Antimalarial Activity of Cupredoxins

THE INTERACTION OF PLASMODIUM MEROZOITE SURFACE PROTEIN 1$_{19}$ (MSP1$_{19}$) AND RUSTICYANIN*

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Background: The interaction of MSP$_{19}$ with the cupredoxin azurin inhibits the growth of Plasmodium falciparum in red blood cells.

Results: Rusticyanin forms a well defined complex with MSP$_{19}$ upon binding at the same surface area than inhibitory antibodies.

Conclusion: Rusticyanin becomes an excellent therapeutic agent for malaria.

Significance: Knowing the rusticyanin-MSP$_{19}$ interface will allow the design of novel antimalarial drugs.

The discovery of effective new antimalarial agents is urgently needed. One of the most frequently studied molecules anchored to the parasite surface is the merozoite surface protein-1 (MSP1). At red blood cell invasion MSP1 is proteolytically processed, and the 19-kDa C-terminal fragment (MSP$_{19}$) remains on the surface and is taken into the red blood cell, where it is transferred to the food vacuole and persists until the end of the intracellular cycle. Because a number of specific antibodies inhibit erythrocyte invasion and parasite growth, MSP$_{19}$ is therefore a promising target against malaria. Given the structural homology of cupredoxins with the Fab domain of monoclonal antibodies, an approach combining NMR and isothermal titration calorimetry (ITC) measurements with docking calculations based on BiGGER is employed on MSP$_{19}$-cupredoxin complexes. Among the cupredoxins tested, rusticyanin forms a well defined complex with MSP$_{19}$ at a site that overlaps with the surface recognized by the inhibitory antibodies. The addition of holo-rusticyanin to infected cells results in parasitemia inhibition, but negligible effects on parasite growth can be observed for apo-rusticyanin and other proteins of the cupredoxin family. These findings point to rusticyanin as an excellent therapeutic tool for malaria treatment and provide valuable information for drug design.

Malaria is a widely spread disease causing morbidity and mortality throughout a large part of the world. The increasing resistance of Plasmodium falciparum, the causative agent of the most deadly form of the disease, to current drugs has only increased the urgency for finding new antimalarial agents (1, 2), including an effective vaccine and new drug therapies (3, 4). There are five Plasmodium species that infect humans, whereas others infect other primates or rodents. Among this latter group, rodent parasites such as Plasmodium yoelii provide useful laboratory models for the study of malaria. The disease is caused by the replication and multiplication of the asexual blood stages in red blood cells. The merozoite form of the parasite invades the host cell, where it develops and replicates to form several new merozoites that then burst out of the cell to continue the cycle of invasion and multiplication. The invasion of red blood cells requires an initial recognition and binding mediated by parasite surface ligands, followed by reorientation and the formation of a moving junction between the erythrocyte and merozoite surfaces as the parasite enters the cell. Merozoite surface protein-1 (MSP1)$^8$ has been implicated in this initial binding between parasite and host cell.

Located on the surface of the asexual blood-stage schizont and merozoite, MSP1 is one of the most frequently studied molecules of the parasite (5). It is synthesized as a ~200-kDa

8 The abbreviations used are: MSP1, merozoite surface protein-1; Az, azurin; BiGGER, bimolecular complex generation with global evaluation and rank- ing; HSQC, heteronuclear single-quantum coherence; ITC, isothermal titration calorimetry; mAb, monoclonal antibody; MSP$_{19}$, MSP1 19-kDa C-terminal fragment; Pc, plastocyanin; PDB, Protein Data Bank; Rc, rusticyanin.

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precursor attached to the surface of the parasite via a glycosylphosphatidylinositol anchor, which undergoes a two-step proteolytic process: first, at merozoite release and then at erythrocyte invasion (6). As a result of this processing, the MSP1 is cleaved into several polypeptides that are shed from the surface in the final processing step, save a 19-kDa C-terminal fragment (MSP119). MSP119 is retained on the parasite surface by the glycosylphosphatidylinositol anchor and taken into the red blood cell at invasion (7–9). The role of MSP119 in the subsequent intracellular development of the parasite is poorly understood, although it is transferred to the developing food vacuole, where it remains until the end of the intracellular cycle and is discarded in the residual body together with products of hemoglobin digestion such as hemozoin (10). MSP119 is considered a promising malaria vaccine candidate due to the abundant evidence of specific antibodies inhibiting erythrocyte invasion and parasite growth, for instance, via the disruption of MSP1 proteolytic processing and intracellular parasite development (11).

