

1 **Estimation of the in-vivo minimum inhibitory concentration of cipargamin in**
2 **uncomplicated *Plasmodium falciparum* malaria**

3

4 **Running title:** Estimated MIC of cipargamin in malaria

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24 **Abstract**

25 The minimum inhibitory concentration (MIC) of an antimalarial drug for a particular
26 infection is the drug level associated with a net parasite multiplication rate of one per
27 asexual cycle. To ensure cure of malaria the MIC must be exceeded until all parasites
28 have been eliminated. The development of highly sensitive and accurate polymerase
29 chain reaction quantitation of low-density malaria parasitemia enables prospective
30 pharmacokinetic–pharmacodynamic (PK–PD) characterization of antimalarial drug
31 effects, and now allows identification of the in-vivo MIC. An adaptive design and PK–PD
32 modeling approach was used to determine prospectively the MIC of the new
33 antimalarial cipargamin (KAE609) in adults with uncomplicated *Plasmodium falciparum*
34 malaria, in an open-label, dose-ranging phase 2a study. Vietnamese adults with acute
35 *P. falciparum* malaria were allocated sequentially to treatment with single 30 mg ($n = 6$),
36 20 mg ($n = 5$), 10 mg ($n = 7$), or 15 mg ($n = 7$) doses of cipargamin. Artemisinin-based
37 combination therapy was given after parasite densities had fallen and then risen as
38 cipargamin levels declined below the MIC, but before a return of signs or symptoms.
39 The rates of parasite clearance were dose-dependent with near saturation of effect at
40 an adult dose of 30 mg. The developed PK–PD model accurately predicted the
41 therapeutic responses in 23/25 patients. The predicted median in-vivo MIC was
42 0.126 ng/mL (range 0.038–0.803 ng/mL). Pharmacometric characterization of the
43 relationship between antimalarial drug concentrations and parasite clearance rates
44 following graded sub-therapeutic antimalarial drug dosing is safe, and provides a
45 rational framework for dose-finding in antimalarial drug development.

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48 **Keywords:** malaria; resistance; cipargamin; pharmacokinetic–pharmacodynamic
49 model; clinical trial

50 INTRODUCTION

51 The emergence of resistance to current antimalarial drugs threatens to reverse recent
52 substantial gains in the control and elimination of malaria. Several factors contribute to
53 the emergence and spread of resistance, notably uncontrolled use of monotherapies,
54 poor quality medicines, and systematic under-dosing (1, 2). Therefore, maximizing the
55 lifetime of any new antimalarial drug depends not only on the propensity for resistance
56 to arise or to share cross-resistance with existing drug classes but also on finding the
57 best treatment dose during drug development (2).

58 An alternative to previous, largely empirical approaches to dose-finding for new
59 antimalarial drugs is to determine prospectively, in vivo, the minimum inhibitory
60 concentration (MIC) (2). The MIC has been defined as the plasma or blood
61 concentration associated with a parasite multiplication rate of one per cycle, and
62 therefore represents a therapeutic target that must be exceeded for a sufficient duration
63 to guarantee cure (3). In recent years, ex-vivo experimental systems, animal models,
64 and more recently, human challenge models have provided valuable information on
65 antimalarial pharmacokinetic–pharmacodynamic (PK–PD) relationships, although their
66 direct relevance to the treatment of symptomatic malaria remains uncertain (4). Ideally,
67 the key PK–PD determinants of therapeutic response should be determined in the
68 natural disease.

69 The spiroindolone cipargamin (formerly KAE609) is a new antimalarial drug with potent
70 activity against *Plasmodium falciparum* and *Plasmodium vivax* (5–7). Cipargamin
71 inhibits the P-type cation-translocating ATP-ase PfATP4, disturbing parasite sodium

72 homeostasis and causing osmotic dysregulation (5, 8, 9). This novel mechanism of
73 action affecting all stages of intraerythrocytic parasite development probably explains
74 why cipargamin treatment causes extremely rapid parasite clearance (5, 6, 10).

75 In the first study of its kind, we aimed to estimate prospectively the in-vivo MIC of
76 cipargamin in acute uncomplicated *P. falciparum* malaria. This was made possible by
77 the development of sensitive and accurate quantitative polymerase chain reaction
78 (qPCR) measurement of parasite nucleic acids, which permits tracking of parasitemia at
79 densities well below those causing illness, and thus, characterization of recrudescence
80 without discomfort or risk for the patient (11–13).

81

82 MATERIALS AND METHODS

83 Patients

84 Adult Vietnamese patients aged 20–60 years and weighing between 40 and 90 kg, with
85 acute *P. falciparum* mono-infection confirmed by microscopy (asexual parasite count
86 5,000–50,000/μL), were recruited if they could take oral medications reliably and gave
87 fully informed written consent to the study procedures, and if their axillary or
88 oral/tympanic/rectal temperature was higher than $\geq 37.5^{\circ}\text{C}$ or $\geq 38^{\circ}\text{C}$, respectively, at
89 screening or during the previous 24 hours. Exclusion criteria included signs/symptoms
90 of severe malaria, mixed *Plasmodium* infection, and use of an antimalarial drug within 2
91 months (see appendix).

