

be stored in active condition for long time. The development of functional protein microarrays for practical use, therefore, requires relatively easy methods for the functional immobilization and purification of freshly prepared proteins on the microplate. We recently developed a high-throughput method for protein synthesis using the wheat germ cell-free protein synthesis and an automatic protein synthesizer (4–6) and demonstrated that the automatic synthesizer is very useful for the production of freshly prepared proteins.

To create a new type of protein microarray, we developed a novel tag using a DNA-binding protein and a newly designed microplate consisting of agarose and commercially available genomic DNAs (7). The new tag, named here as DBtag, is the *Arabidopsis* transcription factor HY5 having a basic leucine-zipper domain (8). We found that the HY5 protein had high binding affinity to commercially available salmon sperm and calf DNAs. Here, we used this DNA-binding ability of HY5 to immobilize and purify the fusion protein on the microplate.

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## 2. Materials

### 2.1. DBtag Protein Production

1. PCR thermocycler MP (Takarabio Inc., Otsu, Japan).
2. ExTaq DNA polymerase (Takarabio Inc.).
3. pEU-DBtag (accession no. AB369281) or *Arabidopsis HY5* gene (GenBANK accession no. NM\_121164).
4. cDNA for synthesized protein.
5. Oligonucleotide primers.
6. Exonuclease I (1 U/10  $\mu$ L reaction mixture, GE Healthcare, Little Chalfont, UK).
7. PCR product purification kit (Gel-M<sup>®</sup>Extraction, Viogene, Shijr, Taipei).
8. 5 $\times$  Transcription buffer (TB): 400 mM HEPES-KOH, pH 7.8, 80 mM magnesium acetate, 10 mM spermidine, and 50 mM DTT.
9. Nucleotide tri-phosphates (NTPs) mix: a solution containing 25 mM each of ATP, GTP, CTP, and UTP.
10. SP6 RNA polymerase (80 units/ $\mu$ L, Promega; Madison, WI).
11. RNasin (80 units/ $\mu$ L, Promega; Madison, WI).
12. Microcon (YM-50; Millipore, Bedford, USA).

13. 10 mg/mL creatine kinase (Roche Diagnostics K. K.).
14. 4× Translational substrate buffer (TSB): 120 mM HEPES-KOH, pH 7.8, 400 mM potassium acetate, 10.8 mM magnesium acetate, 1.6 mM spermidine, 16 mM DTT, 1.2 mM amino acid mix, 4.8 mM ATP, 1 mM GTP, and 64 mM creatine phosphate. Or, 4× SUB-AMIX® (CellFree Sciences Co., Ltd., Matsuyama, Japan).
15. 1× TSB: 30 mM HEPES-KOH, pH 7.8, 100 mM potassium acetate, 2.7 mM magnesium acetate, 0.4 mM spermidine, 4 mM DTT, 0.3 mM amino acid mix, 1.2 mM ATP, 0.25 mM GTP, and 16 mM creatine phosphate. Or, 1× SUB-AMIX® (CellFree Sciences Co., Ltd.).
16. Wheat embryo extract (240 OD/mL, described in Chapter 3) or WEPRO®1240 (CellFree Sciences Co., Ltd.).
17. *Escherichia coli* biotin protein ligase (BirA, Genbank Accession no. NP\_312927).
18. Biotin (Nakalai Tesque, Inc., Kyoto, Japan).

### **2.2. Protein Microarray Using Agarose/DNA Microplate**

1. Agarose (SeaKem Gold, Takarabio, Inc.).
2. Salmon sperm DNA (Sigma-Aldrich Corp, MO).
3. 1× TMD buffer: 20 mM Tris-HCl at pH 7.8, 2 mM MgCl<sub>2</sub>, and 1 mM DTT.
4. Slide glass (Asahi glass, Japan).
5. Lab-Tek II Chamber slide (one-well, Nalge Nunc International Co., Naperville, IL).
6. Pin-type spotter like MultiSPRinter™ spotter (Toyobo Bio Instruments, Tsuruga, Japan) or comparable product.
7. Wash buffer: 20 mM Tris-HCl at pH 7.8, 200 mM NaCl, 2 mM MgCl<sub>2</sub>, and 1 mM DTT.
8. Tupperware box.

### **2.3. Functional Protein Analysis Using the Protein Microarray**

1. cDNAs.
2. 1× PBS buffer: 137 mM NaCl, 2.7 mM KCl, 10 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.8 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.4.
3. Kination solution: 50 mM Tris-HCl at pH 7.8, 100 mM NaCl, 10 mM MgCl<sub>2</sub>, and 0.1 mM DTT, 10,000 Ci/μl [ $\gamma$ -<sup>32</sup>P]-ATP, 0.05% DMSO (plus protein kinase inhibitor for inhibitor solution, if need be).
4. Caspase-3 solution: 20 mM Tris-HCl at pH 7.8, 200 mM NaCl, 2 mM MgCl<sub>2</sub>, 1 mM DTT, and 17.4 ng/μL caspase 3 (human, Sigma-Aldrich Corp)].
5. 10 μg/ml Alexa488-streptavidin (STA) (Invitrogen Corp., Carlsbad, CA).

6. Typhoon 9400 imaging system (GE Healthcare, Little Chalfont, UK) or comparable product.

### 3. Methods

#### 3.1. Construction of DNA Template for DBtagged Protein Production

Arabidopsis *HY5* gene was inserted into pEU vector (4) as pEU-DBtag (Fig. 7.1a). The DBtag fragment (accession no. AB369281) was isolated (Subheading 3.1.1.) and fused on N-terminal of purpose gene by split-PCR (Subheading 3.1.2.). We have optimized a PCR-based linear template DNA generation by designing a set of universal primers for fusions of SP6 promoter and translational enhancer (E02) (9). For production of biotinylated protein, biotinylation site (amino acid sequence: GLNDIFEAQKIEWHE)

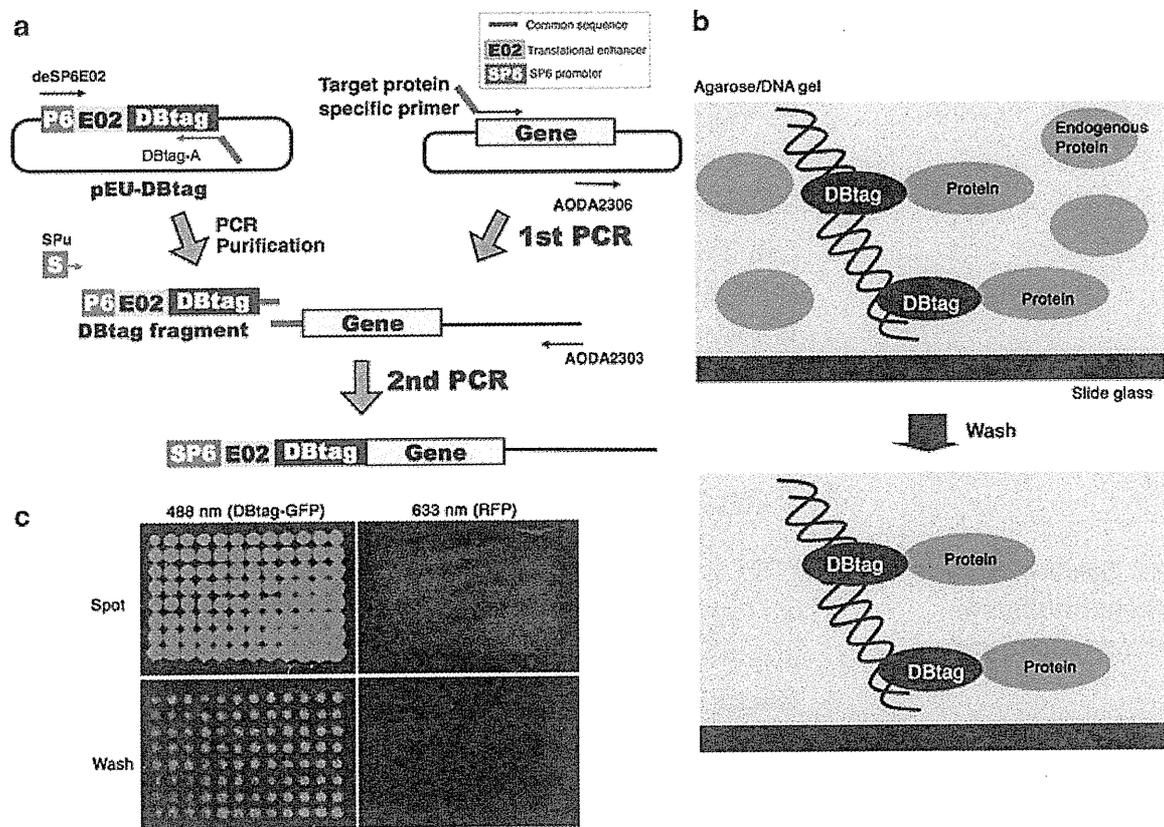


Fig. 7.1. (a) Scheme for DBtag-fusion method by the “split-primer” PCR. The DBtag fragment includes partial SP6 promoter. DNA amplification by SPu primer makes full-length SP6 promoter. (b) Schematic showing immobilized DBtag-fusion proteins on the microplate before and after washing. (c) DBtag-GFP and RFP (untagged) were mixed together and the mixture was spotted on the microplate. The DBtag-GFP was immobilized on the microplate, while the RFP was washed out and no RFP fluorescence was observed. Reproduced from ref. (7) with permission.

is inserted into N- or C-terminal of purpose gene by PCR or general recombinant method.

### 3.1.1. Isolation of DBtag Fragment

1. Prepare 100  $\mu$ L of PCR reaction mixture as the manufacturer's instructions (Takarabio Inc.) by mixing 100 pg/ $\mu$ L of plasmid (pEU-DBtag) and 200 nM of deSP6E02 (5'-GGTGACAC TATAGAACTCACCTATCTCTCTACACA) and DBtag-A (5'-TGGTGGTGGTGGGTGGAAGCCCTGGAAG TACAGGTTCTC), 200  $\mu$ M of each dNTP, 1.25 units of ExTaq DNA polymerase.
2. Set the mixture to PCR thermocycler for 1 min denaturation at 96°C followed by 25 cycles of amplification: 98°C for 10 s, 55°C for 30 s, and 72°C for 1 min.
3. Incubate the amplified product with exonuclease I (1 U/10  $\mu$ L reaction mixture) for 30 min at 37°C, and then treat for 30 min at 80°C (see Note 1).
4. Purify them with a PCR product purification kit.
5. Check concentration of the DBtag fragment.

