

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 8 Mar 2019 11:56:08 -0700
To: Peter Daszak; Kevin Olival;; Anthony, Simon J.; Letko, Michael (NIH/NIAID) [F]
Subject: FW: Reaching out to EcoHealth
Attachments: Letko_lineageB project.pdf
Importance: High

Hi guys,

I wanted to show you some prelim data from one of my post-docs (Dr. Michael Letko), which we think would be of big interest of you guys and PREDICT. Michael has recently developed a rapid and scalable platform to screen novel beta-coronaviruses related to SARS-CoV (aka, Lineage B) for host-cell entry potential. Literally hundreds of lineage B beta-coronaviruses have been discovered primarily in Rhinolophus bats in Asia. Unfortunately, like many newly-discovered viruses, little is known beyond the sequence – there is almost no information on whether or not the majority of these viruses can even infect human cells. As our approach allows us to quickly move from genotype to phenotype, we feel that this work is of high interest to the field of virus discovery and to programs like EcoHealth Alliance - PREDICT.

While we have now tested all of the variation currently published for lineage B beta-coronaviruses for their ability to enter primate cells, we are seeking additional, unpublished lineage B beta-coronavirus sequences to test in our platform. Attached is a short abstract and figure further describing our approach and demonstrating the powerful results that come from it. We kindly ask that you do not distribute this material further, however, as it is still unpublished and quite competitive.

Let me know what you guys think and whether you have any samples with lineage B sequences of S-genes or lineage B rdp for further characterization of S. I think publishing smtg which bridges the gap between virus discovery and high-throughput initial assessment of zoonotic potential would have great interest from the scientific AND public health communities.

Cheers,

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