Modeling of SARS-CoV-2 treatment effects for informed drug repurposing

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Abstract

Several repurposed drugs are currently under investigation in the fight against coronavirus disease 2019 (COVID-19). Candidates are often selected solely by their effective concentrations *in vitro*, an approach that has largely not lived up to expectations in COVID-19. Cell lines used in *in vitro* experiments are not necessarily representative of lung tissue. Yet, even if the proposed mode of action is indeed true, viral dynamics *in vivo*, host response, and concentration-time profiles must also be considered. Here we address the latter issue and describe a model of human SARS-CoV-2 viral kinetics with acquired immune response to investigate the dynamic impact of timing and dosing regimens of hydroxychloroquine, lopinavir/ritonavir, ivermectin, artemisinin, and nitazoxanide.

We observed greatest benefits when treatments were given immediately at the time of diagnosis. Even interventions with minor antiviral effect may reduce host exposure if timed correctly. Ivermectin seems to be at least partially effective: given on positivity, peak viral load dropped by 0.3-0.6 log units and exposure by 8.8-22.3%. The other drugs had little to no appreciable effect. Given how well previous clinical trial results for hydroxychloroquine and lopinavir/ritonavir are explained by the models presented here, similar strategies should be considered in future drug candidate prioritization efforts.

1 Introduction

Since the beginning of the ongoing global outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) a variety of drug therapies have been proposed. Some are based on expert opinion, some on promising *in vitro* results, some on findings in case series from compassionate or off-label treatments. Unfortunately, whenever they are put through the rigorous process of randomized clinical trials, little evidence for palpable real-world benefits remains.

Novel coronavirus disease 2019 (COVID-19) spreads rapidly not only from host to host but within each host as well. The infection progresses at a staggering speed in individual patients which may become infectious after 2-3 days and reach peak viral loads only a few days after the reverse-

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transcriptase polymerase chain reaction (RT-PCR) test becomes positive (To et al., 2020). The need for early initiation of drug therapy has been recognized as key for successful treatment of infectious diseases, and COVID-19 is unlikely to be an exception (Gonçalves et al., 2020).

The repurposing of drugs with established supply chains and low manufacturing costs seems the straightest path towards a timely pharmacological intervention. Because our understanding of the pathophysiology of COVID-19 is still evolving, the selection of viable candidates is mostly dictated by extrapolations from *in vitro* and *in silico* evidence. Identified drug targets include the viral structural spike (S) protein; the host type 2 transmembrane serine protease (TMPRSS2); 3-chymotrypsin-like (3CL) protease mediating proteolysis; RNA-dependent RNA polymerase; and interleukin-6 receptors (Arshad et al.;Sanders et al., 2020).

A basic tenant of clinical pharmacology states that unbound drug must reach its target at sufficient concentrations (e.g. half-maximal effective target concentrations (EC_{50})) and maintain them to exert effects. This is a common criterion for drug candidate selection and has been applied to COVID-19 early on in well-conducted comprehensive surveys (Arshad et al.). Unfortunately, the candidates with highest probability of success have largely failed in practice, and it appears the EC_{50} approach might be too simplistic for this disease, as it is not only important whether EC_{50} is reached, but also for how long concentrations (above EC_{50}) can be maintained, especially at the target site.

One reason may be failure to account for host factors. For instance, a crucial element of treatment response is host immunity. There are *in vivo* studies on the temporal dynamics of immune response and seroconversion (Long et al., 2020;To et al., 2020;Young et al., 2020). Early suppression of viral load even for brief periods may be beneficial by providing more time for the host to mount a defense and assist in clearing an otherwise overwhelming infection.

The viral kinetics of several diseases have been successfully described mathematically in the past, e.g. influenza, hepatitis C, or Ebola (Beauchemin and Handel, 2011;Canini and Perelson, 2014;Oakes et al., 2018). For COVID-19, Kim et al. used a target cell limited model to show the importance of early initiation of treatment and drug mode of action (Kim et al., 2020b). Other authors arrive at similar results with eclipse models (Czuppon et al., 2020;Gonçalves et al., 2020;Hernandez-Vargas and Velasco-Hernandez, 2020). None of these studies however directly used pharmacokinetic profiles in their models.

