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## ORIGINAL ARTICLE

## Production of recombinant proteins from *Plasmodium falciparum* in *Escherichia coli*

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**Introduction:** The production of recombinant proteins is essential for the characterization and functional study of proteins from *Plasmodium falciparum*. However, the proteins of *P. falciparum* are among the most challenging to express, and when expression is achieved, the recombinant proteins usually fold incorrectly and lead to the formation of inclusion bodies.

**Objective:** To obtain and purify four recombinant proteins and to use them as antigens to produce polyclonal antibodies. The production efficiency and solubility were evaluated as the proteins were expressed in two genetically modified strains of *Escherichia coli* to favor the production of heterologous proteins (BL21-CodonPlus (DE3)-RIL and BL21-pG-KJE8).

**Materials and methods:** The four recombinant *P. falciparum* proteins corresponding to partial sequences of PfMyoA (Myosin A) and PfGAP50 (gliding associated protein 50), and the complete sequences of PfMTIP (myosin tail interacting protein) and PfGAP45 (gliding associated protein 45), were produced as glutathione S-transferase-fusion proteins, purified and used for immunizing mice.

**Results:** The protein expression was much more efficient in BL21-CodonPlus, the strain that contains tRNAs that are rare in wild-type *E. coli*, compared to the expression in BL21-pG-KJE8. In spite of the fact that BL21-pG-KJE8 overexpresses chaperones, this strain did not minimize the formation of inclusion bodies.

**Conclusion:** The use of genetically modified strains of *E. coli* was essential to achieve high expression levels of the four evaluated *P. falciparum* proteins and lead to improved solubility of two of them. The approach used here allowed us to obtain and purify four *P. falciparum* proteins in enough quantity to produce polyclonal antibodies in mice, and a fair amount of two pure and soluble recombinant proteins for future assays.

**Key words:** *Plasmodium falciparum*, recombinant proteins, *Escherichia coli*.

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### Producción de proteínas recombinantes de *Plasmodium falciparum* en *Escherichia coli*

**Introducción.** La producción de proteínas recombinantes es fundamental para el estudio funcional de las proteínas de *Plasmodium falciparum*. Sin embargo, las proteínas recombinantes de *P. falciparum* están entre las más difíciles de expresar y, cuando lo hacen, usualmente se agregan dentro de cuerpos de inclusión insolubles.

**Objetivo.** Evaluar la producción de cuatro proteínas de *P. falciparum* usando como sistema de expresión dos cepas de *Escherichia coli* genéticamente modificadas para favorecer la producción de proteínas heterólogas y establecer una reserva de proteínas recombinantes puras y solubles, y producir anticuerpos policlonales a partir de ellas.

**Materiales y métodos.** Las proteínas recombinantes, las cuales correspondían a secuencias parciales de PfMyoA (Miosina-A) y PfGAP50 (proteína-asociada a glideosoma de 50 kDa) y a las secuencias completas de PfMTIP (proteína de interacción con miosina-A) y PfGAP45 (proteína asociada a glideosoma de 45 kDa), fueron expresadas como proteínas de fusión con la glutatión S-transferasa y luego purificadas y usadas para producir anticuerpos policlonales en ratón.

#### Author's contributions:

Eliana Patricia Calvo, Moisés Wasserman and Jacqueline Chaparro-Olaya conceived the study.

Ángela Patricia Guerra and Eliana Patricia Calvo carried out laboratory procedures.

Ángela Patricia Guerra, Eliana Patricia Calvo and Jacqueline Chaparro-Olaya performed analysis and interpreted the data.

All authors participated in the writing of the paper.

**Resultados.** La expresión de las proteínas recombinantes fue mucho más eficiente en la cepa BL21-CodonPlus (la cual expresa tRNAs escasos en las bacterias silvestres), que en la cepa BL21-pG-KJE8. Por el contrario, aunque la cepa BL21-pG-KJE sobreexpresa chaperonas, no redujo la formación de cuerpos de inclusión.

**Conclusión.** El uso de cepas de *E. coli* genéticamente modificadas fue fundamental para alcanzar altos niveles de expresión de las cuatro proteínas recombinantes evaluadas y permitió obtener dos de ellas en forma soluble. La estrategia utilizada permitió expresar cuatro proteínas recombinantes de *P. falciparum* en cantidad suficiente para inmunizar ratones y producir anticuerpos policlonales y, además, conservar proteína pura y soluble de dos de ellas para ensayos futuros.

**Palabras clave:** *Plasmodium falciparum*, proteínas recombinantes, *Escherichia coli*.

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Malaria is the most important parasitic infection worldwide and one of the greatest public health challenges in developing countries. Of the five species of *Plasmodium* that infect humans, *P. falciparum* is the most lethal and causes 198 million new cases each year and nearly 600,000 deaths (1). Despite the reduction in the incidence and mortality of malaria over the past decade, there is a global emergence and gradual spread of antimalarial drug resistance, which has prompted significant efforts to determine the molecular mechanisms governing the biology of the parasite, either to counter this resistance or to propose alternative therapeutic targets.

*Plasmodium* spp. is an obligate intracellular parasite whose survival and proliferation depends on its ability to invade the host cell. Apicomplexan parasites actively enter host cells making use of a unique form of motility referred to as gliding, powered by an actomyosin-motor immersed into a protein complex termed the glideosome (2,3). Since the proteins in this complex are highly conserved and specific to all Apicomplexa (4), the glideosome has enormous potential as chemotherapeutic target. However, the characterization and functional study of proteins from extracts of parasites in culture is difficult because it is impossible to obtain them in pure form and in sufficient quantities. Thus, many of the current functional studies rely on recombinant protein production in heterologous expression systems, amongst which *Escherichia coli* is the most widely used. Its popularity is primarily a

result of the abundant knowledge of the biology and biochemistry of this bacterium, the facility of its genetic manipulation and the low cost of culture maintenance (5). Despite these advantages, the expression of the recombinant proteins of *Plasmodium* is hampered by the high A/T content in its genome (80%) (6) and the dissimilar codon usage between these two organisms (7), with both issues leading to the production of truncated proteins or inefficient synthesis (8). Moreover, the recombinant proteins can fold incorrectly and lead to the formation of inclusion bodies (9), which hinder their purification.

