significantly up-

regulated IL-6 and IL-8 expression at both transcriptomic and protein levels, respectively, (p < 0.05) (Fig. 1a and b, and Fig. 2). In addition, P. gingivalis LPS₁₆₉₀ at $1 \mu g/ml$ and/or $10 \mu g/ml$ induced higher levels of IL-6 and IL-8 expression than E. coli LPS (Fig. 1a and b, and Fig. 2). Moreover, secretory IL-6 and IL-8 protein levels were higher than those in the cellular compartment (Fig. 2). TNF- α level was only measured at transcriptomic level using O-RT-PCR (Fig. 1c). P. gingivalis LPS₁₆₉₀ significantly up-regulated TNF-α mRNA expression as compared with P. gingivalis LPS_{1435/1449}. However, E. coli LPS induced the highest expression of TNF- α transcripts (Fig. 1c).

Time-dependent assay

Table 1. Nucleotide sequence of primers for real-time quantitative-polymerase chain reaction

Gene	Forward	Reverse
IL-6	AATCATCACTGGTCTTTTGGAG	GCATTTGTGGTTGGGTCA
IL-8	GAACCATCTCACTGTGTGTAAA	CACTCCTTGGCAAAACTG
TNF-α	TCTTCTCCTTCCTGATCGTG	GAAGATGATCTGACTGCCTG
β-actin	TTGGCAATGAGCGGTT	AGTTGAAGGTAGTTTCGTGGAT
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The expression of IL-6 and IL-8 in HGFs was up-regulated by *P. gingivalis* LPS₁₆₉₀ and *E. coli* LPS at different time points. IL-6 and IL-8 transcriptomic levels gradually increased and reached peak at 48 h (Fig. 3). Significantly increased expression of IL-6 and



Fig. 1. Expression of IL-6 (a), IL-8 (b) and TNF- α (c) mRNAs in the cellular fractions of human gingival fibroblasts after the stimulation of *Porphyromonas gingivalis* lipopolysaccharide (LPS) and *Escherichia coli* LPS in a dose-dependent assay (1 ng/ml, 10 ng/ml, 100 ng/ml, 1 μ g/ml and 10 μ g/ml) for 24 h. The expression of mRNAs was measured by quantitative real-time polymerase chain reaction analysis. Each bar represents the mean \pm SD of three independent experiments with three replicates. *Significant difference with a *p*-value <0.05 as compared with the controls without LPS treatment.



Fig. 2. Expression of IL-6 (a and b) and IL-8 (c and d) proteins in the culture supernatants (a and c) and cellular fractions (b and d) of human gingival fibroblasts after the stimulation of *Porphyromonas gingivalis* lipopolysaccharide (LPS) and *Escherichia coli* LPS in a dose-dependent assay (1 ng/ml, 10 ng/ml, 10 ng/ml, 1 μ g/ml and 10 μ g/ml) for 24 h. The protein expression levels were measured by enzyme-linked immunoadsorbent assay. Each bar represents the mean \pm SD of three independent experiments with two replicates. *Significant difference with a *p*-value <0.05 as compared with the controls without LPS treatment.

IL-8 levels were observed with reference to the controls at 24 h and 48 h (Figs. 3a and b. and 4a-c). In contrast, the up-regulation of IL-6 by E. coli LPS was more prompt and the expression reached the peak level within 2h (Fig. 3a and 4b). Prolonged incubation with P. gingivalis LPS₁₆₉₀, induced secretion of comparable levels of IL-6 in the culture supernatant and reached even higher level (but not significant) than that induced by E. coli LPS. In contrast, P. gingivalis LPS_{1435/1449} did not show inducement in IL-8 mRNA or protein (Figs. 3b, 4c and d). P. gingivalis LPS₁₆₉₀ seemed to be a more potent stimulator in inducing IL-8 than E .coli LPS (Fig. 3b, and 4c and d).

TNF- α transcript level was rapidly induced at 2 h when incubated with *P*. *gingivalis* LPS₁₆₉₀ (Fig. 3c). However, this induction gradually decreased with incubation time.

Discussion

P. gingivalis LPS is a pathogen-associated molecular pattern (PAMP) and it

has been a subject of continuous debate over the controversial data on its immuno-modulatory activity (Bainbridge & Darveau 2001, Dixon & Darveau 2005). Hence, some argue P. gingivalis LPS as a PAMP to induce the innate immune response, whilst others state that it facilitates the bacteria evading innate immune system (Yamazaki et al. 1992, Agarwal et al. 1995, Reife et al. 1995, Ogawa et al. 1996, Ogawa & Uchida 1996, Yoshimura et al. 1997). It is only recently that the significant role played by lipid A heterogeneity of Gram-negative bacterial LPS in modulating host innate response came into light (Darveau et al. 2004, Al-Outub et al. 2006, Lu et al. 2009).