At the structural and functional levels, MSP119 is particularly well conserved among Plasmodium species (Fig. 1) (12–17), and its three-dimensional structure has been shown to consist of two epidermal growth factor (EGF)-like domains in close contact. A characteristic disulfide-bridge pattern (Fig. 1) makes MSP119 highly resistant to proteases (19) and may explain why MSP119 remains intact in the digestive food vacuole up to the end of the intracellular cycle (10).

MSP1-specific immunoglobulins react with conformational epitopes of MSP119. Some of these antibodies inhibit parasite invasion of erythrocytes, whereas others do not. Fine structure epitope mapping of different monoclonal antibodies (mAbs) and the use of NMR methods indicates the binding of two inhibitory antibodies to epitopes on one side of the molecule near the interface between the two EGF domains, including residues from both domains (20, 21). By contrast, non-inhibitory neutral mAbs bind elsewhere on the molecule (15, 20).

Here, we have used MSP119, from P. yoelii, a rodent malaria parasite used as a laboratory model for vaccine studies (22) and for which both inhibitory and neutral antibodies have been partially mapped on the structure (23, 24). Independent of the immunoglobulin class, complexes involving MSP119 are kinetically rather stable with dissociation constants in the micromolar to subnanomolar range (15, 25). Because the binding affinity is similar in all cases, it has been assumed that the inhibitory effect depends mainly on steric factors, namely, epitope location, rather than the nature of the antibody.

The present study has been based on the structural homology of cupredoxins with the Fab fragment of an antibody, as well as on reports of a protein from this family interacting directly with MSP119 and blocking the increase of parasitemia in human red blood cells infected by P. falciparum, suggesting a promising treatment (26, 27). We first used the DaliLite pairwise comparison program to identify structural similarities between cupredoxins and the Fab fragment (28). A screening was then performed combining NMR and ITC measurements with docking calculations using BiGGER which indicated that, among the cupredoxins tested, rusticyanin (Rc) provided the most effective binding to MSP119. The two proteins form a well defined complex where Rc interacts at the interface between the two MSP119 subdomains, at a site that overlaps with the surface recognizable by the inhibitory antibodies. Further, P. falciparum growth is inhibited by the presence of Rc in red blood cell cul-

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**FIGURE 1.** MSP119 protein. A, multiple sequence alignment of MSP119 with ClustalW2 (18) from a number of Plasmodium species. Sequences are colored by percent identity: black (100%), dark gray (80%), light gray (60%), and white (<50%). Secondary structure elements of P. yoelii MSP119 are shown. Orange boxes highlight cysteine residues that are conserved across different Plasmodium species, whereas red boxes highlight those present only in P. falciparum. Gold arrows stand for disulfide bonds formed by cysteine residues. The main difference between P. falciparum MSP119 and homologs from other Plasmodium species characterized to date lies in the disulfide bond pattern of the protein from the other species: one of the cysteine pairs in the first EGF domain is substituted by a tryptophan and a nonpolar or aliphatic residue.

B, ribbon representation of the lowest energy NMR structure of P. yoelii MSP119 (BMRB accession number: 19233). Side chains of cysteine residues forming disulfide bridges are represented in gold.
MSP1<sub>19</sub>-Rusticyanin Complex

tures. Interestingly, the copper site plays a key role in complex formation, because apo-Rc is not only unable to interact with MSP1<sub>19</sub>, but also to inhibit parasite invasion and development in infected red blood cells.

EXPERIMENTAL PROCEDURES

Expression and Purification of Proteins—P. yoelii MSP1<sub>19</sub> (15N-labeled or unlabeled) was produced (essentially as described previously (29)) from a synthetic gene optimized for Pichia pastoris expression using as nitrogen source either 15NH<sub>4</sub>Cl or (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> for labeled and unlabeled protein, respectively. The 99-amino acid sequence corresponds to residues 1656–1754 of the UniProtKB entry P13828 containing the metal site.

The interaction of MSP1<sub>19</sub> with cupredoxins was followed by titration of 0.5 mM 15N-MSP1<sub>19</sub> solutions with an increasing concentration from 0.5 to 2 mM, whereas cupredoxins were 1JZG for Az (38), 1NIN for Pc (39), and 1A3Z for Rc. In all cases, the proteins were washed extensively to remove the excess of the reducing/oxidizing agent.

