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Publication Date
2018-11-01

DOI
10.1016/j.ebiom.2018.10.033

Peer reviewed
vWA proteins of *Leptospira interrogans* induce hemorrhage in leptospirosis by competitive inhibition of vWF/GPIb-mediated platelet aggregation

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A R T I C L E   I N F O

Article history:
Received 9 August 2018
Received in revised form 10 October 2018
Accepted 10 October 2018
Available online 15 October 2018

Keywords:
Leptospirosis
Hemorrhage
Leptospira interrogans
vwa-I and vwa-II genes
von Willebrand factor
Platelet aggregation
Competitive inhibition

A B S T R A C T

Background: *Leptospira interrogans* is the major causative agent of leptospirosis, a worldwide zoonotic disease. Hemorrhage is a typical pathological feature of leptospirosis. Binding of von Willebrand factor (vWF) to platelet glycoprotein-1bα (GPIbα) is a crucial step in initiation of platelet aggregation. The products of *L. interrogans* vwa-I and vwa-II genes contain vWF-A domains, but their ability to induce hemorrhage has not been determined.

Methods: Human (Hu)-platelet- and Hu-GPIbα-binding abilities of the recombinant proteins expressed by *L. interrogans* strain Lai vwa-I and vwa-II genes (rLep-vWA-I and rLep-vWA-II) were detected by flowcytometry, surface plasmon resonance (SPR) and isothermal titration calorimetry (ITC). Hu-platelet aggregation and its signaling kinetics and active components were detected by lumiggregateometry, Western analysis, spectrophotometry and confocal microscopy. Hu-GPIbα-binding sites in rLep-vWA-I and rLep-vWA-II were identified by SPR/ITC measurements.

Findings: Both rLep-vWA-I and rLep-vWA-II were able to bind to Hu-platelets and inhibit rHu-vWF/ristocetin-induced Hu-platelet aggregation, but Hu-GPIbα-IgG, rLep-vWA-I-IgG and rLep-vWA-II-IgG blocked this binding or inhibition. SPR and ITC revealed a tight interaction between Hu-GPIbα and rLep-vWA-I/rLep-vWA-II with *Kd* values of $3.87 \times 10^{-7}$-$8.65 \times 10^{-8}$ M. Hu-GPIbα-binding of rL-vWA-I/rL-vWA-II neither activated the PI3K/AKT-ERK and PLC/PKC kinases nor affected the NO, cGMP, ADP, Ca$^{2+}$ and TXA2 levels in Hu-platelets. G13/R36/G47 in Lep-vWA-I and G76/Q126 in Lep-vWA-II were confirmed as the Hu-GPIbα-binding sites. Injection of rLep-vWA-I or rLep-vWA-II in mice resulted in diffuse pulmonary and focal renal hemorrhage but this hemorrhage was blocked by rLep-vWA-I-IgG or rLep-vWA-II-IgG.

Interpretation: The products of *L. interrogans* vwa-I and vwa-II genes induce hemorrhage by competitive inhibition of vWF-mediated Hu-platelet aggregation.

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1. Introduction

Leptospirosis caused by *Leptospira* is a common global zoonotic infectious disease [1,2]. The disease is endemic in Asia, Oceania and South America, but in recent years it has been considered as an emerging infectious disease in Europe, North America and Africa, due to frequent case reports and several outbreaks [3–10].

Many animals such as rats and livestock serve as the natural hosts of pathogenic *Leptospira* genospecies and can persistently shed the spirochetes from their urine for a long period of time [11]. Human individuals...
PKC signaling pathways in platelets are activated by phosphorylation to cause an increase in NO, cGMP and free Ca²⁺ levels, which promote synthesis of thromboxane A₂ (TXA₂) and release of ADP from granules in platelets. High levels of TXA₂ and ADP induce talin and αβ₃ integrin polymerization to cause platelet aggregation [17–19]. Therefore, vWF is a key factor in human blood coagulation.

Among pathogenic *Leptospira* genospecies, *Leptospira interrogans* is the most predominant global genospecies [1,13]. *L. interrogans* has many serogroups and serovars but *L. interrogans* serogroup icterohaemorrhagiae serovar Lai is responsible for disease in over 60% of leptospirosis patients in China [3,14,20]. In the genomic DNA of *L. interrogans* serovar Lai strain Lai, we found that LB054 and LB055 genes contain several vWF type-A (vWF-A) superfamily domains and the two genes were named as vwa-I and vwa-II [21]. Previous studies reported that the vWF-A peptide segment from human vWF can bind to the GPIb subset of human platelets, but it does not evoke platelet functional responses and result in blockage of vWF-induced platelet aggregation [22,23]. Therefore, we hypothesized that the products of *L. interrogans* vwa-I and vwa-II genes may induce hemorrhage in leptospirosis by competitive inhibition of vWF binding to GPIb which blocks platelet aggregation.

In the present study, we therefore investigated the distribution of vwa-I and vwa-II genes in different pathogenic or saprophytic *Leptospira* strains. Subsequently, the platelet GPIb-binding and aggregation-inhibiting ability of *L. interrogans* serovar Lai strain Lai recombinant vwa-I and vwa-II gene products containing vWF-A superfamily domains (rLep-vWA-I and rLep-vWA-II), as well as the expression and secretion of recombinant vwa-I and vwa-II of the spirochete during infection of human vascular endothelial cells was determined. Moreover, rLep-vWA-I and rLep-vWA-II-induced hemorrhage in mice was also demonstrated. The results of this study identify the products of *L. interrogans* vwa-I and vwa-II as hemorrhage inducers in leptospirosis by competitive inhibition of vWF-mediated platelet aggregation.

### 2. Materials and methods

#### 2.1. Ethics statement

All subjects (peripheral blood samples from three volunteers in our laboratory) gave written informed consent, and the study was approved by the Human Ethics Committee of Zhejiang University School of Medicine, and complied with the Declaration of Helsinki. Animal experiments were performed in accordance with the National Regulations for the Administration of Experimental Animals of China (1988–2002) and the National Guidelines for Experimental Animal Welfare of China (2006–398). All the animal experimental protocols were approved by the Ethics Committee for Animal Experiment of Zhejiang University School of Medicine.

#### 2.2. Leptospiral strains and culture

Thirteen strains of pathogenic *Leptospira* belonging to three genospecies for the serological diagnosis of human leptospirosis in China and two strains of non-pathogenic saprophytic *L. biflexa* were shown in Supplementary Data [3]. All the leptospiral strains were cultured in EMJH liquid medium at 28 °C [20].

#### 2.3. Cell line and culture

Human umbilical vein endothelial cell (HUVEC) line was provided by the Cell Bank of Chinese Academy of Sciences. The cells were cultured in RPMI-1640 medium supplemented with 10% fetal calf serum (FCS) (Gibco, USA), 100 U/mL penicillin and 100 µg/mL streptomycin (Sigma, USA) at 37 °C in an atmosphere of 5% CO₂.
2.4. Animals

Female C3H/HeJ mice (15 ± 1 g, three-weeks old), female C57BL/6 mice (18 ± 2 g, four weeks old) for generating *Leptospira*-infected animal model [24], and New Zealand rabbits (3.0–3.5 kg) for preparing rLep-vWA-I-IgG and rLep-vWA-II-IgG were provided by the Laboratory Animal Center of Zhejiang University.

