Table S1. Pairwise ranges of sequence divergence within and between named *Parahaemoproteus* lineages. Shaded values represent named sequences that likely include misnamed lineages.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *balmorali* | *belopolskyi* | *cyanomitrae* | *hoemobelopolskyi* | *lanii* | *magnus* | *majoris* | *micronuclearis* | *minutus* | *motacillae* | *parabelopolskyi* | *sanguinis* |
| *balmorali* | 0.001-0.039 |  |  |  |  |  |  |  |  |  |  |  |
| *belopolskyi* | 0.051-0.086 | 0.002-0.039 |  |  |  |  |  |  |  |  |  |  |
| *cyanomitrae* | 0.020-0.060 | 0.054-0.084 | 0.002-0.035 |  |  |  |  |  |  |  |  |  |
| *hoemobelopolskyi* | 0.027-0.054 | 0.053-0.077 | 0.019-0.040 | 0.002-0.006 |  |  |  |  |  |  |  |  |
| *lanii* | 0.052-0.073 | 0.042-0.067 | 0.054-0.073 | 0.057-0.065 | 0.002-0.020 |  |  |  |  |  |  |  |
| *magnus* | 0.056-0.081 | 0.032-0.069 | 0.058-0.084 | 0.069-0.080 | 0.033-0.048 | 0.002-0.010 |  |  |  |  |  |  |
| *majoris* | 0.039-0.063 | 0.052-0.081 | 0.029-0.051 | 0.027-0.044 | 0.050-0.070 | 0.058-0.086 | 0.002-0.010 |  |  |  |  |  |
| *micronuclearis* | 0.019-0.058 | 0.051-0.086 | 0.020-0.048 | 0.013-0.040 | 0.056-0.081 | 0.057-0.097 | 0.033-0.059 | 0.002-0.024 |  |  |  |  |
| *minutus* | 0.039-0.065 | 0.038-0.068 | 0.032-0.060 | 0.025-0.048 | 0.052-0.073 | 0.059-0.079 | 0.018-0.047 | 0.022-0.059 | 0.000-0.010 |  |  |  |
| *motacillae* | 0.042-0.063 | 0.057-0.094 | 0.022-0.051 | 0.018-0.038 | 0.059-0.073 | 0.071-0.086 | 0.028-0.048 | 0.032-0.057 | 0.043-0.052 | 0.002-0.010 |  |  |
| *parabelopolskyi* | 0.059-0.092 | 0.045-0.089 | 0.056-0.092 | 0.048-0.073 | 0.046-0.068 | 0.058-0.075 | 0.052-0.089 | 0.053-0.090 | 0.025-0.083 | 0.061-0.090 | 0.002-0.041 |  |
| *sanguinis* | 0.050-0.076 | 0.044-0.077 | 0.044-0.061 | 0.042-0.056 | 0.061-0.075 | 0.069-0.083 | 0.035-0.050 | 0.044-0.070 | 0.015-0.028 | 0.050-0.064 | 0.050-0.087 | 0.003-0.010 |

Table S2. *Parahaemoproteus* “species” identified in the phylogeny (Figure 1). Lineages denoted in green are represented as entire clades in the phylogeny; those in orange are problemtic in the tree (see notes and text), and those in white are singletons in the tree.

Figure S1.

Number of publications that reported “avian malaria cytochrome b” lineages from 2000 to 2013 (from Scopus, February, 2014).