The aim of this work was to assess two genetically modified strains of *E. coli*, BL21-CodonPlus (DE3)-RIL and BL21-pG-KJE8, on the expression of four *P. falciparum* glideosome proteins: Myosin A (PfMyoA), the myosin tail interacting protein (MTIP), the gliding-associated protein GAP45 and the gliding-associated protein GAP50. The first strain overexpresses four tRNAs that are typically rare in wild-type strains of *E. coli*, and the second strain overexpresses five chaperones (*dnaK*, *dnaJ*, *grpE*, *groEL*, and *groES*) that promote the correct folding of proteins. The recombinant proteins were obtained as glutathione S-transferase (GST) fusion proteins from the partial sequences of the *PfmyoA* and *gap50* genes and complete sequences of the genes *mtip* and *gap45*.

The results showed that the expression of the four recombinant proteins of *P. falciparum* was much more efficient in strains containing tRNAs normally scarce in wild-type strains of *E. coli*, than in strains that have elevated levels of chaperone proteins. Furthermore, the use of the latter did not diminish the formation of insoluble protein aggregates. Finally, the purified recombinant proteins were produced in suitable quantities for immunizing mice and generating antibodies, which recognized the four proteins of interest in *P. falciparum* protein extracts.

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## Materials and methods

### Bioinformatics

The A/T content of the sequences coding for the recombinant proteins was assessed with the GC Content Calculator (<http://www.biologicscorp.com/tools/GCContent>). The theoretical molecular weight and isoelectric point (pI) of each recombinant protein were calculated with the ExPASy compute pI/Mw tool ([http://web.expasy.org/compute\\_pi/](http://web.expasy.org/compute_pi/)), and the charge and number of acidic aminoacids of the proteins were determined using PEPSTATS ([http://www.ebi.ac.uk/Tools/seqstats/emboss\\_pepstats/](http://www.ebi.ac.uk/Tools/seqstats/emboss_pepstats/)). Finally, as codons are unevenly used in different organisms, the codon usage bias between *E. coli* and *P. falciparum* was examined using the Codon Usage Database at <http://www.kazusa.or.jp/codon/>. To assess preferences for particular synonymous codons, the number and frequency of each codon in the recombinant sequences were calculated using Sequence Manipulation Suite (SMS) (<http://www.bioinformatics.org/sms2/reference.html>).

### Cloning of genes

Based on the sequences of *PfmyoA*, *mtip*, *gap45* and *gap50* (PlasmoDB ID: PF3D7\_1342600, PF3D7\_1246400, PF3D7\_1222700 and PF3D7\_0918000, respectively), gene-specific primers were designed as described in table 1. Each fragment was amplified from genomic DNA of *P. falciparum* (3D7 strain) that was extracted by proteinase K lysis, phenol chloroform treatment and subsequent dialysis against TE buffer (10). The polymerase chain reaction (PCR) conditions were as follows: 200  $\mu$ M dNTPs, 1  $\mu$ M primers, 0.625 U *Pfu* DNA polymerase (Thermo scientific) and 1.5 mM  $MgSO_4$ . The amplification program included an initial denaturation cycle of 94°C x 5 min; 35 cycles of 94°C x 30 s, 50°C x 30 s, and 72°C x 1 min; and a

final extension of 72°C x 7 min. The amplicons were cloned into the vector pGEM-T easy (Promega) using the manufacturer's recommendations.

### Subcloning into pGEX-4T2

The cloned fragments in pGEM-T easy were released by digestion with the enzymes *Bam*HI and *Not*I and ligated into the expression vector pGEX-4T2 (Amersham Pharmacia Biotech) in the presence of T4 DNA ligase (Promega) following the manufacturer's recommendations. The ligation products were transformed into TOP10 bacteria (Invitrogen™) by heat shock. The colonies were confirmed by PCR and the presence of the fragment of interest was verified by sequencing.

### Expression of recombinant proteins

The TOP10 (Invitrogen™), BL21-CodonPlus (DE3)-RIL (Agilent) and BL21-pG-KJE8 (Takara Bio Inc) strains were transformed with the recombinant plasmids. For expression assays, a positive colony for each construct in each strain was grown in LB medium that was supplemented with 100  $\mu$ g/ml ampicillin and 50  $\mu$ g/ml chloramphenicol overnight at 37° C with constant stirring at 200 rpm. The following day, each culture was diluted with fresh medium, and for the BL21-pG-KJE8 system, the medium was supplemented with 1 mg/ml arabinose and 10 ng/ml tetracycline (chaperone expression-inducing agents). The cultures were incubated until they reached an optical density ( $OD_{600}$ ) between 0.6 and 0.8, time at which isopropyl thio-beta-galactopyranoside (IPTG, 0.1 mM) was added, and growth was allowed for 16 h at 37° C.