### 3.1.2. Construction of DNA Template for DBtag Protein by Split-PCR

1. Prepare 50  $\mu$ L of a first PCR reaction mixture by mixing 3 ng of plasmid or 3  $\mu$ L of *Escherichia coli* (overnight culture) as template, 200  $\mu$ M each of dNTP, 1.5 units of ExTaq DNA polymerase, 10 nM of target protein-specific primer (5'-CCACCCACCACCACCAatgnnnnnnnnnnnnnnnnnn; uppercase and lowercase indicate common sequence and the 5'-coding region of the target gene, respectively) and AODA2306 primer (5'-AGCGTCAGACCCCGTAGAAA, this primer is designed on pUC Ori sequence), and the buffer supplied by the manufacturer.
2. Set the first mixture to PCR thermocycler for 4 min denaturation at 94°C followed by 30 cycles of amplification: 98°C for 10 s, 55°C for 30 s, and 72°C for 5 min depending on the length of gene (1 kb per min).
3. Prepare 50  $\mu$ L of a second PCR reaction mixture by mixing 5  $\mu$ L of the first PCR product (without any purification) above as template, 200  $\mu$ M each of dNTP, 1.5 units of ExTaq DNA polymerase, 100 nM SPu primer (5'-GCGTAG CATTAGGTGACACT), 100 nM AODA2303 primer (5'-GTCAGACCCCGTAGAAAAGA, this primer is designed on pUC Ori sequence), and 2 nM DBtag fragment and the buffer supplied by the manufacturer.
4. Set the second PCR mixture to PCR thermocycler for 1 min denaturation at 98°C followed by 30 cycles of amplification: 98°C for 10 s, 55°C for 30 s, and 72°C for 5 min depending on the length of gene (1 kb per min).

5. Check the DNA template production by agarose electrophoresis (see Note 2).

### **3.2. DBtag Protein Production by Wheat Cell-Free System**

We use bilayer method for protein production by the cell-free system (10). In principle, exchange of substrates and dilution of by-products take place between translation mix and TSB by expansion of translation mix.

#### *3.2.1. Preparation of mRNA*

1. Prepare 30  $\mu\text{L}$  of transcription reaction by mixing 3  $\mu\text{L}$  of the PCR mix (without any purification) as template, 6  $\mu\text{L}$  of 5 $\times$  TB, 3  $\mu\text{L}$  of NTPs mix, 25 units of SP6 RNA polymerase, and 25 units of RNasin with Milli-Q water.
2. Incubate the reaction mixture at 37°C for 3 h.
3. Add 3 volumes of Milli-Q water, 1/7.5 vol. of 7.5 M ammonium acetate, and 2.5 vol. of ~99% EtOH, and keep on ice for 10 min after mixing well.
4. Centrifuge the mixture (20,000*g*; 5 min) and discard the supernatant.
5. Wash the pellet with 500  $\mu\text{L}$  of 70% ethanol and then spin for 5 min at 20,000*g*.
6. Dissolve the mRNA pellet in 10  $\mu\text{L}$  of Milli-Q water.

#### *3.2.2. Preparation of DBtagged Proteins by Wheat Cell-Free Protein Production*

1. Prepare 25  $\mu\text{L}$  of translational reaction mixture by combining 6.3  $\mu\text{L}$  of wheat embryo extract (final conc. 60 OD/mL), 1  $\mu\text{L}$  of 10 mg/mL creatine kinase, 4.5  $\mu\text{L}$  of 4 $\times$  TSB, and 10  $\mu\text{L}$  of the dissolved mRNA above.
2. Add 125  $\mu\text{L}$  of 1 $\times$  TSB in the U-shaped titer plate well.
3. Carefully place 25  $\mu\text{L}$  of the reaction mixture at the bottom of titer plate well.
4. Place a coverlet on the plate and then wrap with the Saran Wrap to avoid evaporation.
5. Keep the plate in an incubator at 17°C for 16 h without shaking.

### **3.3. Generation of Protein Microarray Using DBtag Protein**

We designed a new microplate that carries a thin layer of agarose gel containing DNA (agarose/DNA microplate) to immobilize and purify the DBtagged proteins on the microplate (Fig. 7.1b). Non-DBtagged proteins are washed out (Fig. 7.1c).

#### *3.3.1. Preparation of Agarose/DNA Microplate*

1. Melt 0.2% agarose gel in 1 $\times$  TMD buffer, and subsequently add 1 mg/mL (final concentration) salmon sperm DNA.
2. Before the gel is solidified, spread 600 or 400  $\mu\text{L}$  of the agarose gel/DNA mixture above on a slide glass or a Lab-Tek II Chamber slide, respectively, to form a thin layer (0.5–0.6 mm) (see Note 3).

**3.3.2. Preparation of Protein Microarray on Agarose/DNA Microplate**

1. Spot approximately 10 nL of each translational mixture per 0.2 mm<sup>2</sup> (~500 μm in diameter) on the agarose/DNA-coated glass plate by using pin-type spotter according to the instruction manual (see Note 4).
2. Soak the microplate in the wash buffer for 15 min.
3. Use immediately for assay (see Note 5).

**3.4. Functional Analysis of DBtagged Protein on Agarose/DNA Microplate (see Note 5)**

Using this new protein microarray, we demonstrate (a) the autophosphorylation activity of the fusion human protein kinases (Subheading 3.4.1. and Fig. 7.2a), (b) a protein–protein interaction between UBE2N (Accession no. NM\_003348, MGC5063) and UBE2v1 (NM\_022442, MGC8586) (Subheading 3.4.2. and Fig. 7.2b), and (c) specific cleavage of the fusion proteins (PAK2, NM\_002577) by caspase 3 (Subheading 3.4.3. and Fig. 7.2c).

**3.4.1. Inhibition Assay of DBtagged Protein Kinases on Agarose/DNA Microplate**

1. Prepare the protein microarray spotting DBtag-fusion protein kinases on the agarose/DNA-coated glass plate as described above.
2. Cover the microplate with a kination solution or inhibitor solution.
3. Incubate for 30 min at 37°C.
4. Soak the microplate in washing buffer for 10 min.
5. Analyze the microplate by Typhoon 9400 imaging system.

**3.4.2. Protein–Protein Interaction Analysis Between DBtagged Protein and Biotinylated Protein on Agarose/DNA Microplate**

1. Prepare DBtag-UBE2N and biotinylated bls-UBE2V1 proteins by the cell-free system.
2. Mix both proteins with Alexa488-STA (final 10 μg/mL).
3. Incubate for 30 min at 26°C.
4. Spot the mixture on the agarose/DNA-coated glass plate as described above (Subheading 3.3.).
5. Soak the microplate in 1× PBS buffer for 10 min (see Note 6).
6. Analyze the microplate by Typhoon 9400 imaging system.

**3.4.3. Caspase Cleavage Assay of DBtagged Proteins on Agarose/DNA Microplate**

1. Prepare biotinylated substrate proteins (DBtag-PAK2-blis) by the cell-free system.
2. Mix the biotinylated proteins with Alexa488-STA (final 10 μg/ml).
3. Incubate for 30 min at 26°C.
4. Spot the mixture on the agarose/DNA-coated glass plate as described above (Subheading 3.3.).
5. Cover the microplate with caspase-3 solution.
6. Incubate for 30 min at 26°C.