With this modeling and simulation study we aimed to understand the influence of different modes of action, concentration profiles, dosing schedules, and timing of interventions on key parameters of viral load (peak load, duration of positivity, and total exposure as measured by area under the curve (AUC)) in acute COVID-19. We developed a model of the within-host viral kinetics of SARS-CoV-2 from published patient data and drove antiviral effect with simulated pharmacokinetic (PK) profiles of selected drugs with different dose regimens. These drugs include hydroxychloroquine (HCQ, considered a blocker of viral entry), ritonavir-boosted lopinavir (LPV/r, a 3CL inhibitor), ivermectin (IVM, a broad spectrum anthelminthic with antiviral activity), nitazoxanide (NZT, an antiparasitic agent with antiviral activity), and artemisinin (ART, the primary component of sweet wormwood, believed to inhibit viral entry and intracellular reproduction of SARS-CoV-2) (Li et al., 2005;Caly et al., 2020;Choy et al., 2020;Gordon et al., 2020;Liu et al., 2020;Wang et al., 2020a;Wu et al., 2020). Our selection was influenced by perceived research interest (HCQ, LPV/r, NZT) and lay use of drugs in the general public as self-medication (HCQ, IVM, ART) (Martins-Filho et al., 2020;Molento, 2020;Nordling, 2020;Owens, 2020;WHO, 2020). Although remdesivir has so far shown the greatest

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promise, there is currently not enough published data to allow for pharmacometric simulation in the model proposed here, and hence the drug was not included (Beigel et al., 2020).

2 Methods

2.1 Data sources

Viral kinetic profiles of COVID-19 patients were taken from Young et al. (Young et al., 2020), a study that followed the first patients (n=18) in four hospitals in Singapore (Chinese nationals: n=16, Singapore residents: n=2). We read out values using a digitizing software. Most (n=13) were not on specific therapy and were included in the analysis. Viral load was measured from nasopharyngeal swabs with RT-PCR and presented in cycle threshold (Ct) values (Young et al., 2020). As the correlation between Ct values and viral load varies by laboratory and analytical conditions, we chose to relate model output with observed Ct values with a published regression fit (Chu et al., 2020). Since the time of infection was not recorded, this value had to be estimated. Although the incubation period varies between patients, an average incubation period of 5 days fitted well for all patients (Lauer et al., 2020). We fixed the positivity threshold at 35 cycles, corresponding to $10^{1.58}$ copies/mL (Wang et al., 2020b).

2.2 Viral kinetics models

In the standard target cell limited model, virus particles V infect a pool of susceptible (target) cells T with the cellular infection rate β. Infected cells I begin shedding virions at a production rate p (Canini and Perelson, 2014). The parameters c and δ determine the rate of clearance of virus and cell death of infected cells, respectively. The time-dependent number of susceptible cells (Eq. 1), infected cells (Eq. 2) and viral load (Eq. 3) are described by a system of ordinary differential equations as follows:

$$\frac{dT}{dt} = -(1-\eta)\beta TV \qquad (1)$$

$$\frac{dI}{dt} = (1-\eta)\beta TV - \delta I \qquad (2)$$

$$\frac{dV}{dt} = (1-\varepsilon)pI - cV \qquad (3)$$

The effects of pharmacological treatments by different modes of action are described by the following variables: inhibition of viral entry into susceptible cells, by decreasing the cellular infection rate with effectiveness η, and/or by blocking viral production rate within infected cells with effectiveness ε. We modeled treatment effect based on the IC_{50} or EC_{50} values of the drugs on their respective targets using a sigmoidal E_{max} model (Eq. 4), with *C(t)* being the concentration of the drug at a given time:

$$\varepsilon \text{ or } \eta = \frac{E_{max} \times C(t)}{EC_{50} + C(t)} \qquad (4)$$

