The Plasmodium circumsporozoite protein is proteolytically processed during cell invasion

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The circumsporozoite protein (CSP) is the major surface protein of Plasmodium sporozoites, the infective stage of malaria. Although CSP has been extensively studied as a malaria vaccine candidate, little is known about its structure. Here, we show that CSP is proteolytically cleaved by a papain family cysteine protease of parasite origin. Our data suggest that the highly conserved region I, found just before the repeat region, contains the cleavage site. Cleavage occurs on the sporozoite surface when parasites contact target cells. Inhibitors of CSP processing inhibit cell invasion in vitro, and treatment of mice with E-64, a highly specific cysteine protease inhibitor, completely inhibits sporozoite infectivity in vivo.

RESULTS AND DISCUSSION

The NH₂-terminal portion of CSP is proteolytically cleaved by a cysteine protease

Malaria infection is initiated when an infected Anopheline mosquito injects sporozoites during a blood meal. After injection, sporozoites enter the bloodstream and go to the liver, where they invade hepatocytes and develop into exoerythrocytic forms. The circumsporozoite protein (CSP) is the major surface protein of the sporozoite and forms a dense coat on the parasite’s surface. Studies have shown that CSP mediates sporozoite adhesion to target cells (for review see reference 1) and that it is required for sporozoite development in the mosquito (2). In addition, CSP has been extensively studied as a vaccine candidate and, thus far, is the only Plasmodium protein shown to confer protection to immunized individuals (for review see reference 1).

Comparison of the deduced amino acid sequences of CS proteins from all species of Plasmodium shows that they have a similar overall structure (see Fig. 1 A and reference 1). They all contain a central repeat region whose amino acid sequence is species specific and two conserved regions: a five amino acid sequence called region I, immediately before the repeats, and a known cell-adhesive sequence with similarity to the type I thrombospondin repeat (TSR; reference 3). CSP has a canonical glycosylphosphatidylinositol (GPI) anchor addition sequence in its COOH terminus; however, the presence of a GPI anchor has not been demonstrated.

It was noted 20 yr ago that CSP immunoprecipitated from sporozoite lysates consists of one to two high MW bands (that differ by ~1 kD) and a low MW band that is 8–10 kD smaller (4, 5). Biosynthetic studies showed that the initial label is incorporated into the top bands and the lower MW band appears later as a processed product (4, 5). The precise nature of this processing, as well as its functional significance, have remained unknown. In this report, we have determined the structural basis for this conserved feature of CSPs and have explored its role during sporozoite invasion of hepatocytes.

The online version of this article contains supplemental material.
To determine what class of protease was responsible for cleavage, we performed pulse-chase metabolic labeling experiments in the presence of different protease inhibitors. We labeled sporozoites with $[^{35}S]$Cys/Met and chased with cold medium containing the indicated inhibitor (Fig. 1 C). In the absence of protease inhibitors, $\sim$80% of labeled CSP was cleaved after 2 h. In the presence of the metalloprotease inhibitor 1,10 phenanthroline or the aspartyl-protease inhibitor pepstatin, there was no effect on CSP processing. In addition, EDTA had no effect on CSP processing, indicating that divalent cations are not required. L-transepoxysuccinyl-leucylamide-[4-guanido]-butane (E-64), a highly specific cysteine protease inhibitor, and PMSF, a serine protease inhibitor, inhibited CSP processing. Leupeptin and TLCK, inhibitors of both cysteine and serine proteases, also inhibited processing. Although PMSF has been reported to have inhibitory activity against some papain family cysteine proteases (6), it is a prototypical serine protease inhibitor. To further examine the role of serine proteases, we assayed two other serine protease inhibitors, aprotinin and 3,4 dichloroisocoumarin (3,4 DCI). Aprotinin inhibits most classes of serine proteases and would be predicted to inhibit the serine proteases of Plasmodium, which are subtilisin-like (7). 3,4 DCI is a serine protease inhibitor that has some activity against cysteine proteases but does not react with papain-like cysteine proteases (8). Neither compound had an effect on CSP processing.

We also performed pulse-chase metabolic labeling experiments with the human malaria parasite, Plasmodium falciparum, and found that E-64 inhibited CSP processing in this species (Fig. 1 D). These data suggest that CSP cleavage occurs by a similar mechanism in both rodent and human Plasmodium species.

