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1 Alternative Screening Approaches for Discovery of MERS Coronavirus Inhibitors 2

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Abstract: Two coronaviruses causing severe respiratory disease and high mortality rates
emerging within the past dozen years reinforces the need for clinically efficacious antivirals
targeting coronaviruses. Alternative screening approaches for antivirals against the recently
emergent MERS-CoV may provide lead compounds to address this need. Two AAC manuscripts
screened libraries of approved compounds which may potentially be re-purposed as MERS-CoV
antivirals. A third AAC paper showed that a previously described SARS-CoV helicase inhibitor
also has activity against MERS-CoV.

16 (*The views expressed in this Commentary do not necessarily reflect the views of the journal or of* 17 *ASM.*)

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Three papers available in *Antimicrobial Agents and Chemotherapy* address antiviral drug discovery for the recently emergent MERS Coronavirus (1, 2, 3).

23 Over the past few decades, antiviral drug discovery and development has generally followed a 24 path from viral target definition through assay development and subsequent compound screening 25 to find a lead compound. Once a lead is found there are routes for lead optimization to increase 26 efficacy which may involve crystallography or molecular modeling studies and also optimization 27 for an improved pharmacokinetic profile. This route usually includes animal safety studies. 28 Concurrent studies to address cell culture antiviral activity usually include the selection of 29 resistant virus. For viral targets, the question generally is not whether one can select for resistance but rather what does it take to select for resistance. This may include both the number 30 31 of mutations necessary to select for resistant virus and also the replicative fitness of the resistant 32 virus.

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34 Following an approach consistent with the typical pathway described above. Adedeji and 35 colleagues had previously described a SARS-CoV nsp13 helicase inhibitor, SSYA10-001 using a commercially available library and a SARS-CoV biochemical helicase assay (4). The compound 36 37 had low micromolar activity both in the biochemical assay and also in a SARS-CoV replicon 38 assay. In the current study, this compound was tested as a potential inhibitor of MERS-CoV and 39 also the related murine hepatitis coronavirus (MHV) and found be active against both viruses 40 although efficacy was slightly diminished as compared with what had been reported for SARS-41 CoV (3). They also use a molecular modeling approach to address compound interaction with 42 the SARS-CoV helicase and define potential residues which may be involved in compound 43 binding. Amino acid substitutions at these residues were introduced into the SARS-CoV 44 enzyme and these mutated enzymes showed reduced inhibition by SSYA10-001. Virological (or 45 replicon) resistance selection was not addressed in the manuscript and it would be interesting to

see if the virus conforms to ones predictions. This is always an interesting question especially

47 given the efficient replication capacity and the lack of polymerase proofreading capability of 48 these viruses which helps ensure a diverse pool of genomes available for antiviral resistance 49 selection. The author suggest that this compound may serve as a lead for development of a 40 broad-spectrum anti-coronavirus inhibitor. A potential added benefit may be that the definition 51 of a viral helicase inhibitor may stimulate added attention to this function as a validated antiviral 52 target.

Two other papers take a alternative viral target neutral approach by screening small libraries of FDA approved compounds in MERS-CoV antiviral assays (1, 2). Since licensed inhibitors may have previously defined pharmacokinetic and safety profiles, the suggestion is that this repurposing approach may shorten the time to provide clinically useful inhibitors of MERS-CoV. This may be a reasonable suggestion, although there are several points mentioned in both manuscript discussions that should be noted.

1) There have been previous attempts to define licensed compounds as re-purposed antivirals.
 One example relevant to these current papers regards chloroquine which scored as a positive hit
 in their MERS-CoV assays (1, 2). The authors note that this compound was tested previously
 against SARS-CoV infectivity in mouse models and was not efficacious in this system (5).

2) It is important when analyzing screening data to note any related compounds tested in the screen which did not score as hits in an attempt to define some level of structure activity relationship. One example is the description of lopinivir as a low micromolar inhibitor of MERS-CoV. Lopinavir is an HIV protease inhibitor but the proteases of HIV and coronaviruses fall into different mechanistic classes of proteases. Snijder and colleagues provide a list of their compound library as supplemental information and discuss whether inhibition is peculiar to lopinavir or to HIV PIs in general (1).

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73 3) If a licensed compound has been optimized to be an inhibitor of some cellular function, does 74 that mean that inhibition in the virus assay is mediated via inhibition of that defined cellular target. This becomes especially relevant if there is a substantial differential between the cellular 75 target and virological EC50s. Similarly, if the inhibitor found in the screen is a known inhibitor 76 77 of a cellular function, then it may be difficult to select for resistant virus. Given the large 78 replicative pool and the lack of coronavirus polymerase proofreading capability, it is still 79 essential to attempt to select for resistant virus and the authors recognize this concern and note that resistance selection studies are being addressed. While it may be possible to optimize leads 80 81 based on cell culture antiviral activity, if the re-purposed compounds are meant to serve as 82 potential leads for coronavirus inhibitors, then target definition is also an important concern to 83 provide a basis for lead optimization.

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85 Following the SARS Coronavirus outbreak in 2002-3, resolution of the outbreak was largely 86 through the implementation of public health measures. Treatment with antiviral agents did not 87 play a major role as there were no specific coronavirus antivirals available for patient treatment. 88 Snijder and colleagues (1) note that it may take up to 10 years to move from antiviral discovery 89 to clinical development of efficacious antivirals. In the 11-12 years since the SARS outbreak, a 90 clinically useful antiviral has not been defined for SARS-CoV. Now 2 years into the emergence 91 of MERS-CoV, hopefully that timeline can be shortened. By defining potential coronavirus 92 inhibitors these papers may provide re-purposed antivirals or lead structures that can be

developed as coronavirus inhibitors. Whether re-purposed compounds provide clinical benefit
 for an infected patient necessitates input by infectious disease clinicians to determine utility of
 these coronavirus inhibitors.

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