2.5. Detection of vwa-I and vwa-II genes in leptospiral strains

Genomic DNAs from the fifteen leptospiral strains were extracted using a Bacterial Genomic DNA Extraction Kit (Axygen, USA). The entire LB054 (vwa-I) or LB055 (vwa-II) gene was amplified from the DNA templates by PCR with the primers vwa-I-1F/vwa-I-1R or vwa-II-1F/vwa-II-1R (Table 1) using a High-Fidelity PCR Kit (TaKaRa, China). All the PCR products were examined by 1.5% ethidium bromide pre-stained agarose gel electrophoresis and then cloned into pMD19-T plasmid using a PCR Product T-A Cloning Kit (TaKaRa) for sequencing by Invitrogen Co. at Shanghai in China. The sequence identities were analyzed and compared with those in GenBank using BLAST software.

2.6. Bioinformatic analysis of vwa-I and vwa-II genes

The structures and functional domains in the vwa-I and vwa-II genes of *L. interrogans* serogroup Icterohaemorrhagiae serovar Lai strain Lai were analyzed using TMHMM, PsortB, Octopus, SignalP-4.1 and NCBI-Batch CD-Search softwares.

2.7. Expression of vwa-I and vwa-II gene segments

Expression of the vwa-I and vwa-II gene segments containing the entire vWF-A superfamilly domains (vwa-I528 and vwa-II603) from *L. interrogans* serogroup Icterohaemorrhagiae serovar Lai strain Lai in *Escherichia coli* and extraction of the expressed recombinant proteins (rLep-vWA-I and rLep-vWA-II) were shown in Supplementary Information.

2.8. Removal of lipopolysaccharide in rLep-vWA-I and rLep-vWA-II

Possible contaminated *E. coli* LPS in the rLep-vWA-I and rLep-vWA-II extracts were removed with a Detoxi-gel endotoxin removing column chromatography (Thermo Scientific, USA) using pyrogen-free water for elution and then detected using a Limulus Ameboocyte Lysate Test Kit (Lonza, Switzerland) as previously described [24,25].

| Primer | Sequence (5' to 3') | Purpose | Size (bp) |
|--------|---------------------|---------|----------|
| vwa-I-1 | F: ATGATTTTTCAATAATCTTAC | Detection of entire vwa-I gene | 939 |
|        | R: TCTATCTATTATATAGC | | |
| vwa-I-2 | F: GTGATCTCTAAATAGGGA | Detection of entire vwa-II gene | 957 |
|        | R: TCTATTTACAGAAGGAC | | |
| vwa-II-1 | F: GCGCTATATG(Mde I)GAGACCAGTAACTT | Expression of vwa-II-1528 segment | 582 |
|        | GATATATTCC | | |
| vwa-II-2 | F: GCGCTATATG(Mde I)GATAATCTT | Expression of vwa-II603 segment | 603 |
|        | GATATATTCC | | |
| 16S-RNA | F: CTTCTGCTGCTAGCGAGCTAAGA | Inner reference used in qRT-PCRs | 145 |

P: forward primer. R: reverse primer. Underlined areas indicate the sites of endonucleases.

2.9. Preparation of rLep-vWA-I-IgG and rLep-vWA-II-IgG

The preparation of rabbit anti-rLep-vWA-I-IgG or rLep-vWA-II-IgG was shown in Supplementary Data.

2.10. Preparation of human and mouse platelets

Peripheral blood samples from healthy volunteers and C3H/HeJ or C57BL/6 mice were mixed with 0.1 volume of ACD buffer (75 mM sodium citrate, 39 mM citric acid, and 135 mM dextrose, pH 6.5) to prevent pellet self-aggregation, and then diluted with 2 volumes of MTH buffer (20 mM HEPES, 137 mM NaCl, 13.8 mM NaHCO₃, 2.5 mM KCl, 0.36 mM NaH₂PO₄, 5.5 mM glucose, pH 7.4). The diluted blood samples were centrifuged at 180 × g for 10 min at room temperature. The human (Hu) or mouse (Ms) platelet rich plasmas were suspended in ACD buffer and then centrifuged at 750 × g for 15 min at room temperature. The Hu-platelets and Ms-platelets were suspended in MTH buffer for immediate use with no self-aggregation using a lumiaaggregometer (type Model-700, Chrono-Log, USA) [26].

2.11. Determination of Hu/Ms-platelet-binding ability of rLep-vWA-I and rLep-vWA-II

Hu/Ms-platelet-binding ability of rLep-vWA-I or rLep-vWA-II was determined by flow cytometry [27]. Briefly, the Hu/Ms-platelets (10⁵) were incubated with 2 μg rLep-vWA-I or rLep-vWA-II at 22 °C for 0.5, 1, 2 or 4 h, and then thoroughly washed with 0.01 M phosphate buffered saline (PBS, pH 7.4). Using 1:200 diluted rabbit anti-rLep-vWA-I- or rLep-vWA-II-IgG as the primary antibody and FITC-labeled goat anti-rabbit-IgG (Abcam, USA) as the secondary antibody, the Hu/Ms-platelet-binding percentages of rLep-vWA-I and rLep-vWA-II were detected using a flow cytometer (type FC-500MCL, Beckman Coulter, USA) with 485/538 nm excitation/emission wavelengths. In the detection, 10 μg rHu-GPIbα (Abcam) plus 150 μM ristocetin (Sigma), a common cofactor of vWF for binding GPIbα to induce platelet aggregation in vitro [26,28], and rHlpA, a recombinant hemolysin of *L. interrogans* [24], were used as the controls.

2.12. Antibody blockage tests

Hu-platelets were incubated with rabbit rHu-GPIbα-IgG (Abcam) at 22 °C for 3 h while rLep-vWA-I or rLep-vWA-II was incubated with rHu-GPIbα-IgG or rLep-vWA-II-IgG at 37 °C for 1 h. The percentages of rLep-vWA-I or rLep-vWA-II binding to the GPIbα-blocked Hu-platelets and the IgG-combined rLep-vWA-I or rLep-vWA-II binding to Hu-platelets were detected by flow cytometry as above.