Aliquots of 1 ml were collected just before induction (time 0) and at 2, 4, and 16 h after induction. These aliquots were centrifuged at 1,000 x g for 5 min; the pellet was solubilized in 1X loading buffer for sodium dodecyl sulfate polyacrylamide

**Table 1.** Sequences of primers

Gene size (bp)	Sequence 5'-3'	Amplicon size	Position on gene
<i>PfmyoA</i> 2841 pb	F: GGATCCGCAATCCAGTTCCTGAAGCT R: GCGGCCGCTAAAATACTTCAAACCAAAAATATC	766 bp	1062-1812
<i>mtip</i> 615 pb	F: GGATCCATGAAACAAGAATGCAATGTA R: GCGGCCGCTTATTGTAATATATCTTCACAGA	629 bp	Complete gene
<i>gap45</i> 615 pb	F: GGATCCATGGGAAATAAATGTTCAAGAAG R: GCGGCCGCTTAGCTCAATAAAGGTGTATCGG	629 bp	Complete gene
<i>gap50</i> 1191 pb	F: GGATCCATGCAACTACGCTTTGCGTCTTTG R: GCGGCCGCTTAAGCAGCTAAAATCTTTATGGCC	470 bp	75-525

The primers for amplifying the *mtip* and *gap45* genes amplify the complete sequence of the gene, whereas those for *PfmyoA* and *gap50* amplify a partial sequence. bp: base pairs. F: primer forward. R: primer reverse. GGATCC: restriction site for *Bam*HI. GCGGCCGCT: restriction site for *Not*I. TTA CTA: stop codons

gel electrophoresis (SDS-PAGE) and the proteins were denatured at 95° C for 5 min. The resulting extract was run on 10% denaturing acrylamide gels, and the recombinant proteins were detected by Coomassie blue staining and/or western blotting (WB). The expression from the pGEX-4T2 vector results in GST fusion proteins with the GST tag (26 kDa) at the amino terminus and the protein of interest at the carboxyl terminus; thus, a polyclonal anti-GST antibody (Sigma) was used as the primary antibody to detect recombinants in WB. A signal amplification system that involved the use of a secondary anti-rabbit IgG antibody conjugated to biotin (Sigma) and alkaline phosphatase enzyme conjugated to streptavidin (Pierce™) was used.

### **Evaluation of the solubility of the recombinant proteins**

The bacterial culture was centrifuged at 1,000 x g and the pellet was re-suspended in five volumes of buffer R (50 mM NaCl, 50 mM Tris HCl pH 7.5 and 5% glycerol), lysozyme (1 mg/ml) and 1:200 protease inhibitor cocktail (Sigma). Five cycles of freezing and thawing (liquid nitrogen x 45 s, water bath at 37° C x 2 min) were performed, and the suspension was then centrifuged at 15,000 x g for 15 min to separate the supernatant from the particulate fraction. The presence of the protein of interest in both fractions was monitored by SDS-PAGE and WB to determine its solubility.

### **Effect of temperature on the recovery of soluble proteins**

In certain cases, temperature decrease may reduce the formation of protein aggregates and thus improve the solubility of the recombinant proteins (11). Therefore, the protocol previously described for the expression of proteins in *E. coli* BL21-pG-KJE8 was followed with the culture maintained at 30° C.

### **Purification of recombinant proteins**

The soluble recombinant proteins were purified by affinity chromatography with glutathione-agarose resin (Thermo Scientific) from 1 L of the bacterial culture. The purification was performed in a batch with 300 µl of the resin bed per 6 ml extract. Binding was allowed for 30 min at 4° C with gentle shaking; the mixture was then centrifuged at 1,000 x g for 2 min and the supernatant was saved. The resin was washed 10 times each with 10 volumes of wash buffer (50 mM Tris-HCl pH 8.0, 150 mM NaCl) or until the absorbance of the wash solution at 280 nm was at or below 0.010. The recombinant protein was eluted with 300 µl elution buffer (50 mM Tris-

HCl pH 8.0, 150 mM NaCl and 10 mM reduced glutathione). The resulting eluates were analyzed by SDS-PAGE and stored at -70° C.

The insoluble recombinant proteins were purified from the particulate fraction as follows: One gram of pellet was homogenized in wash buffer (100 mM Tris-HCl pH 7, 5 mM EDTA, 5 mM DTT, 2 M urea, 2% triton X-100) and centrifuged at 22,000 x g for 30 min at 4° C. This procedure was repeated twice, and the resulting inclusion bodies were then re-suspended in wash buffer without urea or Triton and centrifuged two times as mentioned above; 0.5 ml of extraction buffer (50 mM Tris-HCl pH 7, 5 mM EDTA, 5 mM DTT, 8 M guanidine-HCl), were added to the pellet and the suspension was then homogenized and centrifuged at 17,000 x g for 1 h at 4° C. The supernatant was dialyzed against 1 L of dialysis buffer (150 mM NaCl and 50 mM Tris-HCl pH 8.0) with two buffer changes. The resulting suspension after dialysis was run under denaturing conditions on a preparative gel. The region of the gel containing each recombinant protein was excised, triturated, and incubated with four volumes of ultrapure water at 37° C for 4 h (12). The purity and concentration of the protein in the eluate were analyzed by SDS-PAGE and WB.

### **Production of polyclonal antibodies**

Each of the purified recombinant proteins was inoculated intraperitoneally into four Balb/c mice of 5-6 weeks of age. The immunization schedule consisted of three injections on days 1, 14 and 35, the first one with 100 µg of protein in Freund's complete adjuvant and two boosts with 50 µg of antigen in incomplete adjuvant. The final bleeding was done on day 42 (13). Then, the four recombinant proteins (50-250 ng/lane) and *P. falciparum* protein extracts (Strain 3D7, 50-100 µg/lane) were separated by SDS-PAGE, transferred onto PVDF or nitrocellulose membranes and immunoblotted with the produced antibodies. The anti-MTIP, anti-GAP50 and anti-GAP45 sera were used at dilutions of 1:500, while the anti-MyoA serum was used at a dilution of 1:5000. The secondary antibody used was biotin goat-anti mouse antibody (Dako) at a dilution of 1:2000 or 1:5000, respectively, and streptavidin conjugated to alkaline phosphatase (1:3000) (Promega) or horseradish peroxidase (1:10000) enzymes (Vector).