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NMR Spectroscopy—All protein samples were concentrated in 10 mM potassium phosphate (pH 6.5) using Millipore 3000 NMWL centrifors and microcon. MSP1<sub>19</sub> samples ranged in concentration from 0.5 to 2 mM, whereas cupredoxins were used in the range of 2–5 mM. All NMR samples contained 10% D<sub>2</sub>O to adjust the lock signal. Reduction of the metal center in samples of copper(I) cupredoxins was achieved by adding sodium ascorbate, whereas oxidation of the metal center in samples of copper(II) proteins was achieved using sodium ferricyanide for Pc and Az, and sodium hexachloroiridate(IV) for Rc. In all cases, the proteins were washed extensively to remove the excess of the reducing/oxidizing agent.

NMR experiments were performed in a Bruker Avance 600 MHz spectrometer at 25 °C. The sequence-specific assignment of the backbone amide groups of 15N MSP1<sub>19</sub> (BMRB accession number: 19233) was achieved using standard backbone experiments (HNCA, HNCA, etc.) and was confirmed using three-dimensional 1H-15N NOESY-HSQC and three-dimensional 1H-15N total correlation spectroscopy-HSQC spectra. The interaction of MSP1<sub>19</sub> with cupredoxins was followed by acquiring two-dimensional 1H-15N HSQC spectra during the titration of 0.5 mM 15N-MSP1<sub>19</sub> solutions with an increasing amount of oxidized or reduced cupredoxins up to a final cupredoxin:MSP1<sub>19</sub> molar ratio of 4:1. The pH value of the sample was verified after each titration step. Prolines, which are invisible resonances in 15N HSQC spectra, are located at the positions 4, 15, 50, 61, 84, and 86, whereas Gly-1, Val-2, Glu-69, and Asn-73 are unassigned residues. All data processing was performed with Bruker TopSpin 2.0, and NMR analysis of line broadening perturbations of the cupredoxin-bound MSP1<sub>19</sub> with respect to free malarial protein was performed in the SPARKY program (36).

NMR Line Width Analysis—To estimate line widths, the peaks were fitted to a Gaussian function for the 15N and 1H dimensions using the program SPARKY with a 10,000 steps minimization and a 0.05% tolerance. In the analysis of the line widths (Δν<sub>1/2</sub>), the overall broadening (Δν<sub>1/2</sub>) obtained from signals displaying only minor line broadening was first subtracted from the line width of the corresponding signal. Then, for each residue, the differences of line widths between free and interacting MSP1<sub>19</sub> were calculated in every titration series (ΔΔν<sub>1/2</sub> Binding). The threshold value, used to identify a specifically broadened residue when data from the titration series were analyzed together, was defined as the average ΔΔν<sub>1/2</sub> Binding for the system plus 2 standard deviations (2s<sub>±</sub>). The average ΔΔν<sub>1/2</sub> Binding and standard deviation were calculated for all amides with values ≤10 Hz on the basis that data >10 Hz clearly indicated a specifically broadened residue, and their inclusion would bias the average to a higher value. Some assigned signals of the free MSP1<sub>19</sub> HSQC spectrum overlap (Val-9, Asn-87, and Cys-95) or exhibit very low intensity (Gly-41 and Asn-42), so they could not be properly integrated to include them in the line width analysis.

ITC—All ITC experiments were performed using VP-ITC and Auto-ITC200 instruments (Microcal; GE Healthcare) at 25 °C titrating Rc with MSP1<sub>19</sub>. The reference cell was filled with distilled water. The experiments consisted of 10-μl or 2-μl injections of 0.3 mM MSP1<sub>19</sub> solution in 10 mM potassium phosphate buffer (pH 6.5) into the sample cell, initially containing 6.67 μM Rc solution (reduced, oxidized, and apo forms) in the same buffer. All of the solutions were degassed before the titrations were performed. Titrant was injected at appropriate time intervals to ensure the thermal power signal returned to the base line prior to the next injection. To achieve homogeneous mixing in the cell, the stirring speed was kept constant at 1000 rpm in the Auto-ITC200 and at 450 rpm in the VP-ITC. The data, specifically the heat per injection normalized per mol of injectant versus molar ratio, were analyzed with Origin 7 (Microcal) using a single-site binding model. Calibration and performance tests of the calorimeter were carried out conducting CaCl<sub>2</sub>-EDTA titrations with solutions provided by the manufacturer.