2.13. Determination of Hu-GPIbα-binding ability of rLep-vWA-I and rLep-vWA-II

Hu-GPIbα-binding ability of rLep-vWA-I or rLep-vWA-II was determined by SPR and ITC [29,30]. For SPR detection, 1 nM rHu-GPIbα (R&D, USA) was cross-linked on the activated CM5 sensing array (GE, USA) [26,28], and rHlpA, a recombinant hemolysin of *L. interrogans* [24], was used as the negative array-linking control. For ITC detection, 1 nM rHu-GPIbα in PBS was added in the sample pool. The KD values were determined by SPR and ITC [29,30]. For SPR detection, 1 nM rHu-GPIbα was cross-linked on the activated CM5 sensing array (GE, USA) and then 0.8 nM rLep-vWA-I or rLep-vWA-II in PBS was flowed through the surface of rHu-GPIbα-binding array. The combination of rLep-vWA-I or rLep-vWA-II with rHu-GPIbα was detected using a SPR-based detector (Type-T200, GE) and quantified by the values of equilibrium association constant (KD). For ITC detection, 1 μM rLep-vWA-I or rLep-vWA-II in PBS was added in the titration pool while 0.1 μM rHu-GPIbα in PBS was added in the sample pool. The KD values reflecting the combination of rLep-vWA-I or rLep-vWA-II with rHu-GPIbα in titrating process were detected using a type VP-ITC microcalorimeter (MicroCal, USA) and then analyzed using Origin software. In the detection, rHlpA, a recombinant hemolysin of *L. interrogans* [24], was used as the negative array-linking fixed and mobile phase controls in SPR and the negative titration control in ITC.
2.14. Co-precipitation assay

The products of vwa-I and vwa-II genes in total leptospiral proteins were pulled down with rHu-GPIbox (R&D) by co-precipitation assay. Briefly, freshly-cultured L. interrogans strain Lai was precipitated by a 10,000 × g centrifugation at 4 °C for 30 min. After washing twice with PBS and centrifugation again, the leptospiral pellet was suspended in distilled water and then ultrasonically broken on ice. The lysate was centrifuged at 10,000 × g for 10 min (4 °C) to remove leptospiral debris and the supernatant containing total leptospiral proteins was collected to detect protein concentration using a BCA Protein Assay Kit (Thermo Scientific). 20 μg mouse anti-rHu-GPIbox-IgG (Abcam) in 500 μL PBS was mixed with 100 μL of 6 mg/mL protein-A-coated agarose beads (Millipore, USA) for incubation in a 90 rpm rotator (4 °C) overnight to form protein-A-GPIbox-IgG beads. After a 10-min centrifugation at 14,000 × g (4 °C) and washing with PBS, the beads were suspended in 500 μL PBS and then incubated with 20 μg rHu-GPIbox (R&D) as above to form protein-A-GPIbox-IgG beads. After centrifugation and washing with PBS as above, the beads were suspended in 500 μL PBS and then incubated with 200 μg total leptospiral proteins in a 90 rpm rotator (4 °C) for 2 h. After centrifugation and washing thoroughly with PBS, the beads were suspended in Laemmli SDS-PAGE sample buffer for a 5-min water-bath at 100 °C to release protein-A-GPIb (Millipore, USA) for incubation in a 90 rpm rotator (4 °C) overnight to form protein-A-GPIbox-IgG beads. After a 10-min centrifugation at 14,000 × g (4 °C), the supernatant was subjected to SDS-PAGE to examine the released proteins.

2.15. Identification of rHu-GPIbox-binding leptospiral proteins

The released proteins from protein-A-GPIbox-IgG beads in co-precipitation assay were identified by liquid chromatography plus a type LC1000-LTQ tandem mass spectrometry (LC-MS/MS, Thermo Scientific). The obtained data were automatically searched against the genomic database of L. interrogans strain Lai in iBank (accession No.: NC_004342.2) using Proteome Discoverer 1.4 software.

2.16. Platelet aggregation and inhibition tests

In the platelet aggregation test, 10 μg rHu-vWF plus 150 μM ristocetin (rHu-vWF/ristocetin) were used as the inducers of Hu-platelet aggregation in vitro [18,26]. Hu-platelets (10^5) were incubated with 5 μg rLep-vWA-I or rLep-vWA-II in MTB at 37 °C for 1 h and then the rHu-vWF/ristocetin-mediated rLep-vWA-I or rLep-vWA-II-treated Hu-platelet aggregation was detected using a lumaggregometer (type Model-700, Chrono-Log, USA). On the other hand, rLep-vWA-I or rLep-vWA-II was pretreated with rLep-vWA-I-IgG or rLep-vWA-II-IgG at 37 °C for 1 h and then the rLep-vWA-I-IgG or rLep-vWA-II-IgG to reverse the role of rLep-vWA-I or rLep-vWA-II on inhibition of rHu-vWF/ristocetin-mediated Hu-platelet aggregation was detected as above.

2.17. Detection of signal kinase phosphorylation in platelet aggregation

Hu-platelets (10^6) were incubated with 5 μg rLep-vWA-I or rLep-vWA-II in MTB at 37 °C for 1 h. The Hu-platelets were lysed and then centrifuged as above. The OD_{540} and OD_{450} values reflecting the nitric oxide (NO) or cGMP levels in the supernatants were measured using a Griess’s Diazotization NO Assay Kit (Promega, USA) or a cGMP Assay Kit (R&D) by spectrophotometry. The supernatants were diluted at 1:50 with the assay buffer and then the OD_{540} values reflecting TXB2 levels were measured using a TXB2 Assay Kit (R&D) by spectrophotometry. Besides, the Hu-platelets were precipitated as above for homogenization in the assay buffer and then centrifuged at 10,000 × g for 10 min. The supernatants were diluted with 50-fold volumes of the assay buffer for detecting the released ADP at the OD_{570} using an ADP Assay Kit (Abcam) by spectrophotometry. In the detection, 10 μg rHu-vWF plus 150 μM ristocetin (rHu-vWF/ristocetin) were used as the control [26,28].

2.18. Measurement of nitric oxide, cGMP, TXA2 and ADP in platelets

Hu-platelets (10^6) were incubated with 5 μg rLep-vWA-I or rLep-vWA-II in MTB at 37 °C for 1 h. The Hu-platelets were lysed and then centrifuged as above. The OD_{540} or OD_{450} values reflecting the nitric oxide (NO) or cGMP levels in the supernatants were measured using a Griess’s Diazotization NO Assay Kit (Promega, USA) or a cGMP Assay Kit (R&D) by spectrophotometry. The supernatants were diluted at 1:50 with the assay buffer and then centrifuged at 10,000 × g for 10 min. The supernatants were diluted with 50-fold volumes of the assay buffer for detecting the released ADP at the OD_{570} using an ADP Assay Kit (Abcam) by spectrophotometry. In the detection, 10 μg rHu-vWF plus 150 μM ristocetin (rHu-vWF/ristocetin) were used as the control [26,28].

2.19. Measurement of free Ca^{2+} in platelets

Hu-platelets (10^6) were incubated with 5 μg rLep-vWA-I or rLep-vWA-II in MTB at 37 °C for 1 h. The Hu-platelets were precipitated and washed as above. The Hu-platelet pellets were suspended in the assay buffer and then incubated with free Ca^{2+}. Fluor-AM fluorescence probe at 37 °C for 30 min, followed by an additional incubation at room temperature for 30 min. The fluorescence intensity (I) values reflecting free Ca^{2+} levels in the Hu-platelets using a Fluor-AM Calcium Assay Kit (Molecular Probes, USA) by laser confocal microscopy (type LSM510, Zeiss, Germany) with 494/516 nm excitation/emission wavelength. In the detection, 10 μg rHu-vWF plus 150 μM ristocetin (rHu-vWF/ristocetin) were used as the control [26,28].

