Stenoparib, an inhibitor of cellular poly (ADP-ribose) polymerases (PARPs), blocks *in*

***vitro* replication of SARS-CoV-2 variants**

Katherine E. Zarn[a]*, Sierra A. Jaramillo[a]*, Anthony R. Zapata[a], Nathan E. Stone[a], Ashley

Jones[a], Haley Nunnally[a], Erik W. Settles[ab], Ken Ng[a], Paul Keim[ab], Steen Knudsen[c], Patricia

Nuijten[d], Aloys Tijsma[d], Christopher T. French[ab]#.

[a]Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, AZ 86011-4073

[b]Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ 86011-5640

[c]Allarity Therapeutics, DK-2970 Hørsholm, Denmark

[d]Viroclinics-DDL, Rotterdam, The Netherlands

Running Head: Stenoparib inhibits SARS-CoV-2 variants *in vitro.*

*These authors contributed equally to the study.

#Address correspondence to Christopher T. French, ctfrench@nau.edu

Keywords

COVID-19, antiviral, SARS-CoV-2, coronavirus, stenoparib, remdesivir

Abstract

We recently published a preliminary assessment of the activity of a poly (ADP-ribose)

polymerase (PARP) inhibitor, stenoparib, also known as 2X-121, which inhibits viral replication

by affecting pathways of the host. Stenoparib is an inhibitor of mammalian poly (ADP-ribose)

polymerases (PARPs). Here we show that stenoparib effectively inhibits additional SARS-CoV-2

variants, including an additional wild-type strain (Germany/BavPat1/2020), and the variants

alpha (B.1.1.7), *beta* (B.1.351) and *gamma* (P.1) *in vitro*, with 50% effective concentration

(EC_{50}) estimates of 4.1 µM, 8.5 µM, 24.2 µM and 13.6 µM, respectively. A second study

focusing on a combination of 10 µM stenoparib and 0.5 µM remdesivir resulted in over 90%

inhibition of the *alpha* (B.1.1.7) variant, which is substantially greater than what was achieved

with stenoparib or remdesivir alone at these concentrations.

Importance

The coronavirus disease (COVID-19) pandemic, caused by SARS-CoV-2, has caused over 247 million infections and over 5 million deaths (1). Although protective vaccines are available, the pandemic continues and both old and new SARS-CoV-2 variants may exhibit degrees of resistance to vaccination. To date, only two antiviral drugs, remdesivir and molnupiravir, or treatment with monoclonal antibodies, have been approved by the United States Food and Drug Administration as COVID-19 therapies in certain situations. Additional effective therapeutics are urgently needed. Here we describe the activity of a small molecule, stenoparib, that effectively inhibits replication of SARS-CoV-2 wild-type and variant strains *in vitro*. Stenoparib is an inhibitor of mammalian poly (ADP-ribose) polymerases (PARPs). A host-targeting therapeutic like stenoparib could be a significant benefit for COVID-19 patients as a standalone therapy, or especially as part of a combinatorial COVID-19 treatment strategy with an antiviral drug such as remdesivir or molnupiravir.

Observation

Since the beginning of the COVID-19 pandemic, SARS-CoV-2 has mutated, which has resulted in different variants of the virus. Only two antiviral drugs - remdesivir and molnupiravir, or treatment with monoclonal antibodies, have been approved by the United States Food and Drug Administration as COVID-19 therapies (2, 3). Remdesivir and molnupiravir are nucleoside analogs that affect the activity of the RNA-dependent RNA polymerase (RdRp). After incorporation into viral RNA, remdesivir stalls the RdRp during elongation (4), while molnupiravir results in the incorporation of mutations that can be functionally deleterious (5). In contrast to inhibitors that target viral replication, we recently published a study on the activity of a poly (ADP-ribose) polymerase (PARP) inhibitor, stenoparib, also known as 2X-121, which inhibits viral replication by affecting pathways of the host (6). ADP-ribosylation (ADPR) pathways may have either anti- or pro-viral properties, and their importance in host-virus interactions is becoming increasingly recognized (7). Unlike remdesivir, which inhibits viral replication downstream of entry into the cell, stenoparib inhibits virus entry and post-entry processes (6). Stenoparib inhibited the SARS-CoV-2 USA-WA1/2020 virus and the HCoV-NL63 human seasonal respiratory coronavirus *in vitro*, exhibiting dose-dependent suppression of virus multiplication and cell-cell spread in cell culture (6). Stenoparib exhibits a unique dual activity against the PARP1, 2 and PARP5a, 5b (tankyrase 1, 2) enzymes, which are important intermediates in the Wnt/β-catenin immune checkpoint (8, 9).