92 Study design

93 An adaptive single-dose de-escalation design was employed. The study was performed
94 at a single center in Vietnam in accordance with the ethical principles of the Declaration
95 of Helsinki. The study protocol was approved by the ethics committee of the
96 Vietnamese Ministry of Health, the Oxford Tropical Research Ethics Committee
97 (OxTREC), and by the study center's institutional review board (ClinicalTrials.gov
98 identifier: NCT01836458).

99 Six cipargamin dose evaluations with approximately eight patients per group, running in
100 descending sequence (30, 20, 10, 5, 2, and 1 mg) until the MIC was identified, were
101 planned, with the option of dose adjustment based on data arising during the study. The
102 30 mg adult dose has been shown previously to clear parasitemia (assessed by

103 microscopy) in less than 24 hours in both *P. falciparum* and *P. vivax* malaria (5). During
104 and after each stratum the data monitoring committee decided whether to reduce,
105 maintain, or increase the dose. Cipargamin capsules were supplied at doses of 1, 10,
106 and 25 mg, and were administered orally as a single dose under direct observation (day
107 1).

108 In order to estimate the in-vivo MIC safely, it is necessary for parasitemia to fall below
109 microscopy level of detection and then rise again as drug levels decline below the MIC.
110 The antimalarial plasma concentration at the vertex of this approximate parabola is
111 considered the MIC (2). Antimalarial treatment was given when there was an
112 unequivocal rise in parasite densities indicating recrudescence, but before a return of
113 signs or symptoms (see appendix). Thus, the national standard antimalarial treatment
114 course of dihydroartemisinin-piperaquine (DHA-PPQ 40 mg/320 mg per tablet
115 [Arterakine[®]]; four, two, and two tablets on days 1, 2, and 3, respectively) and
116 primaquine (four 7.5 mg tablets as a single dose) was given to all patients on day 42, or
117 earlier in the case of early treatment failure (ETF) or rising qPCR parasitemia. ETF was
118 defined as clinical deterioration or lack of clinical/parasitemia improvement at 24 hours,
119 parasitemia >75,000/ μ L at or after 12 hours post-dose, any parasitemia detected by
120 microscopy with fever (\geq 48 hours post-dose), or parasitemia >100/ μ L based on
121 microscopy without fever (\geq 72 hours post-dose).

122 **Study assessments and procedures**

123 Vital signs were recorded and blood samples taken every 4–6 hours until defervescence
124 and two consecutive negative microscopy parasite counts, then once daily until day 8,

125 then on alternate days until day 28, and on days 35 and 42. Serial parasite densities
126 were measured from thick and thin blood film examinations at higher densities and then
127 by a validated real-time qPCR of the *P. falciparum* 18S rRNA gene (limit of detection: 22
128 parasites/mL) conducted in real time on site and reported daily to the clinical
129 investigators (14). Samples for ring-stage and gametocyte (Pfs25) mRNA transcripts
130 were also taken and measured at the Queensland Institute of Medical Research
131 Berghofer Medical Research Institute (15). Blood samples (3 mL) for plasma cipargamin
132 concentration measurements were taken at 0 (pre-dose), 0.5, 1, 2, 3, 4, 5, 6, 8, 10, 12,
133 16, 20, 24, 36, 48, 72, 96, 120, 144, and 168 hours after dosing. Samples were stored
134 at -70°C until analysis using a validated LC-MS/MS assay with a lower limit of
135 quantitation of 1 ng/mL (5, 10). More than 67% of the triplicate quality control samples
136 at five different concentrations were within $\pm 15.0\%$ of the individual values. Safety
137 assessments included monitoring of vital signs, laboratory values, urinalysis,
138 electrocardiogram, and adverse events (AEs) classified according to the Common
139 Terminology Criteria for Adverse Events (CTCAE, version 4.03)
140 ([http://evs.nci.nih.gov/ftp1/CTCAE/CTCAE_4.03_2010-06-](http://evs.nci.nih.gov/ftp1/CTCAE/CTCAE_4.03_2010-06-14_QuickReference_5x7.pdf)
141 [14_QuickReference_5x7.pdf](http://evs.nci.nih.gov/ftp1/CTCAE/CTCAE_4.03_2010-06-14_QuickReference_5x7.pdf)).

142 **In-vitro susceptibility testing**

143 The in-vitro susceptibility of *P. falciparum* to cipargamin was measured in pretreatment
144 blood samples using a 24-hour trophozoite maturation assay (16). Relative parasite
145 maturation and drug concentrations were fitted in GraphPad Prism v.6.01 (La Jolla,
146 California, USA) using the dose–response package. All response data were fitted

147 simultaneously to estimate the population mean slope of the dose–response curve and
148 the IC_{50} value, and to characterize variability. All individual isolate data were fitted
149 separately using the population slope estimate to generate robust estimates of the
150 individual isolate IC_{50} values.

151 **Assessments of parasite clearance**

152 Parasite clearance metrics were assessed using the Worldwide Antimalarial Resistance
153 Network parasite clearance estimator (17). Other efficacy endpoints are described in the
154 appendix.