2.20. Functional determination of products of vwa-I528 and vwa-II603 mutants

Previous studies confirmed that the point-mutation of some certain amino acid residues at the GPIb-binding sites in vWF-A domains of vWF caused the decrease of vWF-platelet combination and vWF-induced platelet aggregation [31,32]. The generation of point-mutated vwa-I and vwa-II gene segments containing entire vWF-A superfamily domains (vwa-I528 and vwa-II603), the expression of vwa-I528 and vwa-II603 segments in E. coli and the extraction of target recombinant products were shown in Supplemental Information. The Hu-GPIbox-binding and Hu-platelet aggregation-inhibiting abilities of point-mutated rLep-vWA-I and rLep-vWA-II proteins were determined by flow cytometry, SPR and ITC detection, and Hu-platelet aggregation inhibition test as described above.

2.21. Measurement of vwa-I and vwa-II mRNAs during infection of HUVEC

HVEC (10^5 per well) was seeded in 6-well culture plates (Corning, USA) for a pre-incubation in an atmosphere of 5% CO₂ at 37 °C overnight. Freshly-cultured L. interrogans strain Lai was centrifuged at 13,800 × g for 15 min at 15 °C and then washed twice with PBS. The harvested leptospires were counted under a dark-field microscope with a Petroff-Hauser counting chamber (Fisher Scientific) [33]. The cells were infected with the spirochete at a multiplicity of infection (MOI) of 100 (100 leptospires per host cell) for 1, 2, 4, 8 or 12 h [33,34], and then lysed with 0.05% NaTDC-PBS. The lysates were centrifuged at 350 × g for 5 min (4 °C) to remove cell debris, and the supernatants were centrifuged at a 10,000 × g for 30 min (4 °C) to precipitate leptospires. Using rabbit anti-L. interrogans strain Lai-IgG as the primary antibody and Alexa-Fluor488-conjugated goat anti-rabbit-IgG (Abcam), the integrity of leptospires were observed under a laser confocal microscope (LSM510-Meta, Zeiss, Germany) with 495/519 nm excitation/emission wavelengths for Alexa-Fluor488 detection [25].
which the leptospires from culture in EMJH medium was used as the control. Total leptospiral RNAs were extracted using a TRIzol® Max™ Bacterial RNA Isolation kit (Invitrogen, USA) plus a gDNA Eraser Kit (TaKaRa) and then quantified by ultraviolet spectrophotometry. cDNAs from the RNAs were synthesized using a RTase CDNA Synthesis Kit (TaKaRa). Using the cDNAs as templates, the vwa-I-mRNA and vwa-II-mRNA levels were assessed by real-time fluorescence quantitative RT-PCR (qRT-PCR) using a SYBR® Premix Ex-Taq™ Kit (TaKaRa) in an ABI 7500 Real-Time PCR System (ABI, USA). The primers used are listed in Table 1. In the qRT-PCR, 16S RNA gene of the spirochete was used as the internal reference while the spirochetes from EMJH medium (28 °C) and incubated in 2.5% FCS RPMI-1640 medium (37 °C) were used as the controls. The qRT-PCR data were analyzed using the ΔΔct model and randomization test in REST 2005 software [20,34].

2.22. Detection of Lep-vWA-I and Lep-vWA-II expression and secretion of L. interrogans during infection of HUVEC

HUVEC was infected with L. interrogans strain Lai as described above. The co-cultures were lysed and then centrifuged as above to separate supernatants and leptospires. Subsequently, the integrity of leptospires from the co-cultures after lysis were detected by confocal microscopy as described above. The total proteins in the supernatants were extracted by trichloroacetic acid-acetone precipitation method [24], while the total leptospiral proteins were extracted by ultrasonical breakage and centrifugation as above, followed by detection of protein concentration as above. Using rabbit rLep-vWA-I-IgG or rLep-vWA-II-IgG as the primary antibody and HRP-conjugated goat anti-rabbit-IgG (Abcam) as the secondary antibody, Western Blot assay was used to detect Lep-vWA-I and Lep-vWA-II in the two protein specimens. The immunoblotting signals were quantified for analysis by densitometry (gray scale determination) using an image analyzer (Bio-Rad, USA) [33]. In the assays, LipL41 or Sph2 and FliY, a stable transmembrane lipoprotein or a secreted hemolysin and cytosolic protein of L. interrogans, were used as the expression or secretion controls [20].

2.23. Secretion inhibition test

L. interrogans strain Lai was pre-treated with 0.1 mM PAαN, a T1SS inhibitor, 2.5 mM NaNO3 and 30 mM NaSCN, the T2SS inhibitors, or 10 mM Aurodox (Sigma), a T3SS inhibitor, for 6 h at 37 °C [35]. The secretion of Lep-vWA-I and Lep-vWA-II of the spirochete during infection of HUVEC cells was detected by Western Blot assay as above.

2.24. Detection of rLep-vWA-I- or rLep-vWA-II-induced hemorrhage in mice

Each of C3H/HeJ or C57BL/6 mice was intravenously injected with 100 μg rLep-vWA-I or rLep-vWA-II in 0.1 mL autoclaved PBS and eight animals were used per group. The animal lung, liver and kidney tissues as well as the peripheral blood plasma samples were collected on days 3 and 7 after injection for histopathological examination after HE-staining as well as for detection of prothrombin time (PT), thrombin time (TT), activated partial thromboplastin time (APTT), thrombin generation time (TGT), fibrinogen (F−I) and fibrin degradation product (D-dimer) concentrations using an Auto-Blood Coagulation Analyzer (Sysmex, Japan) [16,36]. In addition, the coagulation time (CT) using Lee-White method, prothrombin (F−II) and prothrombin fragments 1 and 2 (F1 + 2) concentrations using ELISA, and thrombin generation time (TGT) using a Hemostasis System Analyzer (Haemoscope, USA) of the blood plasma samples were also detected as previously described [16]. On the other hand, the same concentration of rLep-vWA-I or rLep-vWA-II were pre-incubated with rLep-vWA-I-IgG or rLep-vWA-II-IgG at 37 °C for 1 h and then intravenously injected into the mice for histopathological examination as above. In the detection, the mice injected with the same volume of autoclaved PBS were used as the control.

2.25. Statistical analysis

Data from a minimum of three independent experiments were averaged and presented as mean ± standard deviation (SD). One-way analysis of variance (ANOVA) followed by Dunnett’s multiple comparisons test were used to determine significant differences. Statistical significance was defined as p < 0.05.

