A set of independent selectable markers for transfection of the human malaria parasite Plasmodium falciparum

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ABSTRACT Genomic information is rapidly accumulating for the human malaria pathogen, Plasmodium falciparum. Our ability to perform genetic manipulations to understand Plasmodium gene function is limited. Dihydrofolate reductase is the only selectable marker presently available for transfection of P. falciparum. Additional markers are needed for complementation and for expression of mutated forms of essential genes. We tested parasite sensitivity to different drugs for which selectable markers are available. Two of these drugs that were very effective as antiparasomidal inhibitors in culture, blasticidin and genetin (G418), were selected for further study. The genes BSD, encoding blasticidin S deaminase of Aspergillus terreus, and NEO, encoding neomycin phosphotransferase II from transposon Tn 5, were expressed under the histidine-rich protein III (HRP III) gene promoter and tested for their ability to confer resistance to blasticidin or G418, respectively. After transfection, blasticidin and G418-resistant parasites tested positive for plasmid replication and BSD or NEO expression. Cross-resistance assays indicate that these markers are independent. The plasmid copy number and the enzymatic activity depended directly on the concentration of the drug used for selection. These markers set the stage for new methods of functional analysis of the P. falciparum genome.

Malaria is responsible yearly for about 2 million deaths—mostly children under the age of 5 (1). Appearance of widespread resistance to currently used drugs such as chloroquine, fansidar, and mefloquine has stimulated efforts to identify new antimalarial drug and vaccine targets. The Plasmodium falciparum genome is ~30 megabases in size, has a base composition of 82% A+T, and contains 14 chromosomes. Genome sequencing is underway, and genomic as well as expressed-sequence-tag databases have been generated (2). Recently the 0.95-megabase chromosome II of this protozoan has been fully sequenced and is predicted to encode 209 proteins (3). Database analyses indicated that 43% of these proteins have no detectable homologs. On this chromosome, 18 ORFs called rifins have been found, and no function has been assigned to them yet. The paucity of genetic tools to study the parasite’s most important pathways, such as mechanisms of drug resistance, parasite invasion, differentiation, and cell cycle, leaves us with a growing database of genes but difficulty in determining their actual functions.

Genetic manipulation of the malaria parasite has taken major strides forward. Early transfection success with Plasmodium species causing rodent malaria (4, 5) was followed by a breakthrough in transient transfection of P. falciparum (6). Subsequently, electroporation-based transfection of ring-stage P. falciparum has been used for stable expression and disruption of malaria genes (7–11). When these early intraerythrocytic parasites are electroporated in the presence of plasmid, DNA seems to be able to cross the erythrocyte membrane, the double membrane surrounding the parasite, and the nuclear membrane to gain entry into the nucleus. There, episomal plasmid can be maintained indefinitely under selective pressure. At a low frequency, homologous integration occurs, and events can be selected following drug withdrawal and subsequent reintroduction (7, 8). Integration has been shown to occur by single-crossover homologous-recombination events that can be exploited for allelic exchange or gene disruption (9, 11). Transfection of the malaria parasite has relied on a single marker, the human or Toxoplasma gondii dihydrofolate reductase genes that confer resistance to methotrexate or pyrimethamine (6, 12). This paucity of selectable markers limits our ability to carry out disruption of essential genes, complementation of knockouts, or execution of plasmid-shift experiments to select specific mutants in important biological pathways.

In an attempt to prepare tools that can facilitate systematic analysis of the malaria parasite genome, we sought additional genetic markers for P. falciparum transfection. We tested different drugs for their ability to inhibit the growth of the parasite in culture. Based on these results, two drugs were selected, blasticidin S and G418. We sought to construct vectors that would confer stable, episomal resistance to these agents. The present work describes the use of BSD (encoding blasticidin S deaminase of Aspergillus terreus) and NEO (encoding neomycin phosphotransferase II from transposon Tn 5) genes as positive selectable markers for P. falciparum transfection. These markers will facilitate functional analysis of the malaria genome and understanding of the biology of the parasite, which are crucial for developing chemotherapies and vaccines.