155 **Pharmacokinetic modeling**

156 Pharmacokinetics was described initially by non-compartmental analysis using Phoenix
157 WinNonlin version 6.2 (Certara, Princeton, NJ, USA). PK–PD characteristics were then
158 evaluated with nonlinear mixed-effects modeling in the software NONMEM v 7.3 (ICON
159 Development Solutions, Ellicott City, MD, USA). The most appropriate model for
160 pharmacokinetic (PK) characterization was developed by evaluating different
161 absorption, disposition, and covariate models as well as random effects components
162 (see appendix for details) (18, 19). Individual PK parameters from the final model were
163 imputed into the PK–PD model to drive the cipargamin-dependent “parasite clearing”
164 effect.

165 **Pharmacodynamic modeling**

166 Parasite densities (microscopy and qPCR) were transformed to total parasite burdens
167 assuming 80 mL whole blood/kg. In *P. falciparum* malaria, as asexual density declines,
168 gametocytemia rises, because mature gametocytes are released from sequestration
169 (20). DNA density estimates do not discriminate between asexual dividing, refractory,
170 and sexual parasites. To reduce confounding by gametocytemia, the qPCR DNA
171 density estimates were censored when sexual parasite densities (measured by Pfs25
172 mRNA) reached >10% of the total measurement (assuming a conservative estimate of
173 10 mRNA copies per cell in the Pfs25 assay). Recrudescence infections were identified
174 from rising qPCR DNA and confirmed by rising ring-stage mRNA together with
175 unchanged or falling Pfs25 transcript numbers; in some patients this was confirmed by
176 the appearance of asymptomatic microscopy-detectable asexual parasites. There was a
177 good correlation between uncensored PCR and microscopy measurements (data not
178 shown) and these data were therefore pooled for PK–PD modeling. Different structural
179 PK–PD models were evaluated to characterize the relationship between drug exposure
180 and parasite killing (see appendix). The MICs were taken directly from individually
181 predicted profiles in patients with recrudescence.

182 **Statistical analysis**

183 The projected sample size was based on operational rather than statistical
184 considerations (see appendix). Parasite clearance and fever clearance times were
185 analyzed using the Kaplan–Meier method (see appendix). The relationship between
186 cipargamin exposure, defined as observed area under the concentration–time curve
187 between 0 and 24 hours (AUC_{0-24h}) or as observed maximum concentration (C_{max}), and

188 parasite clearance half-life ($PC_{1/2}$) was modelled with a non-linear regression model

189 (illustrated below for AUC_{0-24h}):

190 $PC_{1/2} = a + (b - a) \times e^{(-k \times AUC_{0-24h})}$ where a is the asymptotic maximal effect of

191 cipargamin exposure on the $PC_{1/2}$, b is the longest $PC_{1/2}$ and k is the rate of decrease in

192 $PC_{1/2}$.

193

194 **RESULTS**

195 **Patients**

196 Twenty-five adult Vietnamese male patients with acute uncomplicated falciparum
197 malaria were enrolled between 15 January 2014 and 12 March 2015. The first three
198 groups received cipargamin in descending dose order: 30 mg ($n = 6$), 20 mg ($n = 5$),
199 and 10 mg ($n = 7$) (Table 1). One patient in the 30 mg group received 21 mg in error
200 and was included in the 20 mg group for the analysis. Because of the inadequate
201 therapeutic responses in the 10 mg group, dosing of the fourth group ($n = 7$) was
202 increased to 15 mg. Sixteen patients received early rescue treatment (30 mg, $n = 3/6$;
203 20 mg, $n = 2/5$; 10 mg, $n = 5/7$; 15 mg, $n = 6/7$), four because of ETF and 12 because of
204 later recrudescence (Fig. S1).

205 **Therapeutic responses**

206 Rates of fever and parasite clearance were approximately dose dependent (Table S1).
207 Mean [SD] parasite clearance half-life ($PC_{1/2}$) estimates were 4.35 [2.21], 3.79 [1.22],
208 1.91 [1.64], and 1.47 [0.83] hours for 10, 15, 20, and 30 mg, respectively. An asymptotic
209 non-linear model described the relationship between $PC_{1/2}$ and both AUC_{0-24h} and C_{max}
210 well and suggested saturation of the effect at higher doses of cipargamin (Fig. 1).
211 Despite trends for increased 28-day PCR-corrected cure rate with higher doses and
212 increased exposure (AUC) (Table S1), no individual PK parameter predicted cure (data
213 not shown).

214 **Safety**

215 Nineteen (76%) patients reported at least one AE (Table S2). Three AEs in the 30 mg
216 group were considered related to study treatment (nausea, myalgia, and headache).
217 There were no serious AEs or AEs leading to study discontinuation. Most laboratory
218 abnormalities did not exceed grade 2 severity; six patients had grade 3 abnormalities.
219 One patient with a history of hypertension who received 30 mg had a rise in blood
220 pressure to 160/100 mm Hg that resolved after treatment with furosemide 20 mg.

221 **In-vitro susceptibility to cipargamin**

222 Population estimates (95% CI) for slope and IC_{50} were -1.22 (-1.35 – -1.09) and 2.97
223 (2.70–3.26) ng/mL, respectively, with median (range; IQR) individual estimated IC_{50}
224 values of 2.38 (0.468–17.2; 1.25–4.07) ng/mL.