3. Results

3.1. Extensive distribution of vwa-I and vwa-II genes in pathogenic Leptospira genospecies

The PCR and sequencing data revealed that all the 13 tested strains of pathogenic of L. interrogans, L. borgpetersenii or L. weilii but not the 2 tested strains of saprophytic L. biflexa, possess both the LB054 (vwa-I) and LB055 (vwa-II) genes (Fig. 1A) with the nucleotide or amino acid sequence identities of 98.9%–99.8% or 98.9%–100% and 98.7%–99.9% or 98.0%–100% (GenBank accession No.: MG744315-MG744327 and MG744328-MG744340) compared to the reported same genes (GenBank accession No.: NC_004342.2). Moreover, the vwa-I or vwa-II genes of L. interrogans strain Lai had higher amino acid sequence identities (85.6%–100% or 74.4%–100%) compared to those from all the 13 strains belonging to 9 serogroups and 10 serovars of 5 pathogenic Leptospira genospecies in GenBank (Table 2). Bioinformatic analysis indicated that the vwa-I and vwa-II genes contain vWF-A superfamily domains (Fig. 1B). Although PsortB software predicted that the product of vwa-I gene was located in cytoplasmic membrane and the position of vwa-II gene product was unknown, TMHMM software predicted the two products as exoproteins without signal peptide sequences and transmembrane regions while Octopus software presented the similar possibility of the two products located the inside or outside of leptospiral cells (Supplementary Fig. S1). The data suggested that vwa-I and vwa-II genes are required by pathogenic but non-pathogenic saprophytic Leptospira strains.

3.2. Characterization of recombinant expression products of vwa-I and vwa-II genes

The generated prokaryotic expression systems could express the target recombinant proteins (rLep-vWA-I and rLep-vWA-II) encoded by the wild-type or point-mutated vwa-I and vwa-II genes of L. interrogans strain Lai (Supplementary Fig. S2A and S4B). The spectroscopic analysis of recombinant hemoglobin was detectable in all the rLep-vWA-I and rLep-vWA-II extracts after endotoxin-removing treatment (Supplementary Fig. S2C and S4D).

3.3. Hu-Platelet- and GPIbα-binding ability of rLep-vWA-I and rLep-vWA-II

The flow cytometric examination confirmed that both the rLep-vWA-I and rLep-vWA-II rapidly combined with Hu-platelets with the 94.7% and 92.4% maximal human (Hu)-platelet-binding percentages (Fig. 2A and Table 3). When the Hu-platelets were blocked with rHu-GPIbα-IgG, as well as the rLep-vWA-I or rLep-vWA-II was blocked with rLep-vWA-I-IgG or rLep-vWA-II-IgG, the Hu-platelet-binding ability of rLep-vWA-I or rLep-vWA-II was absent (Fig. 2A and Table 3). The surface plasma resonance (SPR) and isothermal titration calorimetric (ITC) detection, the two sensitive and reliable methods to determine protein-protein binding [29,30], revealed that the equilibrium association constant (Kη) values reflecting the binding ability of rLep-vWA-I or rLep-vWA-II with rHu-GPIbα were 5.56 × 10−8 and 3.87 × 10−8 M or 8.65 × 10−8 and 6.42 × 10−7 M (Fig. 2B and C). In particular, the co-precipitation test showed that the rHu-GPIbα captured five protein bands from total proteins of L. interrogans strain Lai (Fig. 2D), and the LC-MS/MS identified two of the captured proteins (~36 kDa) as the
products of *vwa*-I and *vwa*-II genes according to their cleaved peptide sequences (LGLVVFAGAAYLQAPLTGDR, SKVIVLITDGVSNTGK, IDPVTATDLAEQIGAK and EDGSYNEIFIQELSANTGGR for *vwa*-I, and GLVDVM VGDRTDSLQAFTK, GTDLSQAFTKAEALLR and DGTLLSNSNSPGIIHSK for *vwa*-II) (Supplementary Fig. S3A and 3B). The other three captured proteins were identified as the products of LA2066 (~32 kDa, hypothetical protein), LA4255 (~21 kDa, FolE) and LA2836 (~19 kDa, hypothetical protein) (Supplementary Fig. S3C). The data suggested that the products of *L. interrogans* *vwa*-I and *vwa*-II genes have a specific Hu-platelet- or Hu-GPIb-binding ability.

### 3.4. Inhibition of rLep-*vwa*-I and rLep-*vwa*-II on vWF-mediated platelet aggregation

Lumiaggregometer is commonly used to detect platelet aggregation in vitro [26]. Ristocetin, a co-coagulation factor, is necessary for vWF to induce platelet aggregation in vitro [37]. The platelet aggregation test showed that rLep-*vwa*-I and rLep-*vwa*-II did not cause Hu-platelet aggregation, but could inhibit the rHu-vWF/ristocetin-induced Hu-platelet aggregation (Fig. 3A). However, the inhibition of rLep-*vwa*-I or rLep-*vwa*-II could be removed by rLep-*vwa*-I-igg or rLep-*vwa*-II-igg pre-blockage (Fig. 3B). Moreover, no phosphorylation of the AKT, ERK, PLC and PKC as well as no increase of the NO, cGMP, TXA2, free Ca²⁺ and ADP levels in the rLep-*vwa*-I- or rLep-*vwa*-II-binding Hu-platelets could be found (Fig. 3C and D). The data suggested that the products of *L. interrogans* *vwa*-I and *vwa*-II genes can not induce human platelet aggregation but block the vWF-mediated platelet aggregation.

### 3.5. GPIbα-binding sites in Lep-*vwa*-I and Lep-*vwa*-II

Previous studies reported that the point-mutation of some certain amino acid residues in the region-A of human vWF caused the decrease of vWF-platelet binding and attenuation of vWF-mediated platelet aggregation [31,32]. The flow cytometric examination revealed that the recombinant single point-mutated products of *L. interrogans* *vwa*-I and *vwa*-II genes, rLep-*vwa*-I-G13S, rLep-*vwa*-I-R36Q, rLep-*vwa*-I-G47S, rLep-*vwa*-I-S48G, rLep-*vwa*-I-M130V and rLep-*vwa*-I-G144C showed a much weaker binding ability than the rLep-*vwa*-I (Fig. 3E). Moreover, the inhibition of rLep-*vwa*-I or rLep-*vwa*-II could be removed by rLep-*vwa*-I-igg or rLep-*vwa*-II-igg pre-blockage (Fig. 3F).