Molecular Docking Simulations—A soft docking algorithm implemented in the BiGGER software package (37) was used to determine in silico a model of the complexes MSP1<sub>19</sub>-Az, MSP1<sub>19</sub>-Pc, and MSP1<sub>19</sub>-Rc. The PDB coordinates files of cupredoxins were 1JZG for Az (38), 1NIN for Pc (39), and 1A3Z for Rc (40). For each run, 5000 docking geometric solutions were generated based on the complementarity of the protein surfaces. These solutions were evaluated and ranked according to their “global score” and different interaction criteria including electrostatic energy of interaction, relative solvation energy, and the relative propensity of side chains to interact. For the MSP1<sub>19</sub>-Rc adduct, NMR restraints were introduced in the docking calculations. All complexes graphic images were generated using the UCSF Chimera package (41).

P. falciparum Cultures—Synchronized P. falciparum 3D7 late stage trophozoites at 33–36 h were used. The final parasitemia and hematocrit were between 0.1–0.2 and 2%, respectively. Red blood cells used for the assay were centrifuged to remove theuffy coat and washed twice in RPMI 1640 medium so that no white blood cells were present. The cul-
tured medium contained RPMI 1640 medium supplemented with 5 g/liter albumax, 0.025 g/liter gentamycin, and 0.292 g/liter L-glutamine.

*P. falciparum* Growth Inhibition Assay—Sterile 96-well black tissue culture plates (Costar) were used routinely for every assay. The holo- or apo-species of Rc and *Nostoc* Pc were diluted in culture medium and used in duplicate wells for each dilution (200, 100, 50, and 25 μM, respectively) in a final volume of 100 μl/well. Two control sets were used in duplicate wells, one set with no added cupredoxin (positive control) and one with uninfected red blood cells (negative control). The plates were incubated at 37 °C for 48 h in a gas chamber flushed with 5% CO₂, 5% O₂, and 90% N₂. After 48 h, supernatants were removed from each well, replaced with fresh medium containing protein, and incubated for a further 48 h in the same manner. At the end of the 96-h incubation, 25 μl of SYBR Green I dye (SYBR Green I nucleic acid gel stain 10,000×, in dimethyl sulfoxide from Invitrogen) in lysis buffer (1 μl dye to 1 ml lysis buffer), was added to each well and stored overnight at 20 °C.

The lysis buffer contained Tris-HCl (20 mM, pH 8.0), EDTA (2 mM), Saponin (0.16% w/v) and Triton X-100 (1.6% v/v). Plates were thawed at room temperature, and fluorescence intensity was measured with a FLUO Star Omega microplate fluorescence reader (BMG Labtech). Values were expressed in relative fluorescence units. Binding of SYBR Green is specific for parasite DNA as mature erythrocytes lack DNA and RNA. Fluorescence intensity unit was converted to percentage (%) of growth as follows: % growth = (culture under Rc or Pc − (uninfected RBC)/(culture with no Rc or Pc − (uninfected RBC) × 100, where RBC are red blood cells.

FIGURE 2. Conserved structural motifs. A, ribbon representation of the Fab fragment of mAb G17.12 (PDB ID code 1OB1). Domain A is depicted in light gray and domain B in gold. B, structural alignment of Az (upper, PDB ID code 1JZG) and A1 fragment of Fab (lower) built by DaliLite pairwise comparison server. Matching regions, with a Dali Z-score of 2.9, appear in orange. C, ribbon representation of Rc (upper, PDB ID code 1A3Z) and Pc (lower, PDB ID code 1NIN). Dali Z-scores for Rc and Pc are 2.6 and 3.1, respectively. Copper atoms are colored in blue.