225 **Pharmacokinetic modeling**

226 The PK properties of cipargamin were well described by a flexible transit-absorption
227 model followed by a one-compartment disposition model (Fig. 2). Allowing inter-
228 individual variability on the relative bioavailability significantly improved model fit. Body
229 weight was incorporated as a fixed allometric function on clearance and volume
230 parameters. Dose did not significantly affect the PK properties, suggesting dose-linear
231 kinetics (Table 2, Table 3 and Fig. S2). The final PK model (Table 3) showed excellent
232 overall diagnostic performance (Fig. S3 and S4).

233 **Pharmacodynamic modeling**

234 As individual-patient malaria-parasite multiplication rates (K_{GROW}) before drug
235 administration are unknown, K_{GROW} was fixed to 10 per life-cycle (i.e. 48 hours) (21, 22).
236 The initial implementation of the PK–PD model assumed a homogenous parasite
237 population and first-order drug-dependent parasite removal (K_{KILL}). However, individual
238 and population parasite clearance curves showed a clearly biphasic parasitemia decline
239 that could not be explained adequately by gametocytemia. A small, refractory parasite
240 subpopulation was considered the most likely explanation, and its incorporation
241 significantly improved the model fit. The fraction of all asexual parasites that were
242 refractory ($1-F_{\text{SEN}}$) was estimated but allowed for inter-individual variability. Their
243 activation (“awakening”; K_{ACT}) and then removal was also estimated to explain cures.
244 Higher doses and correspondingly higher plasma concentrations were associated with
245 significantly faster maximum parasite killing rates (E_{MAX}). The final PK–PD model (Table
246 3) showed adequate overall diagnostic performance (Fig. S3 and S4) and characterized
247 therapeutic responses correctly for 23 of the 25 patients (i.e. cure, ETF or later
248 recrudescence; Fig. 3). The estimated median in-vivo MIC was 0.126 ng/mL (range
249 0.0375–0.803 ng/mL; IQR 0.0786–0.273 ng/mL), occurring at a median interval of 7.45
250 days (5.29–11.4 days; IQR 6.51–9.32 days) after drug administration for patients
251 predicted correctly as having recrudescence ($n = 12$). Time to MIC is a function
252 of dose as lower doses, and subsequently lower drug concentrations, will reach MIC
253 values more rapidly than higher doses, assuming similar PK and parasite
254 characteristics. Patients correctly predicted as cured ($n = 7$) showed a maximum
255 median MIC value of 0.236 ng/mL (range 0.03–6.33 ng/mL; IQR 0.08–1.47 ng/mL),
256 defined as the ciprofloxacin concentration when predicted parasite numbers fell below 10.

257 **DISCUSSION**

258 Antimalarial drugs are deployed in combinations both to optimize efficacy and to prevent
259 or delay the emergence of resistance
260 (<http://www.who.int/malaria/publications/atoz/9789241549127/en/>). Fixed-dose
261 combinations (FDCs) are needed to ensure adherence to both components and prevent
262 use of monotherapies that could select individual drug resistance. It is essential that the
263 optimum dose of a newly developed compound is chosen before the drug is tied in a
264 FDC. While patients with partial immunity may clear partially treated infections, to
265 ensure cure with the individual drug component in all patients, plasma concentrations
266 must exceed the MIC for a sufficient time to eliminate all the blood stage parasites.
267 Identifying the dose and dosing strategy that achieves this requires characterization of
268 two independent variables: the population PK properties of the antimalarial drugs in the
269 target populations, and the in-vivo drug susceptibility of infecting malaria parasite
270 populations. The MIC can only be estimated accurately in vivo if there is recrudescence.
271 As the MIC depends both on host factors, notably immunity, and the susceptibility of the
272 infecting parasites, it is best assessed in patients from an area of low malaria
273 transmission and consequently low background immunity where multidrug-resistant
274 parasites are prevalent, such as in the present study. The final dosage in a combination
275 regimen will be determined by the predicted duration for which the MIC is exceeded in
276 all relevant patient groups (based on population PK modelling), global variations in
277 malaria parasite susceptibility, practical considerations such as weight banding, any
278 interactions with the partner drugs, and safety and tolerability (2). This first prospective
279 determination of the in-vivo MIC in a dose-finding study was made possible by the

280 recent development of sensitive PCR quantitation methods. The MIC of cipargamin was
281 determined safely without discomfort to the patients, all of whom received curative
282 treatment before any signs or symptoms developed.

283 In this study the PK properties of the novel spiroindolone antimalarial, cipargamin, were
284 described satisfactorily by a one-compartment disposition model with flexible
285 absorption, and were similar to results from previous studies in malaria patients (5).
286 Exposure to cipargamin was approximately dose proportional, as demonstrated
287 previously in human volunteers (10). In the first exploratory studies conducted in Thai
288 patients with *P. falciparum* or *P. vivax* malaria, cipargamin cleared parasitemia more
289 rapidly than any other known antimalarial drug (5). In the current study, parasite
290 clearance rates increased with increasing cipargamin exposure approaching a plateau
291 with the 30 mg dose. The PK–PD modeling predicted MIC values ranging from 0.0375
292 to 0.803 ng/mL (median 0.126 ng/mL). In-vitro susceptibility was assessed by the
293 trophozoite maturation test, which measures ring-stage susceptibility, the main
294 determinant of parasite clearance. In the current study, conventional 48-hour in-vitro
295 tests, which assess the full asexual cycle, mean IC₅₀ values ranged from 0.195 to
296 0.546 ng/mL in laboratory isolates and were all below 3.9 ng/mL in fresh isolates from
297 malaria patients. The results of this study suggest that the in-vivo MIC for cipargamin is
298 in a concentration range associated with approximately 10% inhibition of trophozoite
299 development and 20–50% inhibition of schizont maturation in ex-vivo systems (although
300 the milieu and notably protein binding are different between the two).

