On the Mechanism of Chloroquine Resistance in Plasmodium falciparum

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Introduction

In the last decades, due to its effectiveness and reasonable cost, chloroquine has represented the best and more widely used antimalarial drug. Unfortunately, within a decade of its introduction, *P. falciparum* parasite resistance to chloroquine was observed in most of the malaria-endemic countries. Nowadays, insurgence of resistance against chloroquine is a considerable hurdle for malaria control [1].

In its erythrocyte stage, *P. falciparum* invades the red blood cells where it forms a lysosomal isolated acidic compartment known as the digestive vacuole (DV). In the erythrocyte, the parasite grows by ingesting haemoglobin from the host cell cytosol and deposing it in the DV, where the protein is degraded to its component peptides and heme, which is incorporated into the inert and harmless crystalline polymer haemozoin [2].

Chloroquine is a diprotic weak base and, at physiological pH (~7.4), can be found in its un-protonated (CQ), mono-protonated (CQ\(^+\)) and di-protonated (CQ\(^{2+}\)) forms. The uncharged chloroquine is the only membrane permeable form of the molecule and it freely diffuses into the erythrocyte up to the DV. In this compartment, chloroquine molecules become protonated and, since membranes are not permeable to charged species, the drug accumulates into the acidic digestive vacuole [3,4] where it is believed to bind haematin, a toxic byproduct of the haemoglobin proteolysis [5,6], preventing its incorporation into the haemozoin crystal [2,7,8,9,10]. The free haematin seems to interfere with the parasite detoxification processes and thereby damage the plasmid membranes [11].

Chloroquine sensitive parasites (CQS) accumulate much more chloroquine in the DV than chloroquine resistant strains (CQR) [4,12,13]. Recent studies have associated the reduced chloroquine accumulation observed in the parasite vacuole of resistant strains [12] with point mutations in the gene encoding for the *P. falciparum* chloroquine resistance transporter (PfCRT) protein (for a review see [14,15]). PfCRT is localized in the digestive vacuole membrane and contains 10 predicted membrane-spanning domains [16,17]. CQR phenotype isolates have all been found to carry the PfCRT critical charge-loss mutation K76T or, in two single cases, K76N or K76I [18,19,20,21]. Another mutation, S163R, restores the chloroquine sensitivity of CQR parasites [22,23]. The K76T amino acid mutation might allow the interaction of PfCRT with the positively charged chloroquine (CQ\(^+\) or CQ\(^{2+}\)) and allow its exit from the vacuole, with the net result of decreasing the chloroquine concentration within the DV [16,24]. The single amino acid change S163R, by reintroducing a positive charge, is thought to block the leak of charged chloroquine from the DV, thus restoring chloroquine sensitivity [22,23]. In a recent work, Martin and collaborators [25] were able to express both wild-type and resistant forms of PfCRT on the surface of
Xenopus laevis oocytes and clearly demonstrated that chloroquine resistance is due to the direct transport of a protonated form of the drug out of the parasite vacuole via the K76T PfCRT mutant. Interestingly, they also showed that the introduction of the K76T single mutation in PfCRT of CQS parasites is necessary but not sufficient for the transport of chloroquine via PfCRT. These evidences are however compatible with two alternative models for PfCRT [26]: (1) the channel model (i.e., a passive channel that enables charged chloroquine to leak out of the food vacuole down its electrochemical gradient) or (2) the carrier model (i.e., an active efflux carrier extruding chloroquine from the food vacuole).

Several experimental set-ups have been used to answer the question of whether PfCRT is a channel or a carrier, namely measures of chloroquine accumulation, trans-stimulation and measures of chloroquine efflux. However, the available data have been interpreted in different ways by different authors and the debate about the nature of PfCRT is still ongoing.

Sanchez and collaborators showed that chloroquine accumulation is energy dependent in both CQR and CQS [27]. These authors monitored the time course of labeled chloroquine uptake in the absence and in the presence of glucose. Glucose was added 20 min after chloroquine addition (i.e., when the stationary state was reached). They found that, after glucose addition, the time courses of chloroquine uptake were markedly different in CQS and CQR: chloroquine accumulated to an increased extent in the CQS strain, but decreased in the CQR strain. A similar experiment was repeated by the same authors in 2004 [28] using a broader range of different antimalarial drugs. The authors concluded that the data are compatible with most models that attempt to account for chloroquine resistance and that some energy-dependent mechanism leads to loss of chloroquine from CQR cells and to its accumulation in CQS cells.

Bray et al. [29], in 2006, measured the Cellular Accumulation Ratio (CAR) of chloroquine in six experimental conditions, namely in sensitive and resistant strains, in the absence and presence of carboxylic anhydride p-trifluoromethoxyphenylhydrazone (FCCP), a nonionic uncoupler, and in the absence and presence of glucose. In particular they found that, in absence of glucose, chloroquine the CAR is equal in CQS and CQR strains (~700), reaching a level that is approximately intermediate between that observed in CQS (~1200) and CQR (~350) strains in the presence of glucose. They used several different Plasmodium strains and showed that, in the absence of FCCP, i.e., when the pH of the vacuole is lower than the external pH, the chloroquine CAR is three to four times higher (about 1200 versus about 350) in sensitive strains with respect to resistant strains, while addition of FCCP abolishes the differences leading to a CAR value of about 700 in both cases. They also demonstrate that, in the absence of glucose, the CAR is identical to that obtained in the presence of FCCP suggesting that the energy provided by the glucose is needed to maintain the pH difference between the cytoplasm and the DV. According to the authors, the hypothesis that PfCRT is an active efflux carrier does not appear to fully explain their findings.

