Dear All,

Please find attached the updated manuscript and supplementary info. The documents are clean (no track changes) but contain some comment replies to some authors' questions. I have also included a copy of each document that includes the final track changes relative to the original draft (i.e. "HPG paper - Manuscript Aug-20-2019.docx").

A big thank you to everyone who helped throughout the editing process!
We intend to submit on Wednesday (~CoB, AEST), so if we don't hear from you we will assume you are happy with the manuscripts.

Best regards,
Josh

Joshua Hayward PhD
Research Officer
Retroviral Biology and Antivirals Research Laboratory
Burnet Institute
Disease Elimination and Maternal & Child Health Programs
Thanks Josh and good luck.

I have no further edits/comments.

Linfa (Lin-Fa) Wang, PhD FTSE
Professor & Director
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
Dear All,

I wanted to follow up Josh’s email to thank you all for your invaluable contributions to this manuscript. It has been an incredible team effort. We are really excited with the outcome and cannot wait to see it in print.

I especially want to highlight the contributions of a several individuals—the first being Mary—this whole study would not have been possible without her discovery of a gammaretrovirus sequence in bat scat as well as her determination and ingenuity in developing a method to amplify very low levels of viral RNA from the bat poo sample coupled with development of a pipeline that enabled de novo assembly of the full length HPG genome. Her efforts converge with Ina’s expertise in the purification and identification of viruses in bats and of course the “bat pack” group for collecting the samples as well as the beautiful HPG EM images from Megan and her team at AAHL.

I also want to acknowledge Linfa’s role in recognising that bat retroviral sequences are fascinating and encouraging Mary to “go talk to her sister who is a retrovirologist” which got the ball rolling on Mary’s “side project” thank you so much Linfa for supporting and catalysing this study!

Claudia, many thanks to you and your team for generously allowing us to include the Daintree bat sequencing data that was important for identifying the Australian “HPG-related clade” and Cecilia for your early work on HPG.

Eddie, with your prowess in phylogenetics we have a far more compelling story demonstrating that HPG-related viruses are basal to KoRV and GalV as well as the gammaretroviruses found in Asian bats identified by Josh.

The Burnet Institute Fusion lab members Christina, Andy, and Heidi brilliant work with expressing the HPG trimeric envelope which was pivotal for the bat serological studies.

To past and present members of my lab many thanks for your efforts, including Adam J our molecular go to person and last but not least, Josh for his monumental effort in helping to drive this study, his studies on the full length HPG infectious molecular clone, as well as writing the first draft and coordinating the edits on this paper.

Fingers crossed with the PNAS submission!

Best

Gilda