FIGURE 3. Ab initio docking of cupredoxins with MSP1₁₉ performed by BIGGER. Left, Az. Center, Pc. Right, Rc. Light yellow spheres represent the geometry centers of MSP1₁₉ in the 100 best solutions generated for each complex. All cupredoxins are oriented with respect to their copper center. Robertson diagrams of the cupredoxins are colored according to secondary structures: α-helices in red and β-strands in blue. Copper atoms are represented as blue spheres and the residues bonding to them are in gray sticks.
RESULTS

Structural Similarities between Cupredoxins and the Fab Fragment of a mAb—The Fab fragment crystal structure of mAb G17.12 (15), shown to bind MSP119, is composed of two domains, A and B, containing two regions, variable (symbolized by 1) and constant (symbolized by 2), with the canonical β-sandwich fold of the immunoglobulin superfamily (Fig. 2A). Consistent with previous reports, the DaliLite pairwise comparison program (28) identified significant structural similarities between the A1 fragment of the mAb and copper-containing redox proteins with immunoglobulin fold, such as Az, Pc, and Rc. In particular, the structural alignment between the A1 fragment and Az reveals a matching region, which is localized mainly at the two antiparallel β-sheets, as described previously (26; Fig. 2B), and with a Dali Z-score of 2.9. For the two other cupredoxins, Pc and Rc, this structural match is extended to the loops connecting β-strands yielding Z-scores of 3.1 and 2.6, respectively (Fig. 2C).

Given the structural similarity between various cupredoxins and the Fab fragment, ab initio docking approaches were performed with no experimental restraints (Fig. 3) to explore the capability of the metalloproteins to interact with MSP119 from P. yoelii. MSP119 is well conserved among the species with >50% sequence identity (Fig. 1A), with conserved three-dimensional structure and common functional features (17). We used the BiGGER rigid docking algorithm to generate sets of possible orientations for the different cupredoxin probes around MSP119 (the target). Fig. 3 shows the distribution of MSP119 mass centers resulting from the 100 best solutions from each computation around the corresponding copper protein. For Az and Pc, we observe a remarkably broad dispersion of the MSP119 geometry centers, suggesting the lack of specific surface complementarity. By contrast, molecular docking for the Rc-MSP119 interaction indicates that MSP119 explores a well defined area of Rc surrounding its copper center.

MSP119 Interactions with Cupredoxins by NMR—The MSP119-cupredoxin interaction was monitored by recording two-dimensional 15N HSQC NMR spectra on 15N-MSP119, both free and following the addition of Az, Pc, or Rc. The absence of changes in MSP119 resonances, either chemical shift perturbations or line broadening, indicates no detectable binding to Az and Pc in any of their oxidation states (Fig. 4, top and middle panels). By contrast, line width changes of certain MSP119 amide signals upon addition of Rc(Cu+) suggest a specific MSP119-Rc interaction (Fig. 4, bottom panel). Such observations coincide with ab initio docking simulations performed (Fig. 3) which suggested a well defined complex only between Rc and MSP119.

To probe in greater detail the interaction of MSP119 with either oxidized or reduced Rc, we analyzed the line widths of MSP119 resonances from 15N HSQC spectra across several titrations. Binding to Rc results in general signal broadening due to the increase in the rotational correlation time of MSP119 when interacting with Rc. In addition, several MSP119 backbone amides clustered in one area of the structure undergo larger changes in line widths (ΔΔν1/2_Binding) upon Rc binding (Figs. 5 and 6). These resonances are expected to be at or in the proximity of the area of MSP119 interacting with Rc. To selectively define resonances most likely to be part of the interface, threshold values (specifically, ΔΔν1/2_Binding ≥ 5Hz for 15N and ≥ 11Hz for 1H dimension) were set (see “Experimental Procedures”). As expected, the distribution of line width changes (Δν1/2) becomes broader as the Rc:MSP119 ratio increases (data not shown).
At the Rc(Cu¹⁺):MSP1₁₉ ratio of 1.5:1, 14 amino acids show considerable ¹⁵N line width changes in MSP1₁₉ HSQC spectra (Fig. 5, A and B). These residues are distributed mainly along two regions of MSP1₁₉, namely, at the beginning of N-terminal EGF domain involving Asp-3, Lys-5, His-6, Val-7, Asp-10, and at the end of C-terminal domain comprising Thr-85, Ala-88, Tyr-89, Phe-94, and Ser-97. In addition, Asp-24, Asp-25, and Arg-31 at the two first antiparallel β-strands, along with Cys-59, are also altered. Fig. 5C shows the map of MSP1₁₉ residues affected by Rc addition, with colors corresponding to line broadening in the ¹⁵N dimension. The sequential stretches of residues detailed above form the main cluster on the MSP1₁₉ surface, which surrounds the two EGF domain interface. Interestingly, some of these affected residues (Asp-24, Asp-25, Arg-31, and Cys-59) are located at the rear of the protein (Fig. 5A). Notably, the strength of the broadening observed for a 4:1 Rc(Cu²⁺):MSP1₁₉ ratio is comparable with the one observed at a 1.5:1 Rc(Cu¹⁺):MSP1₁₉ ratio, indicating that MSP1₁₉ binds more weakly to the oxidized Rc. However, the MSP1₁₉ interacting surface involved in Rc recognition at a Rc:MSP1₁₉ ratio of 4:1 is independent of the cupredoxin redox state (Fig. 6).