In this hypothesis, in fact, a single mutation would transform an energy-dependent chloroquine uptake process in an energy-dependent chloroquine efflux process. Therefore they favor the hypothesis that the chloroquine movement through PfCRT is not an active process.

Trans-stimulation of labeled chloroquine ([3H]-CQ) uptake after the parasites were pre-loaded with increasing concentrations of unlabelled chloroquine [27,28,29,30] was observed in CQR strains and not in CQS isolates. Sanchez and collaborators conclude that the trans-stimulation phenomenon is unequivocally characteristic of saturable, carrier-mediated transport systems [31]. On the other hand, Bray and colleagues [29] propose that the trans-stimulation data reported by Sanchez et al cannot by themselves be used to conclude whether the chloroquine transport is in the inward or outward direction: stimulation of [3H]-CQ uptake could indeed be due to acceleration of the transporter cycle by the outgoing unlabelled chloroquine or, as Sanchez et al assert, it could result from reduced efflux of [3H]-CQ due to the carrier competitive inhibition from the pre-loaded unlabelled CQ. In the latter model, labeled and unlabelled chloroquine should be on the same side of the membrane when they interact with the carrier, i.e., they are mixed together. In order to verify this hypothesis, Bray et al [29] incubated CQR lines with premixed chloroquine (labeled and unlabelled), but did not observe trans-stimulation of chloroquine uptake, thus suggesting that labeled and unlabelled chloroquine must be on opposite sides of the membrane for the trans-stimulation effect to take place, i.e., transport of unlabelled chloroquine via the carrier would be in the outward direction while labeled chloroquine transport would occur in the inward direction; in other words, mutant PfCRT would act as a bidirectional carrier, which is not compatible with an active efflux pump. In particular, these authors conjecture that trans-stimulation results might also be explained in terms of a gated channel.

Many authors measured chloroquine efflux from CQS and CQR isolates [27,29,32,33] under different conditions: in presence and absence of glucose, with or without proton gradient uncoupling, with or without Verapamil, an L-type calcium channel blocker of the Phenylalkylamine class. The results of these experiments have been interpreted in different ways by different authors and did not lead to a consensus view about the nature of PfCRT.

Sanchez et al. [34] studied the kinetics of chloroquine efflux in ‘reverse varying-trans’ conditions [31] from CQR and CQS isolates. This procedure investigates whether extracellular unlabelled chloroquine would stimulate the release of pre-loaded [3H]-CQ. These authors expected that, in the presence of an active carrier, trans chloroquine should increase the initial efflux rate. They found an increasing initial efflux rate for both CQR and CQS lines and accordingly proposed that both CQR and CQS parasites possess a carrier of chloroquine with different transport properties.

It should appear clear from this survey that qualitative interpretations of the experimental findings are insufficient to draw conclusions about the nature of PfCRT and that more quantitative analyses are required.

A quantitative model cannot be derived from transient experiments because kinetic parameters, such as the rate of the vacuole pH equilibration during chloroquine uptake and the kinetic constants of chloroquine-hemozoine binding, are unknown and impossible to extract from the available data in an unambiguous way. The only data that can be used to derive a quantitative model without making an unreasonable number of hypotheses on the unknown parameters are those measured at equilibrium.

As we will show, the analytical model that we developed and used here indicates that equilibrium data are compatible with both the carrier and channel model for PfCRT, which explains why they could be interpreted differently by different authors. On the other hand, the carrier and channel hypotheses are only compatible with specific assumptions on the protonation state of the transported species and of the species binding to haeme of haeme-related molecules in the vacuole. For example, a carrier model is only compatible with the data if the transported molecule is protonated.
Another route to understand the nature of the macromolecule is to study its evolutionary relationship with other proteins of known function. Also in this case, data interpretation is controversial. Previous computational analyses of PfCRT [14,16] suggested that PfCRT belongs to the drug/metabolite transporter (DMT) superfamily, whereas other studies proposed that it resembles to ClC chloride channels [33]. Here, we use state-of-the-art bioinformatics tools to identify PfCRT homology relationships and provide evidence that it is indeed a member of the DMT superfamily. This finding is also supported by the observation that a three-dimensional model of the protein based on a DMT-like fold is consistent with experimental data about the mutations involved in insertion and reversion of CQ resistance in Plasmodium.

By combining this latter conclusion with the results of the analytical method, we propose that PfCRT is a carrier of CQ\textsuperscript{+}, CQ\textsuperscript{2+} or both and that either all chloroquine species or only the uncharged one can bind heme of heme related species inside the vacuole.

### Results

We selected to use the data from the Cellular Accumulation Ratio (CAR) experiments described by [29] because, as mentioned above, the experimental conditions (stable and controlled pH values) allow the model to be built using a number of parameters comparable with the number of observations.

Our approach consists in testing the consistency of all plausible hypotheses about the binding mode of the drug to the heme related species inside the vacuole and the mechanism of action of PfCRT with experimental data. Our reasoning does not require any assumption on which heme form or heme related molecule binds to chloroquine and, for this reason, we refer to the heme related species bound by chloroquine inside the vacuole as HM.

