

Serologic Evidence of Fruit Bat Exposure to Filoviruses, Singapore, 2011–2016

Technical Appendix

Determination of Median Fluorescence Intensity (MFI) Cutoff Value

A Bayesian mixture model was first fitted to the data for individual glycoproteins within each bat species using Markov chain Monte Carlo. The model was implemented in R (1) with code provided by Alison Peel (2) that was adapted for use with the software packages JAGS (3) and rjags (4). The parameters of the fit were then used to calculate the MFI at which the p value of being seronegative was 0.001, as well as the p value at an MFI of 200 (Figure).

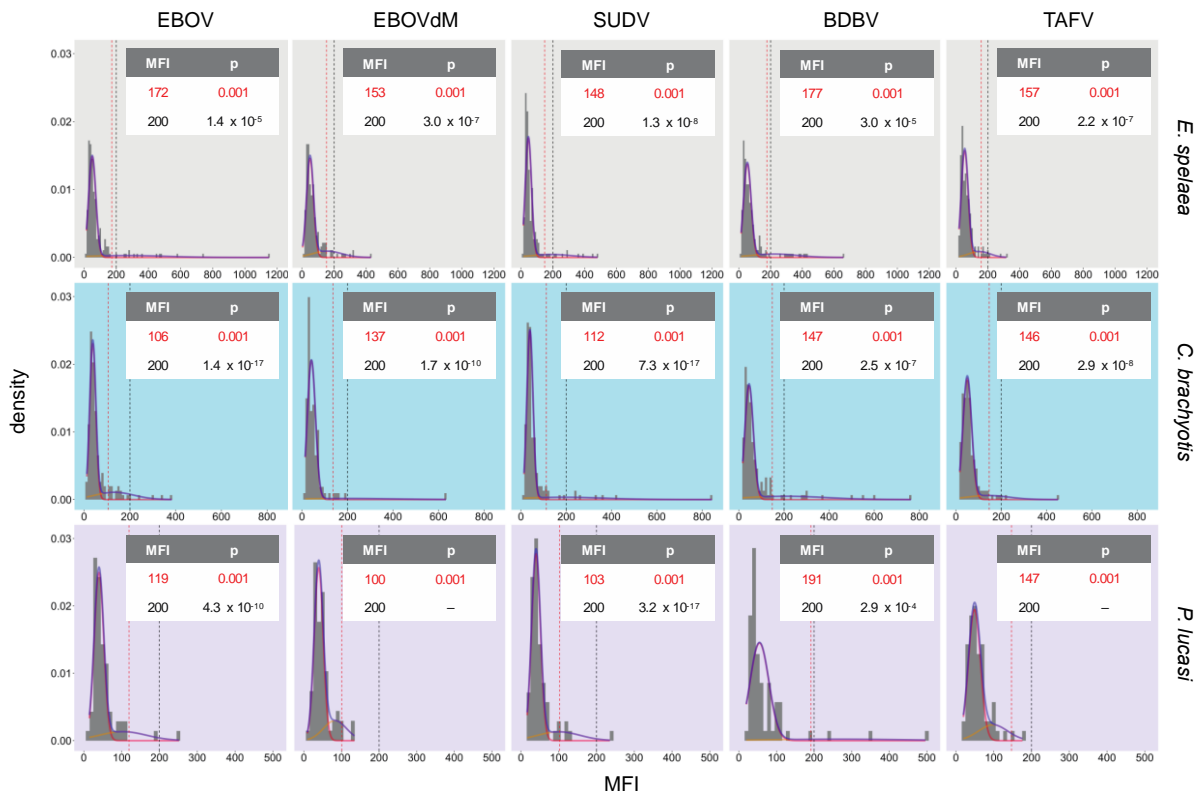


Figure. Median fluorescence intensity (MFI).

References

1. R Core Team, 2016. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna. <https://www.R-project.org/>
2. Peel AJ, McKinley TJ, Baker KS, Barr JA, Crameri G, Hayman DTS, et al. Use of cross-reactive serological assays for detecting novel pathogens in wildlife: assessing an appropriate cutoff for henipavirus assays in African bats. *J Virol Methods*. 2013;193:295–303. [PubMed](#)
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3. Plummer M, 2003. JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling.
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