 Binding of MSP1₁₉ to Halo-Rc by ITC—ITC measurements reveal that MSP1₁₉ binds to Rc either in its reduced or oxidized state with a 1:1 stoichiometry at 25 °C (Fig. 7). Notably, the interaction of MSP1₁₉ with Rc(Cu²⁺) is exothermic with a dissociation affinity constant (Kₐ) of 2 μM, whereas that with Rc(Cu¹⁺) is an endothermic process with lower binding affinity.
Such differences in $K_d$ values are in agreement with NMR titrations and suggest that MSP1$_{19}$ binds to reduced Rc with a greater affinity than to oxidized Rc. Further experiments need to be performed to explain the opposite sign in the enthalpy of both processes as it could be related to (i) changes in the protonation/deprotonation equilibrium of ionizable groups of the interacting proteins; (ii) variations in the hydrogen-bonding networks; (iii) differences in water arrangement in the vicinity of oxidized or reduced cofactors; and (iv) slight conformational modifications altering the number of solvent molecules excluded from the protein interface.
The affinity of a protein-protein interaction is defined by the Gibbs energy of the binding: \( \Delta G = -RT \ln K_d \). \( \Delta G \) has two different contributions, \( \Delta H \) and \( \Delta S \), according to the equation: \( \Delta G = \Delta H - T \Delta S \). Thus, several combinations of those values could yield similar binding affinities. The complex formation is entropically driven in both cases, being the enthalpic contribution to the binding unfavorable (15 kcal/mol). The stoichiometry value (n) was fixed to avoid degeneracy in the nonlinear regression data analysis. Typical relative errors are 20–25% for the dissociation constant and 5–10% for the stoichiometry.

### TABLE 1

Thermodynamic values inferred from ITC experiments

| MSP1_{19} complex | \( \Delta G \) (kcal/mol) | \( \Delta H \) (kcal/mol) | \( -T \Delta S \) (kcal/mol) | \( K_d \) (\( \mu \)M) |
|-------------------|--------------------------|--------------------------|-----------------------------|--------------------|
| Oxidized Rc       | -6.3                     | 15.0                     | -21.3                       | 25.0               |
| Reduced Rc        | -7.8                     | -1.7                     | -6.1                        | 2.0                |

The Case of Apo-Rc—To determine the role of the copper center, NMR and ITC titrations were carried out using MSP1_{19} and apo-Rc. Surprisingly, NMR titrations showed no substantial line width changes even at an apo-Rc:MSP1_{19} ratio of 4:1 (Fig. 8). The finding was further corroborated by ITC measurements, as the weak calorimetric profile suggests a lack of interaction (Fig. 8). Altogether, these data indicate the relevance of the copper center in the binding to MSP1_{19}. Despite the small structural differences in cupredoxins reported previously in solid state, there exists a high degree of mobility of the metal-binding loops in solution in the apo form, as recently demonstrated by NMR (42, 43). The different pattern between apo- and holo-Rc versus MSP1_{19} could be related with the found differences in the dynamics of this site in the two forms.