301 In murine models, in which two compartment disposition models were fitted, cipargamin
302 exposure (AUC) was a better determinant of parasite clearance than C_{\max} after single
303 doses (23). In this clinical study, a clear dose-response relationship was evident and a
304 single compartment model fitted the concentration data satisfactorily. So, C_{\max} and AUC
305 were closely related and there was no clear superiority of one over the other as
306 predictors of the parasitological response.

307 There are several limitations to PK–PD modeling based upon quantitative DNA
308 estimates. First, DNA measurements do not distinguish between asexual and sexual
309 stage parasites, nor between quiescent and dividing parasites. However, the drug effect
310 being assessed is on dividing asexual stage parasites, and in the case of cipargamin
311 reflects splenic clearance of red blood cells containing damaged, osmotically
312 dysregulated parasites (24). As parasite densities decline, the more slowly cleared
313 sexual stage parasites and any drug-refractory forms comprise an increasing proportion
314 of the DNA signal. Recent ex-vivo studies suggest that cipargamin does not induce the
315 same refractory forms observed with artemisinin drugs (25), so the nature of the
316 parasite forms, which persist despite exposure to high cipargamin concentrations,
317 clearly requires further study (25, 26). Low-dose primaquine was not given as a rapid
318 gametocytocide in this study because cipargamin was considered to have
319 gametocytocidal activity, but this was insufficient. Thus, in some cases, both as a result
320 of drug-refractory parasite stages and persistent gametocytemia, the fall and
321 subsequent rise in the observed DNA signal was “flat bottomed” rather than parabolic.
322 Second, while ultrasensitive PCR is 1000 times more sensitive than microscopy, and
323 can detect parasites down to densities of $\sim 20/\text{mL}$, parasite densities at MIC were

324 sometimes lower than this detection threshold; in both cases the MIC had to be
325 extrapolated rather than observed. Detection of mRNA is potentially more sensitive than
326 detection of DNA as there are potentially thousands of mRNA transcripts per cell, but
327 their numbers vary with time, making accurate parasite quantitation potentially difficult.
328 However, changing values are very useful as indicators of trend, and so informed the
329 DNA-based assessments. For example, rising parasite DNA at a time of rising numbers
330 of ring-stage mRNA transcripts and falling gametocyte mRNA unequivocally identified
331 parasite multiplication.

332 In conclusion, the rates of *P. falciparum* parasite clearance were dose dependent, with
333 near saturation of the maximum effect at a cipargamin dose of 30 mg. The PK–PD
334 model developed accurately predicted the therapeutic responses in the majority of
335 falciparum malaria patients.

336

337 **CONTRIBUTORS**

338 NJW, BM, JPJ, and KH were involved in protocol design. TTH, NTTN, NTH, and PDT
339 were involved in data collection. TTH, NJW, JT, FN, BM, JPJ, and KH were involved in
340 data analysis. Each author reviewed and/or edited drafts of the manuscript, and each
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342

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352

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354 The sponsor was involved in study design and in data collection, analysis, and
355 interpretation. All authors had full access to the data and are responsible for their
356 accuracy and completeness. The corresponding author had final responsibility for the
357 decision to submit this report for publication.

358

359 **DECLARATION OF INTERESTS**

360 TTH, NJW, NTTN, NTH, PDT, JT and FN have no conflicts of interest to declare. BM is
361 an employee of Novartis Pharma AG, Basel, Switzerland. JPJ is an employee of
362 Novartis Healthcare Private, Ltd., Hyderabad, India. KH is an employee of Novartis
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459 **Tables and figures**

460

461 **TABLE 1** Patient demographics and baseline characteristics by cipargamin dose

	Dose 1:	Dose 2:	Dose 3:	Dose 4:	
	30 mg	20 mg	10 mg	15 mg	Total
	(n = 6)	(n = 5^a)	(n = 7)	(n = 7)	(n = 25)
Age, years					
Mean (SD)	33.2 (12.91)	32.2 (6.98)	30.6 (8.24)	34.7 (8.79)	32.7 (9.04)
Median (range)	33.5 (20–52)	30.0 (23–41)	30.0 (20–42)	35.0 (20–46)	31.0 (20–52)
Sex					
Male, <i>n</i> (%)	6 (100)	5 (100)	7 (100)	7 (100)	25 (100)
Predominant race					
Asian, <i>n</i> (%)	6 (100)	5 (100)	7 (100)	7 (100)	25 (100)
Height, cm					
Mean (SD)	168.8 (5.49)	163.8 (5.36)	163.7 (8.30)	161.9 (2.41)	164.4 (6.06)
Median (range)	167.5 (163–176)	162.0 (157–171)	162.0 (150–175)	161.0 (159–165)	164.0 (150–176)
Weight, kg					