The present study examined for the first time the functional relevance of this structural heterogeneity of *P. gingivalis* LPS isoforms in HGFs as a modulator of the cytokine network. Penta-acylated *P. gingivalis* LPS₁₆₉₀ induced a significant host innate response in HGFs as evident from the higher levels of IL-6 and IL-8 expressions at both transcriptomic and protein levels. In contrast, when *P. gingivalis* LPS_{1435/1449} interacted with

HGFs, none of the aforementioned proinflammatory cytokines was expressed significantly. Hence, it appears that lipid A heterogeneity imparts a different immuno-modulatory activity on P. gingivalis LPS isoforms. Although no in vitro studies have been performed in HGFs, similar observations have been made when other cell types are induced with heterogeneous lipid A structure (Reife et al. 2006, Lu et al. 2009). For instance, P. gingivalis LPS with pentaacylated lipid A induces E-selection expression in human endothelial cells, whereas P. gingivalis LPS with tetraacylated lipid A structures does not (Reife et al. 2006). Furthermore, P. gingivalis LPS with tetra- and pentaacylated lipid A structures interacts differently with TLR4, where P. gingivalis LPS_{1435/1449} acts as a TLR4 antogonist for E-selection expression in human endothelial cells. We recently showed that the human β -defensins (hBD)-1, -2 and -3 levels in the reconstituted human gingival epithelia are significantly upregulated by P. gingivalis LPS₁₆₉₀. Conversely, hBD expression is downregulated by P. gingivalis LPS_{1435/1449}



Fig. 3. Expression of IL-6 (a), IL-8 (b) and TNF- α (c) mRNAs in the cellular fractions of human gingival fibroblasts after the stimulation of *Porphyromonas gingivalis* lipopolysaccharide (LPS) (1 µg/ml) and *Escherichia coli* LPS (1 µg/ml) in a time-dependent assay (2–48 h). The expression of mRNAs was measured by quantitative real-time polymerase chain reaction analysis. Each bar represents the mean \pm SD of three independent experiments with three replicates. *Significant difference with a *p*-value <0.05 as compared with the controls without LPS treatment.

(Lu et al. 2009) It is also noteworthy that P. gingivalis LPS₁₆₉₀ elicits a higher and more persistent hBD-2 expression than E. coli LPS. Similarly, the present study shows that the HGFs exhibit a relatively prompt responsiveness to the hexa-acyl diphosphorylated lipid A of E. coli LPS, but a persistent responsiveness to the penta-acylated P. gingivalis LPS_{1690} . It could be hypothesized that the delayed response of IL-6 induction by *P. gingivalis* LPS₁₆₉₀ observed in the present study might induce a delayed host response which may facilitate P. gingivalis colonization and persistence. Further study is required to clarify this point.

Although lipid A is considered to be the most conserved moiety of the LPS molecule, recent studies have shown that relatively small changes in lipid A structure can greatly influence the host innate immune response (Dixon & Darveau 2005). In a previous study, Darveau and colleagues showed that the ability of *E. coli* LPS to orchestrate the innate immune response is considerably weak, when C12 fatty acid in the lipid A structure is replaced with C16 fatty acid as measured by the secretion of IL-8 levels (Bainbridge et al. 2006). Hence, it is conceivable that the lipid A structural changes in *P. gingivalis* LPS evoke a markedly different host innate response in HGFs as shown in the present study. Therefore, it is imperative to further discuss the implications of these findings along several lines.

Firstly, the present study provides additional evidence on the role of HGFs as a part of innate defense of gingival tissues. The primary function of HGFs is to maintain the tissue integrity and homeostasis by producing structural components such as collagen, elastin, glycoprotein and glycosaminoglycans. However, HGFs could also act as a regulator of the innate immune response by identifying the PAMP-like P. gingivalis LPS and respond by mounting an immuno-inflammatory response (Ara et al. 2009). Hence, HGFs are capable of expressing IL-6, IL-8 and TNF- α upon stimulation with LPS from oral bacteria (Tamura et al. 1992, Yamazaki et al. 1992, Kent et al. 1998, Tabeta et al. 2000, Ren et al. 2005, Mahanonda et al. 2007, Morandini et al. 2010). The present study demonstrates that E. coli LPS is also

able to induce an immune response in HGFs, but the effect is more pronounced when *P. gingivalis* LPS₁₆₉₀ is used. Secondly, the present study for the first time reveals that lipid A heterogeneity in P. gingivalis LPS elicits a significantly different innate immune response in HGFs as measured by pro-inflammatory cytokines. IL-6 and IL-8 have been shown to be the active pro-inflammatory periodontal mediator of diseases (Ozmeric et al. 1998, Trevilatto et al. 2003). IL-6 is a multifunctional interleukin which activates the down-stream cascades related to immuno-inflammatory pathways. IL-8 induces the microbicidal activity by chemoattracting PMNs through the CXCR1 receptors, and it helps migration of neutrophils through the wall of blood vessels. It has been shown that Gram-negative bacterial LPS such as of E. coli and P. gingivalis could stimulate the IL-6 and IL-8 production in HGFs, although no attempts have been made to determine how the structural heterogeneity of P. gingivalis LPS can affect the expression of these cytokines (Kent et al. 1999, Ren et al. 2005, Ara et al. 2009, Lu et al. 2009, Morandini et al. 2010). Further, it