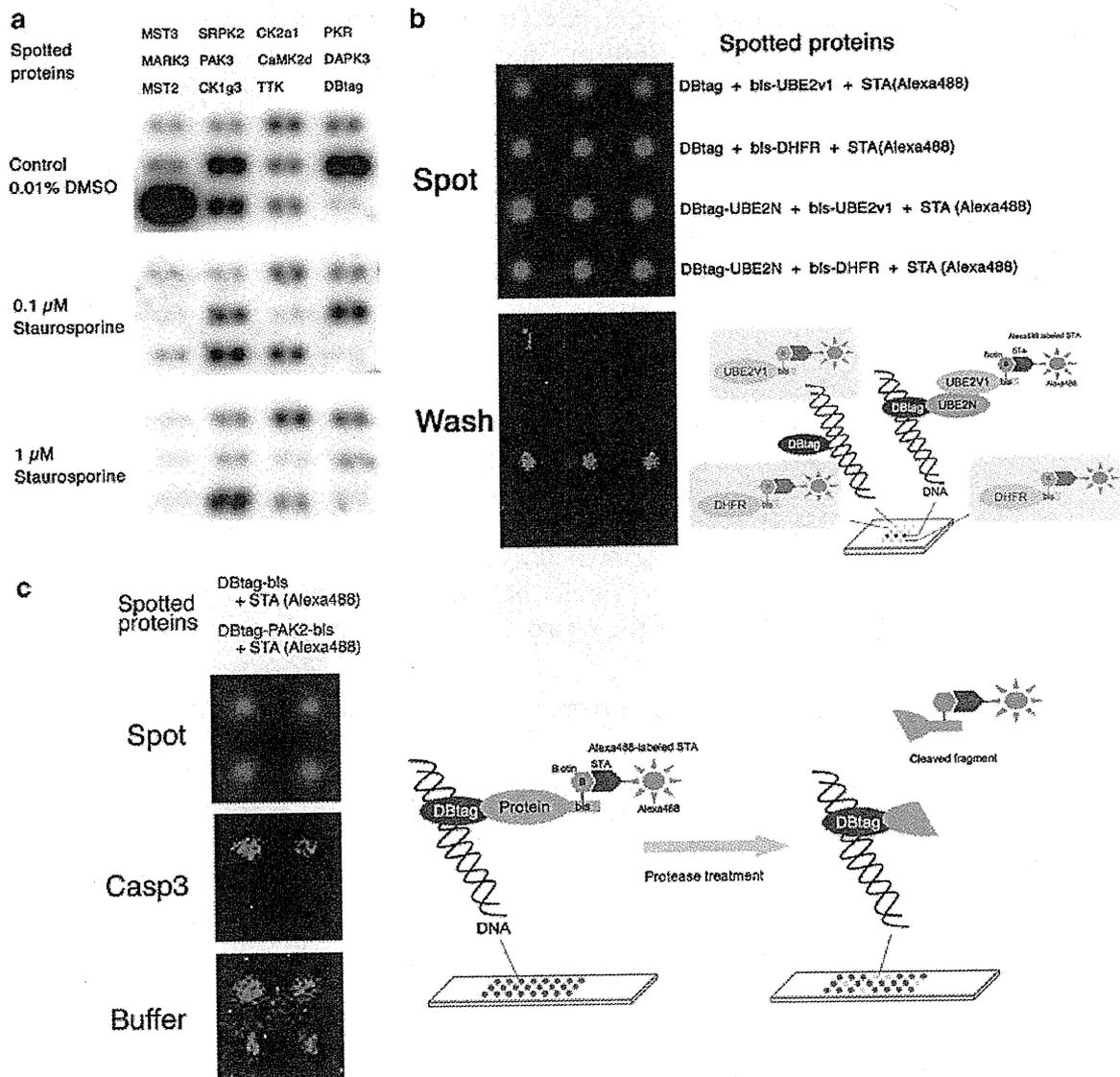


Fig. 7.2. (a) Detection and specific inhibition of the autophosphorylation activity of 11 human protein kinases on agarose/DNA microplate. The DBtagged human protein kinases were analyzed in duplicates. "DBtag" indicates the tag protein by itself (control). (b) Detection of a protein-protein interaction between UBE2N and UBE2v1 on the agarose/DNA microplate. Four samples (DBtag + biotin-labeled bls-UBE2v1 + STA(Alexa488), DBtag + biotin-labeled bls-DHFR + STA(Alexa488), DBtag-UBE2N + the bls-UBE2v1 + STA(Alexa488) and DBtag-UBE2N + the bls-DHFR + STA(Alexa488) from the top in "spot" panel] were spotted with three spots on the microplate. The first, second, and fourth samples lost the fluorescence after washing ("wash" panel). The third sample showed the fluorescence in "wash" panel, indicating a heterodimer as a protein-protein interaction between UBE2N and UBE2v1 proteins. An image from this result was shown in the *right panel*. (c) Two proteins including PAK2 (*lower spots* in each panel: DBtag-PAK2-bis labeled with Alexa488-STA) lost the fluorescence after the caspase 3 (casp3) treatment ("Casp3" panel). DBtag-bis proteins (*upper spots* in each panel: DBtag-bis labeled with Alexa488-STA) and buffer without the casp3 ("buffer" panel) showed fluorescence because they were not recognized by the casp3. *Right panel* indicates the schematic that the fluorescence-labeled region is released by the protease cleavage, and as a result, the fluorescence was lost upon washing.

7. Soak the microplate in 1× PBS buffer for 10 min (see Note 6).
8. Analyze the microplate by Typhoon 9400 imaging system.

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#### 4. Notes

1. Exonuclease I degrades extra primers after the PCR reaction. We often found primer contaminant in samples after Purification kit. The exonuclease I is very convenient to remove the extra primers because it is inactivated by simple heat treatment.
2. If DNA template is of low production, increase of primer concentration could provide higher production. In our case, the concentration increases to 100 nM from 10 nM as final concentration.
3. The agarose/slide-coated glass should be used within 1 day.
4. During spotting process, humidity inside the spotter should be kept. MultiSPRinter™ spotter can control high-humidity condition.
5. During making of the microplate and the assay, the microplate should be kept in a Tupperware box containing wet papers to prevent it from drying. Dried microplate could not be used for the functional analysis of proteins.
6. If soaking time is too long, assay sensitivity is decreased.

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## Adenovirus-vectored *Plasmodium vivax* ookinete surface protein, Pvs25, as a potential transmission-blocking vaccine

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### ABSTRACT

Adjuvants or delivery vehicles are essential components to expedite malaria vaccine development. In this study, replication-defective human adenovirus serotype 5 (rAd) was genetically engineered to express the *Plasmodium vivax* ookinete surface protein (OSP), Pvs25 (AdPvs25). BALB/c mice immunized with the AdPvs25 through various routes including intramuscular, subcutaneous and intranasal routes were analyzed for induction of antigen-specific transmission-blocking immunity. Parenteral but not mucosal immunization induced high serum immunoglobulin G (IgG) responses specific to *P. vivax* ookinetes isolated from *P. vivax* volunteer patients from Thailand. The membrane feeding assay revealed that antisera conferred a transmission blockade of up to 99% reduction in the average oocyst numbers per mosquito, while immunization with a rAd expressing Pfs25 from *Plasmodium falciparum*, a homolog of Pvs25, conferred only a background level of blockade, suggesting that a species-specific transmission-blocking immunity was induced. Vaccine efficacy of AdPvs25 was slightly higher than to a recombinant Pvs25 protein mixed with aluminum hydroxide, but less efficacious than the protein emulsified with incomplete Freund's adjuvant. This study, the first preclinical evaluation of adenovirus-vectored malaria OSps, implicates a potential inclusion of malaria transmission-blocking vaccine antigens in viral vector systems.

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### 1. Introduction

Malaria is one of the most serious infectious diseases with high mortality and morbidity in large areas of tropical regions of the world. There were estimated 189–327 million cases and 881,000 malaria deaths in 2006 [1]. The majority of victims of malaria are children in sub-Saharan Africa. Implementation of various control measures including drug therapy and insecticide-treated bednets have made a substantial contribution to reduction of malaria cases over the past decades; however, these control measures are not sufficient partly due to the emergence of parasites resistant to

antimalarial drugs and mosquito strains resistant to insecticides, and hence new prevention tools need to be developed for local elimination and the ultimate eradication of the disease [2–4]. The development of effective and affordable vaccines is therefore believed to benefit global public health by closing the gap left by the current malaria intervention measures [5].

Several promising vaccine candidates have been intensively investigated [6,7], such as those targeting sporozoite [8], hepatic and erythrocytic stages [9], which are designed to prevent infection and to reduce disease severity. On the other hand, transmission-blocking vaccines (TBVs) that target the sexual stage, in which the parasite undergoes sporogonic development in anopheline mosquitoes, prevent parasite transmission in the mosquito [10–12]. TBVs induce antibodies that react with the ookinete surface proteins (OSPs) of malaria parasites within the mosquito midgut, and as such they do not directly protect vaccinated individuals from infection. They could however contribute to elimination of the disease by lowering the parasite transmission

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frequency below the threshold at which the parasite can maintain its life cycle [2,13,14]. Additionally, TBVs, if combined with vaccines targeting other infection stages, could prevent transmission of escape mutants that emerge during infection. Therefore, TBVs might function as a “safety net” for pre-erythrocytic and erythrocytic vaccines, as well as other non-vaccine interventions.

*Plasmodium falciparum* causes the highest mortality rates among the four *Plasmodium* species known to infect humans; however *Plasmodium vivax*, the second most prevalent malaria species, causes 80–300 million clinical cases every year [15], has the highest morbidity and is a major cause of recurrent malaria. Its clinical manifestations range from asymptomatic to severe diseases that in some cases lead to death. Additionally, an increase in the number of severe cases of *P. vivax* infection casts doubts regarding what was thought to be its relatively benign nature [16]. This species is therefore an important target of malaria control efforts [5,13–15,17]. Furthermore, because global malaria eradication is the ultimate goal, the value of developing vaccines against *P. vivax* can no longer be underestimated [5,13–15,17].

The majority of malaria vaccine candidate antigens currently under preclinical and clinical evaluation are recombinant in origin [6,7], and therefore they are only marginally immunogenic by themselves. This has been demonstrated to be true for the two *P. vivax* candidate vaccine antigens recently tested in clinical trials, the circumsporozoite protein (CSP) [13,18] and Pvs25 OSP [13,19,20]. Therefore, appropriate adjuvant formulations or employment of delivery systems seem to be extremely important in inducing an optimal antiparasite immune response.

Replication-defective human adenovirus has been intensively evaluated for the delivery of foreign genes in gene therapy and for vaccine development against infectious diseases including malaria [21–23]. The ability to induce both cell-mediated and humoral immunities as well as a long-lasting memory T cell response are generally considered advantages of the viral vector systems in vaccine development against malaria [21,23,24]. Those immunities are important to confer solid protection against infection [25]. Attenuated adenovirus has been used for US military recruits to prevent respiratory infection [23,26], therefore safety issues may not be a serious concern for this viral vector system. *P. falciparum* antigens at the pre-erythrocytic stage such as CSP and liver-stage antigen-1 (LSA1), and antigens at the erythrocytic stage such as apical membrane antigen-1 (AMA1) and merozoite surface protein-1 (MSP1) are being tested in clinical trials as adenovirus-vectored antigens [7,23].

Since TBVs require efficient antibody-inducing capacity [10–12,27–30], we therefore hypothesized that the adenovirus vector system is beneficial for this purpose. In this study we evaluated potential application of a replication-defective human adenovirus serotype 5 to induce transmission-blocking immunity against *P. vivax* malaria. The vaccine efficacy of the induced mouse antisera was evaluated by a membrane-feeding assay using field strains of parasites obtained from *P. vivax* volunteer patients in Thailand.

## 2. Materials and methods

### 2.1. Immunization with a recombinant adenovirus expressing Pvs25

AdPvs25 is a replication-defective human adenovirus serotype 5, expressing the Pvs25 gene under the regulation of the cytomegalovirus enhancer and promoter [31]. Genetic engineering of AdPvs25 was conducted based on a COS-TPC method, according to the manufacturer's instructions (TAKARA Bio, Otsu, Japan). Recombinant Pvs25 (rPvs25) protein expressed and purified from

the methylotrophic yeast *Pichia pastoris* [27] was used to comparatively evaluate immunogenicity of AdPvs25.

Eight-week-old female BALB/c mice were purchased from Japan SLC (Shizuoka, Japan), and housed in a special pathogen-free environment in our research institute. Mice were immunized four times at weeks 0, 3, 5 and 7 via subcutaneous (s.c.; 100  $\mu$ l at a single injection site), intramuscular (i.m.; 50  $\mu$ l at two injection sites), intranasal (i.n.; 15  $\mu$ l into each nostril), or intragastric (i.g.; 200  $\mu$ l) route with  $5.1 \times 10^9$  plaque forming units/ml of AdPvs25, or three times at weeks 0, 2 and 4 via the s.c. route with 30  $\mu$ g of the rPvs25 protein alone, or with incomplete Freund's adjuvant (IFA; Difco Laboratories, Detroit, MI, USA) or aluminum hydroxide (Alum; Pierce, Rockford, IL, USA) as controls.

All animal experimental protocols used in this study were approved by the Institutional Animal Care and Use Committee of the University of the Ryukyus, and the experiments were conducted according to the Ethical Guidelines for Animal Experiments of the University of the Ryukyus.