To ensure that the protease inhibitors were not toxic to sporozoites, we incubated sporozoites with the different inhibitors and added propidium iodide, a dye that is excluded by viable cells but penetrates membranes of dying cells. The percentage of sporozoites that took up the dye in the presence of any of the protease inhibitors was no different from controls (unpublished data). In addition, we tested whether sporozoites incubated with protease inhibitors were less metabolically active. Analysis of CSP synthesis after sporozoites had been incubated with individual inhibitors for 2 h showed that it was not affected by E-64, leupeptin, or PMSF (Fig. S2, available at http://www.jem.org/cgi/content/full/jem.20040989/DC1).

Our data suggest that the processing enzyme is a cysteine protease. The cysteine proteases found in parasites are members of two clans, CA (papain-like) and CD (legumin-like) (for review see reference 9), which can be distinguished by their sensitivity to E-64. The protease that cleaves CSP is inhibited by E-64 and, therefore, is a Clan CA, papain family cysteine protease. However, we found that PMSF, a serine protease inhibitor, also inhibited processing. As stated before, PMSF has been reported to have activity against papain family cysteine proteases and this could explain its inhibitory activity in our processing assay. Nonetheless, it is also possible that CSP cleavage is a complex multistep process involving distinct proteases.

**Region I likely contains the cleavage site**

To determine where CSP is cleaved, we mapped the epitopes recognized by the NH$_2$-terminal antiserum using overlapping peptides. As shown in Fig. 2 A, the NH$_2$-terminal antiserum recognized peptides interspersed throughout the NH$_2$-terminal third of the protein, suggesting that the processed form lacks this entire region. These data raised the intriguing possibility that region I, found at the end of the NH$_2$ terminus, contained the cleavage site. To test this, we used a recombinant *P. berghei* parasite in which the last 21 amino acids of the NH$_2$ terminus and the entire repeat region had been replaced by the orthologous region from *P. falciparum* CSP [Pf/Pb sporozoites; Fig. 2 B and reference 10]. A Western blot of Pf/Pb sporozoites shows that both

![Figure 1](https://rupress.org/jem/article-pdf/201/1/27/994513/jem201127.pdf)
CSP forms are present, suggesting it is processed (Fig. 2 C). We performed pulse-chase metabolic labeling experiments with Pf/Pb sporozoites and found that after a 4-h chase, 50–80% of the high MW CSP is processed to the low MW form (unpublished data). When we tested whether E-64 could inhibit processing of the hybrid CSP, we found that it did (Fig. 2 D), indicating that the same protease cleaves both the native and hybrid CS proteins.

These data suggest that the cleavage site is found within region I because this sequence remains unchanged in the hybrid protein. Although it is possible that the cleavage site is outside of the swapped region, this is unlikely because the NH2-terminal antiserum, which recognized peptides throughout the NH2-terminal third of CSP, did not recognize the low MW CSP form. Previous studies have shown that the difference in size, by SDS-PAGE, between the high and low MW forms is ~8–10 kDa (4, 5, 11–13). The NH2-terminal portion of CSP, beginning after the signal sequence and ending just before the repeat region, is predicted to be this size.

CSP cleavage occurs extracellularly by a sporozoite protease

We investigated the cellular location of CSP processing. Immunofluorescence experiments with live sporozoites showed that they were recognized by the NH2-terminal antiserum, demonstrating that full-length CSP was on the surface (Fig. 3 A). To confirm this, we biotinylated sporozoites expressing GFP with a reagent that does not enter cells. As shown in Fig. 3 B, the high MW CSP form is biotinylated, indicating that it is on the surface. As a control, we immunoprecipitated CSP from sporozoites that were metabolically labeled and trypsinized. When compared with controls, trypsin-treated sporozoites were primarily missing the low MW CS band, indicating that the high MW CSP form was intracellular. However, in these experiments, trypsin was added immediately after labeling, which may not have allowed sufficient time for export of all the labeled CSP to the sporozoite surface. To investigate whether this was the case, we repeated this experiment and incorporated a chase into the experimental design. Sporozoites were metabolically labeled and kept on ice or chased in the presence of cyclohexamide to prevent further protein

