

## Baricitinib as potential treatment for 2019-nCoV acute respiratory disease

Given the scale and rapid spread of the 2019 novel coronavirus (2019-nCoV) acute respiratory disease, there is an immediate need for medicines that can help before a vaccine can be produced. Results of rapid sequencing of 2019-nCoV, coupled with molecular modelling based on the genomes of related virus proteins,<sup>1</sup> have suggested a few compounds that are likely to be effective, including the anti-HIV lopinavir plus ritonavir combination.

BenevolentAI's knowledge graph is a large repository of structured medical information, including numerous connections extracted from scientific literature by machine learning.<sup>2</sup> Together with customisations bespoke to 2019-nCoV, we used BenevolentAI to search for approved drugs that could help, focusing on those that

might block the viral infection process. We identified baricitinib, which is predicted to reduce the ability of the virus to infect lung cells.

Most viruses enter cells through receptor-mediated endocytosis. The receptor that 2019-nCoV uses to infect lung cells might be ACE2, a cell-surface protein on cells in the kidney, blood vessels, heart, and, importantly, lung AT2 alveolar epithelial cells (figure). These AT2 cells are particularly prone to viral infection.<sup>3</sup> One of the known regulators of endocytosis is the AP2-associated protein kinase 1 (AAK1). Disruption of AAK1 might, in turn, interrupt the passage of the virus into cells and also the intracellular assembly of virus particles.<sup>4</sup>

Of 378 AAK1 inhibitors in the knowledge graph, 47 have been approved for medical use and six inhibited AAK1 with high affinity. These included a number of oncology drugs such as sunitinib and erlotinib, both of which have been shown to inhibit viral infection of cells through

the inhibition of AAK1.<sup>5</sup> However, these compounds bring serious side-effects, and our data infer high doses to inhibit AAK1 effectively. We do not consider these drugs would be a safe therapy for a population of sick and infected people.

By contrast, one of the six high-affinity AAK1-binding drugs was the janus kinase inhibitor baricitinib, which also binds the cyclin G-associated kinase, another regulator of endocytosis.<sup>6</sup> Because the plasma concentration of baricitinib on therapeutic dosing (either as 2 mg or 4 mg once daily) is sufficient to inhibit AAK1, we suggest it could be trialled, using an appropriate patient population with 2019-nCoV acute respiratory disease, to reduce both the viral entry and the inflammation in patients, using endpoints such as the MuLBSTA score, an early warning model for predicting mortality in viral pneumonia.<sup>7</sup>

JS is editor-in-chief of *Oncogene*. JS has previously sat on a number of scientific advisory boards, including BenevolentAI, and has consulted with Lansdowne partners, Vitruvian, and Social Impact Capital; he now sits on the Board of Directors for BB Biotech Healthcare Trust and chairs Xerion Healthcare. All other authors are employees of BenevolentAI. Events in relation to the 2019-nCoV outbreak are evolving rapidly, and we make our initial thoughts available in this Correspondence in good faith and to assist in the global response. Our early investigations and suggestions require further detailed work and analysis and should not be relied on as constituting any kind of medical or other advice or recommendation.

Peter Richardson, Ivan Griffin, Catherine Tucker, Dan Smith, Olly Oechsle, Anne Phelan, \*Justin Stebbing

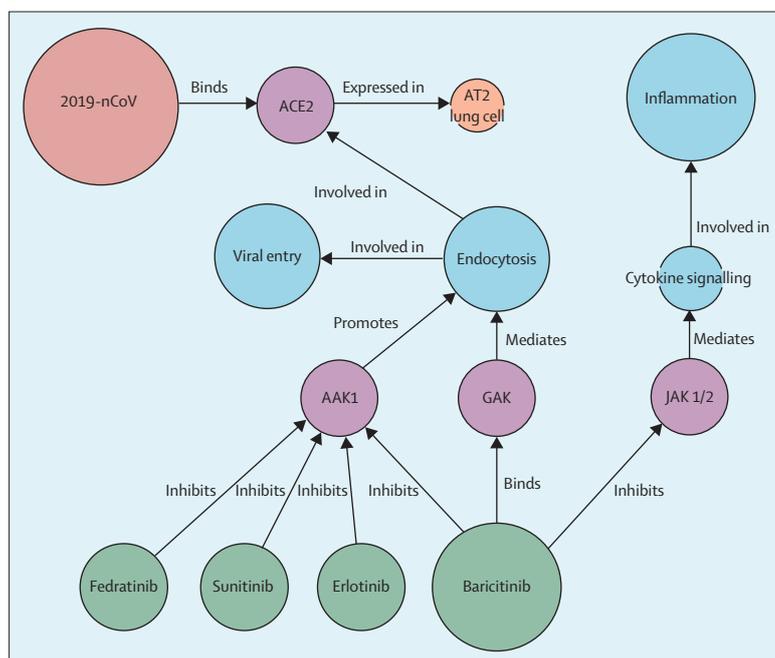
j.stebbing@imperial.ac.uk

BenevolentAI, London, UK (PR, IG, CT, DS, OO, AP); and Department of Surgery and Cancer, Imperial College London, London SW7 2AZ, UK (JS)

- 1 Gruber CC, Steinkellner G. Wuhan coronavirus 2019-nCoV—what we can find out on a structural bioinformatics level. Jan 23, 2020. <https://innophore.com/2019-ncov/> (accessed Feb 3, 2020).
- 2 Segler MHS, Preuss M, Waller P. Planning chemical syntheses with deep neural networks and symbolic AI. *Nature* 2018; **555**: 604–10.
- 3 Zhao Y, Zhao Z, Wang Y, et al. Single-cell RNA expression profiling of ACE2, the putative receptor of Wuhan 2019-nCoV. *BioRxiv* 2020; published online Jan 26. DOI:<https://doi.org/10.1101/2020.01.26.311200>



Published Online  
February 3, 2020  
[https://doi.org/10.1016/S0140-6736\(20\)30304-4](https://doi.org/10.1016/S0140-6736(20)30304-4)



**Figure: The BenevolentAI knowledge graph**

The BenevolentAI knowledge graph integrates biomedical data from structured and unstructured sources. It is queried by a fleet of algorithms to identify new relationships to suggest new ways of tackling disease. 2019-nCoV=2019 novel coronavirus. AAK1=AP2-associated protein kinase 1. GAK=cyclin G-associated kinase. JAK1/2=janus kinase 1/2.

Submissions should be made via our electronic submission system at <http://ees.elsevier.com/thelancet/>

- 4 Lu R, Zhao X, Li J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020; published online Jan 30. [https://doi.org/10.1016/S0140-6736\(20\)30251-8](https://doi.org/10.1016/S0140-6736(20)30251-8).
- 5 Pu SY, Xiao F, Schor S, et al. Feasibility and biological rationale of repurposing sunitinib and erlotinib for dengue treatment. *Antiviral Res* 2018, **155**: 67–75.
- 6 Sorrell F, Szklarz M, Abdul Areez KR, et al. Family-wide structural analysis of human numb-associated protein kinases. *Structure* 2016; **24**: 401–11.
- 7 Chen N, Zhou M, Dong X, et al. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. *Lancet* 2020; published online Jan 29. [https://doi.org/10.1016/S0140-6736\(20\)30211-7](https://doi.org/10.1016/S0140-6736(20)30211-7).