Fig. 4. Expression of IL-6 (a and b) and IL-8 (c and d) proteins in the culture supernatants (a and c) and cellular fractions (b and d) of human gingival fibroblasts after the stimulation of *Porphyromonas gingivalis* lipopolysaccharide (LPS) (1 μ g/ml) and *Escherichia coli* LPS (1 μ g/ml) in a time-dependent assay (2–48 h). The protein expression levels were measured by enzyme-linked immunoadsorbent assay. Each bar represents the mean \pm SD of three independent experiments with two replicates. *Significant difference with a *p*-value <0.05 as compared with the controls without LPS treatment.

is observed that HGFs do not develop LPS tolerance during repetitive exposure (Ara et al. 2009). Therefore, as shown in the present study it is imperative to determine LPS structure, before embarking on studies of LPS, as the structural difference may elicit a markedly different host response. Thirdly, this study shows that TNF- α level is rapidly induced by P. gingivalis LPS_{1690} and gradually declined with time. TNF- α is an acute phase cytokine and induces the production of IL-6. But when IL-6 level is increased it acts as a negative feedback to inhibit TNF-a production (Leal-Berumen et al. 1996, Starkie et al. 2003). TNF- α mediates its biological activity via two receptors known as TNFR55 and TNFR75, which can be found in both soluble and membrane-bound forms (Martel-Pelletier et al. 1995). Interestingly TNF- α binding to the HGFs markedly reduces with the presence of TNF- α mediated by shedding the TNFR75 as sTNFR75 (Ohe et al. 2000). Therefore, it could be speculated that the gradual decline in TNF- α activity observed in the present study may be due to the increased

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shedding of sTNFR, inhibitory effect of IL-6 or other mechanisms to be defined in further studies.

P. gingivalis residing in the dental plaque biofilms perpetually interacts with gingival tissues. P. gingivalis or its LPS is sensed by the HGFs and subsequently they activate innate response by releasing pro-inflammatory cytokines such as IL-6, IL-8 and TNF-α. It has currently been concerned that the significant changes in bacterial composition may occur as a result of inflammation rather than being its cause (Wade 2011). Darveau and colleagues have recently showed that haemin acts as a crucial environmental regulator for P. gingivalis to change its TLR4 agonist penta-acylated LPS₁₆₉₀ structure TLR4 antagonist tetra-acylated to LPS_{1435/1449} structure, where LPS₁₆₉₀ and LPS_{1435/1449} are produced predominantly under low and high haemin concentrations, respectively (Al-Qutub et al. 2006). As the haemin concentrations increase markedly in uncontrolled periodontal inflammation, this structural modification of P. gingivalis LPS may disguise the host innate mechanisms and

facilitate invasion of *P. gingivalis* into the gingival tissues. Hence, local cytokine paralysis could lead to devastating effects on host defense in the periodontium, where bacterial exposure is constant and the host may no longer be able to detect the presence of pathogenic bacteria like *P. gingivalis* and direct leucocytes for their removal, thereby contributing to periodontal destruction.

The present study suggests that *P. gingivalis* LPS heterogeneity may differentially modulate the pro-inflammatory cytokine expression in HGFs. It is reasonable to speculate that *P. gingivalis* may utilize its ability of transformation of LPS lipid A structure, and hence modulate innate host response in a favourable way to gain access and multiply inside the gingival tissues under certain conditions, subsequently leading to periodontal destruction.

Acknowledgements

The authors are grateful to Ivy Law and Joanne Yip for technical assistance. This work received the International Association for Dental Research (IADR)/Lion Dental Research Award in July 2010.

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Address: Lijian Jin Faculty of Dentistry, The University of Hong Kong 34 Hospital Road Hong Kong SAR China E-mail: Ijjin@hkucc.hku.hk

Clinical Relevance

Scientific rationale for the study: P. gingivalis LPS is one of the major virulent attributes strongly involved in periodontal pathogenesis. It displays a significant amount of structural heterogeneity, containing both tetra- (LPS_{1435/1449}) and penta-acy-lated (LPS₁₆₉₀) lipid A structures. The impacts of both isoforms of P. gingivalis LPS on innate host response remain elusive. This study investigated the modulatory effects

of *P. gingivalis* LPS heterogeneity on the expression of IL-6, IL-8 and TNF- α in HGFs.

Principal findings: P. gingivalis LPS₁₆₉₀ significantly up-regulated the mRNA and protein expression of IL-6 and IL-8, whereas *P. gingivalis* LPS_{1435/1449} did not induce significant host response. The expression levels of IL-6 and IL-8 up-regulated by *P. gingivalis* LPS₁₆₉₀ continuously increased with time course.

Practical implications: P. gingivalis LPS heterogeneity may differentially modulate the immuno-inflammatory response in HGFs and contribute to periodontal pathogenesis. This finding enhances the understanding on the molecular mechanisms of bacteria-host interactions that are crucial for development of novel treatment approaches to controlling periodontal diseases. This document is a scanned copy of a printed document. No warranty is given about the accuracy of the copy. Users should refer to the original published version of the material.