Two mechanisms are thought to be involved in chloroquine accumulation into the *P. falciparum* vacuole: acidic trapping due to low vacuolar pH and chloroquine binding to heme or heme related species. It is reasonable to assume that PfCRT does not directly affect the molecular mechanism of chloroquine-HM binding. Recent studies [36,37,38] indicate that the vacuolar pH of CQS and CQR strains are similar, hence the reduction of chloroquine accumulation in resistant strains cannot be explained in terms of different acidic trapping and PfCRT must be directly involved in releasing chloroquine out of the vacuole. A proof of this hypothesis has been recently provided by Martin and collaborators [25].

#### The analytical approach

In this study we formulate an analytical model describing different combinations of the two sets of hypotheses described below, the first related to the mode of chloroquine binding to HM, the second to the mechanism of action of the mutated PfCRT. We test all possible combinations of these hypotheses for their consistency with the available experimental data provided by [29] and summarized in Table 1. Abbreviations used throughout the manuscript are reported in Table 2.

Concerning the chloroquine binding to HM we consider two possibilities:

**H1** The concentration of the complex chloroquine:HM inside the vacuole, [CQ:HM]\textsubscript{DV}, linearly increases with the concentration of the binding form of chloroquine in the vacuole. According to which chloroquine species reacts with HM, this can be expressed as [CQ:HM]\textsubscript{DV} = \alpha \times [CQ]\textsubscript{DV} or [CQ:HM]\textsubscript{DV} = \alpha \times [CQ\textsuperscript{+}]\textsubscript{DV}, or [CQ:HM]\textsubscript{DV} = \alpha \times [CQ\textsuperscript{2+}]\textsubscript{DV} or [CQ:HM]\textsubscript{DV} = \alpha \times [CQ\textsuperscript{3+}]\textsubscript{DV}, where [CQ\textsuperscript{TOT}] = [CQ] + [CQ\textsuperscript{+}] + [CQ\textsuperscript{2+}] + [CQ\textsuperscript{3+}]. The latter representing the case of chloroquine binding HM regardless of its protonation state.

**H2** The concentration of the complex chloroquine:HM increases non linearly with the concentration of the binding chloroquine form in the vacuole and reaches saturation at concentrations of chloroquine above a given threshold. If we define the threshold concentrations as t\textsubscript{HM,CQ}, t\textsubscript{HM,CQ}\textsuperscript{+}, or t\textsubscript{HM,CQ}\textsuperscript{2+} or simply t\textsubscript{HM} when the species is clear from the context, the above hypothesis can be expressed as: [CQ:HM]\textsubscript{DV} = f([CQ]\textsubscript{DV}), where, for [CQ] > t\textsubscript{HM,CQ} reads [CQ:HM]\textsubscript{DV} = constant. Similar expressions hold for [CQ\textsuperscript{+}] and [CQ\textsuperscript{2+}] and [CQ\textsuperscript{3+}]

#### Table 1. Values of the chloroquine cellular accumulation ratio in sensitive and resistant strains, in the presence and absence of FCCP, as estimated from figures 1A and 2A in Bray et al [29].

<table>
<thead>
<tr>
<th>CAR</th>
<th>−FCCP</th>
<th>+FCCP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sensitive</td>
<td></td>
<td></td>
</tr>
<tr>
<td>strain (CQS)</td>
<td>1200 (B)</td>
<td>700 (A)</td>
</tr>
<tr>
<td>GC03 strain</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Resistant</td>
<td></td>
<td></td>
</tr>
<tr>
<td>strain (CQR)</td>
<td>350 (C)</td>
<td>700 (D)</td>
</tr>
</tbody>
</table>

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Table 2. List of abbreviations used throughout the paper.

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>CQS</td>
<td>Chloroquine Sensitive Strain</td>
</tr>
<tr>
<td>CQR</td>
<td>Chloroquine Resistant Strain</td>
</tr>
<tr>
<td>CAR</td>
<td>Cellular Accumulation Ratio</td>
</tr>
<tr>
<td>CQ</td>
<td>un-protonated form of chloroquine</td>
</tr>
<tr>
<td>CQ*</td>
<td>mono-protonated form of chloroquine</td>
</tr>
<tr>
<td>CQ**</td>
<td>di-protonated form of chloroquine</td>
</tr>
<tr>
<td>CQTOT</td>
<td>CQ+ and CQ++</td>
</tr>
<tr>
<td>[H+]-CQ</td>
<td>labeled chloroquine</td>
</tr>
<tr>
<td>DV</td>
<td>Digestive Vacuole</td>
</tr>
<tr>
<td>HM</td>
<td>heme related species bound by chloroquine inside the vacuole</td>
</tr>
<tr>
<td>[CQ], [CQ'], [CQ**], [CQTOT]</td>
<td>Concentration of CQ, CQ', CQ**, CQTOT</td>
</tr>
<tr>
<td>[CQHM]DV</td>
<td>concentration of the complex chloroquine:HM inside the vacuole</td>
</tr>
<tr>
<td>[H+]</td>
<td>concentration of H+</td>
</tr>
<tr>
<td>FCCP</td>
<td>carbonylcyanide</td>
</tr>
<tr>
<td>p-trifluoromethoxyphenylhydrazone, a ionophoric uncoupling agent</td>
<td></td>
</tr>
<tr>
<td>JPfCRT</td>
<td>chloroquine flux through PfCRT</td>
</tr>
<tr>
<td>HMM</td>
<td>Hidden Markov Model</td>
</tr>
</tbody>
</table>

doi:10.1371/journal.pone.0014064.t002

The membrane equilibrium equation is:

\[ P_{eq}(CQ)_e - [CQ]_{DV} = J_{PfCRT} \] (1)

where \( P_{eq} \) is the membrane permeability to unprotonated chloroquine; equation (1) has been obtained taking into account that the system has reached a steady state in the analysed experimental conditions. Consequently, the net chloroquine flux across the membranes is zero. The only form of chloroquine for which the erythrocyte and the external plasmodium membranes are permeable is the un-protonated one and this implies that CQ concentrations are the same on the two sides of these membranes.