**Figure 2.** The conserved region I likely contains the proteolytic cleavage site. (A) The epitopes recognized by the NH2-terminal antiserum were determined by ELISA by testing its reactivity to overlapping peptides encompassing the NH2-terminal third of CSP. Pep 1, GYGQNKSIQAQRNLNE; Pep 2, RNLNELCYNEGNDNKL; Pep 3, NDNKLYHVLNSKNGKI; Pep 4, KNGKIYIRNTVNRLLA; Pep 5, NRRLLADEQGGKNEKK; Pep 6, KNEKKNKIERNNKLK; and N-term, full-length NH2-terminal peptide. (B–D) Proteolytic cleavage of hybrid CSP. (B) Structure of CSP from Pf/Pb sporozoites. The portion of P. berghei CSP that has been replaced with the orthologous sequence of P. falciparum CSP is shown in orange and includes region I, which is shown in black. (C) Western blot of Pf/Pb sporozoites probed with mAb 2A10, directed against the P. falciparum CSP repeat region. (D) Pf/Pb sporozoites were metabolically labeled and kept on ice (lane 1) or chased with cold medium for 4 h, in the absence or presence of E-64. Samples were processed as outlined in Fig. 1.

**Figure 3.** CSP is processed extracellularly by a parasite protease. (A) Staining of live sporozoites with the NH2-terminal antiserum. Phase contrast and fluorescence views are shown. Bar, 10 µm. (B and C) P. berghei sporozoites expressing GFP were biotinylated, lysed, and CSP (B) and GFP (C) were immunoprecipitated. A Western blot of the immunoprecipitated material was probed with streptavidin (B and C, lane 1), mAb 3D11 (B, lane 2), or polyclonal antiserum to GFP (C, lane 2). The membrane was cut where indicated so that it could be probed with individual antisera and, the membrane strips were developed together. (D) Metabolically labeled P. berghei sporozoites were kept on ice (time = 0) or chased for 1 h, and incubated in medium containing pronase (+) or pronase plus pronase inhibitor cocktail (−). CSP was immunoprecipitated from sporozoite lysates and analyzed by SDS-PAGE and autoradiography. (E) P. berghei sporozoites were dissected and purified in the absence (−) or presence (+) of E-64, washed, metabolically labeled, and either kept on ice (time = 0) or chased for 2 h. Sporozoites were lysed, and CSP was immunoprecipitated and analyzed by SDS-PAGE and autoradiography.
synthesis. Next, they were treated with pronase or pronase plus an inhibitor cocktail. As shown in Fig. 3 D, if the parasites were kept on ice after labeling, the high MW CSP was not digested by pronase. However, if sporozoites were chased before pronase treatment, both CSP forms were digested, indicating that both forms were found on the sporozoite’s surface, making this the likely location of processing.

Sporozoites isolated from salivary glands of infected mosquitoes are invariably contaminated with mosquito debris, raising the possibility that the protease that cleaves CSP is of mosquito origin. To address this question, we dissected and purified sporozoites in the presence of E-64, and then metabolically labeled them in medium without E-64. Cysteine proteases of mosquito origin would be extracellular and, therefore, irreversibly inhibited by the E-64 present during sporozoite isolation. However, we found that CSP was processed with the same kinetics regardless of whether sporozoites were purified in the presence or absence of E-64. These data suggest that the protease was synthesized (or secreted) after the removal of E-64 and, therefore, was of sporozoite origin (Fig. 3 E).

**CSP cleavage is required for cell invasion**

Proteolytic cleavage of cell surface and secreted proteins occurs during invasion of erythrocytes by the merozoite stage of *Plasmodium* (for review see reference 14). To determine whether CSP cleavage was required for sporozoite entry into cells, a variety of protease inhibitors were tested for their ability to inhibit sporozoite invasion of a hepatocyte cell line. As shown in Fig. 4 A, E-64 inhibited invasion by 90% and PMSF and leupeptin also had inhibitory activity. Pepstatin had no effect on invasion and the serine protease inhibitors aprotinin and DCI, which do not have activity against the papain family cysteine proteases, also did not have inhibitory activity on invasion. Importantly, pretreatment of target cells with E-64 had no inhibitory effect on sporozoite invasion. The ability of E-64 to inhibit invasion was not restricted to *P. berghei* sporozoites, as invasion by both *P. yoelii* and *P. falciparum* sporozoites was also inhibited by E-64. Notably, the number of extracellular sporozoites was always enhanced in the presence of E-64, suggesting that there was an accumulation of attached sporozoites that were prevented from entering (Fig. 4 B). Because attachment to cells is a distinct stage
of sporozoite invasion (15), these results suggest that E-64 specifically blocks invasion and that attachment to cells does not require proteolytic cleavage of CSP.