Mean (SD)	60.7 (7.45)	56.8 (3.35)	60.8 (11.41)	56.9 (5.44)	58.9 (7.56)
Median (range)	63.5 (50–69)	57.0 (53–62)	60.0 (42–78)	59.0 (50–65)	59.0 (42–78)

Body mass index, kg/m²

Mean (SD)	21.3 (2.65)	21.2 (1.16)	22.5 (2.42)	21.7 (2.07)	21.7 (2.12)
Median (range)	20.8 (18.8–25.7)	21.0 (20.2–23.1)	22.9 (18.7–26.4)	23.0 (18.6–23.9)	21.2 (18.6–26.4)

462 ^aOne patient in the 30 mg cohort received 21 mg in error (a 1 mg capsule was
463 mistakenly administered in place of the required 10 mg capsule). This patient was
464 analyzed with the 20 mg cohort for all analyses.

465 SD, standard deviation.

466

467 **TABLE 2** Summary of individual pharmacokinetic parameter estimates from the final
 468 model describing cipargamin pharmacokinetics in patients with uncomplicated
 469 *P. falciparum* malaria

Parameter ^a	Dose 30 mg	Dose 20 mg	Dose 15 mg	Dose 10 mg
	(n = 6)	(n = 5)	(n = 7)	(n = 7)
C _{max} (ng/mL)	597 (248–687)	535 (434–678)	442 (312–618)	247 (155–413)
T _{max} (h)	3.51 (2–10)	3.00 (2–4)	3.00 (2–4)	4.02 (2–6)
AUC _{inf} (μg.h/mL)	16.7 (7.75–18.80)	10.1 (8.30–15.60)	11.3 (5.28–14.40)	6.4 (3.87–9.10)
T _{1/2} (h)	16.7 (12.2–29.2)	15.4 (12.0–16.2)	14.9 (11.4–28.8)	17.3 (15.6–25.0)

470 All values are reported as median (range).

471 C_{max}, maximum (peak) plasma drug concentration after drug administration; T_{max}, time
 472 to reach C_{max}; AUC_{inf}, accumulated area under the plasma concentration–time curve
 473 from time zero to infinity; T_{1/2}, terminal elimination half-life.

474 ^a Individual post-hoc empirical Bayes estimates from the final population
 475 pharmacokinetic model.

476

477 **TABLE 3** Population parameter estimates of the final model describing cipargamin
 478 pharmacokinetics and pharmacodynamics in patients with uncomplicated *P. falciparum*
 479 malaria

Parameter	Population estimate ^a (% RSE ^b)	95% CI ^b	% CV for IIV ^a (% RSE ^b)	95% CI ^b
Pharmacokinetic model				
CL/F (L/h)	1.72 (5.69)	1.55–1.94	18.5 (12.4)	13.5–21.8
V/F (L)	40.6 (4.71)	37.3–44.7	–	–
Nr. trans comp	3 <i>fix</i>	–	–	–
MTT (h)	0.867 (12.6)	0.682–1.11	65.2 (13.5)	47.5–79.9
Ka (h ⁻¹)	1.65 (25.2)	1.04–2.81	176 (30.4)	107–312
F (%)	100 <i>fix</i>	–	26.2 (25.3)	13.6–37.6
σ (% CV)	17.5 (10.3)	14.3–21.1	–	–
Pharmacodynamic model				
K _{GROW} (h ⁻¹)	0.0479 <i>fix</i>	–	–	–
E _{MAX} (h ⁻¹)	0.564 (12.9)	0.383–0.710	62.2 (33.6)	45.1–90.2
EC ₅₀ (ng/mL)	0.354 (16.7)	0.222–0.466	–	–
F _{SEN} (%)	99.1 (0.132)	98.8–99.4	81.8 (39.2)	58.9–194
K _{ACT} (h ⁻¹)	0.0987 (14.7)	0.0592–0.123	41.5 (42.0)	30.2–67.7
COV _{Dose_Emax}	0.0463 (14.9)	0.0318–0.0604	–	–
σ (%)	109 (17.0)	94.8–178	–	–

480 CL/F, apparent elimination clearance; V/F, apparent volume of distribution; Nr. trans
481 comp, number of transit compartments in the absorption model; MTT, mean transit time
482 through the transit compartments; Ka, first-order absorption rate constant from the last
483 transit compartment to the central compartment; F, relative oral bioavailability; σ ,
484 unexplained residual error. K_{GROW} , parasite multiplication rate, fixed to 10-fold
485 multiplication per 48-hour cycle; E_{MAX} , maximum effect (maximum parasite reduction
486 rate); EC_{50} , concentration needed for 50% of maximum effect; F_{SEN} , fraction of total
487 asexual parasites which were fully drug sensitive; K_{ACT} , first-order rate constant for
488 refractory parasites to become active; $COV_{\text{Dose_E}_{\text{max}}}$, exponent of the relationship
489 between dose and E_{MAX} (i.e. $\theta_i = \theta_{\text{TVE}_{\text{max}}} \times (\text{Dose}/10)^{COV_{\text{Dose_E}_{\text{max}}}}$).