The expression for CAR is:

\[ CAR = \frac{[C]_{in}}{[C]_{out}} = \frac{[C]_{DV}V_{DV} + [C]_{e}(V_{in} - V_{DV})}{[C]_{e}V_{in}} \] (2)

where the total concentration of chloroquine inside the vacuole is:

\[ [C]_{DV} = [CQ]_{DV} + [CQ^+]_{DV} + [CQ^{++}]_{DV} + [CQ : HM]_{DV} \] (3)

being [CQ:HM]_{DV} the concentration of chloroquine bound to HM.

\[ [C]_e = [C]_{out} = [CQ^{TOT}]_e = [CQ]_e + [CQ^+]_e + [CQ^{++}]_e \] (4)

is the concentration of chloroquine outside the vacuole; [C]_{in} is the average chloroquine concentration in the infected erythrocyte, \( V_{in} \) is the volume of the infected erythrocyte and \( V_{DV} \) is the volume of the digestive vacuole. The analytical derivation of eqs (1) and (2) is detailed in Text S1, sections S2 and S3, respectively. The proof of the first equality of eq (4) ([C]_e = [C]_{out}) is reported in Text S1, section S4.

Finally, the relationships between the concentrations of the three forms of chloroquine given by the two-base dissociation equilibrium are:

\[ [CQ^+] = \frac{[CQ][H^+]}{k} = \frac{[CQ]10^{-pH}}{k'} \] (5)

\[ [CQ^{++}] = \frac{[CQ][H^+]^2}{k''} = \frac{[CQ]10^{-2pH}}{k''} \] (6)

with \( 1/k' = (1/k_2 + 1/k_3) \) and \( k'' = k_1 k_2 \) and \( k_1 \) and \( k_2 \) are the two dissociation constants.

Experimentally determined values for the constants used in Eqs (2) to (6) are reported in Table 3.

Figure 1 summarizes the various hypotheses tested here. The columns refer to the mode of binding of the chloroquine to HM, assuming either that the experimental data have been obtained in non saturation conditions (linear regime, hypothesis H1) or that the concentration of the chloroquine species is above the (unknown) saturation concentration for HM (saturation conditions, hypothesis H2). The rows are related to assumptions about the concentration of CQ*. The mutated PfCRT function considering the possibility that the experimental data have been obtained in non saturation conditions (linear regime, hypothesis H1) or that the concentration of the chloroquine species is above the (unknown) saturation concentration for HM (saturation conditions, hypothesis H2). The rows are related to assumptions about the mutated PfCRT function considering the possibility that the latter is a channel (first row, hypothesis J1) or an active carrier (remaining rows, hypotheses J2) and, in the case of active carrier, considering the possibility that the considered chloroquine species concentration into the vacuole is or is not above the (unknown) threshold needed to saturate PfCRT.

In the following we will show the procedure used to test the hypotheses summarized in Figure 1. We use the symbol CQ* in equations that hold for all four forms of chloroquine (CQ, CQ*, CQ**, and CQTOT).

We examined the consequences of each of the hypotheses reported in Figure 1. As a general strategy, we used the values of
CAR in experiments A, B and C reported in Table 1 (CAR\textsubscript{A}, CAR\textsubscript{B} and CAR\textsubscript{C}, respectively) to calibrate the model, inferred a CAR value for experiment D (CAR\textsubscript{D}) and compared it with the experimental one. In some cases, the value of CAR\textsubscript{A} and CAR\textsubscript{B} was used to infer the value of the vacuolar pH (\textit{pH\textsubscript{DV}}) subsequently compared with the experimental one. When the results show that a hypothesis is inconsistent with the experimental data and has to be discarded, the corresponding cell in Figure 1 is shaded. Inferred values of CAR\textsubscript{D} and their agreement or disagreement with experimental values are shown in Figure 2B.

**Test of hypothesis H1** ([CQ:HM]\textsubscript{DV} = \alpha[CQ\textsuperscript{*}]\textsubscript{DV}). Here, we use the values of CAR\textsubscript{A} and CAR\textsubscript{B} to infer the \textit{pH\textsubscript{DV}} value. Notice that, since CAR\textsubscript{A} and CAR\textsubscript{B} refer to CQS strains, here we are not making any assumption on PfCRT.