### **Ethics**

This study was approved by the Ethics Committees of the Colombian *Instituto Nacional de Salud*

(approval 9, October 7<sup>th</sup>, 2010) and of the *Facultad de Ciencias* of the *Universidad Nacional de Colombia* (approval 5, October 11<sup>th</sup>, 2010).

## Results

### Bioinformatics

The A/T content of the sequences coding for the recombinant proteins was about 65% in all the cases. The theoretical molecular weight and pI of the four recombinants: GST-PfMyoA, GST-PfMTIP, GST-PfGAP45 and GST-PfGAP50, were 54.6 kDa/5.67, 49.8 kDa/4.71, 49.9 kDa/4.83 and 43.6 kDa/6.33, respectively. The PEPSTATS tool found 70, 77, 90 and 51 acidic amino acids equivalent to 15%, 18%, 21% and 13% of the total amino acids in the named proteins. As stated above, BL21-CodonPlus (DE3)-RIL strain overexpresses four tRNAs that are typically rare in wild-type strains of *E. coli*; then, the Codon Usage Database was used to get the frequency of use of AGA, AGG, AUA and CUA codons in *E. coli* and *P. falciparum*. The relative abundance of these codons in the expressed sequences was also calculated (table 2).

### Effect of host strain on the production of recombinant proteins

This study evaluated the expression of four proteins from *P. falciparum* in three different strains of *E. coli*: TOP10, BL21-CodonPlus (DE3)-RIL (hereinafter called CodonPlus), and BL21-pG-KJE8 (hereinafter called pG-KJE8). The IPTG-induced expression of each protein was evaluated by SDS-PAGE and WB with an anti-GST antibody; GST-PfMyoA, GST-PfMTIP, GST-PfGAP45 and GST-PfGAP50 proteins were detected as bands of ~52 kDa, ~55 kDa, ~60 kDa and ~43 kDa, respectively.

The recombinant GST-PfGAP45 had the same molecular weight (~60 kDa) as one of the molecular chaperones (groEL) expressed in the pG-KJE8 strain, resulting in bands overlapping; thus, at time zero, a band was observed that corresponded to the chaperone groEL. Expression of this recombinant was confirmed by WB that showed a weak expression in this strain. In contrast to the other three proteins, GST-PfMTIP was not successfully expressed in *E. coli* pG-KJE8 (figure 1).

Regarding the incubation time for the CodonPlus system, GST-PfGAP45 was expressed from 2 h post incubation; however, at 16 h a decreased signal was observed, which suggests proteolytic degradation. GST-PfMTIP was expressed quite well from 2 h after incubation and increased until 16 h. For GST-PfGAP50, expression was significantly higher compared to that of the other two recombinant proteins, and it was produced in large amounts beginning at 2 h after incubation and continuing until 16 h (figure 1). The expression of GST-PfMyoA did not increase in the CodonPlus strain and was almost undetectable by Coomassie blue staining; conversely, in the pG-KJE8 strain, protein synthesis was evident between 2 and 4 h of incubation (figure 1).

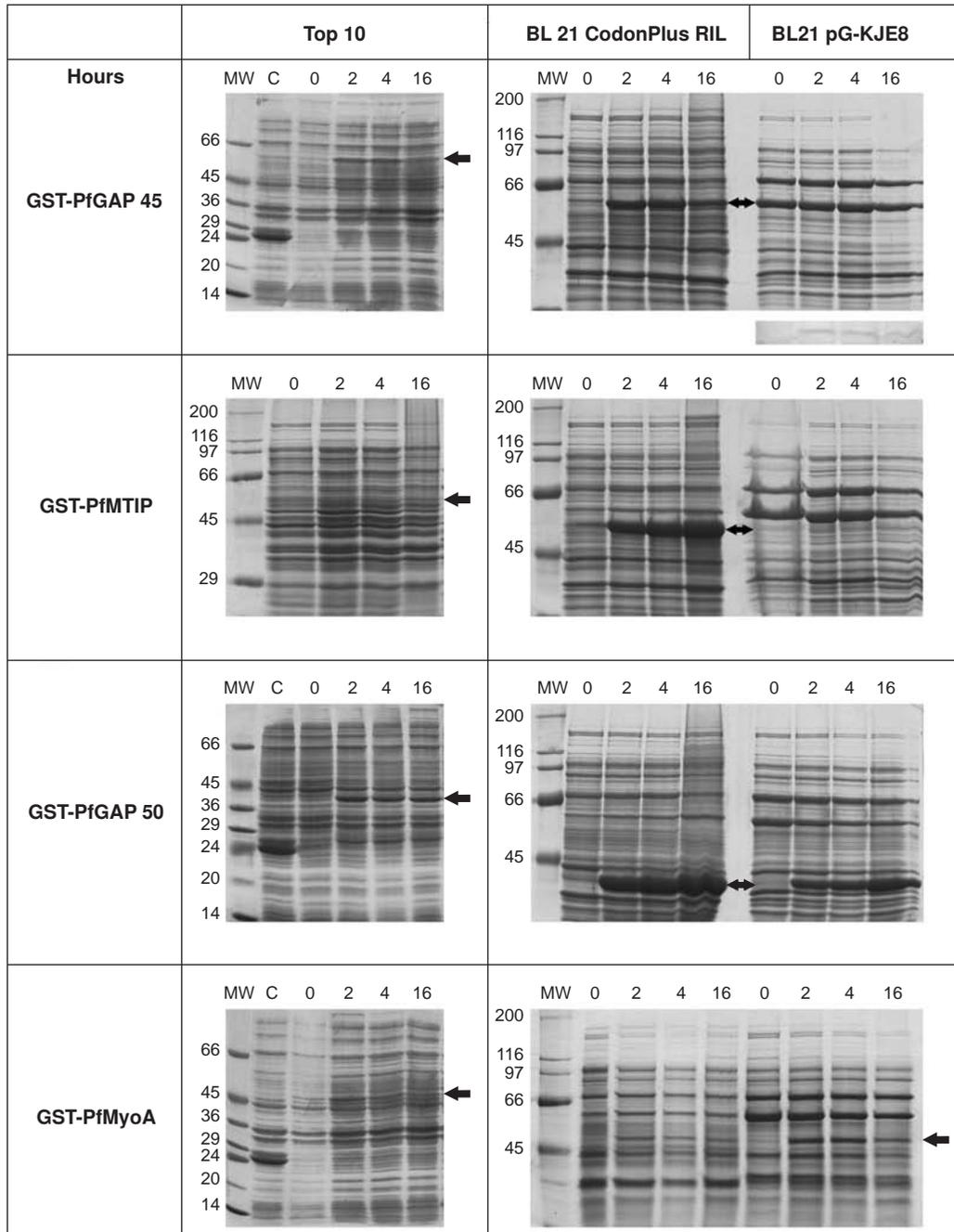
### Effect of host strain on the solubility of the recombinant proteins