SARS-CoV-2 variants may carry mutations throughout the genome, particularly in the sequence coding for the spike (S) protein. As a host-targeting therapeutic, we hypothesized that the antiviral activity of stenoparib should be able to inhibit all variant strains. We explored the activity of stenoparib against four additional SARS-CoV-2 variants of concern; SARS-CoV-2 Germany/BavPat1/2020 wild-type strain (wt) and variant strains (B.1.1.7 [*alpha*], B.1.351 [*beta*], and P1 [*gamma*] – hereafter referred to using the Greek nomenclature). SARS-CoV-2 virus variants were mixed with serial dilutions of compound and transferred to Vero E6 *Cercopithecus*

aethiops kidney cells, which were fixed and stained 20 hours (h) later with a SARS-CoV/SARS-

CoV-2 Nucleocapsid monoclonal antibody (Sino Biological) followed by a horseradish

peroxidase (HRP)-labeled Goat anti-Mouse IgG (Thermo Scientific) and TrueBlue substrate.

The 2 controls included on all assay plates were 1) infected and untreated cells and 2)

uninfected and untreated cells. The experiment was conducted in quadruplicate and the results

were calculated as the average fraction of wells that showed positive staining for the virus using

ViroSpot assay (10). Inhibition of virus replication by stenoparib was dose-dependent, with EC_{50}

ranging between 4.1 µM to 24.2 µM across the 4 variants tested (Fig. 1A). Interestingly, the

EC_{50} for the *beta* variant (24.2 µM) was 1.8- to 5.8-fold higher than for the wt, *alpha*, and

gamma variants (4.1, 8.5, and 13.6 µM, respectively). A similar phenomenon was noted for

remdesivir (Fig. 1B), where the EC_{50} for the *beta* variant (9.9 µM) was 2.0- to 2.6-fold higher

than for the wt, *alpha*, and *gamma* variants (3.8, 5.0, and 4.3 µM, respectively). According to a

recent report, the *beta* variant appears to exhibit a significantly reduced eclipse period and more

rapid replication *in vitro* (11), which would likely affect its dose response toward stenoparib and

remdesivir. The *beta* variant carries numerous changes to the S protein, several of which affect

the receptor binding domain and are also common to the *alpha* and *gamma* variants. In addition

to these changes, the *beta* variant carries mutations in the N protein and in the Nsp3 polyprotein

(ORF1a), which may be involved in ADPR following infection (12). Differential susceptibility to

ADPR may contribute to the altered replication kinetics of the *beta* variant, although this awaits

experimental validation.

In an additional set of experiments, we focused on the SARS-CoV-2 *alpha* variant. Vero

E6 cells were infected with the *alpha* variant using a multiplicity of infection of 0.1, and the

activity of stenoparib was assessed using the plaque reduction assay. Plaques are areas of

dead or destroyed cells and appear as small, clear regions in an infected cell monolayer after

fixation and staining with crystal violet. Following infection and treatment with an inhibitor, cells

were overlaid with low melting point agarose, fixed at 120 h post infection, stained with crystal

violet, and plaques were manually counted. The 3 control types were 1) infected and untreated

cells, 2) uninfected and untreated cells, and 3) infected cells treated with a combination of

camostat mesylate and E64d (CE), which are protease inhibitors that prevent spike protein

cleavage and virus entry into the cell (13). For the analysis shown in Fig. 2A and 2B, we

combined lower doses of stenoparib (2.5, 5.0, and 10 µM) with the previously reported 50%

effective concentration (EC_{50}) of remdesivir (0.5 µM) (6). In Fig. 2A and 2B, neither 10 µM

stenoparib nor 0.5 µM remdesivir achieved greater than a 50% reduction in plaquing efficiency

compared to the infected, untreated cells. When combined, however, synergy occurred as

plaque inhibition increased to over 90% - superior to what was achievable with either drug alone

(P < 0.01) at these doses. Notably, this was accomplished without significant cytotoxicity (Fig.