Let us consider the hypothesis that the concentration of the complex CQ\textsuperscript{*}:HM linearly increases with the vacuolar concentration of CQ\textsuperscript{*}, i.e. hypothesis H1 corresponding to the twenty cells C\textsubscript{1–5,5–8} in Figure 1 in the columns labeled as “Linear regime”. We can have four different expressions for the total chloroquine accumulated in the vacuole [C]\textsubscript{DV} depending on which chloroquine form reacts with HM, namely

\begin{align}
\text{case 1 : } [C]\textsubscript{DV} &= [CQ\textsuperscript{TOT}]\textsubscript{DV} + \alpha[CQ]\textsubscript{DV} & (7) \\
\text{case 2 : } [C]\textsubscript{DV} &= [CQ\textsuperscript{TOT}]\textsubscript{DV} + \alpha[CQ\textsuperscript{++}]\textsubscript{DV} & (8) \\
\text{case 3 : } [C]\textsubscript{DV} &= [CQ\textsuperscript{TOT}]\textsubscript{DV} + \alpha[CQ\textsuperscript{*}]\textsubscript{DV} & (9) \\
\text{case 4 : } [C]\textsubscript{DV} &= (1 + \alpha)[CQ\textsuperscript{TOT}]\textsubscript{DV} & (10)
\end{align}

Corresponding to columns 5, 6, 7 and 8 of Figure 1, respectively.

Combining these equations with (2), (3), (4), (5), and (6) an expression for CAR as a function of the binding constant \alpha and of \textit{pH\textsubscript{DV}} can be obtained. For instance, in case 1 (eq. (7)), we have:

\begin{align}
CAR &= \frac{V_e - V_{DV}}{V_e + V_{DV}} \left(1 + \frac{[H^+]\textsubscript{DV}}{k'} + \frac{[H^+]\textsubscript{DV}^2}{k'^2}\right) & (11)
\end{align}

where \(V_e = V_{in} - V_{DV}\).

Let us consider the behavior of CQS strains. In this case, [CQ]\textsubscript{DV} \equiv [CQ]. Knowing \alpha and using the experimental value of CAR for sensitive strains (experiment A in Table 1), we can compute the parameter \alpha. Knowing \alpha and using the experimental value of CAR in the absence of FCCP (experiment B in Table 1) we can solve the second order equation (11) in \textit{pH\textsubscript{DV}}, which is found to have only one positive solution. The same procedure can be applied to equations (8–10) to derive the equivalent of (11) for cases 2–4 (see also Text S1, section S5). The results for the four cases are:

\begin{align}
\text{Case 1 : } \alpha &= 5.311 \times 10^7 \quad \text{pH\textsubscript{DV}} = 5.36 \\
\text{Case 2 : } \alpha &= 8.352 \times 10^4 \quad \text{pH\textsubscript{DV}} = 7.17 \\
\text{Case 3 : } \alpha &= 1.680 \times 10^4 \quad \text{pH\textsubscript{DV}} = 7.28 \\
\text{Case 4 : } \alpha &= 1.398 \times 10^4 \quad \text{pH\textsubscript{DV}} = 7.27
\end{align}

**Figure 1. Summary of the hypotheses analysed throughout the manuscript.** The columns refer to the mode of binding of the chloroquine to HM, the rows to mutated PfCRT, considering the possibility that the latter is a channel or an active carrier. Shaded cells correspond to combination of hypotheses inconsistent with the analysed data.

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Only the pHDV value obtained in case 1 is compatible with the experimental data for pHDV (Figure 2A and Table 3) and therefore we can conclude that, if the data are obtained in non-saturating conditions for HM binding, the non-protonated form of chloroquine binds to HM, regardless of the mechanism of action of the mutated PfCRT. The C_{1,5,6,8} cells in Figure 1 are therefore shaded since they correspond to cases not compatible with the experimental data.

**Test of hypotheses J1 (PfCRT is a channel) and J2 (PfCRT is a carrier) [cells C_{1,3,5} Figure 1 and Figure 2B].** Let us now consider the data obtained for resistant strains (C and D in Table 1). We can use the values of pHDV and \( z \) to calculate the concentration of the un-protonated chloroquine inside the vacuole for CQR strains in the absence of FCCP (experiment C Table 1) using equation (11). We call this value [CQ]_{DV,C} to indicate that it is related to experiment C and use eq (1) to calculate the outward flux due to PfCRT, i.e.

\[
J_{PfCRT} = P_{eq} \left( [CQ]_{e} [CQ]_{DV,C} \right)
\]

obtaining [CQ]_{DV,C} = 1.53 \times 10^{-12} \text{M} and \( J_{PfCRT} = 2.799 \times 10^{-3} \text{nM cm/s}.\)

Next, we examine the specific hypotheses for PfCRT.

If PfCRT is a channel and the DV membrane potential is zero, the transport is only driven by the difference in concentration of the transported chloroquine form.

As a paradigm of our procedure, we describe the case where the transported form is CQ\(^{+}\). A similar reasoning can be applied if the transported species is CQ\(^{++}\) or a combination of CQ\(^{+}\) and CQ\(^{++}\).

We have

\[
J_{PfCRT} = f\left( [CQ^{+}]_{DV} - [CQ^{+}]_{e} \right)
\]

The function \( f(x) \) is increasing and it is zero when its argument is zero. The presence of FCCP in experiment D (Table 1) implies that pHDV = pHe, i.e. that the concentrations of the three chloroquine forms are the same inside and outside the vacuole. Combining this observation with eq. (12) and the membrane balance equation (eq. (1)), we obtain that [CQ]_{DV,D} = [CQ]_{e}, [CQ^{+}]_{DV,D} = [CQ^{+}]_{e}, and [CQ^{++}]_{DV,D} = [CQ^{++}]_{e}, i.e. both the chloroquine diffusive flux through the vacuolar membrane and through PfCRT (eq [12]) are zero (for detailed calculations see Text S1, section S6). These findings imply that CAR_{D} = CAR_{A}, which is consistent with the experimental data (Figure 2B). Accordingly, cell C_{1,5} of Figure 1 and Figure 2B is not shaded.