We also considered an eclipse model, an extension in which infected cells enter an eclipse phase (E) for an average duration k^{-1} until they begin shedding virions. Initial conditions were set as

$$T(0) = T_0,$$

$$V(0) = V_0,$$

$$I(0) = 0,$$

and additionally, for the eclipse model,

$$E(0) = 0$$

where T_0 is the number of susceptible cells fixed to 1×10^5 (based on prior modeling efforts and accounting for ~1% of alveolar cells expressing ACE2, the main point of entry for SARS-CoV-2) (Baccam et al., 2006;Li et al., 2020b), V_0 the initial viral load on inoculation (fixed at 1×10^0 copies/mL), and E_0 the number of cells in eclipse state. The within-host reproduction number R_0 was set to 3.79 (Li et al., 2020a). This value is also approximately in the same range as other within-host virus kinetic models (Hernandez-Vargas and Velasco-Hernandez, 2020;Kim et al., 2020b). Other parameters need to be estimated by numerical optimization, i.e. viral clearance c, the production rate p, and the death rate of infected cells δ. The cellular infection rate β of the virus is dynamically calculated (Eq. 5).

$$\beta = \frac{c\delta R_0}{(p-\delta R_0)T_0} \qquad (5)$$

Supplementary Table S2 shows all model parameters and sources.

2.3 Immune response

Our understanding of SARS-CoV-2 immunity is still evolving. Immunity could involve cells entering into a refractory state or an antibody mediated increase in viral clearance. Adding an additional state would increase model complexity beyond what seems supported by the source data. We therefore chose to enter acquired immune response as a time-dependent covariate effect on viral clearance c. Temporal dynamics are based on Long et al. (Long et al., 2020) who evaluated seroconversion for IgM and IgG in 285 patients from three hospitals in Chongqing (neighboring Hubei Province). Data were extracted with a digitizing software and fitted to a sigmoidal E_{max} model. As effect size of the immune response in SARS-CoV-2 infection ($E_{max,\ immunity}$) is unknown, we estimated this value together with the models of viral kinetics.

2.4 Pharmacokinetic models

We simulated pharmacokinetics (PK) of HCQ, IVM, LPV/r and ART from published population pharmacokinetics models. Profiles for HCQ were simulated from healthy volunteers reported by Lim et al. (Lim et al., 2009) The IVM model was taken from Duthaler et al. and simulated using fed state dosing (Duthaler et al., 2019). The LPV/r model by Dickinson et al. (Dickinson et al., 2011) was built from data of healthy volunteers receiving 400/100mg, the dose that was under investigation in WHO Solidarity. For ART we directly implemented the model developed by Birgersson et al. in healthy male volunteers with a dosing regimen of 500 mg daily for 5 days (similar to historical dosing recommendations in malaria) (Birgersson et al., 2016). No published pharmacometric model is available for NTZ. The drug is rapidly and completely hydrolysed to an active metabolite, tizoxanide (TZ). We therefore extracted the mean TZ pharmacokinetic profile from a study in healthy Mexican volunteers with a digitizing software, fitted a one-compartment oral absorption model with lag time, and used this for simulation (Balderas-Acata et al., 2011).

As the protein-bound fraction of a drug is considered not to interact with its target, we considered only the unbound fraction of the drugs where available (**Supplementary Table S2**). i.e. 50% for

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153 HCQ (Furst, 1996), 7% for IVM (Klotz et al., 1990), 1% for NTZ (FDA, 2005), and 1% for LPV
154 (Boffito et al., 2004). No human *in vivo* data exist for lung concentrations in any of the drugs in this
155 study. We used literature-based approximations to adjust for differences between plasma and lung
156 concentration profiles. The issue of lung tissue concentrations is particularly contentious for HCQ,
157 with some reports of lung:plasma ratio ranging from 27 to 177 in macaques (Maisonnasse et al.,
158 2020). Recent evidence suggests that in COVID-19 HCQ plasma concentrations are more
159 representative (Fan et al., 2020). For IVM lung accumulation, we used cattle data published by
160 Lifschitz et al., an approach also used in another publication discussing the potential role of IVM in
161 COVID-19 (Lifschitz et al., 2000;Schmith et al., 2020). LPV concentrations in lung tissue were
162 assumed to be 1.78 times higher than in plasma, and protein binding was set to 99% (Atzori et al.,
163 2003;FDA, 2013). For NTZ we used estimates from a recently pre-published physiology-based
164 pharmacokinetic (PBPK) model for lung partitioning (Rajoli et al., 2020).