2C). Combinations of two or more drugs may lead to synergism through different mechanisms

of action, which has the potential benefit of reducing individual doses of each drug and

minimizing undesirable side effects.

Besides the known roles for the PARP1 and PARP2 enzymes in DNA repair (14, 15),

members of the PARP family have numerous additional functions (16). The 18 known human

PARPs appear to differentially affect viral replication; some exhibit proviral activity and others

exhibit antiviral roles (7, 17-21). In coronavirus, the N protein is mono (ADP) ribosylated

(MARylated) during infection. Stability of the N protein is critical for viral genome replication,

translation, packaging, and modulation of the host cell cycle (22). The N protein is the only

ADPR target definitively identified in coronavirus thus far (17), and the prevalence of this

modification across multiple coronavirus families suggests an important role in virus stability

(17). Despite this, the role of N protein MARylation, and of ADPR in general with regards to

coronavirus stability, is not well characterized. Possibly ADPR has a role in regulating virus

genome structure, similar to ADPR of histones or the adenovirus core proteins (23, 24). While

remdesivir and molnupiravir inhibit the viral replicon, stenoparib likely acts through multiple

targets. A combination of stenoparib and remdesivir or molnupiravir may be highly potent at

inhibiting SARS-family coronaviruses including SARS-CoV-2.

Acknowledgements

This research was supported by a grant from The Flinn Foundation, the Cowden Endowment for

Microbiology, and an Arizona Board of Regents TRIF award. Core experiments were supported

by service fees paid by Allarity Therapeutics.

Conflict of Interest Statement

SK is employed by and holds a financial interest in Allarity Therapeutics, which stands to

potentially benefit from these results.