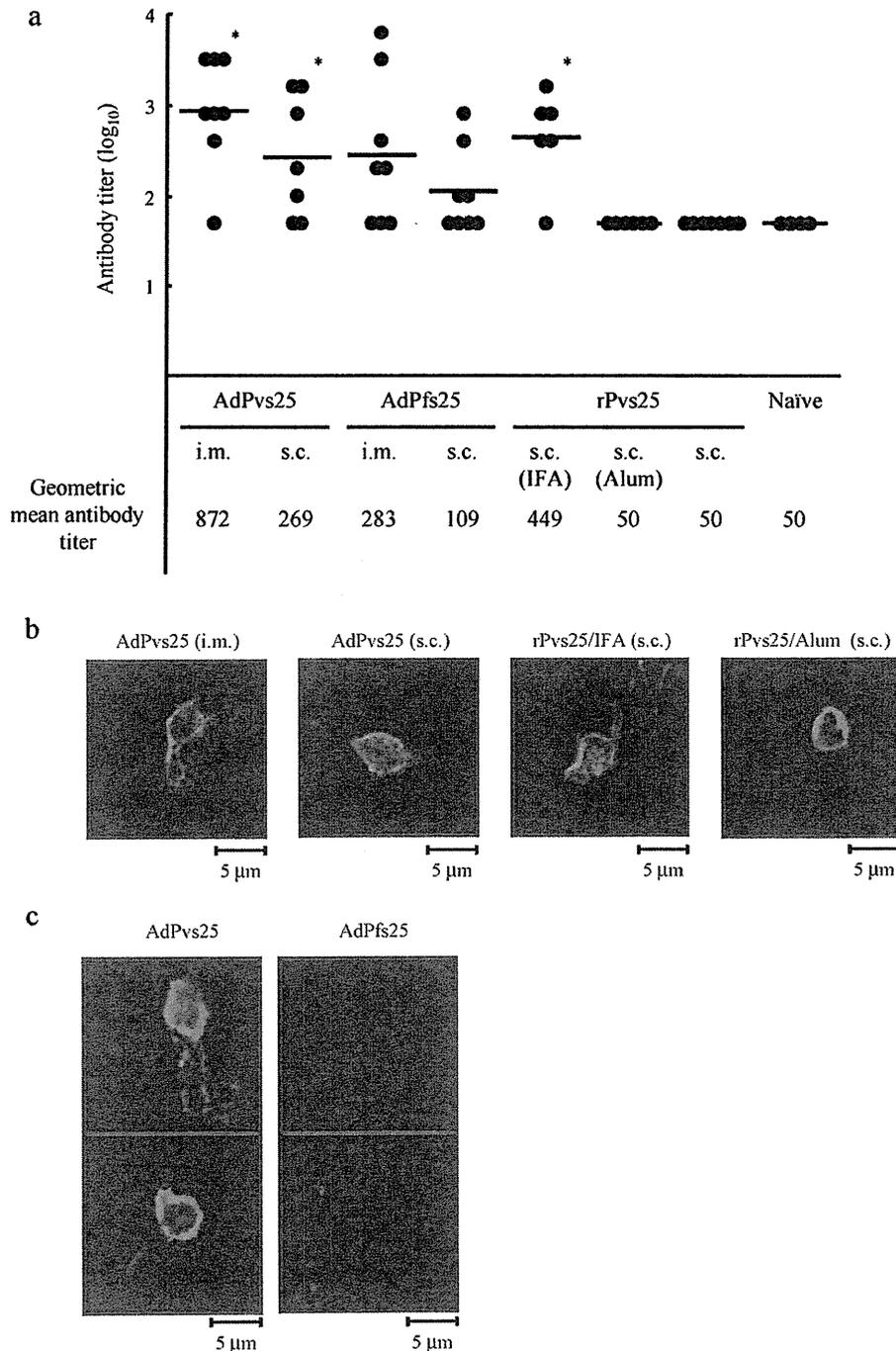
### 2.2. ELISA for antibody titer determination

Mouse antisera were collected 1–2 weeks after the last immunization (week 8 or 6 for AdPvs25 or rPvs25 protein, respectively), and Pvs25-specific serum IgG was analyzed by ELISA as described previously [27–30]. Briefly, the ELISA plates (Sumilon; Sumitomo Bakelite Co., Ltd., Tokyo, Japan) were coated with 5  $\mu$ g/ml of rPvs25 in bicarbonate buffer overnight at 4°C and blocked with 1% (w/v) bovine serum albumin (BSA) in phosphate buffered saline (PBS) for 2 h at 37°C. Two-fold serial dilutions of the antisera, commencing with an initial 50-fold dilution with 0.5% (w/v) BSA in PBS, were applied to wells (2 h, 37°C). Anti-mouse IgG conjugated to alkaline phosphatase (1/4000; Sigma–Aldrich, St. Louis, MO, USA) was added to the wells and incubated for 2 h at 37°C, before its substrate *p*-nitrophenylphosphate (Bio-Rad Laboratories, Inc., Redmond, WA, USA) was applied for 20 min at 37°C and the absorbance at 415 nm (OD<sub>415</sub>) was read on a microplate reader (Bio-Rad). The plates were washed twice with PBS containing 0.05% Tween-20 (PBS-T) and once with PBS between each incubation step. The antibody titer was defined as the serum dilution that gave an OD<sub>415</sub> value equal to 0.1, or as the serum dilution where a one magnitude higher dilution gave an OD<sub>415</sub> value less than 0.1.

### 2.3. Mosquito membrane feeding assay

The membrane feeding assay was conducted as described previously [27–29]. Briefly, peripheral blood was collected, with written informed consent, from *P. vivax* volunteer patients who came to a malaria clinic in the Mae Sod district in the Tak province of north-western Thailand. Plasma was removed from the collected blood. Single species infection with *P. vivax* was confirmed by Giemsa stain prior to the assay. The vaccine-induced mouse antisera were mixed with an equal volume of heat-inactivated human AB serum obtained from malaria-naïve volunteers. Then, the mouse antisera and the human AB serum mixture was added to the parasitized blood cells obtained from the patients (1:1 v/v ratio), and incubated for 15 min at room temperature. The mixture was applied to a membrane feeding apparatus kept at 37°C to feed *Anopheles dirus* A mosquitoes (Bangkok colony, Armed Forces Research Institute of Medical Sciences) for 30 min. Fully engorged mosquitoes were maintained for a week in an insectary kept at 26°C. For each test sample, 20 mosquitoes were analyzed to count the number of oocysts that had developed in the midgut.

Human subject research conducted in this study was reviewed and approved by the Ethics Committee of the Thai Ministry of Public Health and the Institutional Review Board of the Walter Reed Army Institute of Research.



**Fig. 1.** Immunogenicity of AdPvs25 in mice. (a) Eight-week-old female BALB/c mice were immunized four times at weeks 0, 3, 5 and 7 via subcutaneous (s.c.) or intramuscular (i.m.) route with  $5.1 \times 10^8$  plaque forming units of the AdPvs25, or three times at weeks 0, 2 and 4 via the s.c. route with  $30 \mu\text{g}$  of recombinant Pvs25 (rPvs25) protein alone, or with incomplete Freund's adjuvant (IFA) or aluminum hydroxide (Alum), as controls. Serum samples were collected at week 8 or 6 for the adenovirus-vectored or the recombinant protein immunization, respectively, and evaluated for Pvs25-specific IgG titers. Serum from naïve mice was used as a negative control for the ELISA. Antibody titers were defined as the serum dilution that resulted in an  $\text{OD}_{415}$  of 0.1, or as the serum dilution where a one magnitude higher dilution gave an  $\text{OD}_{415}$  value less than 0.1. \* indicates a significant difference to non-immune serum by the Wilcoxon–Mann–Whitney test ( $P < 0.05$ ). (b) Ookinete-specific reactivity of the induced antisera as analyzed by immunofluorescence. The antisera derived from i.m. or s.c. immunization with the AdPvs25, or s.c. immunization with the rPvs25 protein emulsified with IFA or the rPvs25 protein mixed with Alum specifically recognized native Pvs25 protein expressed on the surface of *P. vivax* zygote/immature ookinetes. (c) The antisera derived from i.m. immunization with the AdPvs25 or the AdPfs25 were reacted to *P. vivax* zygote/immature ookinetes, indicating the specificity of the AdPvs25 antisera.

#### 2.4. Detection of native Pvs25 using mouse antisera

Peripheral blood of *P. vivax*-infected volunteer patients was collected as described above. The gametocytemic blood was used to

grow zygotes and ookinetes *in vitro* [32], then samples were spotted onto slides and fixed with acetone as described previously [27–30]. The slides were then blocked with 5% nonfat milk in PBS, and incubated with the mouse antiserum derived from immunization with

the AdPvs25, AdPfs25, or the rPvs25 protein emulsified with IFA, or the rPvs25 protein mixed with Alum, after diluting the antisera 100-fold with 5% nonfat milk in PBS. The samples were washed with ice-cold PBS and incubated with Alexa488-conjugated anti-mouse antibody (Invitrogen, Carlsbad, CA, USA). After washing with ice-cold PBS, slides were viewed by confocal scanning laser microscopy (LSM5 PASCAL; Carl Zeiss MicroImaging, Thornwood, NY, USA).

2.5. Statistical analysis

Statistical analyses were conducted by the Wilcoxon–Mann–Whitney test or the Kruskal–Wallis test using JMP software version 8.0 (SAS Institute, Inc., Cary, NC, USA).

3. Results and discussion

There is an increasing demand for the development of effective recombinant vaccine platform technologies to enhance vaccine efficacy by the innovation of new adjuvants or delivery systems [33]. This would seem to be particularly true for OSPs, because they are low-molecular-weight proteins that are by themselves not sufficiently immunogenic.

In this study, we engineered replication-defective human adenovirus serotype 5 for expression of a *P. vivax* OSP, Pvs25, to test its efficacy to induce transmission-blocking immunity. We immunized BALB/c mice through various routes including i.m., s.c., i.n. and i.g., and the Pvs25-specific serum IgG response was measured (Fig. 1a and Table 1). Parenteral (i.m. and s.c.) but not mucosal (i.n. and i.g.) immunization (Supplementary data Fig. 1) with the AdPvs25 induced robust IgG responses comparable in titers to those induced by the rPvs25 protein administered s.c. with IFA. Immunization by the i.m. route with the AdPvs25 tended to induce higher IgG response than s.c. immunization, and at least three booster injections seemed to be necessary to induce the maximal level of response (Supplementary data Fig. 1). AdPvs25-induced antisera could efficiently recognize the *P. vivax* ookinete surface as determined by the immunofluorescence assay (Fig. 1b). Although, rPvs25 protein immunization with aluminum hydroxide induced only a background level of IgG response as compared with the unimmunized naïve control serum (Fig. 1a), the induced antiserum could recognize the parasite surface as efficiently as the AdPvs25 or the rPvs25/IFA induced antiserum (Fig. 1b).