Docking Simulations with BiGGER—Along with the \textit{ab initio} docking calculations run on the MSP1_{19}-Rc(Cu\(^+\)) complex, revealing how the MSP1_{19} mass center docks on the Rc metal crevice (Fig. 3), an NMR-restrained docking with BiGGER was also performed. Line width data for those MSP1_{19} residues in contact with Rc at a Rc:MSP1_{19} ratio of 1.5:1 were included in the run. The output is a set of docked solutions that can be ranked according to the BiGGER global score or individual scores, such as hydrophobic criteria, electrostatics, and geometrical parameters. Fig. 9 shows the best 100 solutions, as represented by Rc geometry centers, according to the global and hydrophobic scores from the program (Fig. 9A). The best scoring models predicted by restrained docking reveal how MSP1_{19} leans its EGF domain interface to approach Rc (Fig. 9A). Indeed, the proximity of the surfaces on both proteins in the complex is shown in the space-filling representation (Fig. 9A). In addition to the copper center, loops connecting Rc \( \beta \)-strands are in close contact with MSP1_{19}. A deep analysis of the complex interface predicted by docking points to the N-terminal and C-terminal regions of the MSP1_{19} as driving complex formation as some NMR restraints are satisfied (Fig. 9B). In the model reported, some electrostatic interactions occur (Fig. 9C) because Rc residues Lys-81 and Lys-116 are close to Glu-91 and Glu-83 in MSP1_{19}. Furthermore, Lys-5 of MSP1_{19} can interact with Glu-9 of Rc, although the Glu is partially buried. The Rc interaction surface is mainly hydrophobic with the exception of a single positive spot, Lys-81 and Lys-116, surrounded by Phe-83, Gly-82, and Trp-7 and the copper center, which, in turn, is enclosed by Met-99, Val-98, and Pro-141. This interaction mode resembles those of the copper protein Pc and cytochrome \( c_6 \) with their photosynthetic partners, cytochrome \( f \) and photosystem I. In such complexes, Pc and cytochrome \( c_6 \) use the hydrophobic site surrounding the copper center and the heme group (site 1) as well as their charged patch (site 2; 44, 45).

Inhibition of \textit{P. falciparum} Growth by Holo-Rc—To assess the physiological relevance of the MSP1_{19} binding to Rc, the growth of \textit{P. falciparum} within red blood cells was followed in...
the presence of either holo- or apo-Rc (see “Experimental Procedures”). The addition of holo-Rc to infected cells resulted in parasitemia inhibition, as culture growth decreased significantly (Fig. 10) at a concentration of 100 μM until the point of complete inhibition at 200 μM holo-Rc. In contrast, the apo form even at high concentrations did not have a significant effect on P. falciparum growth. These data fully corroborate previous observations using NMR or ITC as much as apo-Rc is unable to bind to MSP119.

To discard the theory that such a parasitemia inhibition could be ascribed to the well known apoptotic role of several cupredoxins (46, 47), control experiments were run with the holo- or apo-form of Pc. Holo-Pc was chosen as it does not bind to MSP119, as inferred from the herein presented NMR screening (see above), but it is structurally very similar to Rc: the two proteins belong to the type I blue copper-protein family, with almost identical folding and tetrahedral copper center. Upon addition of either holo- or apo-Pc (25 μM) under the same culture conditions, the Plasmodium growth first slightly decays to further reach a constant value until the end of the experiment. So the Plasmodium growth does not depend on protein concentration (the percentage of growth is maintained at approximately 70% even at 200 μM Pc) and is practically the same with either holo- or apo-Pc. Altogether these results indicate that holo-Rc inhibits parasitemia upon specific binding to MSP119.
DISCUSSION

Proteins from the cupredoxin family have demonstrated antimalarial activity and potential as therapeutic agents (26, 27). We have shown here that the cupredoxin rusticyanin interacts with MSP1\textsubscript{19} with micromolar \(K_d\), forming a well defined complex. The interaction takes place on the same surface as that targeted by inhibitory antibodies, suggesting that a similar mechanism could take place. Its strength is dependent on the presence and, to a lesser extent, on the oxidation state of the metal center, which is consistent with the need for an intact interaction surface and charge conservation. Furthermore, we have observed the inhibition of \textit{P. falciparum} parasitemia in infected cells where holo-Rc is present as a result of the interaction with MSP1\textsubscript{19}. However, negligible effect on parasite growth could be observed for apo-Rc and Pc forms.