These data suggest that CSP is cleaved during cell invasion. Therefore, we predicted that intracellular sporozoites would lose their reactivity to the NH$_2$-terminal antiserum, which recognizes only full-length CSP. However, we found that the majority of sporozoites associated with cells lost their reactivity to the NH$_2$-terminal antiserum regardless of whether they were intracellular or extracellular (unpublished data). In the absence of cells, 80–90% of sporozoites stained with this antiserum (unpublished data), suggesting that cell contact was the trigger for CSP cleavage. To test this, sporozoites were preincubated with cytochalasin D (CD), an inhibitor of sporozoite invasion but not attachment to cells (15), in the presence or absence of E-64 and added to cells. As shown in Table I, sporozoites incubated with CD plus E-64 stained with the NH$_2$-terminal antiserum, whereas those incubated with CD alone did not. mAb 3D11, directed against the repeat region of CSP, bound to both E-64-treated and untreated sporozoites. Controls in which sporozoites were incubated without cells showed that neither elevated temperature nor serum alone had a significant effect on CSP cleavage (Table I).

In this assay, sporozoites were incubated with cells for only 2 min before being fixed and stained. The rapid loss of reactivity to the NH$_2$-terminal antiserum indicates that there is a dramatic increase in the kinetics of CSP cleavage when parasites are added to cells. In the absence of cells, the half-life of newly synthesized CSP is ~1 h (Fig. 1 and references 4, 5). These data indicate that the secretion of the protease that cleaves CSP is regulated. It is likely that the low level cleavage observed in the absence of cells is due to leaky secretion from apical organelles, whereas exocytosis of larger amounts of protease is mediated by specific signals that are transduced upon contact with target cells.

CSP cleavage is not required for migration through cells

It has been shown that sporozoites interact with cells in two distinct ways: they either rupture the plasma membrane and migrate through a cell or they enter with a vacuole and productively invade the cell (16). To study whether CSP processing was preferentially associated with one of these processes, we tested whether E-64 inhibited sporozoite migration through cells. Migration can be quantified by including a high MW fluorescent tracer in the medium because it will enter cells that are wounded by sporozoites as they pass through. As shown in Fig. 4 C, E-64 had no effect on sporozoite migration through cells.

These data indicate that CSP cleavage is associated with productive invasion of cells and suggests that sporozoites differentially recognize cells that they will invade; a finding that makes sense given that, in vivo, they travel through several cell barriers to reach their target, the hepatocyte. One question raised by these findings is how do sporozoites recognize hepatocytes? Previous work has shown that CSP binds to heparan sulfate proteoglycans (HSPGs) found on hepatocytes, making these molecules likely candidates for target cell recognition (for review see reference 1). We are currently investigating whether binding of CSP to HSPGs triggers cleavage and initiates the cascade of events leading to productive invasion of cells.

Inhibition of cysteine proteases prevents malaria infection

Lastly, we tested E-64 as an inhibitor of malaria infection in vivo using a rodent model of the disease. Using a quantitative PCR assay, we compared the amounts of parasite rRNA in the livers of mice pretreated with E-64 or buffer and infected with Plasmodium sporozoites. We found that mice injected with E-64 were completely protected from malaria infection (Fig. 4 D). Although inhibitors of cysteine and serine proteases have not yet been used for the treatment of human disease, animal studies have shown the feasibility of using these inhibitors as drugs in the treatment of parasitic infections (for review see references 17, 18). Our finding that we can completely prevent malaria infection by targeting the cysteine proteases of the sporozoite stage could lead to the development of new prophylactic agents for malaria.

In conclusion, we have shown that the high MW CSP form is proteolytically cleaved by a papain family cysteine protease of parasite origin. Several lines of evidence support a role for CSP cleavage during cell invasion. First, under conditions in which CSP cleavage is inhibited, cell invasion is similarly inhibited. Second, rapid and complete CSP cleavage occurs when sporozoites contact target cells, indicating that cleavage is temporally associated with invasion.

### Table I. Contact with hepatocytes triggers cleavage of CSP

<table>
<thead>
<tr>
<th>Experiment</th>
<th>Cells</th>
<th>Condition$^a$</th>
<th>Method for sporozoite visualization</th>
<th>Number of sporozoites visualized$^b$</th>
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<tr>
<td>1</td>
<td>Hepa 1-6</td>
<td>CD</td>
<td>3D11</td>
<td>244 ± 3</td>
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<td>Hepa 1-6</td>
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<td>230 ± 4</td>
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<td>CD</td>
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<td>no cells</td>
<td>E-64</td>
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<td>90% ± 4.1</td>
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<td></td>
<td>no cells</td>
<td>CD + E-64</td>
<td>α-N</td>
<td>84% ± 0.5</td>
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<td></td>
<td>no cells</td>
<td>CD + 10% serum</td>
<td>α-N</td>
<td>80% ± 3.7</td>
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$^a$P. berghei sporozoites (wild type in experiment 1; GFP in experiment 2) were preincubated ± E-64, and before addition to coverslips, CD was added to the indicated samples. Sporozoites were spun onto coverslips, with or without cells as indicated, brought to 37°C for 2 min, fixed, and stained with the indicated antisera.