EXPERIMENTAL PROCEDURES

Strains. The clones 3D7 (The Netherlands), HB3 (Honduras), Dd2 (Indochina), and W2 (Indochina) were used in this study. These parasites were kindly provided by Tom Wellems (National Institutes of Health, Bethesda, MD; HB3 and Dd2) and Pradip Rathod (Catholic University, Washington, DC; 3D7 and W2).

Cell Culture and Materials. All enzyme reactions and DNA preparations were performed as described by Maniatis et al. (13). Parasites were cultured by the method of Trager and Jensen (14) by using a gas mixture of 3% O2, 3% CO2, and 94% N2. RPMI medium 1640 was supplemented with 30 mg/liter hypoxanthine (Sigma), 25 mM Hepes (Sigma), 0.225% NaHCO3 (Sigma), 0.5% Albumax I (Life Technologies, Grand Island, NY), and 10 µg/ml gentamycin (Life Technologies).

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Blasticidin S and zeocin were from Invitrogen. Phosphinothri-
ycin, geneticin, kanamycin, hygromycin, and paromomycin were
purchased from Sigma. Puromycin was from CLONTECH;
nourseothricin from Hans-Knoll-Institut for Natural Products
Research (Jena, Germany); and phleomycin from Cayla (Tou-
louse, France).

**Plasmid Constructs.** PCR with the primer pair 5’-GGA
AGA TGC ATG CCA AGC CTT TGT ACG AAG AAT
CCA CCC TC-3’ and 5’-GAC GGG AAG CTT TGC TCC
TGG GCC ACG AAG TGC-3’ was used to amplify the BSD
gene of *A. terreus* from pDNA6/V5-His plasmid (Invitrogen).
The neomycin phosphotransferase gene of transposon Tn 5
was used to amplify the
9
CTG TCT TTT
AAG CTT
A TGC AT
GGA AG
9
y
70% (vol/vol) ethanol and resuspended in TE buffer. DNA (5
µg) was digested with *ScaI* or *ScaI* + *DpnI*. Digested products
were separated by electrophoresis on 1% agarose gels, trans-
ferred to Hybond N+ Nylon membrane (Amersham Phar-
cma), and hybridized with 32P-labeled pBluescript II SK(+) probe (Stratagene). For plasmid recovery, 500 ng of genomic
DNA was electroporated into *Escherichia coli* cells.

**BSD Enzyme Assay.** Cultured parasitized red blood cells (12
µl) at 10% parasitemia and 2% hematocrit were washed with
assay buffer (10 mM Tris-HCl, pH 7.5), suspended in 0.75 ml
of assay buffer, and lysed by sonication on ice. The superna-
tants were recovered by centrifugation at 25,000 × g for 10 min
at 4°C and subsequently used for measurement of enzyme
activity. A spectrophotometric assay based on the differential
absorbance of the cytosine nucleus in the substrate (blasticidin
S) and uracil in the product (deaminohydroxyblasticidin S) was
used (19). The assay mixture contained 6 µl of 10 mM
blasticidin S and an appropriate amount of assay buffer to
adjust the total volume to 600 µl. The reaction was initiated by
adding 200 µg of crude enzyme extract to the mixture. The
reaction was carried out at 30°C, after which it was stopped by
adding 4.4 ml of 0.1 M HCl, and the decrease in absorbance at
282 nm was monitored (20). We determined that an OD282 of
30 nmol of blasticidin S cleaved. Samples
were normalized to protein concentration, measured by using
a bicinchoninic acid protein assay kit (Sigma).

**Neomycin Phosphotransferase Assay.** To assay neomycin
phosphotransferase, we used the procedure developed by
Ramesh and Osborne (21) with the following adjustments. The
parasitized red blood cells were washed with PBS; resuspended
in 0.4 ml of the assay buffer containing 10 mM Tris-HCl (pH
7.4), 10 mM MgCl2, 25 mM NH4Cl, and 0.6 mM β-mercap-
tetoethanol; and lysed by sonication on ice. The superna-
tants were recovered by centrifugation at 25,000 × g for 10 min
at 4°C. In a 60-µl final volume, 10 µl of cell extracts were added
to 40 µl of the reaction mix [3.3 µl of 1 M Tris-Maleate, pH
7.1/2.1 µl of 1 M MgCl2/20 µl of 0.4 M NH4Cl/2.2 µl (20 µCi)
of [γ-32P]ATP (6,00 Ci/mmol)/12.4 µl H2O] and 10 µl of 5