165 **2.5 Pharmacodynamic effects**

166 The effectiveness of HCQ was shown *in vitro* in Vero E6 cells by Liu et al. (Liu et al., 2020). The
167 EC_{50} values at 48h ranged between 4.06 and 12.96 µM, depending on the amount inoculated. We
168 enter the mean of these values (8.51 µM) as an effect on the reduction of the cellular infection rate β.
169 We simulated dosages of 200 mg q8h for 10 days as proposed by Gautret et al. and the scheme
170 previously employed in the WHO Solidarity trial, 800 mg q12h on the first day (loading dose) and
171 400 mg q12h on day 2-10 (Gautret et al., 2020;WHO, 2020).

172 For IVM, we assumed two pharmacodynamic effects: the inhibition of RNA helicase and inhibition
173 of nicotinic acetylcholine receptors (nAChR). The inhibitory effect of IVM on helicase has been
174 previously reported for flaviviridae, i.e. yellow fever virus (YFV, IC_{50} 0.12 µM), Dengue virus
175 (DENV, IC_{50} 0.5 µM), and West Nile Virus (WNV, IC_{50} 0.35 µM) (Mastrangelo et al., 2012). There
176 are no *in vitro* data for SARS-CoV-2 yet, although Caly et al. (Caly et al., 2020) have reported a
177 strong maximal inhibition of virus replication in the Vero E6 cell line with an IC_{50} of about 2 µM.
178 Higher concentrations (10-25 µM) need to be achieved for similar inhibition of DENV replication
179 (Wagstaff et al., 2012). The difficulties in achieving micromolar concentrations have led some
180 authors to speculate IVM is not druggable in the context of COVID-19 (Bray et al., 2020). Strikingly,
181 despite the higher IC_{50} in DENV infected Vero E6 cells, a small trial of IVM 3x400 µg/kg in DENV
182 patients demonstrated antiviral effects *in vivo* (Yamasmith et al., 2018). Due to the higher
183 susceptibility of SARS-CoV-2 to IVM than DENV in Vero E6 cells, we used a conservatively
184 reduced IC_{50} of 0.1 µM in the simulations as an inhibitory influence on viral production p.

185 In addition, IVM interacts with nAChR (IC_{50} 156 nM) (Degani-Katzav et al., 2017). It has been
186 hypothesized that inhibition of nAChR downregulates angiotensin-converting enzyme 2 (ACE2)
187 expression and thus reduces the points of entry for SARS-CoV-2 (Oakes et al., 2018). We enter this
188 as a net inhibitory effect on the cellular infection rate β. In contrast to direct inhibition of viral entry,
189 this is an antiviral activity mediated by the host and therefore not easily captured in *in vitro* assays.
190 For IVM, we evaluated 300 µg/kg and 600 µg/kg q24h for three days. These dosages are not
191 approved, but safety and tolerability of single fixed doses of 120 mg were shown previously in
192 healthy volunteers (Guzzo et al., 2002).

193 LPV and RTV are both protease inhibitors. Their use in COVID-19 was investigated as a now
194 discontinued arm of the WHO solidarity trial (LPV 400 mg and RTV 100 mg q12h for 14 d) (WHO,
195 2020). LPV reduced the viral RNA copies of SARS-CoV-2 *in vitro* with an EC_{50} of 26.1 µM,
196 whereas RTV has an EC_{50}>100 µM (Choy et al., 2020). As RTV in this co-formulation (LPV/r) is

197 only intended to boost the bioavailability of LPV, we only consider the antiviral effect of LPV on the
198 viral production rate *p* (Chandwani and Shuter, 2008).

199 ART as the main component of *A. annua* (sweet wormwood) extract has not been studied in SARS-
200 CoV-2. Nair et al. reported an antiviral effect in Vero E6 cells of artesiminin on SARS-CoV-2 with
201 an EC_{50} of 19.8 µg/ml (=70 µM) (Nair et al., 2021). Studies suggest that artemisinin interferes with
202 viral entry by interaction with the spike protein (Sehailia and Chemat, 2020), but also effects post-
203 entry steps of infection (Cao et al., 2020b;Nair et al., 2021) We entered this as an effect on viral
204 production rate *p* and the cellular infection rate β.

205 NTZ has shown in vitro activity against SARS-CoV-2 in Vero E6 cells at an EC_{50} of 2.12 µM (Wang
206 et al., 2020a). The mechanism of action is unclear but it has been hypothesized that NTZ inhibits
207 viral entry as well as replication. We used both effects in the simulations (Arshad et al.).

