## Appendix: Non-phylogenetic and Multivariate Tests

### (a) Non-phylogenetic results.

Appendix Table 1. Effect of D-index, Home Range Overlap and Body Mass on Parasite Richness in Nonphylogenetic Tests

| | **D-Index** | | | | **Home Range Overlap** | | | |
|---|---|---|---|---|---|---|---|---|
| | **Slope: D-index** | **F-ratio** | **P-value** | **Mass Significant?** | **Slope: Range Overlap** | **F-ratio** | **P-value** | **Mass Significant?** |
| **Parasite Taxonomic Groups:** | | | | | | | | |
| All combined | 0.33 | 1.92 | 0.17 | yes | -0.0013 | 0 | 0.63 | yes |
| Helminths | 0.39 | 2.28 | 0.14 | yes | 0.007 | 0.002 | 0.61 | no |
| Viruses | 0.24 | 1.48 | 0.23 | yes | -0.0034 | 0.0007 | 0.64 | no |
| Protozoa | 0.37 | 2.53 | 0.12 | yes | 0.023 | 0.03 | 0.54 | no[1] |
| **Parasite Transmission Modes:** | | | | | | | | |
| Direct (all combined) | 0.21 | 0.79 | 0.38 | yes | 0.035 | 0.06 | 0.51 | no[1] |
| Non-vector (helm.) | 0.47 | 3.58 | 0.063 | yes | 0.033 | 0.04 | 0.52 | no |

Notes: Analyses were run using species values, with $n$=68 for analyses of the D-index and $n$=38 for analyses of home range overlap. Parasite richness served as the dependent variable in a statistical model with D-index (or home range overlap), body mass and sampling effort as predictor variables. Sampling effort was statistically significant in all analyses involving the D-index, but not in all tests of home range overlap, possibly because of the smaller sample sizes.

Summary: In comparison to phylogenetic tests, the D-index was not significant in non-phylogenetic analyses (Table 1). This could reflect a confounding effect of body mass, which is negatively correlated with the D-index. Body mass was also found to be a phylogenetic artifact in a previous analysis of parasite richness in anthropoid primates (Nunn et al. 2003). Consistent with this possibility, body mass was significant in most non-phylogenetic tests but largely non-significant after controlling for phylogeny (Table 1), and the D-index was non-significant in phylogenetic tests without body mass as a covariate.

**(b) Multivariate Results**

Appendix Table 2. Multivariate Tests Involving D-Index (Independent Contrasts, n=47)

| | D-index | Mass | Age 1st Reprod. | Geo. Range | Latitude | Popln. Density | Group Size | Home Range | Sampl. Effort |
|---|---|---|---|---|---|---|---|---|---|
| All Combined | b=0.40, P=0.09 | b=0.34, P=0.09 | ---- | b=0.17, P=0.01 | ---- | ---- | ---- | ---- | b=0.44, P<0.001 |
| Helminths | b=0.74, P=0.007[a] | b=0.48, P=0.03 | ---- | ---- | ---- | ---- | ---- | ---- | b=0.34, P=0.001 |
| Viruses | ---- | b≈0, P=0.98 | ---- | b=0.20, P<0.001 | ---- | ---- | ---- | ---- | b=0.27, P=0.014 |
| Protozoa | ---- | b=0.06, P=0.72 | ---- | ---- | ---- | ---- | ---- | ---- | b=0.45, P<0.001 |
| Direct (all combined) | ---- | b=0.21, P=0.22 | ---- | b=0.20, P=0.006 | ---- | ---- | ---- | ---- | b=0.34, P=0.003 |
| Non-vector (helm.) | b=0.86, P=0.004[a] | b=0.61, P=0.013 | ---- | ---- | ---- | ---- | ---- | ---- | b=0.29, P=0.008 |

Table shows slope and p-value for variables entered into the stepwise model (or forced in the case of body mass and sampling effort). Dashes indicate that the variable was not entered into the regression model.

[a]: Significant after implementing false discovery rate control (Verhoeven et al. 2005); only applied to D-index, with tests involving viruses, protozoa and directly transmitted parasites included as non-significant in the false discovery rate test (i.e., n=6 tests).

Appendix Table 3. Multivariate Tests Involving Home Range Overlap (Independent Contrasts, n=27)

| | Range Overlap | Mass | Age 1st Reprod. | Geo. Range | Latitude | Popln. Density | Group Size | Home Range | Sampl. Effort |
|---|---|---|---|---|---|---|---|---|---|
| All Combined | ---- | b=0.31, P=0.23 | b=0.89, P=0.08 | b=0.24, P=0.007 | ---- | ---- | b=0.77, P=0.005 | b=-0.22, P=0.08 | b=0.17, P=0.20 |
| Helminths | ---- | b=0.24, P=0.10 | ---- | ---- | ---- | ---- | ---- | ---- | b=0.22, P=0.39 |
| Viruses | ---- | b=0.13, P=0.44 | ---- | b=0.19, P=0.008 | ---- | b=0.14, P=0.07 | ---- | ---- | b=0.05, P=0.62 |
| Protozoa | ---- | b=0.17, P=0.43 | ---- | b=0.16, P=0.08 | ---- | ---- | ---- | ---- | b=0.08, P=0.54 |
| Direct (all combined) | ---- | b=0.08, P=0.68 | b=0.95, P=0.05 | b=0.23, P=0.007 | ---- | ---- | b=0.49, P=0.01 | ---- | b=0.28, P=0.02 |
| Non-vector (helm.) | ---- | b=0.13, P=0.60 | ---- | ---- | ---- | ---- | ---- | ---- | P=0.22, P=0.13 |

Table shows slope and p-value for variables entered into the stepwise model (or forced in the case of body mass and sampling effort). Dashes indicate that the variable was not entered into the regression model.

General Summary and Notes: We checked for collinearity among predictor variables using variance inflation factors (VIF) and assessment of correlations among variables (Petraitis et al. 1996). Using protozoa as a dependent variable and all other host characteristics and sampling effort as independent variables, VIFs are below 3 for the main results that use independent

contrasts. Moreover, while some predictor variables are correlated significantly, the maximum $R^2$ is 0.367. Thus, collinearity is unlikely to impact our results. Results here differ from some previous results of the dataset, possibly because of different sample sizes (generally smaller here) and an expansion in the number of primate taxa that are included in the parasite database (for example, Nunn et al. 2003 examined only anthropoid primates). Although results are not always directly comparable, one general pattern that emerges from studying all primates is that geographic range is more commonly significant than in a previous study, while population density was more often found to be the key variable that emerges in studies of anthropoid primates (Nunn et al. 2003). This could reflect that drivers of parasite richness differ among taxa, or that parasite richness is really driven by *total population size*, measured as density multiplied by geographic range, with tests in different subsets of taxa detecting different elements of this underlying factor (geographic range or density; see discussion of this possibility in Nunn et al. 2003). Latitude is only significant in the subset of the database used here when examining vector-borne parasites in analyses of home range overlap (results not shown; cf. Nunn et al. 2005).

**References Cited in Appendix:**


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