AdPfs25 immunization, particularly for the i.m. route, induced relatively high IgG response to the rPvs25 protein as determined by ELISA (Fig. 1a and Supplementary data Fig. 2), implicating that the induced antisera are somewhat cross-reactive at least at the recombinant protein level; however, the differences in IgG titers between AdPfs25 and the unimmunized naïve control groups did not reach statistically significant levels. Further, AdPfs25 antisera failed to react to the *P. vivax* ookinete (Fig. 1c), indicating the specificity of the AdPvs25 antisera.

Next, we evaluated the TBV efficacy of the induced mouse antisera against field isolates of *P. vivax* parasites in infected blood samples from volunteer patients in Thailand by the membrane feeding assay as described previously [28,29]. The same experiments were performed three times using blood samples from three different *P. vivax* (Pv)-infected volunteer donors (Pv-infected blood donors 1–3; Fig. 2a–c and Table 1). The average number of oocysts per mosquito fed on parasitized blood mixed with the antisera induced by parenteral immunization (i.m. or s.c.) with the AdPvs25 was reduced by 82–99% as compared with the unimmunized naïve control serum when parasite burden was low (Fig. 2a and b and Table 1). Although, the rPvs25/Alum induced no detectable Pvs25-specific serum IgG response (Fig. 1a and Table 1), its TBV efficacy (92–97% blockade; Fig. 2a and b and Table 1) was com-

Table 1  
Summary of immunization experiments outlining antibody titers and transmission-blocking effects.

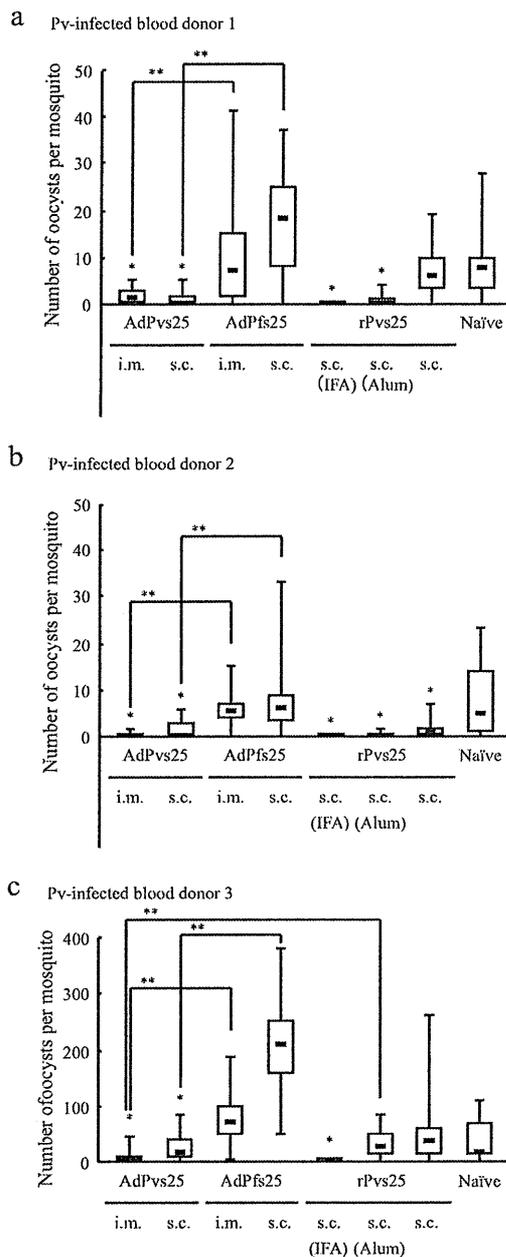
Immunization group	Immunization route	Adjuvant	Geometric mean antibody titer	TBV effect (Pv-infected blood donor 1)			TBV effect (Pv-infected blood donor 2)			TBV effect (Pv-infected blood donor 3)		
				Average oocyst number per mosquito (median oocyst number)	% Reduction in average oocyst number per mosquito (oocyst-free mosquitoes per 20 mosquitoes)	Average oocyst number per mosquito (median oocyst number)	% Reduction in average oocyst number per mosquito (oocyst-free mosquitoes per 20 mosquitoes)	Average oocyst number per mosquito (median oocyst number)	% Reduction in average oocyst number per mosquito (oocyst-free mosquitoes per 20 mosquitoes)	Average oocyst number per mosquito (median oocyst number)	% Reduction in average oocyst number per mosquito (oocyst-free mosquitoes per 20 mosquitoes)	
AdPvs25	i.m.	–	872 <sup>§</sup>	1.5 <sup>*</sup> (1.0)	82.3 (9)	0.1 <sup>*</sup> (0)	98.6 (19)	10.0 <sup>*</sup> (3.0)	71.4 (7)	10.0 <sup>*</sup> (3.0)	71.4 (7)	
	s.c.	–	269 <sup>§</sup>	1.0 <sup>*</sup> (0)	87.8 (11)	1.3 <sup>*</sup> (0)	82.4 (13)	25.0 (14.5)	28.5 (1)	25.0 (14.5)	28.5 (1)	
AdPfs25	i.m.	–	283	10.0 (7.0)	0 (4)	5.5 (5.0)	25.7 (3)	85.3 (71.5)	0 (0)	85.3 (71.5)	0 (0)	
	s.c.	–	109	16.6 (18.0)	0 (1)	7.9 (6.0)	0 (1)	207.3 (206.0)	0 (0)	207.3 (206.0)	0 (0)	
rPvs25	s.c.	IFA	449 <sup>§</sup>	0 <sup>*</sup> (0)	100 (20)							
	s.c.	Alum	50	0.7 (0)	91.5 (13)	0.2 (0)	97.3 (17)	31.2 (24.5)	10.9 (1)	31.2 (24.5)	10.9 (1)	
Naïve	s.c.	–	50	7.0 (6.0)	14.6 (1)	1.4 <sup>*</sup> (0.5)	81.1 (10)	53.5 (34.0)	0 (1)	53.5 (34.0)	0 (1)	
	s.c.	–	50	8.2 (7.5)	0 (3)	7.4 (4.5)	0 (5)	35.0 (14.5)	0 (0)	35.0 (14.5)	0 (0)	

i.m.: intramuscular; s.c.: subcutaneous; IFA: incomplete Freund's adjuvant; Alum: aluminum hydroxide; TBV: transmission-blocking vaccine; Pv: *Plasmodium vivax*.

\* P < 0.001 vs. naïve.

§ P < 0.005 vs. naïve.

% Reduction is calculated as the reduction in the average oocyst number for each immunization group compared to the average oocyst number for the unimmunized naïve control group.



**Fig. 2.** Transmission-blocking effects induced by antisera (1/2 dilution) derived from mice immunized with the AdPvs25, the AdPfs25, or the rPvs25 protein were evaluated. The data were expressed as the median values of oocyst number per mosquito (black bar within the box) with 25% and 75% quartiles (box) and ranges (error bars). Three independent experiments were performed, using three blood samples from Pv-infected blood donors 1–3. \*  $P < 0.001$  vs. naïve mice by the Wilcoxon–Mann–Whitney test; \*\*  $P < 0.001$  between the indicated two groups by the Wilcoxon–Mann–Whitney test.

parable to those attained by the AdPvs25. We do not know why the rPvs25/Alum immunization conferred substantial TBV efficacy without inducing antibody response detectable in ELISA (Fig. 1a); however, when the level of parasite burden increased as seen in the case for donor 3, the AdPvs25 appeared to become significantly more efficacious than the rPvs25/Alum, particularly for the i.m. immunization regimen (Fig. 2c and Table 1). These results suggest that adenovirus-vectored Pvs25 has potentially higher vaccine efficacy than the Alum-adjuvanted rPvs25 protein.

The rPvs25/IFA immunization consistently conferred a complete blockade regardless of the level of parasite burden; however, the local reactogenicity was considerably higher than Alum-adjuvanted or adenovirus-vectored immunization regimen.

Intraperitoneal or intravenous immunization with the AdPvs25 induced a robust serum IgG response, although its TBV effect was not assessed in this study. In contrast, despite the fact that adenoviruses mainly affect the respiratory system, the AdPvs25 administered by the i.n. route failed to induce a specific serum IgG response as determined by the ELISA (Supplementary Fig. 1). This might be due to the fact that only a low virus dose was able to be administered. However, the rPvs25 protein administered i.n. with a minute amount of cholera toxin (CT) adjuvant consistently induced a strong IgG response in mice, and as such its level of efficacy was very similar to that attained by the i.m. administered AdPvs25 immunization regimen (data not shown). Thus, it seems that adenovirus-vectored i.n. immunization is much less effective than the recombinant protein antigen administered through the same route with a potent mucosal adjuvant like CT. Administration through the i.g. route was also tested in this study, but failed to induce any antibody response, probably because the gastrointestinal environment is too destructive for the virus to effectively transduce the foreign gene. The intravaginal route was found to be another ineffective route to induce an antibody response by adenovirus immunization, and as such no specific serum IgG was observed. The reason for this failure might be the same as those for i.n. immunization.

In this study we concomitantly engineered a replication-defective adenovirus expressing Pfs25, an ortholog gene of Pvs25. Its immunization induced low but detectable cross-reactive serum IgG to the rPvs25 protein, although it did not reach a level of statistical significance as compared with the naïve control serum (Fig. 1a). However, the membrane feeding assay confirmed that no TBV effect was induced against *P. vivax* species (Fig. 2), suggesting that induction of interspecies cross-blocking immunity cannot be expected. However, a mixed administration of the two adenovirus vectors each expressing Pfs25 and Pvs25, or engineering of a single virus vector that co-expresses both P25 genes should be technically feasible, implicating that multi-species TBVs could be constructed. To address this possibility, we conducted a preliminary immunization experiment in which a mixture of the two adenoviruses, AdPfs25 and AdPvs25, were administered through various routes, and assessed immunogenicity towards both proteins. The results implicated that the existence of multiple viral vectors did not have a negative impact on the induction of specific IgG responses against the individual protein (data not shown).

Heterologous prime–boost regimens employing different viral vectors, different administration routes, or different vaccine formulations such as those using plasmid DNA or recombinant proteins, is thought to be a promising approach to enhance vaccine efficacy of malaria antigens [23,34–38]. To determine whether the prime–boost regimen is also applicable to OSP-based TBVs, we tested a DNA prime–adenovirus vector boost (one DNA injection and three consecutive adenovirus injections). The results implicated however that DNA immunization does not adequately replace adenovirus vector immunization, because the level of antibody remained lower than the adenovirus vector only immunization regimen (data not shown). Similarly, a combination of different immunization routes was evaluated and from our results, we concluded that replacement of parenteral with mucosal immunization induced a lower immune response (data not shown). Taken together, these results implicate that DNA or mucosal immunization, which was by itself found not to be sufficiently immunogenic, when combined with the parenteral adenovirus vector immunization, ablated to varying degrees the

overall vaccine efficacy. However, we were unable to make a final conclusive statement, at this preliminary stage of evaluation, regarding the suitability of a prime–boost regimen and whether or not it could be applied for TBVs. This is because there are other various possible combinations that need to be tested, such as an adenovirus prime–vaccinia virus boost regimen, which is known to be one of the most effective combinations [36,38].