Once the optimal conditions for the production of each recombinant protein had been established, solubility was assessed. For this test, protein extracts were prepared under non-denaturing conditions, and the presence of the protein of interest in both the cytosolic extract and pellet was evaluated. GST-PfGAP45 and GST-PfMTIP

**Table 2.** Frequency of AGA, AGG, AUA and CUA codons in the four recombinant proteins

AA	Codon	Frequency per 1000 AA		How many times this AA/How many times this codon Percentage of this codon in the expressed sequence			
		In <i>E. coli</i>	In <i>P. fal.</i>	PfMyoA 250 AA	PfMTIP 204 AA	PfGAP45 204 AA	PfGAP50 150 AA
Arg	AGA	2.4	15.9	11/7 2.8%	3/1 0.5%	9/6 2.9%	3/2 1.3%
	AGG	2.1	4.3	11/2 0.8%	3/1 0.5%	9/0 0%	3/0 0%
Ile	AUA	5.0	50	21/11 <b>4.4%</b>	13/6 2.9%	10/5 2.5%	9/5 <b>3.3%</b>
Leu	CUA	3.4	6	15/0 0%	18/0 0%	9/1 0.5%	24/0 0%

The AGA and AGG codons for arginine (Arg), AUA codon for isoleucine (Ile) and CUA codon for leucine (Leu), are rarely used in *E. coli*. The table shows how many times Arg, Ile and Leu are present in the expressed sequence, how many of these arginines, isoleucines and leucines are coded by AGA, AGG, AUA or CUA, and the percentage of each one of these codons (with one hundred percent considered to be the number of amino acids of the expressed sequence). Percentages  $\geq 3\%$  are highlighted in bold. The codon usage frequencies were taken from <http://www.kazusa.or.jp/codon/>. AA: Amino acid. P. fal: *Plasmodium falciparum*



**Figure 1.** SDS-PAGE of the whole bacterial extracts from each expression system. The production of GST-PfGAP45, GST-PfMTIP, GST-PfGAP50 and GST-PfMyoA proteins was monitored 2, 4, and 16 h after IPTG-induced expression. The expression was evaluated in three different strains of *E. coli*: TOP10, BL21-CodonPlus (DE3)-RIL and BL21-pG-KJE8. In the upper part of the figure, the strain and induction time (h) are specified. For GST-PfGAP45, the WB using an anti-GST antibody is found below the gel and corresponds exactly to the electrophoresis lanes. MW: Molecular weight marker in kDa (Sigma). C: Control cells expressing only the GST tag (26 kDa). The black arrow indicates the protein of interest.

were found in both the cytosolic fraction and pellet, whereas GST-PfGAP50 and GST-PfMyoA were found in the pellet (figure 2). These two proteins were only soluble in the presence of strong chaotropic agents such as 8 M guanidine, which

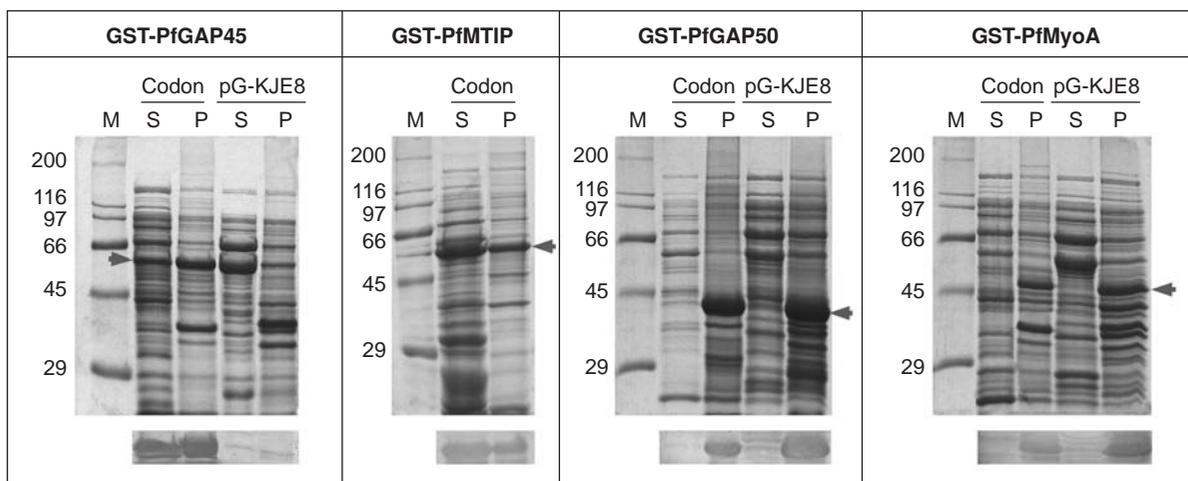
indicated that insoluble protein aggregates or inclusion bodies (IB) had formed. No differences in solubility were observed between the host strain that co-expressed the chaperones and strains that only had basal levels of these proteins.