208 **2.6 Software**

209 We modelled and simulated pharmacokinetic profiles with Pkanalix and mlxR (version 4.1.3), an R
210 package for interfacing with Monolix (version 2019R2, http://www.lixoft.com, Antony, France).
211 Data for viral loads and NTZ were read out with WebPlotDigitizer (version 4.2,
212 https://automeris.io/WebPlotDigitizer). Immunity E_{max} and EC_{50} were estimated using the R package
213 rstanemax (version 0.1.2). Data checkout, analysis and visualization were performed in GNU R
214 (version 3.6.3, R Foundation for Statistical Computing, http://www.R-project.org, Vienna, Austria).
215 Ordinary differential equation (ODE) systems and parameter estimations were implemented with the
216 R packages deSolve (version 1.28) and dfoptim (version 2018.2-1).

217 **3 Results**

218 **3.1 Viral kinetics models**

219 We used the viral load profiles of untreated patients published by Young et al. (n=13, supplemental
220 material) (Young et al., 2020). We evaluated target cell limited and eclipse models, both with a time-
221 varying effect on viral clearance *c* following a sigmoidal E_{max} model fitted to reported seroconversion
222 data (Long et al., 2020). The averaged parameters estimates from individual profiles with the Nelder-
223 Mead method were (see also **Supplementary Table S1** and **Supplementary Figure S1**):

224 - viral clearance *c:* 5.07,
225 - production rate *p:* 10.2,
226 - death rate of infected cells δ: 0.54, and
227 - maximal immune effect on clearance $E_{max,immunity}$: 57.0

228 Non-linear mixed effects implementations of these models proved less robust to changes in initial
229 estimates and suffered from numerical identifiability problems.

230 Profiles were best described by a standard target cell limited model. The addition of an eclipse phase
231 did not improve fits and also introduced identifiability issues, as was already noted in another study
232 (Hernandez-Vargas and Velasco-Hernandez, 2020). Left untreated, viral load exceeds the RT-PCR
233 positivity threshold of 35 cycles at 5.4 dpi, peaks at 10.4 dpi with a Ct value of 28.4 cycles, and drops
234 below the positivity limit at 18.9 dpi, similar to reports from clinical studies (Kim et al., 2020a;Lauer
235 et al., 2020;To et al., 2020). Total viral exposure (measured as AUC) was
236 12’003 days*log(copies/mL).

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3.2 Dosage and effectiveness of treatment

Temporal impact of treatment is shown as individual curves in **Figure 1**. Effect on viral exposure as difference in area under the curve (AUC), relative change in duration, and change in peak cycle (Ct) are presented in **Figure 2**. Full results including changes in peak viral load and duration of disease are available in **Supplementary Table S3** and **Supplementary Figure S2**. The PK curves of the treatments and the corresponding effect on SARS-CoV-2 viral kinetics are shown in **Supplementary Figure S2 – S5**.

HCQ reduced peak viral load by 0.2-0.3 log units and exposure by 4.6-8.2% when given on positivity. Treatment started around peak viral load (10.2 dpi) had no appreciable effect on total viral load or duration of disease. Between both dose regimens, the WHO Solidarity trial arm resulted in the more pronounced reduction in total viral load. Effects of IVM were more pronounced: given on positivity, peak viral load dropped by 0.3-0.6 log units and exposure by 8.8-22.3 %. Exposure reductions are associated with slightly prolonged durations of shedding from 13.5 days (untreated) to 14.2-15.6 days for IVM and 14.1-14.5 days for HCQ, and a shift of T_{max} from day 10.2 (untreated) to day 10.9-12.3 and day 10.5-10.9, respectively. Interestingly – and in contrast to HCQ – some effects remain when treatment is initiated around peak viral load (3.4-13.2 % difference in exposure). LPV/r, ART and NTZ had no influence on viral dynamics, independent of time of initiation.

4 Discussion

Our modeling and simulation study described patient viral load well and captured the essential milestones of SARS-CoV-2 viral kinetics, e.g. duration of viral shedding, and peak viral loads. It also shows that the window of opportunity to treat COVID-19 is narrow. As the infection spreads rapidly throughout the host, the pool of susceptible cells is quickly depleted. Drugs inhibiting viral entry (like HCQ) therefore only appear to have a role, if any, in the first days after inoculation (post-exposure prophylaxis) or as primary prophylactic agents handed out to at-risk individuals.