MSP1\textsubscript{19} signals show slow exchange in the presence of the Fab fragments of the inhibitory mAb12.8 and mAb12.10, indicating the kinetic stability of complexes involving MSP1\textsubscript{19} with binding affinity constants in the micromolar to subnanomolar range (20). Rc binds specifically with a \(K_d\) of 2 \(\mu\)M to the interface between the two MSP1\textsubscript{19} EGF domains, overlapping the surface recognized by these inhibitory antibodies (20, 21), as indicated by our NMR-based mapping. A detailed comparison of MSP1\textsubscript{19} bound to either Rc or mAb12.10 and mAb12.8 reveals that the common interacting surfaces are located in the first EGF domain along with the first \(\beta\)-sheet and at the end of the second EGF domain. Interestingly, these regions of MSP1\textsubscript{19} form a shallow pocket (Fig. 1B) that may have a role in erythrocyte invasion (21). In addition, these residues involved in the formation of protein complexes with MSP1\textsubscript{19} are distributed in three segments: His-6 to Val-9, Lys-16 to Arg-22, and Tyr-89 to Cys-95 (numbering according to the \textit{P. yoelii} MSP1\textsubscript{19} sequence; Fig. 1A), and they are strongly conserved in different species (21), supporting the idea that this is a functional site. The presence of additional perturbed residues identified in this study may be explained by the flat structure of MSP1\textsubscript{19} (5) because perturbations as a result of a protein-protein interaction may be transferred from one MSP1\textsubscript{19} face to the other.

Another point of interest arising from this study is the mode of interaction of MSP1\textsubscript{19} with Rc, compared with the interaction with mAbs. The study took as starting point a structural alignment of Rc with the Fab fragment of the non-inhibitory mAb G17.12 whose interaction with MSP1\textsubscript{19} has been solved through x-ray crystallography (15). The similarities with the \(\beta\)-barrel, as well as the loops connecting them, are clear (Fig. 2). However, the relative orientation between the mAb and MSP1\textsubscript{19} does not match that defined for the MSP1\textsubscript{19}-Rc complex (Fig. 11A). In contrast, the models of mAb12.8-MSP1\textsubscript{19} and mAb12.10-MSP1\textsubscript{19} complexes built by Autore \textit{et al.} (48) using NMR-based docking calculations match well with the Rc-MSP1\textsubscript{19} model reported here. In looking for structural sim-
similarities between Rc and mAb12.10 with the DaliLite pairwise comparison server, the Z-score 2.8 (Fig. 11, B and C) suggested strong structural similarities, especially in the loops that interact with MSP119. In this paper, MSP119 complexes with mAb12.10 and Rc demonstrate (Fig. 11) a similar MSP119 orientation with respect to the other molecule (mAb12.10 or Rc) within each complex. The A1 region of mAb12.10 forms the main interaction with MSP119, similar to the structurally related region of Rc, especially at the level of β-strand connecting loops. As proposed by Autore et al. (48), a positively charged electrostatic spot on the antibody surface is required in the interaction and binding to MSP119. A similar positively charged area is located on the Rc surface, Lys-81 and Lys-116 in the complex interface, as inferred from our docking simulations (Fig. 9C). The Rc-MSP119 interface also involves hydrophobic contacts in the region surrounding the Rc copper center that presumably plays a key role in complex formation, as indicated by the NMR and ITC experiments. Reduced Rc binds MSP119 more efficiently than the oxidized form, suggesting that both electrostatic potential properties and protein folding depend on the metal redox state. This effect is even more drastic for apo-Rc, which is unable to interact with MSP119.

The practical significance of these observations can be found in the potential antimalarial role of the binding of Rc to MSP119 on the parasite surface, thereby blocking parasite growth and interfering directly with parasite invasion of red blood cells. In fact, the interaction might sterically interfere with the recognition between MSP1 and an erythrocyte surface molecule or with the proteolytic processing of MSP1, which occurs during invasion and can be inhibited by antibodies binding to MSP119. Such a role has been shown previously in the drug suramin (49). An alternative hypothesis, based on the fact that MSP119 is internalized with the malaria parasite during invasion and then trafficked to the food vacuole where it persists until the end of the next intraerythrocytic cycle (10), is that MSP119-bound Rc would be internalized and interfere with MSP119 functioning inside the cell, as shown for an antibody (11). Supporting this possibility, it has been reported that Rc is not only able to enter mammalian cells, but also to induce caspase-8-mediated apoptosis and/or to inhibit the cell cycle (47). Furthermore and unlike other cupredoxins, Rc is a copper protein with high acid stability and is biologically functional at a pH below 1.0 (50). The extreme acid stability of Rc may be important in understanding its function of blocking MSP119, because pH is ~4.5–5.5 inside the Plasmodium food vacuole. Altogether, Rc could be an excellent therapeutic tool for malaria treatment and expand our understanding of MSP119 function. In this way, as well, it could provide beneficial information for drug design.

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