**Effect of temperature on the solubility of recombinant proteins expressed in the strain pG-KJE8**

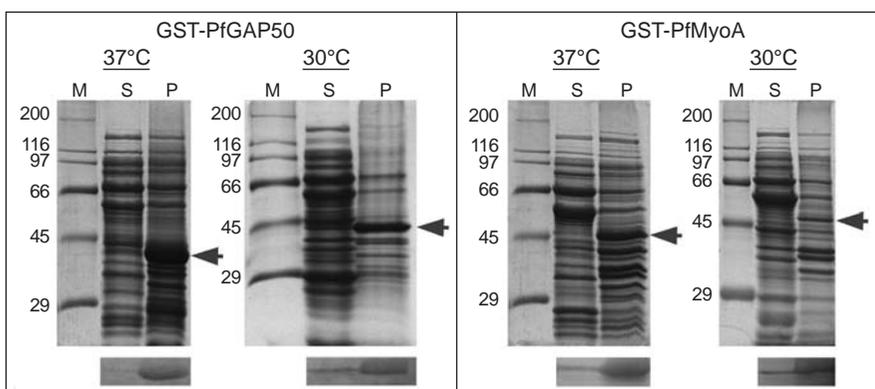
Because the activity of certain chaperones of *E. coli* is increased at temperatures of approximately 30° C, and temperature reduction at the time of induction has been used favorably to improve the solubility of the recombinant proteins (11,14,15), an expression assay was conducted by incubating at 30° C proteins GST-PfMyoA and GST-PfGAP50 producing pG-KJE8 clones. Despite this modification, no increase in the solubility of the two proteins was observed (figure 3).

**Purification of recombinant proteins**

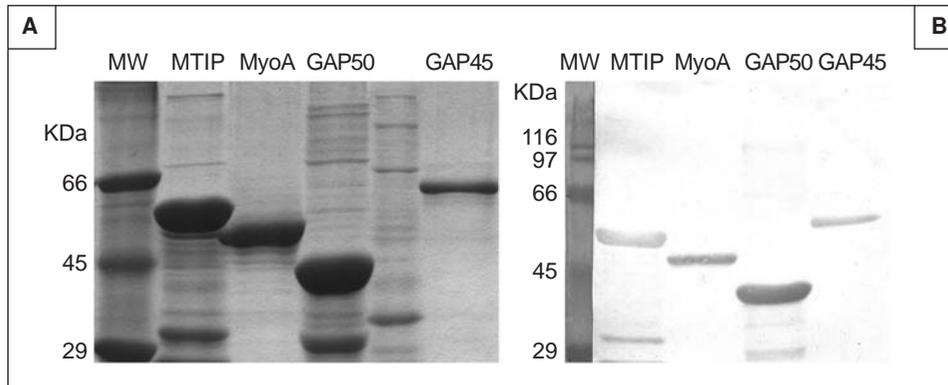
The culture was scaled up to 1 L to obtain sufficient raw material to begin the purification process. The soluble GST-PfMTIP protein was purified by affinity chromatography (Pierce™ Glutathione Agarose), and although other lower-weight bands were found using SDS-PAGE, GST-PfMTIP was always found in greater amounts than the others (figure 4). The bands of different molecular weights were most likely degraded or truncated proteins whose GST tag at the amino terminus allowed their co-purification by affinity chromatography and recognition by the anti-GST antibody. Furthermore, although GST-



**Figure 2.** SDS-PAGE of soluble and insoluble fractions of *Escherichia coli* cultures expressing each one of the recombinant proteins. Bacteria were grown at 37°C and then harvested and disrupted 2 hours post induction (hpi) for GST-PfMyoA and GST-PfGAP45, or 16 hpi for GST-PfMTIP and GST-PfGAP50. The presence of the protein of interest in the soluble fraction (S) and/or pellet (P) was detected by SDS-PAGE and WB with anti-GST. M: Molecular weight marker in kDa (Sigma). The WB membranes located under each gel correspond to exactly the same order of the gel electrophoresis lanes.



**Figure 3.** SDS-PAGE analysis of temperature effect on the solubility of GST-PfMyoA and GST-PfGAP50. The *Escherichia coli* cultures (strain pG-KJE8) expressing GST-PfMyoA or GST-PfGAP50 were grown at 30°C and harvested at 2 hours post induction (hpi) in the case of GST-PfMyoA and at 16 hpi for GST-PfGAP50. The presence of the protein of interest was detected in the soluble fraction (S) and/or the insoluble pellet (P) by SDS-PAGE and WB with anti-GST. M: Molecular weight marker in kDa (Sigma). The WB membranes located under each gel correspond to exactly the same order as the gel electrophoresis lanes.



**Figure 4.** SDS-PAGE and Western blot of the four purified recombinant proteins.

The purified proteins were subjected to SDS-PAGE in A and WB in B. The primary antibody used was a polyclonal anti-GST antibody (Sigma).

PfGAP45 was detected in the cytosolic extract, it was not purified by affinity with glutathione-agarose resin and had to be excised from acrylamide gels. Seven milligrams of GST-PfMTIP were obtained, whereas 1 mg was recovered for GST-PfGAP45.

GST-PfMyoA and GST-PfGAP50 were solubilized from inclusion bodies with guanidinium hydrochloride (8 M) and analyzed by SDS-PAGE. GST-PfMyoA, unlike GST-PfGAP50, presented several contaminating proteins; therefore, it was necessary to extract it from acrylamide gels. Approximately 3.2 mg of GST-PfGAP50 was recovered, whereas 800 µg of GST-PfMyoA was recovered. Once purified, all of the proteins were confirmed by WB with anti-GST (figure 4).