### Table 2

| Genospecies  | Serogroup       | Serovar | Strain | Genes          | GenBank No.              | Sequence Identity (%) |
|--------------|-----------------|---------|--------|----------------|-------------------------|-----------------------|
| *L. interrogans* | Icterohaemorrhagiae | Lai     | Lai    | vwa-I/vwa-II | MG744315/744328          | 100/100***            |
| *Canicola*    | Canicola        | Lin     | vwa-I   | MG744316/744329 | 99.7/99.9               |
| *Pyrogenes*   | Pyrogenes       | Tian    | vwa-I   | MG744317/744330 | 99.7/99.9               |
| *Autumnalis*  | Autumnalis      | Lin4    | vwa-I   | MG744318/744331 | 99.7/99.7               |
| *Australis*   | Australis       | 65-9    | vwa-I   | MG744319/744332 | 100/99.7                |
| *Pomona*      | Pomona          | Luo     | vwa-I   | MG744320/744333 | 99.7/98.0               |
| *Grippotyphosa* | Grippotyphosa  | Lin6    | vwa-I   | MG744321/744334 | 99.0/98.7               |
| *Hebdonias*   | Hebdonias       | 56,069  | vwa-I   | MG744322/744335 | 99.7/99.0               |
| *L. interrogans* | Icterohaemorrhagiae | Lai     | IPV     | RS18585/18590  | NC_017552.1             | 100/100               |
| *Canicola*    | Canicola        | 114     | vwa-I   | RS18115/18190  | NC_005824.1             | 100/99.4              |
| *Pyrogenes*   | Pyrogenes       | UP-MMC-NIID | RS17985/17990 | 99.7/99.7             |
| *Australis*   | Australis       | Pegk151 | RS18650/18655 | 99.7/100              |
| *Grippotyphosa* | Grippotyphosa  | Linhai  | RS18625/18630 | 99.7/98.4             |
| *Sejroe*      | Hardjo-prajitno | RS18258/18290 | 99.7/98.4 |             |
| *L. borgpetersenii* | Javanica       | Javanica | M10   | vwa-I/vwa-II | MG744323/744336         | 99.3/100              |
| *Ballum*      | Ballum          | 56,604  | vwa-I   | MG744324/744337 | 99.7/100               |
| *Tarassovi*   | Tarassovi       | 55-52   | vwa-I   | MG744325/744338 | 99.7/99.7               |
| *Mini*        | Mini            | Nano10  | vwa-I   | MG744326/744339 | 99.7/100               |
| *L. borgpetersenii* | Ballum         | Ballum  | 56,604  | RS16395/16400 | NC_0010230.1            | 86.2/76.7             |
| *Sejroe*      | Hardjo          | BK-6    | vwa-I   | RS16740/16745 | NC_0013045.1            | 85.6/74.4             |
| *Manhao*      | Manhao          | L105    | vwa-I   | MG744327/744340 | 100/90.3               |
| *L. australis* | Shermani        | LT821   | vwa-I   | RS17415/17420 | NC_006695.1             | 87.8/73.5             |
| *L. mayottensis* | Mini            | GMO1   | vwa-I   | RS19530/19535 | NC_001218.1             | 83.0/66.9             |
| *Mini*        | MD1272          | 19,315,19320 | 99.7/100 | MG744327/744340 | 87.5/75.8             |

** The sequences from the present study by PCR and sequencing.
** The sequences from GenBank.
*** The amino acid sequence identity from LB_054 (vwa-I) and LB_055 (vwa-II) genes in GenBank (NC_0043432.3).
Fig. 2. Platelet- and GPIbα-binding ability of rLep-vWA-I and rLep-vWA-II. (A). Hu-platelet-binding ability of rLep-vWA-I and rLep-vWA-II, determined by flow cytometry. rHu-vWF and rHlpA, a commercial recombinant human vWF and a recombinant hemolysin of L. interrogans, were used as the controls. (B). rHu-GPIbα-binding ability of rLep-vWA-I and rLep-vWA-II, determined by SPR. rHlpA, a recombinant hemolysin of L. interrogans, was used as the control. (C). rHu-GPIbα-binding ability of rLep-vWA-I and rLep-vWA-II, determined by ITC. The legend is the same as shown in C. (D). rHu-GPIbα-captured leptospiral proteins, determined by co-precipitation test. Lane M: protein marker. Lane 1: total proteins from L. interrogans strain Lai. Lane 2: proteins released from protein-A-GPIbα-IgG beads. Lane 3: rHu-GPIbα control.
T112A, rLep-vWA-II-G48S and rLep-vWA-II-V75D, presented a significant decrease of Hu-platelet-binding and rHu-vWF/ristocetin-induced Hu-platelet aggregation-inhibiting abilities, compared to the prototypes of rLep-vWA-I and rLep-vWA-II (Fig. 4). In addition, the multiple point-mutated rLep-vWA-I-G13S/R36Q/G47S and rLep-vWA-II-G76S/Q126R could not bind to Hu-platelets and inhibit rHu-vWF/ristocetin-induced Hu-platelet aggregation (Fig. 4). The SPR and ITC detection also confirmed the significant attenuation of rHu-GPIbα-binding ability of the five single point-mutated rLep-vWA-I or rLep-vWA-II proteins and absence of rHu-GPIbα-binding ability of the two multiple point-mutated rLep-vWA-I or rLep-vWA-II protein (Supplementary Fig. S5). The data suggested that the G13/R36/G47 in Lep-vWA-I and G76/126R in Lep-vWA-II act as human platelet GPIbα-binding sites.

### 3.6. Increase of expression and secretion of Lep-vWA-I and Lep-vWA-II during infection

The confocal microscopic examination confirmed the integrity of leptospires from the lysates of *Leptospira*-cell co-cultures (Fig. 5A). The qRT-PCR and Western Blot assay showed that the Lep-vWA-I or Lep-vWA-II mRNA level and protein expression of *L. interrogans* strain Lai were significantly increased during infection of human umbilical vein endothelial cells (HUVEC) (Fig. 5B and C). In particular, the secretion of Lep-vWA-I and Lep-vWA-II was also observed during infection (Fig. 5D). The Aurodox, a type 3 secretion system (T3SS) inhibitor, but not the T1SS and T2SS inhibitors (PAβN, NaN3 and NASCN) [38], caused a significant decrease in Lep-vWA-

### Table 3

Hu-platelet-binding percentages of rLep-vWA-I and rLep-vWA-IIΔ.

| Group | Platelet-binding percentage (% of 10⁴ platelets) |
|-------|-----------------------------------------------|
|       | 0.5 h | 1 h | 2 h | 4 h |
| rLep-vWA-I | 89.9 ± 3.6 | 90.7 ± 3.8 | 94.7 ± 4.2 | 93.3 ± 5.6 |
| rLep-vWA-II | 88.2 ± 3.1 | 90.2 ± 2.9 | 92.4 ± 3.5 | 90.7 ± 2.8 |
| rHu-vWF | 93.7 ± 3.5 | 94.4 ± 2.5 | 95.2 ± 2.1 | 93.5 ± 2.9 |
| rHu-GPIbα-IgG-blocked rLep-vWA-I | 3.5 ± 0.5* | 3.7 ± 0.4* | 4.2 ± 0.4* | 5.4 ± 0.5* |
| rHu-GPIbα-IgG-blocked rLep-vWA-II | 3.9 ± 0.5* | 4.2 ± 0.6* | 4.4 ± 0.6* | 5.5 ± 0.5* |
| rHu-vWF/IgG-blocked rLep-vWA-I | 2.5 ± 0.1* | 2.7 ± 0.1* | 3.0 ± 0.2* | 3.1 ± 0.2* |
| rHu-vWF/IgG-blocked rLep-vWA-II | 1.5 ± 0.1* | 1.7 ± 0.1* | 1.9 ± 0.1* | 2.0 ± 0.2* |
| rHu-GPIbα-IgG-blocked rLep-vWA-I | 1.7 ± 0.1* | 1.8 ± 0.1* | 2.0 ± 0.1* | 2.1 ± 0.2* |
| rHu-GPIbα-IgG-blocked rLep-vWA-II | 1.4 ± 0.1* | 1.7 ± 0.1* | 2.1 ± 0.2* | 3.9 ± 0.2* |

* The data from experiments such as shown in the Fig. 2A.

* p < 0.05 vs the Hu-platelet-binding percentages of specific IgG-unclocked rLep-vWA-I, rLep-vWA-II or rHu-vWF.

