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(b)(3):50 USC 3024(i)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

(U) The WIV was funded to conduct reverse genetics studies on bat Coronaviruses.

The WIV received funding to conduct research to exchange the receptor binding domain (RBD) of a template bat Coronaviruses with the RBDs of other bat Coronaviruses to understand the impact on infectivity. This work was funded by the NIH via EcoHealth Alliance (9). Specific Aim # 3 of the WIV NIH Grant included studies to conduct Gain of Function (GoF) studies on chimeric Bat Coronaviruses.

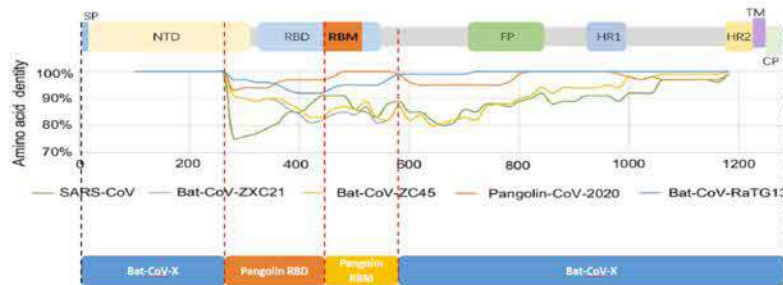
- Viral work conducted at BSL-2 level
- Specific Aim 1: Characterize the diversity of high spillover-risk SARSr-CoVs in bats in southern China... We will sequence receptor binding domains (spike proteins) to identify viruses with the highest potential for spillover which we will include in our experimental investigations (Aim 3).
- Specific Aim 3: *In vitro* and *in vivo* characterization of SARSr-CoV spillover risk, coupled with spatial and phylogenetic analyses to identify regions and viruses of public health concern. We will use S protein sequence data, infectious clone technology, in vitro and in vivo infection experiments and analysis of receptor binding to test the hypothesis that % divergence thresholds in S protein sequences predict spillover potential.

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