Notice that, as a by-product of our calculations, the J_{PfCRT} permeability can be explicitly calculated in the hypothesis that f(x) is a linear function of \([CQ^{+}]_{DV} - [CQ^{+}]_{e}\) (see Text S1, section S7).

The argument used to demonstrate that CAR_{D} = CAR_{A} when the membrane potential is zero also holds if the membrane potential is different from zero. According to [26,29] we assume that the DV membrane potential is mainly due to a proton gradient; therefore, the presence of the proton un-coupler FCCP in experiments A and D (Table 1) lowers the membrane potential to a negligible value. On the other hand, a non zero membrane potential should only be taken into account when analyzing the results of experiments B and C, whose data are not used here to demonstrate that CAR_{D} = CAR_{A}. In other words, the presence of a non-zero membrane potential, that would require the addition of a term in equation (12), does not affect experiments A and D. Consequently it would have no effect on eq (12) and on our whole reasoning.

For testing the hypothesis that PfCRT is a carrier, corresponding to cells C_{2,5,5} in Figure 1, we need to consider the case of the CQ\(^{+}\) concentration inside the vacuole being lower (or not) than the threshold value t_{PfCRT}, i.e. being insufficient (or sufficient) to saturate the carrier (hypotheses J2a and J2b).

In the first case, corresponding to cells C_{2,5,5} in Figure 1, the outward flux is a linear function of the concentration of the
transferred chloroquine form \( \text{CQ}^* \), i.e.

\[
J_{\text{PCRT}} = \lambda ([\text{CQ}]_{\text{DV}}) \tag{13}
\]

As shown in Text S1, section S8, the \( \text{CARD} \) values for each of the chloroquine forms can be computed from eqs. (1), (11) and (13). In particular:

\[
\text{CARD} = 204 \quad \text{for} \quad J_{\text{PCRT}} = \lambda ([\text{CQ}]_{\text{DV}}) \\
\text{CARD} = 684 \quad \text{for} \quad J_{\text{PCRT}} = \lambda ([\text{CQ}^+]_{\text{DV}}) \\
\text{CARD} = 689 \quad \text{for} \quad J_{\text{PCRT}} = \lambda ([\text{CQ}^{++}]_{\text{DV}})
\]

Corresponding to cells C1,5 in Figure 1, respectively. The only cases where the results are consistent with the data reported in Table 1 are that \( \text{PCRT} \) is an active carrier for either \( \text{CQ}^o \) or \( \text{CQ}^{++} \) in a linear regime (Figure 2B). This implies that only cell C2,5 is shaded in Figure 1 and Figure 2B.

A similar line of reasoning allows the \( \text{CARD} \) value to be computed in the hypothesis that the \( \text{CQ}^o \) concentration inside the vacuole is not lower than the threshold value \( t_{\text{PCRT}} \). In this case (corresponding to cell C2,5 in Figure 1) we have:

\[
J_{\text{PCRT}} = \text{constant} \tag{14}
\]

In particular, \( J_{\text{PCRT,C}} \equiv J_{\text{PCRT,D}} \) where the suffix C and D refer to the experiments shown in Table 1. Eq. (14) and the CQ membrane balance equation (eq (1)) implies \( [\text{CQ}]_{\text{DV,C}} = [\text{CQ}]_{\text{DV,D}} \). By substituting the values for \( [\text{CQ}]_{\text{DV,D}} \) and \( \sigma \) in equation (11) and remembering that \( \text{pH}_{\text{DV}} = \text{pH}_i \) in the presence of FCCP, we obtain \( \text{CARD} = 204 \). This value significantly differs from the experimental one indicating that hypothesis J2b is not plausible, regardless of the chloroquine species involved in the chloroquine:HM binding and of the mechanism of action of the mutated \( \text{PCRT} \). Consequently, none of the 20 cells C1–5,1–4 can be shaded at this stage.

**Test of hypotheses J1 (PCRT is a channel) and J2 (PCRT is a carrier) [cells C1,1–4, Figure 1]**. As shown before, if experiment A has been performed in saturation conditions, the same is true for experiment B. We now need to infer what are the conditions of experiment C, i.e. whether

\[
[\text{CQ} : \text{HM}]_{\text{DV,A}} = [\text{CQ} : \text{HM}]_{\text{DV,C}} \tag{16}
\]

Notice that in experiment A there is no effect of \( \text{PCRT} \) (being this the case of a sensitive strain) or of \( \text{pH} \) differences (because of the presence of FCCP), therefore all the chloroquine accumulation is due to the chloroquine bound to \( \text{HM} \). In particular, it is apparent from eq. (15) that, without the \( [\text{CQ} : \text{HM}]_{\text{DV}} \) contribution, \( \text{CAR}_x \) would be 1. Equation (16) implies that the \( [\text{CQ} : \text{HM}]_{\text{DV}} \) contribution to \( \text{CAR}_x \) is equal to the \( [\text{CQ} : \text{HM}]_{\text{DV}} \) contribution to \( \text{CAR}_\text{C} \) hence, due to the additional contribution of \( \text{pH} \) to chloroquine accumulation in C, we would have \( \text{CAR}_\text{C} > \text{CAR}_\text{A} \). Since the experimental data show that \( \text{CAR}_\text{C} < \text{CAR}_\text{A} \), we can reject the hypothesis represented by equation (16) and conclude that the concentration of chloroquine in experiment C is not in the saturation region (detailed numeric calculation can be found in Text S1, section S9). In conclusion, if experiment A was performed at saturating chloroquine:HM concentration, the same holds for experiment B, but not for experiment C. This implies that, in experiment C, we have \( [\text{CQ} : \text{HM}]_{\text{DV}} = f_{\text{CQ}^o} \), where \( f_{\text{CQ}^o} \) is a monotonic increasing function of one of the chloroquine species.