These findings may help to explain the disappointing results of clinical trials with HCQ: by the time patients are hospitalized or even transferred to critical care, few susceptible cells are left, so little impact can be made at this point (Annie et al., 2020;Cavalcanti et al., 2020 ;Molina et al., 2020;Tang et al., 2020a). The WHO Solidarity trial's dosing scheme was clearly more effective than the one proposed by Gautret et al. (Gautret et al., 2020). However, even with the higher dosing scheme used in the WHO Solidarity trial, no appreciable effect of HCQ was observed and the treatment arm was prematurely terminated on June 18, 2020 (Pan et al., 2020). Of note, recent trials have also failed to find benefits for HCQ in pre- and post-exposure prophylactic indications (Boulware et al., 2020;Rajasingham et al., 2020). Since viral load is not the only determinant of disease state, one cannot directly deduce clinical effect of any of the regimens from these simulations. Given the negative results of previous trials with HCQ, we suggest that HCQ results should be used as a lower threshold to rank other drugs against.

We found greatest effects for IVM. Again, the earlier and longer the exposure, the better, but compounds like IVM still convey some benefit if initiated at a later stage. When held to the HCQ benchmark, IVM 600 µg/kg daily for 3 days, particularly when given around time of positivity, may have meaningful impact whereas IVM 300 µg/kg daily for 3 days had efficacy comparable to HCQ regimens. This finding is in contrast to other analyses suggesting IVM is poorly druggable in COVID-19, e.g. (Schmith et al., 2020). It is important to stress that these IVM doses, while apparently safe in healthy volunteers, are far higher than any dose approved for other indications (1x200 µg/kg to 1x400 µg/kg). At 3x600 µg/kg in a 70 kg patient, doses are similar to the maximum

281 doses (120 mg single administration) described by Guzzo et al. (Guzzo et al., 2002). Boosting
282 exposure to IVM by co-administering inhibitors of its metabolism or elimination (such as the
283 CYP3A4 and P-glycoprotein (P-gp) inhibitor ritonavir) is a theoretical option (Chaccour et al., 2017).
284 However, there are concerns that inhibition of P-gp as an integral part of the functional blood brain
285 barrier could lead to more central nervous adverse events (Chandler, 2018). Until this interaction has
286 been studied systematically, it seems unwise to explore this strategy. For IVM, no results of clinical
287 trials regarding its effectiveness in Covid-19 have been published yet.

288 ART, NTZ and LPV/r had no noteworthy effect and do not appear suitable candidates for follow-up
289 at this point. We attribute this in part to their strong protein binding (88-99%), leaving little free drug
290 to engage with targets. Additionally, the EC_{50} for ART is rather high at 70 µM and not likely to be
291 even partially achieved. For LPV/r our findings are confirmed by clinical trial results (Cao et al.,
292 2020a, 24), notably the RECOVERY trial (University of Oxford, 2020) and the WHO Solidarity trial,
293 who discontinued the LPV/r treatment arm on July 4, 2020 (Pan et al., 2020). As of now, no trials on
294 NTZ and ART have reported results.

295 Our study has several limitations. Our model parameter estimates are based on assumptions of
296 incubation time and number of target cells in the lungs, both of which introduce bias. Covid-19 was
297 initially described from a cluster of pneumonia cases, and while symptoms of the upper and lower
298 airways are most recognizable, vascular, thromboembolic, gastrointestinal, and neurological
299 symptoms have been widely described (Klok et al., 2020;Mao et al., 2020;Struyf et al., 2020;Zhang
300 et al., 2020). Expression levels of ACE2 are also much higher in other tissues, e.g. the small intestine,
301 the kidneys, and the heart (Li et al., 2020b). Hence it seems unlikely that systemic viral loads are
302 solely a product of alveolar epithelial cells. Extent of viral burden is dependent on disease severity
303 and also site of sampling (e.g. oropharyngeal, nasopharyngeal, plasma (Fajnzylber et al., 2020)).
304 Ethnicity is thought to affect clinical outcomes (Sze et al., 2020), yet there is inconclusive evidence
305 as to the impact of ethnicity on viral load (Magleby et al., 2020). In conclusion, we suggest that the
306 size of the pool of target cells be re-estimated in different populations.