![FIG. 1. Maps of pCBM-BSD and pCBM-NEO vectors.](image)
mM neomycin sulfate or kanamycin sulfate (Sigma). The reaction was carried out at 37°C for 60 min, after which it was stopped by the addition of an equal volume of phenol-chloroform-isomyl alcohol (25:24:1, vol/vol). A 30-μl aliquot of the aqueous phase was applied to P81 paper, washed twice with water for 10 min each, and then washed twice with 50 mM sodium phosphate (pH 7.4) for 2 h. The radioactivity was then determined by liquid scintillation counter. Samples were normalized to protein concentration, measured by using a bicinechonic acid protein assay kit (Sigma). One unit of activity is defined as 5 fmol (62,500 cpn) of product formed per milligram of protein.

RESULTS

P. falciparum Growth Inhibition by Blasticidin S and G418.

In an effort to develop tools for genomic analysis of the human malaria parasite P. falciparum, we tested different drugs for their ability to inhibit the growth of the 3D7 parasite clone in culture. Because the parasite lives in an anucleate host erythrocyte, the range of drugs that can be used for selection is not limited generally by toxicity to the host cell. There were 10 drugs tested at concentrations up to 1 mg/ml (Table 1). Puromycin, nourseothricin, zeocin, phleomycin, phosphinothricin, blasticidin S, and G418 were found to be inhibitory.

For the purpose of this study, we focused our work on two drugs, blasticidin S and G418. Both drugs had an antiplasmodial effect with IC_{50} values for P. falciparum clone 3D7 of 0.35 μg/ml and 150 μg/ml, respectively (Table 1). Blasticidin S was chosen, because it is potent in culture and its resistance determinant is encoded by a small (399 bp) ORF, enhancing the probability of efficient expression and leaving room for cloning of larger DNA fragments. G418 was chosen, because it has been used successfully as a selectable marker in a broad range of eukaryotic organisms. We tested the effect of both drugs on P. falciparum lines with different chloroquine sensitivity. Four different parasite lines (3D7, HB3, W2, and Dd2) ranged in sensitivity (IC_{50}) to blasticidin S from 0.15 to 0.45 μg/ml (Fig. 2A) and to G418 from 150 to 380 μg/ml (Fig. 2B). There was no correlation with chloroquine sensitivity.

**BSD and NEO: Selectable Markers for P. falciparum Transfection.** The transfection vectors pCBM-BSD and pCBM-NEO contain the BSD or NEO (also called APH(3')-II) genes under the regulatory control of P. falciparum promoter and terminator sequences (Fig. 1). After individual electroporation of these vectors into P. falciparum, the pCBM-BSD culture was split into three lines (BS1, BS2, and BS5), and blasticidin S (1 μg/ml, 2 μg/ml, and 5 μg/ml, respectively) was added 48 h later. The pCBM-NEO culture was also split into three lines (G3, G5, and G10) and G418 (300 μg/ml, 500 μg/ml, and 1 mg/ml, respectively) was added 48 h later. Parasites were detected in all three pCBM-BSD plates by microscopy 4 weeks after transfection. Parasites were detected in the G3 and G5 lines at 4 weeks, but no parasites were obtained from the G10 culture up to 7 weeks. Drug pressure was maintained throughout the culture period. As a control, the 3D7 strain was transfected with the pBluescript vector and grown under the same conditions. No resistant parasites were detected at any of the drug concentrations used.

To confirm that the transfected plasmids had been replicated by P. falciparum, we tested susceptibility of the episomes to DpnI, an enzyme that cleaves GATC sequences only when the adenine is methylated. Because the necessary methylation activity (Dam methylase) is absent from eukaryotes but present in E. coli, replication of plasmid DNA in P. falciparum would lead to resistance to DpnI digestion. There was a failure of DpnI cleavage of plasmid sequences present in the parasite genomic DNA preparations, whereas this enzyme produced multiple fragments from E. coli-replicated DNA (Fig. 3). The absence of methylation identified by DpnI resistance indicates that the transfected plasmid DNA had been replicating episomally in P. falciparum. ScaI digestion alone gave the expected size of the linearized construct (Fig. 3).