490

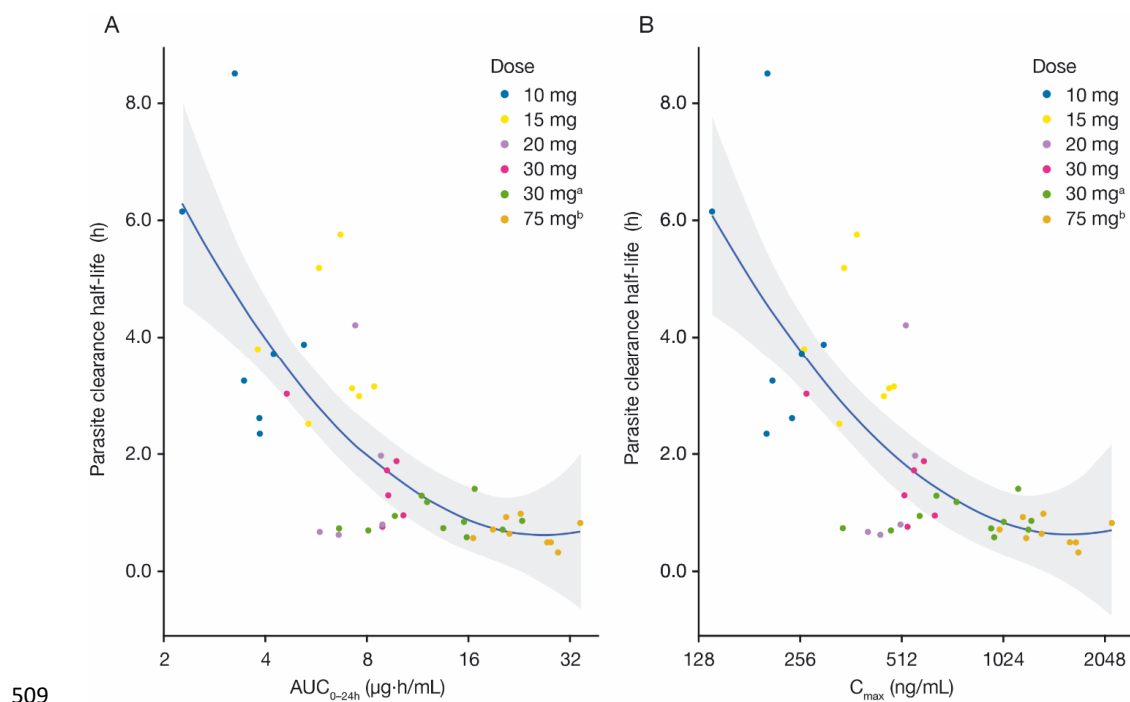
491 ^a Population mean values and inter-individual variability (IIV) were estimated by
492 NONMEM. Coefficient of variation (% CV) for IIV was calculated as $100 \times \sqrt{e^{\text{estimate}} - 1}$.
493 Population mean parameter estimates were calculated for a typical patient with a body
494 weight of 59 kg receiving a study drug dose of 10 mg.

495

496 ^b Relative standard error (RSE) was calculated as $100 \times (\text{standard deviation}/\text{mean}$
497 parameter estimate) from 1,000 and 500 successful iterations for the PK and PK-PD
498 models, respectively, of a nonparametric bootstrap diagnostic. The 95% confidence
499 interval (95% CI) was characterized as the 2.5 to 97.5 percentiles of the bootstrap
500 estimates.

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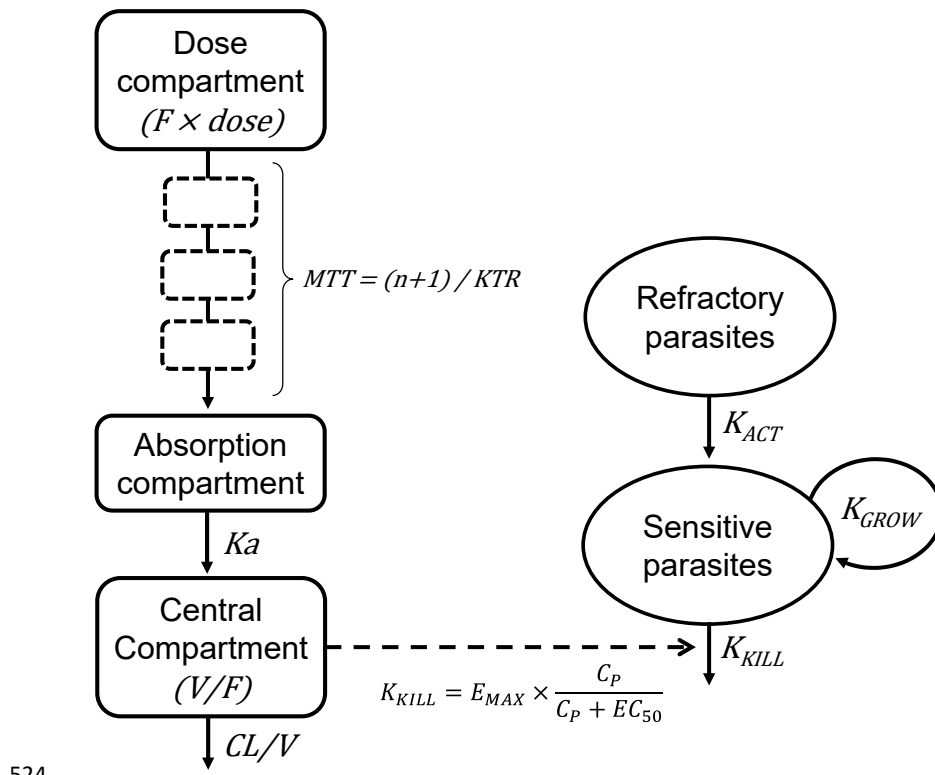
502 **FIG 1** A) Parasite clearance half-life vs AUC_{0-24h} and B) parasite clearance half-life vs
503 C_{max}
504
505 Circles represent individual AUCs, the color represents the corresponding cipargamin
506 dose, and the blue line and shaded area represents LOESS smooth with the uncertainty
507 band. ^a From study X2201; ^bFrom study X2202. AUC_{0-24h} , area under the plasma
508 concentration–time curve during from time zero to 24 hours post-dose.