$^b$Each point was plated in duplicate, 50 fields/coverslip were counted, and the percentage staining with the NH$_2$-terminal antiserum is shown.

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And lastly, the conservation of this process across the genus indicates that it is of importance to the parasite.

These data are part of a growing body of work demonstrating that proteolytic processing of secreted and surface proteins is required for cell invasion by Plasmodium and other Apicomplexan parasites such as Toxoplasma (14, 19, 20). One of the most well-studied examples is MSP-1, the major surface protein of Plasmodium merozoites, the infective form of the erythrocytic stage (for review see reference 1). Interestingly, both CSP and MSP-1 have known cell-adhesive domains in their COOH termini, raising the possibility that cleavage controls the exposure of these domains. In CSP, the COOH terminus contains the TSR, a known cell-adhesive sequence that has been shown to bind with high affinity to HSPGs (for review see reference 1). Previous studies have shown that the NH2-terminal portion of CSP also binds to HSPGs (21). Our data suggest a model for CSP cleavage that explains why this protein has two heparin-binding domains. Our hypothesis is that an initial interaction between cell surface HSPGs and the NH2-terminal portion of CSP crosses the protein and provides the signal for cleavage. In turn, cleavage exposes the cell-adhesive TSR, which binds with high affinity to HSPGs, initiating a cascade of events that ultimately lead to cell entry.

**MATERIALS AND METHODS**

**Antibodies and peptides.** mAb 3D11 is directed against the repeat region of P. berghei CSP (22); mAb NYS1 is directed against the repeat region of P. yoelii CSP (23); and mAb 2A10 is directed against the repeat region of P. falciparum CSP (11). For immunoprecipitations, mAbs 3D11 and 2A10 were conjugated to sepharose as outlined previously (24). Antibody to the NH2-terminal and COOH-terminal thirds of P. berghei CSP were generated in rabbits using peptides that were provided by G. Corradin and M. Roggero (Institute of Biochemistry, Lausanne, Switzerland). The sequences of the NH2- and COOH-terminal peptides were GYGQNKSIQAQRNLN-ELCYNEGNNDNKLKYHVLNSNKGKYRINTVRKLLDAPEGKKNEKKNIERNNKKL and NDDSIESPAKEIFVKQRIDSITETWSSQCNVTCGSRIRVKKKGSKNKAEDLTLEDITIECKMDKCS, respectively. Overlapping peptides and repeat peptides were synthesized and purified by Midwest Bio-Tech.

**Sporozoites.** P. yoelii, P. berghei, P. berghei–expressing GFP (25), and recombinant P. berghei sporozoites expressing a hybrid P. berghei–P. falciparum CSP (Pf/Pb sporozoites; reference 10) were grown in the presence or absence of the indicated protease inhibitor. For the pronase experiment, sporozoites were incubated with mAb 3D11 agrose overnight at 4°C and washed with lysis buffer and lysed with buffer with 500 μM NaCl and preclusion buffer (0.5% Triton X-100, 10 mM Tris-HCl, pH 6.8). CSP was eluted with 1% SDS in 0.1 M glycine, pH 1.8, neutralized with Tris-HCl, pH 8.8, and run on a 7.5% SDS–polyacrylamide gel under nonreducing conditions. For experiments with P. falciparum or Pf/Pb sporozoites, a 10% SDS–polyacrylamide gel was used. Gels were fixed, enhanced with Amplify (Amersham Biosciences), dried, and exposed to film.

**Immunoprecipitation and SDS-PAGE analysis.** Metabolically labeled sporozoites were lysed in lysis buffer (1% Triton X-100, 150 mM NaCl, 50 mM Tris-HCl, pH 8.0) with protease inhibitors for 1 h at 4°C, and lysates were incubated with mAb 3D11 agrose overnight at 4°C and washed with lysis buffer and lysed buffer with 500 mM NaCl and preclusion buffer (0.5% Triton X-100, 10 mM Tris-HCl, pH 6.8). CSP was eluted with 1% SDS in 0.1 M glycine, pH 1.8, neutralized with Tris-HCl, pH 8.8, and run on a 7.5% SDS–polyacrylamide gel under nonreducing conditions. For experiments with P. falciparum or Pf/Pb sporozoites, a 10% SDS–polyacrylamide gel was used. Gels were fixed, enhanced with Amplify (Amersham Biosciences), dried, and exposed to film.