Since OSP-based TBVs do not directly protect vaccinated individuals from infection, it should not be used as a “standalone” malaria vaccine. Researchers are beginning to realize that a single antigen, a single stage, or even a single species malaria vaccine developmental strategy can no longer be considered as a practical or realistic strategy, as was previously believed [5], and therefore a combination of heterologous immunization regimens, including the prime–boost method, need to be pursued more vigorously for future malaria vaccine development. In this sense, it is very feasible and should be technically possible to combine adenovirus–vectored TBVs with other virus vectored vaccines, such as vaccinia virus, or with viral vectors targeting the pre-erythrocytic or erythrocytic stages of single or multiple malaria species, or even in combination with vaccines targeting other infectious diseases.

Of course, there is still much scope for optimizing adenovirus–vectored OSP-based TBVs. For example, adenovirus serotype 5 used in the present study may need to be changed to other serotypes for future clinical application in malaria endemic areas in Africa, because a large proportion of African population has high serotype 5 antibody [37]. However, the present study should at least support the notion that malaria OSP antigens can be included in adenovirus–vectored or possibly other viral vectored immunization regimens, and that they are able to induce comparable levels of humoral immunity compared with those induced by the recombinant proteins combined with the Alum adjuvant.

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## Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.vaccine.2011.01.083.

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## Plasmodial ortholog of *Toxoplasma gondii* rhopty neck protein 3 is localized to the rhopty body

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### ABSTRACT

The proteins in apical organelles of *Plasmodium falciparum* merozoite play an important role in invasion into erythrocytes. Several rhopty neck (RON) proteins have been identified in rhopty proteome of the closely-related apicomplexan parasite, *Toxoplasma gondii*. Recently, three of *P. falciparum* proteins orthologous to *TgRON* proteins, *PfRON2*, 4 and 5, were found to be located in the rhopty neck and interact with the micronemal protein apical membrane antigen 1 (*PfAMA1*) to form a moving junction complex that helps the invasion of merozoite into erythrocyte. However, the other *P. falciparum* RON proteins have yet to be characterized. Here, we determined that “PFL2505c” (hereafter referred to as *pfRon3*) is the ortholog of the *tRon3* in *P. falciparum* and characterized its protein expression profile, subcellular localization, and complex formation. Protein expression analysis revealed that *PfRON3* was expressed primarily in late schizont stage parasites. Immunofluorescence microscopy (IFA) showed that *PfRON3* localizes in the apical region of *P. falciparum* merozoites. Results from immunoelectron microscopy, along with IFA, clarified that *PfRON3* localizes in the rhopty body and not in the rhopty neck. Even after erythrocyte invasion, *PfRON3* was still detectable at the parasite ring stage in the parasitophorous vacuole. Moreover, co-immunoprecipitation studies indicated that *PfRON3* interacts with *PfRON2* and *PfRON4*, but not with *PfAMA1*. These results suggest that *PfRON3* partakes in the novel *PfRON* complex formation (*PfRON2*, 3, and 4), but not in the moving junction complex (*PfRON2*, 4, 5, and *PfAMA1*). The novel *PfRON* complex, as well as the moving junction complex, might play a fundamental role in erythrocyte invasion by merozoite stage parasites.

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### 1. Introduction

Malaria is caused by the replication of protozoan parasites of the genus *Plasmodium* in circulating host erythrocytes [1]. The invasion process of merozoite stage parasite into erythrocyte requires the discharge of contents of apical secretory organelles (micronemes and rhopties) to form an irreversible contact, called a tight junction, between the merozoite and the erythrocyte membrane. This tight junction migrates from the anterior to posterior poles of the merozoite. According to this moving junction, the host membrane invaginates the merozoites to eventually form a parasitophorous vacuole [2,3]. The moving junction is one of the most distinctive features of apicomplexan invasion into host cells, and was first

observed in *Plasmodium* species [4]. Studies in apicomplexan parasite *Toxoplasma gondii* identified a total of four proteins from distinct apical secretory organelles to form a moving junction complex; micronemal protein apical membrane antigen 1 (*AMA1*) and three rhopty neck (RON) proteins, *RON2*, *RON4*, and *RON5* [5,6]. Recently, this RON–*AMA1* complex (*PfRON2*, *PfRON4*, *PfRON5*, and *PfAMA1*) was also identified in *Plasmodium falciparum* [7–9]. Attempts to knockout the *AMA1* gene locus were unsuccessful in both *Plasmodium* [10] and *T. gondii* [11]. *AMA1*-binding peptide R1 not only prevents RON–*AMA1* complex interaction, but also blocks *P. falciparum* merozoite invasion into erythrocytes [9].

Although the cumulative evidence above strongly suggests that the conserved RON–*AMA1* complex plays an essential role in merozoite invasion, it is yet to be clarified whether molecules other than *RON2*, *RON4*, and *RON5*, play roles in the formation of the moving junction complex and in the invasion process. The report on *T. gondii* rhopty proteome identified the presence of other RON proteins, *RON1* and *RON3* [12]. Therefore, we were interested in

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identifying the ortholog of *tgron3* in *P. falciparum* and in characterizing its protein expression profile, subcellular localization, and role in the formation of the RON–AMA1 complex.

## 2. Materials and methods

### 2.1. Parasites

*P. falciparum* asexual stages (3D7 strain) were maintained in human erythrocytes (blood group O<sup>+</sup>) *in vitro*, as previously described [13].

### 2.2. RNA isolation and cDNA synthesis

Total RNA was extracted from *P. falciparum* schizont-infected erythrocytes (purified by differential centrifugation on a 70%/40% Percoll/sorbitol gradient) using the TRIzol Reagent (Invitrogen, Carlsbad, CA). Following DNase treatment, cDNA was generated with a random hexamer using the SuperScriptIII® First Strand Synthesis System (Invitrogen).

### 2.3. Antibodies

Recombinant *Pf*RON3 proteins were produced using the wheat germ cell-free translation system (CellFree Sciences, Matsuyama, Japan) as described previously [14–16]. Briefly, regions of the *Pf*RON3 gene encoding the deduced amino acid sequence, 927–1056 (*Pf*RON3\_1) and 1686–1884 (*Pf*RON3\_2), were PCR-amplified from *P. falciparum* 3D7 blood-stage cDNA and ligated into pEU-E01-GST-(TEV)-N2 (CellFree Sciences), an expression plasmid with an N-terminal glutathione S transferase (GST)-tag followed by a tobacco etch virus (TEV) protease cleavage site, designed specifically for the wheat germ cell-free protein expression. Oligonucleotide primers used in the PCR amplification were *Pf*RON3\_XhoI1 (5'-ctcgagGATATTCATTAAAGAAACCTATAAATT-3') and *Pf*RON3\_BamHI1 (5'-ggatccCTAATGTGGGAACATTTTCATGATTGGTA-3') for *Pf*RON3\_1, and *Pf*RON3\_XhoI2 (5'-ctcgagGATTTTAAAGATAATCAGATGATGATC-3') and *Pf*RON3\_BamHI2 (5'-ggatccCTATTTTTAGGTACATATATATATATGTC-3') for *Pf*RON3\_2 (XhoI and BamHI restriction sites are underlined). Both GST-*Pf*RON3\_1 and GST-*Pf*RON3\_2 were captured using a glutathione-Sepharose 4B column (GE Healthcare, Camarillo, CA), and eluted by on-column cleavage with 60 U of AcTEV protease (Invitrogen) after extensive washing with PBS. To generate anti-*Pf*RON3\_1 and anti-*Pf*RON3\_2 sera, female BALB/c mice were immunized subcutaneously with 20 µg of purified *Pf*RON3\_1 or *Pf*RON3\_2 emulsified with Freund's adjuvant. A Japanese white rabbit was also immunized subcutaneously with 250 µg of purified *Pf*RON3\_1 or *Pf*RON3\_2 emulsified with Freund's adjuvant. All immunizations were performed 3 times at 3-week intervals, and then antisera were collected 2 weeks after the third immunization. In a similar manner, mouse anti-*Pf*RAP1 (aa 1–782) antibody, mouse anti-*Pf*EXP2 (aa 25–287) antibody, mouse and rabbit anti-*Pf*FAMA1 (aa 25–546) antibodies, and rabbit anti-GST antibody, were generated as control. Rabbit antisera against the *Pf*RON3\_1 and *Pf*RON3\_2 proteins were affinity purified using a column conjugated with recombinant *Pf*RON3\_1 or *Pf*RON3\_2 as ligands, respectively. Briefly, recombinant *Pf*RON3\_1 or *Pf*RON3\_2 was covalently linked to a HiTrap™ NHS-activated HP column (GE Healthcare) as manufacturer's recommendation. Rabbit antiserum was then applied to either the *Pf*RON3\_1- or the *Pf*RON3\_2-conjugated column. After an extensive washing step with 20 mM phosphate buffer (pH 7.0), antigen-specific IgGs were eluted with 0.1 M glycine-HCl (pH 2.5), and then immediately neutralized with 1 M Tris (pH 9.0). Mouse monoclonal anti-*Pf*RON4 antibody (26C64F12) [7] and anti-*Pf*RESA antibody (23/9) [17] were kind gifts from Jean F. Dubremetz (Université de Montpellier 2, France) and Robin F. Anders (La Trobe University, Australia), respectively.

### 2.4. SDS-PAGE and western blot analysis

*P. falciparum* cultured parasites were harvested after tetanolysin (List Biological Laboratories, Inc., Campbell, CA) treatment that can remove the hemoglobin without loss of parasite proteins present in the parasitophorous vacuolar space [18]. The parasite proteins were then extracted in SDS-PAGE loading buffer, incubated at 4 °C for 6 h, and subjected to electrophoresis under reducing condition on a 12.5% polyacrylamide gel (ATTO, Tokyo, Japan). Proteins were then transferred to a 0.2-µm PVDF membrane (GE Healthcare). The proteins were immunostained with antisera followed by horseradish peroxidase-conjugated secondary antibody (GE Healthcare) and visualized with Immobilon Western Chemiluminescent HRP Substrate (Millipore, Billerica, MA) on a LAS 4000 mini luminescent image analyzer (GE Healthcare). The relative molecular masses of the proteins were estimated with reference to Precision Plus Protein Standards (BioRad, Hercules, CA).