### Immunoblotting

The MTIP (~32 kDa), GAP50 (~45 kDa), GAP45 (~50 kDa) and PfMyoA (~90 kDa) proteins were identified in immunoblots of parasite protein extracts by the antibodies raised against GST-PfMTIP, GST-PfGAP50, GST-PfGAP45 and GST-PfMyoA respectively (figure 5).

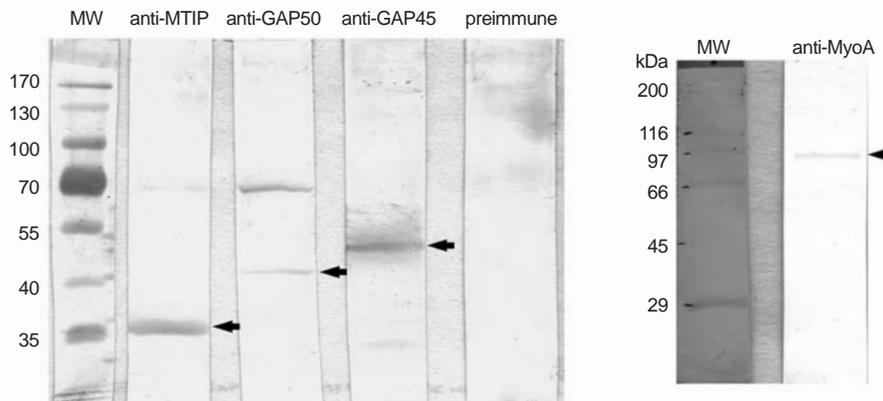
### Discussion

The expression of *P. falciparum* proteins in heterologous systems typically results in a lack of expression or in insoluble expression. This problem was highlighted by a large-scale study where 1,000 *P. falciparum* open reading frames were selected for expression in *E. coli* (16). Of these ORFs, only 30% were expressed and only 6.3% of the resulting proteins were soluble. Higher molecular weight and protein disorder were negatively correlated with expression, hydrophobicity did not correlate with either expression or solubility, and pI was the

only one factor associated with both expression and solubility. Notably, the high A/T content and the codon usage of *P. falciparum*, both usually correlated with lack of expression, did not affect significantly either the expression or solubility (16).

Later, Vedadi, *et al.* (17) selected 1,008 apicomplexan genes to be expressed in codon-enhanced *E. coli* strains. These genes were selected using *P. falciparum* as a model and looking for orthologous genes from *P. vivax*, *P. yoelii*, *P. berghei*, *P. knowlesi*, *Toxoplasma gondii* and *Cryptosporidium parvum*. Of these 1,008 genes, 304 (30.2%) were produced as soluble proteins, and when the seven genomes were analyzed as a “super Apicomplexan genome”, 229 (49%) out of the 468 target genes were produced as soluble proteins. Vedadi, *et al.* (17) found that protein size, A/T content or pI do not have any impact in the soluble expression and concluded that *E. coli* is in effect a suitable expression system for Apicomplexan proteins, including those from *Plasmodium*.

The present study evaluated the expression of four proteins from *P. falciparum* in three different strains of *E. coli*: TOP10, CodonPlus and pG-KJE8. TOP10 is a strain that allows for stable replication and a high copy number of plasmids; the other two strains are used extensively in protein expression and not only have a decreased protease activity but also facilitate translation (CodonPlus) or protein folding (pG-KJE8). By using this approach, the four recombinant proteins were successfully expressed (figure 1). GST-PfMyoA and GST-PfGAP50 proteins were detected in SDS-PAGE and immunoblotting experiments about the expected sizes. On the other hand, GST-PfMTIP and



**Figure 5.** Immunoblot on protein extracts of *Plasmodium falciparum* to detect PfMTIP, PfGAP50, PfGAP45 and PfMyoA. Protein extracts from 3D7 strain of *Plasmodium falciparum* were subjected to denaturing electrophoresis and transferred onto PVDF or nitrocellulose membranes. Membranes were probed with the anti-MTIP, anti-GAP50, anti-GAP45 and anti-MyoA antibodies raised against the GST-PfMTIP, GST-PfGAP50, GST-PfGAP45 and GST-PfMyoA recombinant proteins, respectively.

GST-PfGAP45 migrated with apparent molecular masses of ~55 kDa and ~60 kDa, although they were predicted to encode proteins of ~50 kDa (figure 4). This behavior can be explained by their content of acidic amino acids, whose interactions with SDS have been reported to slow down the rate of migration (18-20).

In fact, GST-PfMTIP and GST-PfGAP45 exhibited the highest contents of acidic amino acids (18% and 21%), the lowest pI values (4.71 and 4.83) and the most negative charge (-25 and -26). In contrast, the charge and pI values were estimated at -4.5 / 5.67 for GST-PfMyoA and 1.5 / 6.33 for GST-PfGAP50. In spite of their anomalous migration, the GST-PfMTIP and GST-PfGAP45 identity was validated by sequencing the recombinant plasmids, and because the antibodies raised against these two recombinant proteins recognized their target proteins on *P. falciparum* extracts. The PfMyoA, MTIP, GAP45 and GAP50 proteins have theoretical masses of ~92, ~23.5, ~23.6 and ~45 kDa, respectively, and they were detected at ~90, ~32, ~50 and ~45 kDa in WB assays using protein extracts of *P. falciparum* (3D7 strain) (figure 5). The anomalous migration of MTIP and GAP45 was expected since both proteins typically run at molecular weights greater than would be predicted by their sequence. This phenomenon has been extensively reported and thought to result from post-translational modifications of the proteins (21,22). The GST-PfMyoA, GST-PfGAP45 and GST-PfGAP50 proteins were expressed in all three strains of *E. coli*, GST-PfMTIP could only be expressed by one strain (CodonPlus), and among the three strains tested, CodonPlus showed the

most efficient expression for three of the four recombinant proteins (GST-PfMTIP, GST-PfGAP45, and GST-PfGAP50).