**Biotinylation of sporozoite lysates.** Sporozoite lysates were separated by SDS-PAGE, transferred to PVDF membrane, and incubated with either 4 μg/ml mAb 3D11, NH2-terminal antiserum (1:3,000), COOH-terminal antiserum (1:3,000), or 4 μg/ml mAb 2A10 followed by anti-mouse or anti-rabbit Ig conjugated to horseradish peroxidase (HRP; 1:100,000). Bound antibodies were visualized using the enhanced chemiluminescence detection system (ECL).

**Immunoblot of sporozoite lysates.** Sporozoite lysates were separated by SDS-PAGE, transferred to PVDF membrane, and incubated with either 4 μg/ml mAb 3D11, NH2-terminal antiserum (1:3,000), COOH-terminal antiserum (1:3,000), or 4 μg/ml mAb 2A10 followed by anti-mouse or anti-rabbit Ig conjugated to horseradish peroxidase (HRP; 1:100,000). Bound antibodies were visualized using ECL.

**Immunofluorescence assay.** Live P. berghei sporozoites were incubated with NH2-terminal antiserum (1:500 in DMEM/BSA) at 4°C for 2 h, washed at 4°C, and allowed to air dry on slides at 4°C. They were incubated with anti-rabbit Ig–FITC, washed, and mounted.

**Sporozoite invasion assay.** Invasion assays were performed as described previously (15), with some modifications. For assays with P. berghei and P. yoelii, Hepa 1–6 cells (CRL-1830; American Type Culture Collection) were used, and for assays with P. falciparum, HepG2 cells (HB-8065; American Type Culture Collection) were used. Sporozoites were precoated with the indicated protease inhibitor for 2 h at 28°C and plated on cells in the continued presence of the inhibitor for 1 h at 37°C. In a control, Hepa 1–6 cells were incubated with 10 μM E-64 for 2 h at 37°C, the medium was removed, and untreated P. berghei sporozoites were added. After incubation with sporozoites, cells were washed and fixed, and sporozoites were stained with a double-staining assay that distinguishes between extracellular and intracellular sporozoites.

**Cell contact assay.** P. berghei sporozoites were incubated in DMEM ± 10 μM E-64 at 4°C for 2 h and added to Hepa 1–6 cells on glass coverslips. 30 min before sporozoites were added to coverslips, CD was added to all samples (final concentration, 1 μM). Sporozoites were centrifuged onto coverslips (1,250 g) for 5 min at 4°C. Coverslips were brought to 37°C for 2 min, fixed with 4% paraformaldehyde, and stained with either mAb 3D11 followed by anti-mouse Ig FITC or the NH2-terminal antiserum followed by anti-rabbit Ig FITC. When P. berghei sporozoites expressing GFP were used, the cells were only stained with the NH2-terminal antiserum. As a
control, sporozoites were spun onto coverslips without cells using the aforementioned protocol.

**Sporozoite migration assay.** Sporozoites were preincubated ±10 μM E-64 for 2 h at 28°C and added to Hepa 1–6 cells in the continued presence of inhibitor with 1 μg/ml rhodamine-dextran. After 1 h at 37°C, the cells were washed and fixed, and rhodamine-positive cells were counted as outlined previously (16).

**Assay for sporozoite infectivity in vivo.** Swiss/Webster mice were given three i.p. injections of DMEM ± E-64 (50 mg/kg/injection) at 16, 2.5, and 1 h before i.v. injection of 15,000 *P. yoelii* sporozoites. 40 h later, livers were harvested, total RNA was isolated, and malaria infection was quantified using reverse transcription followed by real-time PCR using primers that recognize *P. yoelii*-specific sequences within the 18S rRNA as outlined previously (27). 10-fold dilutions of a plasmid construct containing the *P. yoelii* 18S rRNA gene were used to create a standard curve.

**Online supplemental material.** Fig. S1 shows the specificity of the NH$_2$- and COOH-terminal antisera as determined by ELISA. Fig. S2 shows that the protease inhibitors that inhibited CSP processing are not toxic to sporozoites. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20040989/DC1.

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