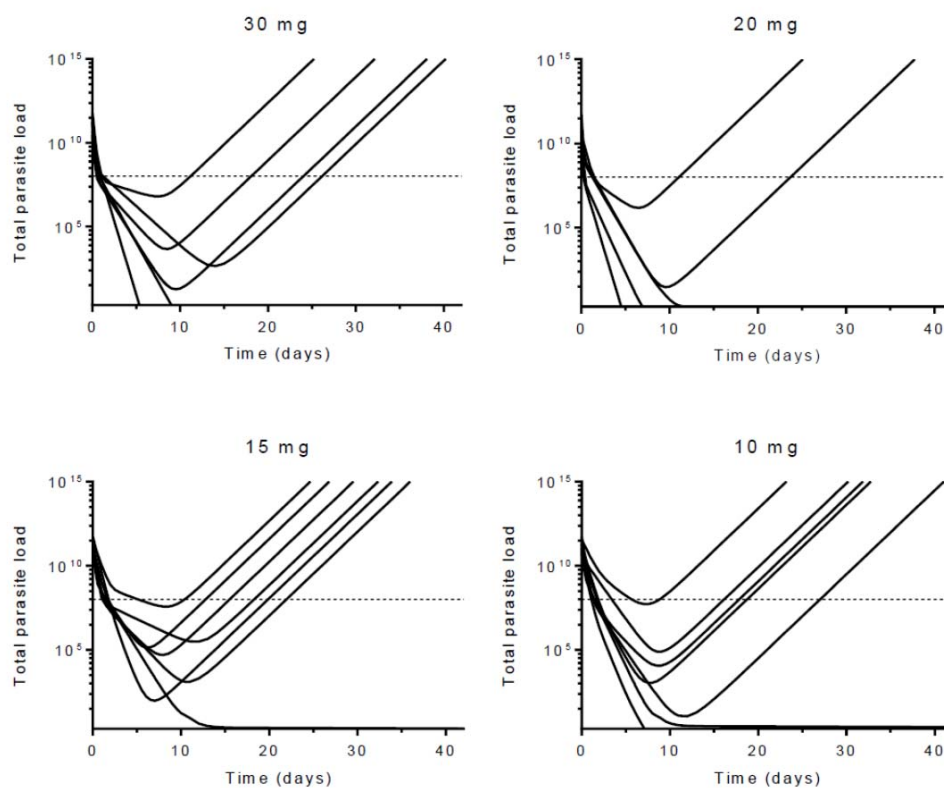
510 **FIG 2** Schematic representation the final model describing cipargamin pharmacokinetics
511 and pharmacodynamics in patients with uncomplicated *P. falciparum* malaria

512 The fraction of asexual parasites that were fully drug sensitive was estimated at
513 enrollment, and the observed total parasitemia is the sum of sensitive and refractory
514 parasites.

515 CL/V , apparent elimination clearance; C_p , cipargamin plasma concentration; EC_{50} ,
516 concentration needed for 50% of maximum effect; E_{MAX} , maximum effect (maximum
517 parasite reduction rate; dose-dependent as specified in Table 3); F , relative oral
518 bioavailability; K_a , first-order absorption rate constant from the last transit compartment
519 to the central compartment; K_{ACT} , first-order rate constant for refractory parasites to
520 become active; K_{GROW} , parasite multiplication rate, fixed to 10-fold multiplication per 48-
521 hour cycle; K_{KILL} , first-order rate constant for cipargamin-dependent parasite kill; KTR ,
522 first-order transit rate constant; MTT , mean transit time through the transit
523 compartments; V/F , apparent volume of distribution.



526 **FIG 3** Individually predicted parasite clearance curves, using the final model describing
527 cipargamin pharmacokinetics and pharmacodynamics in patients with uncomplicated
528 *P. falciparum* malaria
529
530 Each solid line represents predicted total parasite load after dosing over time for an
531 individual patient. The broken horizontal lines indicate the level of microscopy detection.



532