In the hypothesis that \( \text{PCRT} \) is a channel, the reasoning is identical to that of section 1.1.1 for cell C1,5 of Figure 1 and leads to the same conclusions: we cannot exclude that \( \text{PCRT} \) is a channel (Figure 2B) therefore, cells C1,1–4 in Figure 1 are not shaded. Notice that no hypothesis on the chloroquine:HM binding is required in the reasoning of section 1.1.1.

We now discuss the case when the transported form is \( \text{CQ}^o \), i.e. \( \text{PCRT} \) is an active carrier that transports \( \text{CQ}^o \) in the linear regime (cell C1,4 Figure 1). A similar reasoning can be applied if the transported species are \( \text{CQ} \) or \( \text{CQ}^{++} \); the detailed calculations for these other cases are reported in Text S1 (sections S11 and S12).

In the hypothesis that \( \text{PCRT} \) transports \( \text{CQ}^o \) and that the dependency of the \( J_{\text{PCRT}} \) flux is linear in the concentration of vacular \( \text{CQ}^o \) \( \rho_{\text{PCRT}} = \rho([\text{CQ}^o]_{\text{DV}}) \) we need to consider the following cases for chloroquine-HM binding:
We tested how stable our model is with respect to reasonable variations of the CAR values. We repeated the whole procedure using values of CAR derived for other parasite lines and for variation within the experimental error obtaining the same conclusions (data not shown).

In conclusion, ten of the forty cells of Figure 1, each corresponding to a different assumption about the mode of binding of chloroquine to HM in conjunction with a specific form of PfCRT, are not shaded, i.e. they correspond in principle to hypotheses consistent with the experimental data.

Sequence and analysis of PfCRT

Previous bioinformatics analyses of the PfCRT protein were devoted at identifying the functional role of the PfCRT protein, leading to different conclusions. On one hand several authors [14,16] assigned PfCRT to the drug/metabolite transporter (DMT) superfamily and, among the previously defined protein families, reported that PfCRT has the highest similarity with the drug/metabolite exporter (DME) family. On this basis, the authors concluded that PfCRT is likely to function as an exporter of metabolites in sympor with H^+

Other studies proposed that PfCRT might share significant similarity with the CIC chloride channels of other organisms [29,35], which would reinforce the hypothesis that the protein acts as a gated aqueous pore.

As already mentioned by other authors [14], data supporting the CIC similarity hypothesis are not available and were impossible to reproduce using any available sensitive and updated sequence analysis tool. On the contrary, as detailed later, several different and effective methods strongly support the hypothesis that PfCRT is an active carrier.

The HHsearch tool [39,40] identifies three protein families in the Pfam database [41] with the highest similarity to PfCRT: PF06027 (DUF914), E-value 1.2×10^{-23}, PF08449 (UAA transporters), E-value 5.6×10^{-23}, PF04112 (nucleotide-sugar transporters), E-value 7.8×10^{-23}. These all belong to the Drug/Metabolite Transporter clan CL0184, which consists of several families of different secondary carriers, among which drug, sugar and nucleotide antipariters have the highest similarity with PfCRT. The alignment of PfCRT homologues with the closest Pfam family (DUF914) is shown in Figure 3.

Two amino acids of PfCRT are known to be involved in chloroquine resistance, 163 and 76, and therefore expected to be involved in the transport mechanism. To verify whether this is indeed the case, we built a homology model of the protein.

By searching the PDB database [42] with HHsearch, we retrieved two significant hits (e-value<0.1). The significant matches correspond to two solved structures (pdb codes 3B5D and 2I68) of the same protein, EmrE. This protein is a small E.coli multidrug transporter belonging to the same drug/metabolite transporter family described above that acts by exchanging various positively charged aromatic drugs across the plasma membrane with protons. EmrE is a homodimer, each monomer being composed by four membrane spanning helices. Two different regions of PfCRT sequence match three helices of each EmrE monomer, consistently with the presence of an internal sequence symmetry in PfCRT. We also searched for homologous proteins spanning the complete sequence of the protein to use as templates. Three different and sensitive methods (Shrimp [43], Phyre [44] and PROCAIN [45]) all identified the Glycerol-3-phosphate transporter GlpT from E.Coli (PDB code 1PW4) as a homolog of known structure with a significant sequence similarity spanning the whole sequence (e-value<10^{-3} in all cases). The protein was ranked first in the searches performed with Shrimp and
PROCAIN and second by Phyre. The top ranking protein identified by Phyre (LacY) has the same fold and belongs to the same superfamily as the Glycerol-3-phosphate transporter.

GlpT was therefore selected as the template for the model. It is an active transporter presenting a 12-helix trans-membrane helix protein with an internal sequence symmetry.

The final model (shown in Figure 4) was generated according to the target/template alignment shown in Figure 5. The model coordinates can be downloaded from the PMDB database [46] (Id PM0076214).

Mapping of residues 163 and 76 in the three-dimensional model of the protein (Figure 4) shows that they face each other and line the path of the transported molecule. This is consistent with the experimental observations and it appears plausible that the K76T and S163R mutations can permit positive charged species to be transported or not, respectively.