The intensity of the bands corresponding to plasmid increased with the concentration of the drug, which indicates an increase in the copy number of the plasmid in response to the drug. To determine the plasmid copy number in resistant isolates, 0.5 μg of total DNA was slotted onto nylon membrane and hybridized with the BSD or NEO probe (Fig. 4). Varying amounts of either gene were slotted onto the blot, corresponding to the amount of BSD DNA that would be present per microgram of total DNA if there were 1–35 copies of the construct per cell. The data show an increase in copy number out of the culture period.

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![Graph A](image1.png)

**Fig. 2.** Inhibition of 3D7, HB3, W2, and Dd2 parasite clones as a function of blasticidin S (A) or G418 (B) concentrations.

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<table>
<thead>
<tr>
<th>Gene</th>
<th>Drug</th>
<th>IC_{50} μg/ml</th>
</tr>
</thead>
<tbody>
<tr>
<td>NEO</td>
<td>Geneticin (G418)</td>
<td>150</td>
</tr>
<tr>
<td></td>
<td>Paromomycin</td>
<td>&gt;1,000</td>
</tr>
<tr>
<td></td>
<td>Kanamycin</td>
<td>&gt;1,000</td>
</tr>
<tr>
<td>BSD</td>
<td>Blasticidin</td>
<td>0.35</td>
</tr>
<tr>
<td>BLE</td>
<td>Phleomycin</td>
<td>200</td>
</tr>
<tr>
<td></td>
<td>Zeocin</td>
<td>500</td>
</tr>
<tr>
<td>HYG</td>
<td>Hygromycin</td>
<td>&gt;1,000</td>
</tr>
<tr>
<td>SAT</td>
<td>Nourseothricin</td>
<td>75</td>
</tr>
<tr>
<td>BAR</td>
<td>Phosphinothricin</td>
<td>600</td>
</tr>
<tr>
<td>PAC</td>
<td>Puromycin</td>
<td>0.02</td>
</tr>
</tbody>
</table>

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![Graph B](image2.png)
and IC$_{50}$ with increased drug concentration (Table 2). Plasmid rescue performed on genomic DNA prepared 7 weeks after transfection showed a correlation between numbers of E. coli transformants (reflecting episome copy number) and concentration of drug used for selection. Restriction analysis of a dozen plasmid clones from each rescued sample showed no rearrangements of the transfected DNAs (data not shown).

**Enzyme Assays.** To monitor the expression of the BSD gene product, extracts from 3D7 alone or from 3D7-blasticidin S-resistant parasites (BS1, BS2, and BS5) were tested for BSD enzymatic activity. The BSD gene encodes a deaminase that converts the potent inhibitor blasticidin S into a nontoxic deaminohydroxy derivative (20). As shown in Fig. 5A, extracts from BS2 and BS5 produced a significant and time-dependent decrease in the absorbance at 282 nm, indicative of BSD activity within these parasites. No significant activity was detected in BS1 extracts, and no activity was detected in nontransfected 3D7 parasites. The level of the activity was proportional to the concentration of the drug used to select for the transfectants (Fig. 5A), indicating once again that higher drug concentration increases the copy number of the episome and thus the expression of the BSD gene. To monitor the expression of the NEO gene in G3 and G5 cells, we assayed the aminoglycoside phosphotransferase activity of its gene product in vitro by using [$\gamma$-32P]ATP as a phosphate donor and kanamycin as a phosphate acceptor. Both G3 and G5 express activity (Fig. 5B). Here again, the data show a correlation between the drug concentration, plasmid copy number, and enzyme activity. Similar results were obtained by using neomycin sulfate as a phosphate acceptor (not shown).