307 Point estimates of viral kinetics parameters yielded realistic estimates of viral load profiles with
308 reasonable uncertainty around point estimates (%CV: 30-43). We did not normalize the
309 asynchronous dynamics of the source data (e.g. viral peak at different dpi), which might have
310 improved fits. However, currently no accepted procedure exists (Hernandez-Vargas, 2019). Other
311 authors have used more sophisticated methods such as non-linear mixed effects (nlme) modeling on
312 the same source data, implementing other structural models such as eclipse models (Czuppon et al.,
313 2020;Gonçalves et al., 2020). Our nlme implementations of the models suffered from the same
314 numerical identifiability issues seen by other authors (Hernandez-Vargas and Velasco-Hernandez,
315 2020). Given that the model presented here is structurally different from other target cell limited or
316 eclipse models, some point estimates can differ from other implementations (such as the reproduction
317 number R_0, or number of susceptible cells T_0, eg. (Gonçalves et al., 2020)).

318 Virus extinction is not captured by any models like the one proposed here. We therefore decided not
319 to model prophylactic dosing (prior to or on exposure), and resorted to return to negativity on RT-
320 PCR as a surrogate measure for disease duration. This is supported by data suggesting that late stage
321 shedding is of non-infectious virus particles only (Walsh et al., 2020).

322 We made several assumptions on modes of drug action and their efficacy. We used the published
323 mode of action of HCQ on SARS-CoV-2, which were performed in the African green monkey
324 kidney-derived cell line Vero (Wang et al., 2020a), even though there is evidence that this cell line

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325 might not be suitable to represent lung tissue (Hoffmann et al., 2020). The model places HCQ effects
326 only on viral entry, although it might also have other modes of actions which might affect the
327 production of virions within infected cells (Quiros Roldan et al., 2020;Tripathy et al., 2020).
328 Additionally, HCQ has immunomodulatory effects and might hinder the activation of B and T cells
329 and thus inhibit the host-innate immune response (Goldman et al., 2000;Quiros Roldan et al., 2020).
330 No data for SARS-CoV-2 were available for modeling. If relevant at all, our model would be
331 overestimating the effectiveness of HCQ.

332 The *in vitro* evidence of efficacy of IVM against SARS-CoV-2 is not detailed enough to model
333 effects with greater precision. Based on data from other flaviviridae, particularly Dengue virus, the
334 proposed inhibition of replication seems reasonable (Mastrangelo et al., 2012). Inclusion of effects on
335 viral entry follows pathophysiological reasoning and has yet to be confirmed in studies. IVM engages
336 with nAChR, which leads to a reduction of ACE2 and in turn decreases the points of entry for SARS-
337 CoV-2, influencing the cellular infection rate. Even though the IC_{50} for IVM on nAChR has been
338 experimentally determined, we do not know how exactly this relates to the reduction of ACE2
339 expression. Therefore, we decided to model it solely based on plasma levels and the available IC_{50}.

340 In HCQ and IVM, even though total viral load is reduced, the duration of virus shedding might be
341 increased, a consequence of a 'flattening of the curve' similar to what is observed on a population
342 scale. However, this gives the immune response more time to develop an immune response. For this
343 reason, overall total viral load decreases in the simulated models. Changes in peak viral load were
344 moderate at best (< 1 log unit). While convenient endpoints to measure in a clinical setting, AUCs of
345 viral load appear more appropriate for drug discovery.

346 ART and NZT have only recently received attention in COVID-19 treatment. Despite having little
347 effect in our study they would make excellent candidates from economic and logistic points of view.
348 We selected ART as it is the primary active ingredient in sweet wormwood. Herbal concoctions of
349 wormwood are being promoted as a cheap, easily accessible form of self-medication in COVID-19
350 (Deutsche Welle, 2020). *A. annua* and derivatives (artesunate, dihydroartesunate) are widely used as
351 antimalarials. Effective concentrations have yet to be determined for ART and its derivatives,
352 although the large degrees of protein binding imply that effective target concentrations need to be in
353 the low micromolar range. Studies suggest that artemisinin has also anti-inflammatory and
354 immunomodulatory effects, which might be beneficial when treating COVID-19 (Tang et al., 2020b).
355 However, as these effects are not related to the viral kinetic, we were not able to include these in our
356 simulations. Even then its use would have one crucial limitation: the WHO is discouraging use of
357 oral artemisinin monotherapy (AMT) in malaria as it is considered to be a major factor for the
358 development of parasite resistance (WHO, 2014). A renaissance of oral AMT in malaria endemic
359 regions during the ongoing COVID-19 pandemic could cause more harm than good.