In conclusion, sequence analysis strongly suggests that PfCRT is an active carrier belonging to the Drug/Metabolite transporter superfamily and, furthermore, a three-dimensional model based on the basis of this evolutionary relationship is consistent with the experimental data on the protein.

**Discussion**

The ongoing debate on PfCRT, the molecule responsible for chloroquine resistance in Plasmodium, has not yet provided a conclusive answer to the question of whether PfCRT is a channel or a carrier.

The qualitative analysis of chloroquine accumulation, trans-stimulation and chloroquine efflux data has been used to support both the channel and the carrier hypotheses by different authors [26,27,29,30,34]. This is not surprising since we can analytically demonstrate that, at least as far as the chloroquine accumulation ratio experiments are concerned, the data are consistent with both hypotheses. A similarly rigorous approach cannot be used for the other experiment types since the problem is underdetermined.

This notwithstanding, we are able to show here that, if PfCRT is a carrier, it can only transport protonated or di-protonated chloroquine molecules and that chloroquine can either bind heme or heme related species in the digestive vacuole regardless of its charge or in its neutral form.

On the other hand, a reassessment of the evolutionary relationships of the protein with state-of-the-art methods and updated databases strongly suggests that the protein is indeed a member of the Drug/Metabolite transporter clan. This conclusion is further substantiated by the observation that a model based on this detected evolutionary relationship is consistent with experimental data.

Taking together the results of these two interdisciplinary approaches allow us to conclude that the chloroquine species are transported out of the vacuole through PfCRT in their protonated form, in agreement with studies such those presented by Lehane et al [24,47] who provided evidence that the presence of chloroquine increases the leak of H+ from the vacuole.

We would like to emphasize that our analytical approach does not require ad-hoc hypotheses as it would be the case if we were to model data coming from trans-stimulation and chloroquine efflux experiments where parameters such as the rate of the vacuole pH equilibration during chloroquine uptake or the kinetic constants of chloroquine-hemozoine binding are unknown. On the other hand, the model can be used effectively to interpret the results of stationary experiments. As an example, recently Martin and collaborators [25] set up a system in which PfCRT is expressed at the surface of *Xenopus laevis* oocytes and measured the chloroquine uptake which, in this system, is not influenced by chloroquine-HM binding. The available data have been obtained in the pre-stationary state, but the same system could in principle be used to measure chloroquine uptake at equilibrium in a pH-controlled experiment. In this case a simplified version of our analytical model could be employed to derive the systems parameters and provide more detailed information about PfCRT.

Remarkably, our analysis conclusively demonstrates that experimental data on the chloroquine accumulation ratio at equilibrium are consistent with both hypotheses that the mutant
molecule is an active or a passive carrier of the drug and therefore insufficient to distinguish between the two mechanisms, while at the same time they can be used to restrict hypotheses on the nature of the transported and HM-binding species in the two cases. Our computational analysis of the sequence and a structural bioinformatics approach strongly suggests that the mutated protein acts as an active carrier of chloroquine and, in this assumption, we can conclude that the PfCRT mutated protein confers resistance by carrying either the mono or di-protonated chloroquine out of the vacuole. It is tempting to speculate that the mechanism is that the mutated PfCRT uses the $H^+\text{gradient}$ to expel the protonated form of chloroquine from the vacuole. Cationic transport inhibitors could be tested to further support this hypothesis and, perhaps, as starting point for developing novel therapies against resistant malaria strains.

We hope that the example of the power of systems and computational biology analysis of the data presented here will convince the Plasmodium community to take advantage of our results.

**Materials and Methods**

**Ethics Statement:** N/A

We performed sequence similarity searches on the nr database [48] release of October 4th, 2010 using three iterations of CS-Blast [49]. We selected the first 500 hits, all having an e-value lower than 1e-5, and realigned their sequences using the multiple sequence alignment tool MUSCLE [50]. Such alignment was then used to scan the Pfam [41] and PDB [42] databases on October 5th, 2010 with the Hidden Markov Model based search method HHpred [39], the results of which are reported in Table S1. Three distant homology recognition tools, Phyre [51], Shrimp [43] and PROCAIN [45], were used to identify templates spanning the complete PfCRT sequence (see Table S2, Table S3 and S4). In all the cases, a statistically significant similarity of the PfCRT sequence with that of the Glycerol-3-Phosphate transporter GlpT from E.Coli (PDB code 1PW4) spanning the whole sequence of both target and template proteins was detected.

**Supporting Information**

| Text S1 | Details of the calculations presented in the main manuscript. Found at: doi:10.1371/journal.pone.0014064.s001 (1.24 MB PDF) |
| Table S1 | HHpred results on Pfam and PDB databases. Found at: doi:10.1371/journal.pone.0014064.s002 (0.02 MB PDF) |
| Table S2 | Phyre results. Found at: doi:10.1371/journal.pone.0014064.s003 (0.02 MB PDF) |
| Table S3 | PROCAIN results. Found at: doi:10.1371/journal.pone.0014064.s004 (0.02 MB PDF) |
| Table S4 | Shrimp results. Found at: doi:10.1371/journal.pone.0014064.s005 (0.03 MB PDF) |

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**Author Contributions**

Conceived and designed the experiments: MC AV PM AT. Analyzed the data: MC AV PM. Wrote the paper: AV AT.

**References**