References

1. WHO. 2021. https://covid19.who.int/. Accessed 3 Nov 2021.
2. Prevention USCfDCa. 2020. Information for Clinicians on Investigational Therapeutics for Patients with COVID-19, *on* National Center for Immunization and Respiratory Diseases (NCIRD), Division of Viral Diseases. https://www.cdc.gov/coronavirus/2019-ncov/hcp/therapeutic-options.html. Accessed 16 Oct 2021.
3. Beigel JH, Tomashek KM, Dodd LE, Mehta AK, Zingman BS, Kalil AC, Hohmann E, Chu HY, Luetkemeyer A, Kline S, Lopez de Castilla D, Finberg RW, Dierberg K, Tapson V, Hsieh L, Patterson TF, Paredes R, Sweeney DA, Short WR, Touloumi G, Lye DC, Ohmagari N, Oh MD, Ruiz-Palacios GM, Benfield T, Fatkenheuer G, Kortepeter MG, Atmar RL, Creech CB, Lundgren J, Babiker AG, Pett S, Neaton JD, Burgess TH, Bonnett T, Green M, Makowski M, Osinusi A, Nayak S, Lane HC, Members A-SG. 2020. Remdesivir for the Treatment of Covid-19 - Final Report. N Engl J Med 383:1813-1826.
4. Kokic G, Hillen HS, Tegunov D, Dienemann C, Seitz F, Schmitzova J, Farnung L, Siewert A, Hobartner C, Cramer P. 2021. Mechanism of SARS-CoV-2 polymerase stalling by remdesivir. Nat Commun 12:279.
5. Kabinger F, Stiller C, Schmitzova J, Dienemann C, Kokic G, Hillen HS, Hobartner C, Cramer P. 2021. Mechanism of molnupiravir-induced SARS-CoV-2 mutagenesis. Nat Struct Mol Biol 28:740-746.
6. Stone NE, Jaramillo SA, Jones AN, Vazquez AJ, Martz M, Versluis LM, Raniere MO, Nunnally HE, Zarn KE, Nottingham R, Ng KR, Sahl JW, Wagner DM, Knudsen S, Settles EW, Keim P, French CT. 2021. Stenoparib, an Inhibitor of Cellular Poly(ADP-Ribose) Polymerase, Blocks Replication of the SARS-CoV-2 and HCoV-NL63 Human Coronaviruses In Vitro. mBio 12:e03495-20.
7. Kuny CV, Sullivan CS. 2016. Virus-Host Interactions and the ARTD/PARP Family of Enzymes. PLoS Pathog 12:e1005453.
8. McGonigle S, Chen Z, Wu J, Chang P, Kolber-Simonds D, Ackermann K, Twine NC, Shie JL, Miu JT, Huang KC, Moniz GA, Nomoto K. 2015. E7449: A dual inhibitor of PARP1/2 and tankyrase1/2 inhibits growth of DNA repair deficient tumors and antagonizes Wnt signaling. Oncotarget 6:41307-23.
9. Thorsell AG, Ekblad T, Karlberg T, Low M, Pinto AF, Tresaugues L, Moche M, Cohen MS, Schuler H. 2017. Structural Basis for Potency and Promiscuity in Poly(ADP-ribose) Polymerase (PARP) and Tankyrase Inhibitors. J Med Chem 60:1262-1271.
10. van Baalen CA, Jeeninga RE, Penders GH, van Gent B, van Beek R, Koopmans MP, Rimmelzwaan GF. 2017. ViroSpot microneutralization assay for antigenic characterization of human influenza viruses. Vaccine 35:46-52.
11. Pyke AT, Nair N, van den Hurk AF, Burtonclay P, Nguyen S, Barcelon J, Kistler C, Schlebusch S, McMahon J, Moore F. 2021. Replication Kinetics of B.1.351 and B.1.1.7 SARS-CoV-2 Variants of Concern Including Assessment of a B.1.1.7 Mutant Carrying a Defective ORF7a Gene. Viruses 13.
12. Lei J, Kusov Y, Hilgenfeld R. 2018. Nsp3 of coronaviruses: Structures and functions of a large multi-domain protein. Antiviral Res 149:58-74.
13. Hoffmann M, Kleine-Weber H, Schroeder S, Kruger N, Herrler T, Erichsen S, Schiergens TS, Herrler G, Wu NH, Nitsche A, Muller MA, Drosten C, Pohlmann S. 2020. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. Cell 181:271-280 e8.
14. Dziadkowiec KN, Gasiorowska E, Nowak-Markwitz E, Jankowska A. 2016. PARP inhibitors: review of mechanisms of action and BRCA1/2 mutation targeting. Prz Menopauzalny 15:215-219.

15.   Ame JC, Rolli V, Schreiber V, Niedergang C, Apiou F, Decker P, Muller S, Hoger T,
Menissier-de Murcia J, de Murcia G. 1999. PARP-2, A novel mammalian DNA damage-
dependent poly(ADP-ribose) polymerase. J Biol Chem 274:17860-8.

16.   Gupte R, Liu Z, Kraus WL. 2017. PARPs and ADP-ribosylation: recent advances linking
molecular functions to biological outcomes. Genes & development 31:101-126.

17.   Grunewald ME, Fehr AR, Athmer J, Perlman S. 2018. The coronavirus nucleocapsid
protein is ADP-ribosylated. Virology 517:62-68.

18.   Grunewald ME, Chen Y, Kuny C, Maejima T, Lease R, Ferraris D, Aikawa M, Sullivan
CS, Perlman S, Fehr AR. 2019. The coronavirus macrodomain is required to prevent
PARP-mediated inhibition of virus replication and enhancement of IFN expression. PLoS
Pathog 15:e1007756.

19.   Li L, Zhao H, Liu P, Li C, Quanquin N, Ji X, Sun N, Du P, Qin C-F, Lu N, Cheng G. 2018.
PARP12 suppresses Zika virus infection through PARP-dependent degradation of NS1
and NS3 viral proteins. Science signaling 11:eaas9332.

20.   Atasheva S, Frolova EI, Frolov I. 2014. Interferon-stimulated poly(ADP-Ribose)
polymerases are potent inhibitors of cellular translation and virus replication. Journal of
virology 88:2116-2130.