### 2.5. Immunoprecipitation

Immunoprecipitation was carried out as previously described [19]. Briefly, proteins were extracted from late schizont parasite pellets in PBS with 1% Triton X-100 containing Complete Proteinase Inhibitor Cocktail (Roche, Indianapolis, IN). Supernatants (50 µl) were pre-incubated at 4 °C for 1 h with 40 µl of 50% protein G-conjugated beads (GammaBind Plus Sepharose; GE Healthcare) in NETT buffer (50 mM Tris-HCl, 0.15 M NaCl, 1 mM EDTA, and 0.5% Triton X-100) supplemented with 0.5% BSA (fraction V; Sigma-Aldrich Corporation, St. Louis, MO). Aliquots of recovered supernatants were incubated either with rabbit anti-*Pf*RON3\_1, anti-*Pf*FAMA1, anti-*Pf*RON2, or anti-GST antibody, and then 40 µl of 50% protein G-conjugated bead suspension was added. After one-hour incubation at 4 °C, the beads were washed once with NETT-0.5% BSA, once with NETT, once with high-salt NETT (0.5 M NaCl), once with NETT, and once with low-salt NETT (0.05 M NaCl and 0.17% Triton X-100). Finally, proteins were eluted from the protein G-conjugated beads with 0.1 M glycine-HCl (pH 2.5), and then immediately neutralized with 1 M Tris pH 9.0. The supernatants were used for western blot analysis.

### 2.6. Indirect immunofluorescence assay

Thin smears of ring or schizont-enriched *P. falciparum*-infected erythrocytes were prepared on glass slides and stored at –80 °C. The smears were thawed, fixed with 4% formaldehyde at room temperature for 10 min, permeabilized with PBS containing 0.1% Triton X-100 at room temperature for 15 min, and blocked with PBS containing 5% non-fat milk at 37 °C for 30 min. The smears were then incubated with rabbit anti-*Pf*RON3 antibodies (1:500 dilution) and control mouse antibodies at 37 °C for 1 h, followed by incubation with both Alexa Fluor 488-conjugated goat anti-rabbit IgG and Alexa Fluor 546-conjugated goat anti-mouse IgG (Invitrogen) as secondary antibodies (1:500) at 37 °C for 30 min. Nuclei were stained with 4',6-diamidino-2-phenylindole (2 µg/ml, DAPI) mixed with a secondary antibody solution. Slides were mounted in ProLong Gold Antifade reagent (Invitrogen) and viewed under ×63 oil-immersion lens. High-resolution image-capture and processing were performed using a confocal scanning laser microscope (LSM5 PASCAL or LSM710; Carl Zeiss MicroImaging, Thornwood, NY). Images were processed in Adobe Photoshop (Adobe Systems Inc., San José, CA).

### 2.7. Immunoelectron microscopy

Parasites were fixed for 15 min on ice in a mixture of 1% paraformaldehyde and 0.1% glutaraldehyde in 0.1 M phosphate buffer (pH 7.4). Fixed specimens were washed, dehydrated, and embedded in LR White resin (Poliysciences, Inc., Warrington, PA) as previously

have been described [20,21]. Ultrathin sections were blocked in PBS containing 5% non-fat milk and 0.01% Tween 20 (PBS-MT) at 37 °C for 30 min. Grids were then incubated at 4 °C overnight with rabbit anti-PfRON3\_2 or control sera in PBS-MT (1:20). After washing with PBS containing 10% BlockAce (Yukijirushi, Sapporo, Japan) and 0.01% Tween 20 (PBS-BT), the grids were incubated at 37 °C for 1 h with goat anti-rabbit IgG conjugated to 10 nm gold particles (GE Healthcare) diluted 1:20 in PBS-MT, rinsed with PBS-BT, and fixed at room temperature for 10 min in 2.5% glutaraldehyde to stabilize the gold particles. The grids were then rinsed with distilled water, dried, and stained with uranyl acetate and lead citrate. Samples were examined with a transmission electron microscope (JEM-1230; JEOL, Tokyo, Japan).

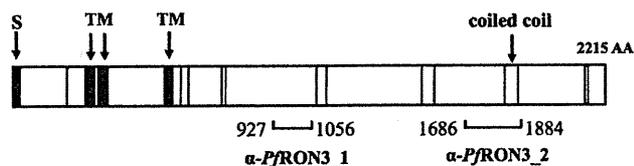
### 3. Results

#### 3.1. Primary structure analysis of the RON3 orthologs

Using TgRON3 (TGME49\_023920) as a query in BLAST analyses [22], we found RON3 orthologs in *P. falciparum* (PfRON3; PFL2505c, PlasmoDB) [23], *P. yoelii* 17XNL strain (PyRON3; PY01808, PlasmoDB), *P. vivax* Sal-I strain (PvRON3; PVX\_101485, PlasmoDB), *P. knowlesi* H strain (PkRON3; PKH\_146960, PlasmoDB), *P. chabaudi* AS strain (PchRON3; PCA\_146710, PlasmoDB), *P. berghei* ANKA strain (PbRON3; PBANKA\_146490, PlasmoDB), and *Eimeria tenella* (EtrON3; CAO79912, Sanger Institute). The full-length PfRON3 protein consists of 2215 amino acid residues, with a putative N-terminal signal peptide sequence predicted by SignalP3.0 [24] to span amino acid residues 1–22. Three transmembrane regions (TM) (aa 250–272, 276–298, and 551–573) were predicted by TMHMM2.0 [25], and one coiled coil region (aa 1822–1847) was predicted by SMART [26]. Alignment of the deduced amino acid sequences of all the RON3 orthologs among the genus *Plasmodium* using Clustal W [27] demonstrated that twelve Cys residues are conserved (Fig. 1), with a 42% overall sequence identity. Moreover, the N-terminal region is highly conserved among the RON3 orthologs in the genus *Plasmodium*, in *T. gondii*, and in *E. tenella* (Fig. 2).

#### 3.2. PfRON3 is expressed in the schizont stage and existed in the ring stage

The PfRON3 protein expression profile was analyzed by stage-specific western blot analysis using tightly synchronized parasites as antigens. Both antibodies ( $\alpha$ -PfRON3\_1 and \_2) recognized a band slightly larger than 250 kDa corresponding to the predicted molecular mass of PfRON3 in late stage parasites, 40–44 h post invasion (Fig. 3A, arrowhead). Furthermore, both antibodies also recognized a prominent 190-kDa band, 40–44 h post invasion (Fig. 3A, arrow). After erythrocyte invasion, the 190-kDa band quickly degraded to 50- and 40-kDa bands (Figs. 3A and 4H). However, a small amount of the 190-kDa band was present throughout the ring (Figs. 3A and 4H) and trophozoite stages (Fig. 3A, 24–36 h). Additionally, only the anti-PfRON3\_2 antibody



**Fig. 1.** Schematic representation of PfRON3. The primary structure of PfRON3 is depicted based on the analyses described in the Results section. S and TM indicate putative signal peptide (black) and transmembrane (blue) sequences, respectively. The yellow color box indicates a coiled coil region. Vertical red bars indicate conserved Cys residues in orthologs among the genus *Plasmodium*. The regions used to generate anti-PfRON3 sera ( $\alpha$ -PfRON3\_1 and  $\alpha$ -PfRON3\_2) are indicated.

recognized a 37-kDa band, 40–44 h post invasion that might represent one of the processed forms of the PfRON3 protein (Fig. 3A). Neither anti-PfRON3\_1 or -PfRON3\_2 had any reactivity against antigens of uninfected erythrocytes (Supplementary Fig. S1).

#### 3.3. PfRON3 localizes in the rhoptry body of merozoites

In order to determine the sub cellular localization of PfRON3, a dual label indirect immunofluorescence assay (IFA) was performed using anti-PfRON3\_2 antibody with anti-PfRAP1 (rhoptry body marker), anti-PfRON2 (rhoptry neck marker), anti-PfAMA1 (microneme marker), and anti-PfRESA (dense granule marker) antibodies as controls (Fig. 4). In mature schizonts, the anti-PfRON3 antibody produced a punctate pattern of fluorescence in the apical end of each developing merozoite. Although some of the PfRON3 signals overlapped with those of PfRON2, PfAMA1, or PfRESA the PfRON3 signals did not completely colocalize with those of the controls, whereas complete colocalization was observed between the signals of PfRON3 and PfRAP1. Negative control sera were always used and these images were found to be negative (data not shown). To confirm the IFA results, the precise subcellular localization of PfRON3 in the merozoite. Using anti-PfRON3 antibody, gold particle signals were detected in the body portion of the rhoptries (Fig. 5).

#### 3.4. PfRON3 is found in the parasitophorous vacuolar space after merozoite invasion into erythrocyte

To investigate PfRON3 localization after the parasite invades erythrocytes, we performed IFA on ring stage parasites. PfRAP1 and PfEXP2 were used as parasitophorous vacuolar (PV) markers because they have been demonstrated to be present in ring stages and to associate with the PV [28–30]. We found that PfRON3 colocalized with the PV markers, PfRAP1 and PfEXP2 in a discrete compartment surrounding the ring stage parasites (Fig. 6A). Next we performed western blot analysis using extracts of tightly synchronized ring or schizont stage parasites (Fig. 6B). PfRON3 was detected in ring and schizont stage parasites together with PfRAP1 and PfEXP2. However PfRON2 and PfRON4 were detected only in schizont stage parasites (Fig. 6B) in agreement with the IFA results (Fig. 6A). Negative control sera were always used and these images were found to be negative (data not shown).

#### 3.5. PfRON3 forms a complex with PfRON2 and PfRON4, but not with PfAMA1

To evaluate the interaction between PfRON3 and the RON-AMA1 complex, we performed immunoprecipitation experiments using mature schizont-rich parasite extracts (Fig. 7). We did not detect PfRON3 in the immunoprecipitate obtained using anti-PfAMA1 antibody. However, PfRON3 was found in the anti-PfRON2 precipitates. In the reciprocal experiment, PfRON2 and PfRON4 were detected in the immunoprecipitate obtained using the anti-PfRON3\_1 antibody; however, PfAMA1 was not detected (Fig. 7). There was negligible crossreactivity between the anti-PfRON3\_1 or anti-PfRON3\_2 IgGs and PfRON2 and PfRON4 (Supplementary Fig. S1). These faint crossreactions were insignificant compared to the reactions with the actual target molecules.

### 4. Discussion

In this study, we characterized the protein expression profile and subcellular localization of *P. falciparum* RON3 as well as its complex formation with PfRON2 and PfRON4.