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Fig. 3. Inhibition of rLep-vWA-I and rLep-vWA-II on vWF-mediated Hu-platelet aggregation. (A). Inhibition of rLep-vWA-I and rLep-vWA-II on vWF/ristocetin-induced Hu-platelet aggregation, determined by platelet aggregation test. (B). Reversed inhibition of rLep-vWA-I-IgG and rLep-vWA-II-IgG on rLep-vWA-I and rLep-vWA-II blockage of vWF/ristocetin-induced Hu-platelet aggregation, determined by platelet aggregation test. (C). No phosphorylation of the AKT, ERK, PLC and PKC in rLep-vWA-I- or rLep-vWA-II-treated Hu-platelets, determined by Western Blot assay. Lane 1: normal Hu-platelets. Lane 2: vWF/ristocetin-treated Hu-platelets. Lanes 3 and 4: rLep-vWA-I- or rLep-vWA-II-treated Hu-platelets. (D). No increase of the NO, cGMP, TXA2, free ADP and Ca2+ levels in rLep-vWA-I- or rLep-vWA-II-treated Hu-platelets, determined by spectrophotometry and confocal microscopy.
The data suggested that \( \text{vwa-I} \) and \( \text{vwa-II} \) genes are required by \( L. \text{interrogans} \) during infection and the \( \text{vwa-I} \) and \( \text{vwa-II} \) gene products can be secreted through leptospiral T3SS.

**4.7. Hemorrhage induced by \( rLep-vWA-I \) and \( rLep-vWA-II \) in mice**

The gross pathological examination showed that all the lungs of \( rLep-vWA-I \)- or \( rLep-vWA-II \)-injected mice presented visible hyperemia.
and swelling but the livers and kidneys had no visible changes compared to those of normal mice (Fig. 6A). The pathological examination showed that both rLep-vWA-I and rLep-vWA-II caused the pulmonary diffuse hemorrhage with interstitial pneumonia and extensive renal focal hemorrhage (Fig. 6B and C). When rLep-vWA-I or rLep-vWA-II was pre-blocked by rLep-vWA-I-IgG or rLep-vWA-II-IgG, the
hemorrhagic phenomenons in the lung and kidney tissues of mice were absent (Supplementary Fig. S6). The data suggested that the products of *L. interrogans vwa*-I and *vwa*-II genes act as hemorrhage inducers in mice.

### 3.8. Ms-platelet-binding ability of rLep-vWA-I and blood coagulation dysfunction

The flow cytometric examination confirmed that rLep-vWA-I and rLep-vWA-II could rapidly bind to Ms-platelets from C3H/HeJ or C57BL/6 mice with the 91.9% and 90.5% or 92.1% and 91.6% maximal human (Hu)-platelet-binding percentages (Fig. 7A and B). On the other hand, the coagulation time (CT), prothrombin time (PT), thrombin time (TT), activated partial thromboplastin time (APTT) and thrombin generation time (TGT) of peripheral blood specimens from the two rLep-vWA-I- or rLep-vWA-II-injected mice presented a 2.36–8.81 fold extension but the fibrinogen (coagulation factor I, F—I), prothrombin (coagulation factor II, F—II), prothrombin degradation fragments (F1 + 2) and fibrin degradation product (D-dimer) levels had no significant changes, compared to the normal mice (Fig. 7C). The data suggested that the products of *L. interrogans vwa*-I and vwa-II genes act as hemorrhage inducers in mice due to attenuation or dysfunction of platelet aggregation.

### 4. Discussion

*Leptospira* is a large group of Gram-negative helical prokaryotic microbes that can be classified into pathogenic and non-pathogenic saprophytic *Leptospira* genospecies [1,2,11]. Both the pathogenic and saprophytic *Leptospira* genospecies express surface LPS (i.e. endotoxin) [39], but only the former is pathogenic due to expression of many invasive and virulence factors such as the ColA collagenase, the LigB adhesin, the Mce invasive protein and the OMP047 apoptotic inducer [20,25,34,40]. Unlike saprophytic *Leptospira*, which live in the natural environment, pathogenic *Leptospira* need to invade into animal hosts for propagation. This requires certain genetic diversity between the saprophytic and pathogenic *Leptospira* genospecies. In the present study,
we found that only the strains from pathogenic *Leptospira*, but not from saprophytic *Leptospira* genospecies, possess sequence-conserved *vwa*-I and *vwa*-II genes. In particular, the expression of *L. interrogans* *vwa*-I and *vwa*-II genes as well as the secretion of their products (Lep-vWA-I and Lep-vWA-II) were observed during infection of human vascular endothelial cells. However, the T3SS inhibitor (Aurodox) but not the T1SS and T2SS inhibitors could inhibit the secretion of Lep-vWA-I and Lep-vWA-II. Earlier studies reported that *L. interrogans* may possess an incomplete type III secretion system (T3SS) because no genes could be predicted to encode a transmembrane channel in the T3SS for transport of proteins [41,42]. However, a recent study showed that the product of the *gspD* gene in *L. interrogans* strain Lai was predicted as a YscC-like protein, a porin for protein secretion in T3SS of *Yersinia pestis* [43]. Our data indicate that the pathogenic but not saprophytic *Leptospira*...
genspecies possess vwa-I and vwa-II genes and the products of vwa-I and vwa-II genes can secrete through T3SS during infection.

Many prokaryotic pathogens, such as *Escherichia coli*, *Shigella dysenteriae*, *Helicobacter pylori*, *Clostridium difficile* and *Rickettsia* species, can cause hemorrhagic injury of infected hosts [44–48]. LPS has been confirmed as a strong causative agent of hemorrhage due to the inflammation-mediated increase of vascular permeability, damage of vascular endothelial cells and basement membrane, and inhibition of platelet adhesion and aggregation [49–51]. However, the biological activity of leptospiral LPS is much lower than that of E. coli LPS, while hemorrhage in leptospirosis is much more severe [6,13,25,39]. Therefore, pathogenic *Leptospira* genspecies must produce some factors other than leptospiral LPS in order to induce hemorrhage during infection.

GPIb is a platelet transmembrane protein composed of two α-subunits and two β-subunits [52]. During the process of VWF-induced platelet aggregation in vivo, VWF first binds to platelets through its VWF-A domain with the leucine-rich repeat N-terminal (LRRTN) domain of GPIbα to form a VWF-GPIb-IX-V complex that further initiates PI3K/AKT-PLC/PKC signaling to cause talin/integrin-dependent platelet aggregation [19,28]. Therefore, the GPIbα-binding ability of rLep-vWA-I and rLep-vWA-II, the products of *L. interrogans* vwa-I and vwa-II containing VWF-A superfamily domains, is the key feature of these two proteins for their ability to induce hemorrhage by competitive blockage of VWF. In the present study, both rLep-vWA-I and rLep-vWA-II were able to interact with Hu-platelets but also bind to rHu-GPIb with Kd values of 3.87 × 10^{-7}–8.65 × 10^{-8} M. Kd values lower than 10^{-6} M generally indicate high-affinity protein-protein interactions [29,30]. In particular, platelet aggregation and aggregation inhibition tests confirmed that rLep-vWA-I and rLep-vWA-II blocked rHu-VWF/ristocetin-induced Hu-platelet aggregation in vitro. Moreover, this study also identified C13, G47 and R36 in Lep-vWA-I and C76 and Q126 in Lep-vWA-II as the rHu-GPIb-binding residues. All the data demonstrate that the *L. interrogans* vwa-I and vwa-II gene products exhibit human platelet GPIbα-binding ability and can cause hemorrhage during leptospirosis by competitive inhibition of VWF-mediated platelet aggregation.