**Independence of BSD, NEO, and DHFR Markers.** To be used for gene replacement or for simultaneous expression of multiple gene products from expression vectors, markers need to be independent, and the resistance conferred by one marker should not interfere with the activity of the second marker. To test this possibility, we measured the IC$_{50}$ of the clones BS5 and G5 on blasticidin S, G418, and pyrimethamine and compared them to the IC$_{50}$s of the untransfected 3D7 strain. Other drugs that have the potential to be used in positive selection of P. falciparum transfection (puromycin and nourseothricin) were also tested in this study. No cross-resistance was detected between these markers; IC$_{50}$ values for parental and transfected strains were indistinguishable with each drug (not shown).

**DISCUSSION**

We have developed two markers for P. falciparum transfection. NEO and BSD genes can be expressed in the human malaria parasite. Table 2. Summary of IC$_{50}$ and plasmid copy number experiments for control (3D7) and transfected lines BS1, BS2, BS5, G3, and G5

<table>
<thead>
<tr>
<th>Line</th>
<th>IC$_{50}$</th>
<th>Copy number per cell</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blasticidin</td>
<td>3D7</td>
<td>0.4 µg/ml</td>
</tr>
<tr>
<td></td>
<td>BS1</td>
<td>3 µg/ml</td>
</tr>
<tr>
<td></td>
<td>BS2</td>
<td>4 µg/ml</td>
</tr>
<tr>
<td></td>
<td>BS5</td>
<td>25 µg/ml</td>
</tr>
<tr>
<td></td>
<td>G418</td>
<td>400 µg/ml</td>
</tr>
<tr>
<td></td>
<td>G3</td>
<td>1 mg/ml</td>
</tr>
<tr>
<td></td>
<td>G5</td>
<td>&gt;1 mg/ml</td>
</tr>
</tbody>
</table>

**FIG. 3.** (A) Detection of pCBM-BSD DNA from parasites selected on 1 µg/ml (BS1), 2 µg/ml (BS2), or 5 µg/ml (BS5) of blasticidin S. Genomic DNA (prepared 7 weeks posttransfection) and DNA from the original plasmid (pCBM-BSD) were restricted with ScaI (S, which cuts once in the vector) or ScaI + DpnI (SD, with 15 pBluescript recognition sites), hybridized with a 32P-labeled pBluescript probe, and detected by autoradiography. A longer exposure of the autoradiograph is also shown. (B) Detection of pCBM-NEO DNA from parasites selected on 500 µg/ml G418 (G5). DNA was prepared as described for A. Untransfected 3D7 served as a control in both A and B.
parasite *P. falciparum* and confer resistance to G418 and blasticidin S, respectively. *NEO* is a widely used marker for eukaryotic transfection, whereas *BSD* has not been used previously for transfection of a parasite (we have now developed it for use in *Leishmania*). For both markers, there is a correlation between the level of enzymatic activity, the episome copy number, and the concentration of the drug used to select for parasite transfectants. This correlation is valuable for heterologous gene expression where the level of expression can be changed by controlling the drug concentration. Parasites harboring the *BSD* plasmid were able to grow in blasticidin S at concentrations up to 25 μg/ml (70× the IC50, data not shown). However, at 1 μg/ml, there is no background resistance in the control culture. Therefore, there is a wide range of drug to use for titration of expression levels.

From our data, we believe that other markers, such as *PAC*, *SAT*, and *BLE*, that confer resistance to puromycin (IC50 = 20 ng/ml), nourseothricin (IC50 = 75 μg/ml), and phleomycin (IC50 = 200 μg/ml) also have the potential to serve as markers for *Plasmodium* transfection. These markers have been used successfully for transfection of other protozoan parasites such as *Leishmania* (22, 23). Neither *NEO* nor *BSD* induces cross-resistance to other drugs that are or might be used for positive selection in *P. falciparum* transfection, suggesting that these independent markers will be useful for gene replacement or for simultaneous expression of multiple gene products from expression vectors.

The ability to use *BSD* and *NEO* markers for malaria transfection will set the stage for rescue of disrupted essential genes, for making gene libraries to complement naturally occurring or induced mutants, or for other techniques that require the presence of multiple independent markers. The development of these resistance markers will allow better exploitation of the accumulating *P. falciparum* genomic information, lead to better understanding of the biology of the parasite, and facilitate development of drug and vaccine targets.

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