360 For NTZ, pharmacokinetic simulations were based on a mean curve of a single dose of NTZ 500 mg.
361 The EC_{50} value was determined for NTZ, not the immediately formed active metabolite tiaxozanide,
362 which would be the active compound expected to reach tissue (Wang et al., 2020a). When more
363 detailed results for tiaxozanide are available, simulated efficacy could change.

364 In conclusion, while *in vitro* studies are very well suited to identify possible modes of actions of
365 potential treatments for COVID-19, they are unable to predict the clinical efficacy of a drug. Our
366 simulation of treatments fitted well with available results from clinical trials, even though several
367 estimations had to be made and limitations accepted. Although early initiation was a strong
368 determinant for treatment effect, none of the interventions studied showed major impact on viral

369 dynamics. Efforts should focus on identification of more efficacious drug candidates and vaccine
370 development. Until then, general social and hygiene measures remain the best interventions to
371 combat COVID-19.

372 **5 Conflict of Interest**

373 The authors declare that the research was conducted in the absence of any commercial or financial
374 relationships that could be construed as a potential conflict of interest.

375 **6 Author Contributions**

376 FH conceived the project; CK, VS, FH performed the analyses; FH, CK, VS wrote the first draft of
377 the manuscript. All authors revised and approved the final manuscript.

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379 None to declare.

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381 None.

382 **9 Supplementary Material**

383 The Supplementary Material for this article can be found online at:

384 [needs to be completed]

385 **10 Data Availability Statement**

386 The original contributions presented in the study are included in the article/supplementary materials,
387 further inquiries can be directed to the corresponding author/s. The source code is available on
388 GitHub: https://github.com/cptbern/sars2-viral-kinetics.

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713

714 **Figure captions**

715 **Figure 1** - Viral load profiles of SARS-CoV-2 following different treatment regimens and initiation
716 of treatment (green: untreated, blue: on positivity (5.4 days post infection), red: on peak (10.2 days
717 post infection)). Lines may overlap so that only one color is visible; simulations were always run for
718 all time points. Ct: serial cycle threshold values; ART: artemisinin; HCQ: hydroxychloroquine IVM:
719 ivermectin; LPV/r: lopinavir/ritonavir; NTZ: nitazoxanide. Dosing of different modeled treatment
720 regimens: HCQ 200: 200 mg every 8h for 10 days; HCQ 800: 800 mg every 12h for 1 day, then 400
721 mg every 12h for 9 days; IVM 300: 300 µg/kg every 24h for 3 days; IVM 600: IVM 600 µg/kg every
722 day for 3 days; NTZ 1200: NTZ 1200 mg every 6h for 5 days; NTZ 2900: NTZ 2900 mg every 12h
723 for 5 days; ART 500: ART 500 mg once a day for 5 days; LPV/r 400/100: LPV/r 400/100 mg every
724 12h for 14 days.

725 **Figure 2** – Treatment effects on viral exposure as difference in area under the curve (AUC), relative
726 change in duration, and change in peak cycles (Ct) following different initiation time of treatment (on
727 positivity: 5.4 days post infection, on peak: 10.2 days post infection). HCQ: hydroxychloroquine;
728 IVM: ivermectin; NTZ: nitazoxanide; ART: artemisinin; LPV/r: lopinavir/ritonavir. Dosing of
729 different modeled treatment regimens: HCQ 200: 200 mg every 8h for 10 days; HCQ 800: 800 mg
730 every 12h for 1 day, then 400 mg every 12h for 9 days; IVM 300: 300 µg/kg every 24h for 3 days;
731 IVM 600: IVM 600 µg/kg every day for 3 days; NTZ 1200: NTZ 1200 mg every 6h for 5 days; NTZ
732 2900: NTZ 2900 mg every 12h for 5 days; ART 500: ART 500 mg once a day for 5 days; LPV/r
733 400/100: LPV/r 400/100 mg every 12h for 14 days.

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