Studies of the apicomplexan parasite *T. gondii* identified various TgRON proteins (RON2, RON4, RON5 [5,6], RON1, and RON3 [12]). The potential orthologs of the TgRON proteins were subsequently

Protein	position	Amino acid sequence	position
<i>Pf</i> RON3	171	NEMNQAI L VYKKA KSDSYVMDAL K KDGL L LARTFLS VSFVQSLRGI I GLINHKLIDL CFTNAYVFNHVASFDKLI MN NIFGVIMSYVFKS	262
<i>Pv</i> RON3	169	NEMDHALMI YKKA KTDAYWGMVDAL KNDG L L LARTFMSV S FVQSLRGI I GVINHELIDL CFSNAYLYNH IASFDKLI MN NTFGVIMSYVFKS	260
<i>Pk</i> RON3	169	NEMDHALMI YKKA KTDAYWGMVDAL KNDG L L LARTFMSV S FVQSLRGM IGVIN YELIDL CFSKAYMYN G IASFDKLI MN NTYGVI I SYVFKS	260
<i>Pb</i> RON3	168	NEMDQALS IYKTRNDSYWNV I DAL KSDGI L LAKTFI SASFIHGI SGGVGLANHELLN I CFSNAFFFN IAPLDKFFVMKNTFGSI I SYVFKS	259
<i>Pch</i> RON3	169	NEMDQALAI YKTRNDSYWNVVDAL KSDGMLLAKTFI SASFAHSVSGI VGVNHELLN I CFSNAYFINHI AP LDKFFVMKNTFGSI I SYVFKS	260
<i>Py</i> RON3	86	NEMDQALL IYKTRNDSYWSVVDAL KSDGI L LAKTFI SASFAHSVSGI VGLANHELLN I CFSNAYFLNHI AP LDKFFVMKNTFGSI I SYVFKS	177
<i>Tg</i> RON3	196	NAPTEAMEVVLGNNTQNMFTWIDSVRQNP FATVKNV VVHAFENGLKGVSGMV EVELNQGCFA I AQQTRH I L PFGSLFPGGI L GKIMQKLMRS	287
<i>Ei</i> RON3	217	NAGGQALDL I LANKSRPLFSWASSLWRNPLATLSNVVTVAFNETFEKTAGFP TDEVKSACFSFGYRVNSI APYTA VLPGGI FGSMLKLSRS	308
		* * * * * : : : : : * * * * * : : : : : * * * * * : : : : : * * * * * : : : : *	
<i>Pf</i> RON3	263	LLLFFYP L I PFRGAF AFA I S AFC I TQLGKIVFA I YK NLRQLYR - I SYRKY I S I V LKVKLRNEPEL KKYAMKLL YGDAL I M I TKIWKLSYV	352
<i>Pv</i> RON3	261	LLLFFYP LVI PFRGAF AFA L S SFC I S QLSKIVFL I YRNI KRLAR - I SYRKL YS T I L KFNVLKFP ELQPYASKLL YGDAL I L VSKIWKLSYV	350
<i>Pk</i> RON3	261	LLLFFYP LVI PFRGAF S FAL S SFC I TQLSKIVFL I YRNI KRLVR - I SYRKL YS T I L KFNVLKFP ELQPYASKLL YGDAL I L VSKIWKLSYV	350
<i>Pb</i> RON3	260	YL I FFYPL I V PFRGAF S F I L S S I C L M Q L G K I V H M I Y R N L K K L Y R - T S R R K F Y Y A I L K V N L L N Q P Q I H V Y A M K L L Y G D A L I L V S K I W K L S Y V	349
<i>Pch</i> RON3	261	Y L I Y F Y P L I V P F R G A F S F M L S S I C L M Q F G K I V H T I Y K N L K R L Y R - V S R R K F Y Y A I L K N L L K Q P E A Q L Y A M K L L Y G D A L V L V S K I W K L S Y V	350
<i>Py</i> RON3	178	Y L T F F Y P L I V P F R G A F S F I L S S I C L M Q F G K I V H M I Y K N L K K L Y R - I S R R K F Y Y A I L K V N L L R Q P Q I H V Y A M K L L Y G D A L V L V S K I W K L S Y V	267
<i>Tg</i> RON3	288	Y I M F F H P V L A N F K G L L A L F L G V L C K V R L P Q L I N A V F G A I F R A K R R A G R Y I H K F F F K T I S L R K D I T G K I L V D D L V R G S G A V M I T L L F Q L H G V	378
<i>Ei</i> RON3	309	F M L V F Y P A Y A S F R G I F A L M I G V I C K T G I I A S F E K L V K T L V N I A R - L G L R G T R M L L R R F A V R G D P V A S P L V Q D L R R S S P A M I T L L F Q L Y A V	398
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Fig. 2. Amino acid alignment of the conserved N-terminal region of RON3 orthologs. Deduced amino acid sequences of RON3 orthologs were aligned using Clustal W with manual correction. "\*" indicates the conserved residues in the aligned sequences. ":" indicates conservative substitutions. Cys residues are highlighted in yellow.

identified in *P. falciparum*. Bradley et al. [12] suggested that *Pf*RON3 (PFL2505c) is an ortholog of *Tg*RON3 (TGME49\_023920). However, Proellocks et al. [31] analyzed the amino acid sequence similarities of the RON orthologs identified in the genera *Plasmodium*, *Toxoplasma*, and some (but not all) *Apicomplexa*, and reported that, they may not be true orthologs because the collective sequence identity is below 12% [31]. In contrast, our pair-wise amino acid alignments between *T. gondii* and *P. falciparum* RON orthologs showed 11% identity between RON1 orthologs (TGME49\_110010 vs. PFD0207c), 14% between RON2 orthologs (TGME49\_100100 vs. PF14\_0495), 12% between RON3 orthologs (TGME49\_023920 vs. PFL2505c), and 10% between RON4

orthologs (TGME49\_029010 vs. PF11\_0168), suggesting that the amino acid identity between RON3 orthologs (*Tg*RON3 and *Pf*RON3) is comparable to that of other RON orthologs. Furthermore, multiple alignments of the deduced amino acid sequences of apicomplexan parasite RON3 orthologs showed that the N-terminal regions are conserved (Fig. 2). Based on these analyses, we conclude that *Pf*RON3 (PFL2505c) is an authentic ortholog of *Tg*RON3 (TGME49\_023920).

*T. gondii* RON3 protein was originally suggested to be localized at the rhoptry neck by immunofluorescence assay [12]. In contrast, our current immunoelectron microscopy results confirmed that *Pf*RON3 localizes in the rhoptry body rather than the rhoptry neck. Since *Pf*RON3 is in the rhoptry body, we are tempted to think that *Tg*RON3 is also localizes in the rhoptry body rather than the rhoptry neck. Therefore we believe that the localization of *Tg*RON3 should be reconfirmed by electron microscopy using quality antibodies. In general, the biggest technical hurdle to obtaining antibodies of adequate quality for use in electron microscopy studies of this sort would be the ability to produce correctly folded recombinant proteins in sufficient quantity and purity [31]. The immunoelectron microscopy results we obtained clearly demonstrate that high quality antibodies can be successfully produced using quality proteins synthesized in the wheat germ cell-free protein production system. We have already [14–16] demonstrated that the wheat germ cell-free protein production system enables the expression of quality recombinant proteins without codon optimization.

In our stage-specific western blot and immunofluorescence microscopy analyses for the *Pf*RON3 expression profile, we detected *Pf*RON3 not only in the merozoite rhoptry body but also in the PV of ring stage parasites (Fig. 6). Previous studies showed that well-characterized rhoptry body proteins (*Pf*RhopH complex, *Pf*RAP complex, and *Pf*RAMA) are discharged into the PV [32–34]. Therefore, the secretory pathway of *Pf*RON3 into the PV might be similar to that of these rhoptry body proteins. Additionally, since the 260-kDa band, corresponding to full-length *Pf*RON3, is only visible at the schizont stage (40–44 h post invasion) (Fig. 3A), the processed 190-kDa fragment may contain the functional domains throughout the parasite's asexual erythrocytic cycle.

Finally, our immunoprecipitation studies demonstrated that *Pf*RON2, *Pf*RON3, and *Pf*RON4, are able to interact and form a novel complex *in vitro*, even in the absence of *Pf*AMA1, indicating that the formation of this novel RON complex is independent of *Pf*AMA1. These results are in agreement with the previously published results showing that *Pf*RON2 and *Pf*RON4 are able to interact and form a complex independently, in the absence of *Pf*AMA1 and in the parasite; most AMA1 is not associated with complexes that contain *Pf*RON2 and *Pf*RON4 [35]. However, in this study we were unable to confirm the

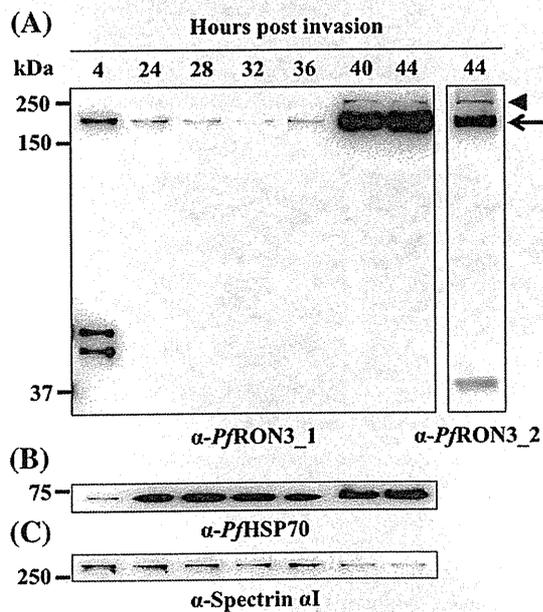


Fig. 3. Stage-specific expression profile of *Pf*RON3. Proteins from synchronized parasite cultures were harvested at each time point and separated by SDS-PAGE on a 12.5% gel under reducing condition. (A) Using either anti-*Pf*RON3\_1- or anti-*Pf*RON3\_2- specific antibodies, a band of approximately 260 kDa (arrowhead) was detected in late stages (40–44 h post invasion) and a 190-kDa band (arrow) was detected in both the schizont, ring, and trophozoite stage parasites. (B and C) Loading controls. To ensure that equal amounts of the stage-specific samples were loaded in each lane for western blot analysis, the membranes were probed with anti-*Pf*HSP70 monoclonal antibody (4C9) as a quantitative parasite protein marker [36], and anti-human spectrin  $\alpha$  I rabbit antibody indicating the number of erythrocytes. The intensity of the *Pf*HSP70 bands indicated that the amount of sample loaded in each lane was comparable.