This CodonPlus strain has a plasmid that contains extra copies of the *argU*, *ileY*, and *leuW* genes that code for tRNA with specific codons for arginine (AGA/AGG), isoleucine (AUA), and leucine (CUA) that are rare in *E. coli*. Since in *P. falciparum* the AGA and AUA codons are used 6.6-fold and 10-fold more often than in *E. coli*, the co-expression of this plasmid provides the bacteria with a supplement of specific tRNAs for the codons of the parasite. In fact, an analysis of the cloned sequences revealed that AGA is the most used codon for arginine and AUA/AUU are the most used codons for isoleucine (table 2). These differences in codon usage can explain why the expression of the GST-PfMTIP, GST-PfGAP45, and GST-PfGAP50 proteins in the CodonPlus strain is increased compared with the expression in the TOP10 and pG-KJE8 strains, which only have basal levels of these tRNAs. These results are consistent with what has been reported in other studies (23,24).

However, in the case of GST-PfMyoA, a significant increase in expression in the CodonPlus strain was not observed. Carstens (25) has proposed that there may be low or no expression if the frequency of at least one type of rare codon in the bacterium is  $\geq 3\%$  in the protein to be expressed. For GST-PfMyoA, three rare codons, AGG, AGA and AUA, were found, and they reached frequencies of 0.8, 2.8 and 4.4%, respectively (table 2). Carstens (25) also suggested that the consecutive presence of rare codons is the most important factor affecting the expression of a heterologous protein in *E.*

*coli*. In GST-PfMyoA, three cases were found: two doublets (AUAAGA) and a triplet (AUAAUAAGA); in GST-PfGAP45, a single case was found (the doublet AGAAGA) and in GST-PfGAP50 and GST-PfMTIP, no cases were found. Goldman, *et al.* (26) reported that the effect of successive rare codons on expression is more noticeable when they are located near the amino terminus of the protein, especially when the codons code for arginine. Chen, *et al.* (27) explain that this result occurs because of instability in the protein synthesis machinery near the beginning of the message. Upon analyzing the four sequences, only GST-PfMyoA (250 amino acids) presented this condition at codons 14-15 and 36-37. All of the above characteristics of the GST-PfMyoA sequence can explain why despite the use of three genetically different strains, an important increase in its production was not achieved.

GST-PfMyoA and GST-PfGAP50 were produced as protein aggregates, while GST-PfMTIP and GST-PfGAP45 were found in the cytoplasmic fraction. The results show that, for these proteins, A/T content, size protein and pI do not have noticeable effect on expression or solubility. Although the CodonPlus strain promotes expression of certain proteins of *P. falciparum*, the insolubility of the recombinant protein has been reported. Because translation is more efficient, the set of available chaperones to assist in protein folding becomes saturated and this may cause the accumulation and aggregation of misfolded proteins in the cytoplasm (28). The *E. coli* pG-KJE8 strain overexpresses both multi-component chaperone complexes present in *E. coli*: the gro proteins EL (60 kDa) and ES (10 kDa), and the KJE complex, which is formed by chaperones *dnaK*, *dnaJ* and *grpE* (29). In this way, if there is poor folding because of the saturation of the chaperone system itself, the presence of additional molecules will facilitate the proper folding of the protein, and it would be reflected in an increase in solubility (30-32). In our case, the evaluation of the solubility of the recombinant proteins produced in CodonPlus and pG-KJE8 strains showed similar results that were independent of the adjusted conditions for expression (temperature, time of incubation and IPTG concentration). Thus, the use of a bacterial system that provides extra chaperones did not prevent the formation of insoluble aggregates of GST-PfMyoA or GST-PfGAP50, indicating that additional factors other than the availability of the folding machinery determined the solubility of these recombinant proteins.

According to Wall, *et al.* (33), the specific role of the co-production of chaperones on the expression of a gene in *E. coli* is unclear and appears to be specific to each protein. In fact, undesirable side effects derived from chaperone gene co-expression, such as growth inhibition, proteolysis, reduced yield, reduced solubility or reduced specific activity, have been reported (34).

With respect to the purification of GST-PfGAP45, we suggest that the protein adopts a three-dimensional structure that prevents free exposure of the GST tag, thus preventing the recombinant protein from interacting with the glutathione agarose resin. This may explain why GST-PfGAP45 could not be purified by affinity chromatography. The detection of GST-PfGAP45 with anti-GST in denaturing conditions allows us to state that the GST tag was present.

In this study, the main purpose of producing the four recombinant proteins was to achieve suitable quantities of proteins for immunizing animals and generating antibodies, and to obtain large quantities of soluble proteins in sight of future in vitro protein-protein interaction studies. To achieve this goal, we used different host cells to establish the conditions in which the most efficient expression might be obtained and sought conditions that would allow us to express the protein in its native conformation. Although it was not possible to obtain all the proteins in soluble form and the use of denaturing agents for solubilization was required in two cases, the four proteins were obtained in high quantity.

Our results indicate that the use of genetically modified strains for the expression of *P. falciparum* proteins was necessary to improve the synthesis and achieve higher expression levels detectable by Coomassie blue staining, but their use did not necessarily have a positive effect on the solubility of the proteins. The CodonPlus strain favored the expression of three proteins, but the solubility varied from a completely soluble protein such as GST-PfMTIP to a completely insoluble protein such as GST-PfGAP50.

Although it is not possible to generalize about heterologous expression strategies, the approach used here led us to obtain four *P. falciparum* proteins corresponding to partial sequences of PfMyoA and GAP50, and the complete sequences of MTIP and GAP45. From 1 L of culture, we were able to produce and purify enough material for immunizing mice and for keeping a large supply for future uses.

### Conflicts of interest

None declared

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