APPENDICIES

I. NOTES ON SURVEYS

Schmidt et al. 1961 reports naturally infected *M. mulatta.* 22 of 228 animals that were imported from Dacca (presumably Dakar, Bangladesh), but originally from East Pakistan, were positive. Whether these individuals were infected from their origin (Pakistan) or infected close to the Assam- Burma (India-Myanmar) border is not known. The author implies that these individuals had been held in a new location before exportation. Thus, infection could have occurred in Northeastern India. This would be less surprising, as it is within the range of the simian malaria vectors *Anopheles leucosphyrus.*

Liu et al. 2011 and Liu et al. 2014 report sensitivities and suspected sampling rates for individuals. We used these probabilities to extrapolate prevalence for chimpanzees and gorillas at each site. The outcomes are given in Table S2 but the conversion file will be made available upon request.

For surveys that included multiple samples from known individuals (i.e. De Nys et al. 2013), we created a dataset from the reported data and sampled randomly from it to estimate prevalence. This was repeated 10,000 times to get an estimate of prevalence in the population and the extrapolated number of infected individuals was used in Table S2.

Lastly, many of the ape malarias have received multiple names throughout the century. Early work was summarized by P.C.C. Garnham in his 1966 textbook and concluded that there were three ape malarias:

- ***P. reichenowi* infects chimpanzees** (Reichenow 1920, Blacklock and Adler 1923, Schwetz 1933). This is the only ape malaria that has both a morphological and molecular characterization. It originally was described as *P. falciparum,* but is morphologically and molecularly distinguishable from human parasites.
- ***P. malariae* infects chimpanzees** (Reichenow 1920, Blacklock and Adler 1923, Schwetz 1933). *P. rodhaini* is also mentioned in the literature, however Garnham (1966) and Coatney et al. (1971) review the literarure and present ample evidence that it was *P. malariae.* It has morphological similarities to human *P. malariae* and multiple researchers were able to infect humans with *'P.*

rodhaini' and chimps with '*P. malariae'.* We changed historical records that identified species as *P. rodhaini* to *P. malariae.*

- ***P. schwetzi* infects chimpanzees and gorillas** (REichenow 1920, Blacklock and Adler 1923, Schwetz 1933). Contacos and colleagues (1970) demonstrated that this species could be transmitted to man, but before that all infection trials had failed. The parasite is usually found coinfecting with other malaria parasites. It has been described as *Plasmodium vivax*-like and *P. ovale*- like in its morphology.

All surveys of apes before 2009, reported only one of three of these malarias (*P. schwetzi* was the only malaria confirmed in *Gorilla gorilla).* While there now seems to be a much greater diversity, we left surveys with the original species identification. Unfortunately, only *P. reichenowi* has been molecularly characterized (Escalante et al. 1994) of the original 3 morphologically described ape malarias.

After 2009, there was an explosion of molecularly characterized malaria species from African apes and monkeys. Five new species have been described based on molecular data in the *Laverania* subgenus. *Laverania* is a monophyletic clade that infects apes and includes the malignant human malaria *P. falciparum*:

- ***P. falciparum* infects humans, but is also found in chimpanzees, gorillas, bonobos, and *Cercopithecus nictitans.*** Following lumping strategies purported by Coatney et al. (1971), we include *P. praefalciparum* within *P. falciparum. P. praefalciparum* has been used to describe *P. falciparum* –like isolates from gorillas. It has been argued that the greater diversity of *P. falciparum* in these apes supports a hypothesis that *P. falciparum* first evolved in gorillas and more recently infected humans through a single host switch event. The diversity found in chimpanzees is much lower. Only one isolate has been found in *C. nictitans.* It is possible that chimpanzees, bonobos, and this monkey are spillover hosts- that the parasites are not endemic in populations. But this requires more study.
- ***P. reichenowi* infects chimpanzees.**
- ***P. billcollinsi* infects chimpanzees.**
- ***P. blacklocki* infects gorillas.**
- ***P. gaboni* infects chimpanzees.**
- ***P. alderi* infects gorillas.**

Additionally, researchers have found parasites that are similar to human parasites. Although new data only has molecular data, morphological data has been used to successfully reconstruct some molecular phylogenies (i.e. Martinsen et al. 2007).

- ***P. vivax* like in chimpanzees & gorillas** (Duval et al. 2010, Kaiser et al. 2010, De Nys et al. 2013, Prugnolle et al. 2013, Liu et al. 2014). In survey data these are identified as *P. vivax*.*
- ***P. ovale* like in chimpanzees** (Duval et al. 2009, Kaiser et al. 2010). In survey data these parasites are recorded as *P. ovale**
    - Either of these could be same as *P. schwetzi* reported by early authors (Reichenow 1920, Adler 1923, Bray (cited by Garnham et al. 1966)). *P. schwetzi* has been described as morphological similar to *P. vivax* and to *P. ovale*- depending on the author. However, *P. schwetzi* was found in both chimpanzees and gorillas across a large geographic range, so it might be more likely that *P. schwetzi* is the same as *P.vivax*-like parasites found in gorillas and chimpanzees (Prugnolle et al. 2013, Liu et al. 2014). We have left the species identification as above- at a later date these can be renamed as paired molecular and morphological data emerge.

- ***P. malariae* like in chimpanzees** (Duval et al. 2010, Kaiser et al. 2010). We assume that this is the same as *P. malariae* reported by early authors (Reichenow 1920, Adler 1923, Bray (cited by Garnham et al. 1966)). However more molecular data should be collected to verify this.

II. SURVEY REFERENCES

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