21.   Westera L, Jennings AM, Maamary J, Schwemmle M, Garcia-Sastre A, Bortz E. 2019.
Poly-ADP Ribosyl Polymerase 1 (PARP1) Regulates Influenza A Virus Polymerase. Adv
Virol 2019:8512363.

22.   McBride R, van Zyl M, Fielding BC. 2014. The coronavirus nucleocapsid is a
multifunctional protein. Viruses 6:2991-3018.

23.   Déry CV, de Murcia G, Lamarre D, Morin N, Poirier GG, Weber J. 1986. Possible role of
ADP-ribosylation of adenovirus core proteins in virus infection. Virus Research 4:313-
329.

24.   Strickfaden H, McDonald D, Kruhlak MJ, Haince J-F, Th'ng JPH, Rouleau M, Ishibashi T,
Corry GN, Ausio J, Underhill DA, Poirier GG, Hendzel MJ. 2016. Poly(ADP-ribosyl)ation-
dependent Transient Chromatin Decondensation and Histone Displacement following
Laser Microirradiation*. Journal of Biological Chemistry 291:1789-1802.

Figures

 Figure 1. Dose-response curves for stenoparib and remdesivir on SARS-CoV-2 variants. **A.**

 stenoparib. **B.** remdesivir. Vero E6 cells (ATCC CRL-1586) were infected for 20 hours with

 SARS-CoV-2 wild type (wt) or the indicated variants in the presence or absence of stenoparib or

 remdesivir as indicated. Results are the average fraction of quadruplicate wells that exhibited

 positive staining for SARS-CoV-2 (y-axis) vs. the concentration of the inhibitors (x-axis). These

 data were used to estimate the EC_{50} of stenoparib and remdesivir. The EC_{50} values were

 approximated with the aid of the online calculator from AAT Bioquest ("Quest Graph™ EC_{50}

 Calculator." AAT Bioquest, Inc, 26 Oct. 2020, https://www.aatbio.com/tools/ec50-calculator).

 Viruses; wild-type (wt): BetaCoV/Munich/BavPat1/2020, European Virus Archive Global. *Alpha*:

 USA/CA_CDC_5574/2020, BEI Resources, Cat# NR-54011. *Beta*: hCoV-19/South

 Africa/KRISP-K005325/2020, BEI Resources. *Gamma*: hCoV-19/Japan/TY7-503/2021 (Brazil

 P.1), BEI Resources.

Figure 2. Activity of stenoparib and remdesivir on the *alpha* (B.1.1.7) variant. **A.** Virus Plaque

assays. Vero E6 cells (ATCC CRL-1586) were infected for 2 hours with SARS-CoV-2 *alpha*

(USA/CA_CDC_5574/2020, BEI Resources, Cat# NR-54011), washed, and overlaid with low-

melting temp agarose/MEM with or without stenoparib and/or remdesivir at the concentrations

indicated. The cell monolayers were fixed with 4% paraformaldehyde and stained with 0.1%

crystal violet prior to manual counting of clear plaques. The experiment was performed using

technical triplicates, and error bars represent the standard deviation of three independent

experiments. Statistical analysis was performed using the Student's unpaired t-test. * P < 0.05,

** P < 0.01 applies where indicated. **B.** Photographs of plate wells after crystal violet staining.

Labels indicate the concentrations of stenoparib or remdesivir. Abbreviations: S = stenoparib, R

= remdesivir at the concentrations indicated (e.g. S2.5 / R0.5 = stenoparib 2.5 µM, remdesivir

0.5 µM, etc.). **C.** Cytotoxicity measurements performed by the lactate dehydrogenase release

assay (Promega Cytotox 96) 48 hours after infection. Inhibitors stenoparib or remdesivir were

used at the indicated concentrations (x-axis). The assays were performed according to the

manufacturer's recommendations. Results from drug treatments were normalized to the fraction

of maximum cytotoxicity (percent cytotoxicity; y-axis) achieved by detergent lysis of cells. The

experiment was performed using technical triplicates, and error bars represent the standard

deviation of three independent experiments.

A

B

C