Hemorrhage can be classified as disruptive hemorrhage due to vessel wall injury and diapedetic hemorrhage due to thrombocytopathy and platelet dysfunction and is usually caused by heredopathia, malnutrition, leukemia or microbial infections [16,53]. Younger guinea pigs and Syrian hamsters are more suitable for leptospirosis animal models [54,55], but C3H/HeJ and C57BL/6 mice are also commonly used as the experimental reagents for mice but not for guinea pigs and Syrian hamsters are readily available. Animal experiments in our study showed that 100 μg rLep-vWA-I or rLep-vWA-II was able to cause severe diffuse diapedetic hemorrhage in lung tissues and extensive focal diapedetic hemorrhage in kidney tissues of mice, while hemorrhage could be blocked by rLep-vWA-I or rLep-vWA-II-lgC. CT, TT, PT, APPT and TGT are common assays to assess coagulation function of blood as well as the prothrombin degradation fragments (F1 + 2) and fibrin degradation product (D-dimer) levels reflect the generation of thrombin from activated prothrombin and formation of fibrin from cleaved fibrinogen [16,36]. Compared to the normal mice, all the coagulation times of peripheral blood specimens from rLep-vWA-I- and rLep-vWA-II-injected mice were extended, but no changes of the fibrinogen (F-I), prothrombin (F-II), F1 + 2 and D-dimer levels were found. In the process of blood coagulation, the aggregated platelets induced by VWF can produce coagulation factor V and combine with coagulation factor X to form a complex that cleaves prothrombin into thrombin to cause the conversion of fibrinogen into fibrin [17,58,59]. Moreover, the rLep-vWA-I- or rLep-vWA-II-injected mice also presented interstitial pneumonia. Previous studies revealed that heme, heat shock protein-60 (HSP60) and adenosine 5′ triphosphate released from erythrocytes can induce inflammation through NLRP3 inflammasome, NF-κB and Ca^{2+}/PKC signaling pathways of macrophages and vascular endothelial cells [60–62]. Therefore, the interstitial pneumonia observed in the mice may be caused by the released components of erythrocytes. All the data indicate that the products of *L. interrogans* vwa-I and vwa-II genes can cause hemorrhage in mice probably due to dysfunction and disorder of platelet aggregation.

Supplementary data to this article can be found online at [https://doi.org/10.1016/j.ebiom.2018.10.033](https://doi.org/10.1016/j.ebiom.2018.10.033).

**Acknowledgements**

We are grateful to professor Stijn van der Veen, a native English speaker working at our university, to modify the English of our manuscript.

**Funding sources**

This work was supported by grants from the National Natural Science Foundation of China (81671974, 81471907, 81501713, 81760366 and 81802021), a grant from the National Key Lab for Diagnosis and Treatment of Infectious Diseases of China (201111845/2013-032) and a grant from Program of High Level Creative Talents Cultivation in Guizhou Province (Qian-Ke-He 2016-4021).

**Declaration of interests**

We declare no competing interests.

**Contributors**

J.Q.F., X.A.L. and J.Y. contributed to the design of this study, J.Q.F., M.I. and W.L.H. performed the experiments. J.Q.F., Y.L., Y.M.G. and K.X.L. analyzed the experimental data. J.Q.F., D.M.O. and J.Y. wrote and modify the manuscript. All authors reviewed and approved the final version of the manuscript.

Potential conflicts of interest

No reported conflicts.

**References**

[1] Bharti AR, Nally JE, Ricaldi JN, et al. Leptospirosis: a zoonotic disease of global importance. Lancet Infect Dis 2003;3(12):757–71.

[2] Adler B, Moctezuma A, Ricaldi JN, et al. Leptospirosis: the dawn of the molecular genetics era for an emerging zoonotic pathogen. Nat Rev Microbiol 2009;7(10):736–47.

[3] Zhang CL, Wang H, Yan J. Leptospirosis prevalence in Chinese populations in the last two decades. Microbes Infect 2012;14(4):317–23.

[4] Smith JK, Young MM, Wilson KL, Craig SB. Leptospirosis following a major flood in Central Queensland, Australia. Epidemiol Infect 2015;143(3):585–90.

[5] Miraglia F, Matsu M, Morais ZM, et al. Molecular characterization, serotyping, and antibiotic susceptibility profile of *Leptospira interrogans* serovar Copenhageni isolates from Brazil. Diagn Microbiol Infect Dis 2015;77(3):195–9.

[6] Forbes AE, Zochowski WJ, Dubrey SW, Sivaprakasam V. Leptospirosis and *Weil’s disease in the UK*. Q J Med 2012;105(12):1151–62.

[7] Goris MG, Boer KR, Duarte TA, Kliffen SJ, Hartskeerl RA. Human leptospirosis trends, the Netherlands, 1925–2008. Emerg Infect Dis 2013;19(3):371–8.

[8] Traxler RM, Callinan LS, Holman RC, Steiner C, Guerra MA. Leptospirosis-associated hospitalizations, United States, 1998–2009. Emerg Infect Dis 2014;20(8):1273–9.

[9] de Vries SG, Visser BJ, Nagel IM, Goris MG, Hartskeerl RA, Grobusch MP. Leptospirosis in Sub-Saharan Africa: a systematic review. Int J Infect Dis 2014;28(1):47–64.

[10] Hartskeerl RA, Collares-Pereira M, Ellis WA. Emergence, control and re-emerging leptospirosis: dynamics of infection in the changing world. Clin Microbiol Infect 2011;17(4):494–501.

[11] Adler B, Moctezuma A, Leptospirosis and leptospirosis. Vet Microbiol 2010;140(3–4):287–96.

[12] McBrine AJ, Athanazio DA, Reis MG, Ko AI. Leptospirosis. Curr Opin Infect Dis 2005;18(5):376–86.

[13] Haake DA, Levet PN. Leptospirosis in humans. Curr Top Microbiol Immunol 2015;387(387):85–97.

[14] Hu WL, Lin XA, Yan J. Leptospirosis and leptospirosis in China. Curr Opin Infect Dis 2014;27(5):432–6.

[15] Palaniappan RU, Ramasujam S, Chang YT. Leptospirosis: pathogenesis, immunity, and diagnosis. Curr Opin Infect Dis 2007;20(3):284–92.

[16] Dahlbäck B. Blood coagulation. Lancer 2000;355(9215):1627–32.

[17] Lenting PJ, Christophe OD, Denis CV, von Willebrand factor biosynthesis, secretion, and clearance: connecting the far ends. Blood 2015;125(13):2019–28.
