Supplementary Information

Supplementary Methods

Determining phylogenetic changes in feeding

Since plant compounds used for medicinal purposes are often evolutionarily conserved, we explored how red colobus foraging choices changed in phylogenetic structure between whipworm-positive and negative intervals. The plant families eaten during this study were used to reconstruct phylogenetic relationships in Phylomatic v.3 using the R20120829 backbone tree for plants, with branch lengths dated in Phylocom v.4.2. [1]. Net relatedness index (NRI) was calculated in the *picante* [2] library, where positive NRI values indicates phylogenetic clustering (*i.e.*, red colobus preferentially feed on closely related plant species), and negative NRI values indicates phylogenetic over-dispersion (*i.e.*, red colobus preferentially feed on distantly related plant species). Mean pairwise distance (MPD) was weighted by the proportion of time red colobus spent feeding on the respective plant family, and statistical significance assessed by comparison to 1000 randomly assembled communities [3].

Supplementary Tables

Supplementary Table 1: Sample size of the five activities included in GLMM and PCA analysis, including the number of individuals with data coverage.

Activity	*N*	% Activity	# INDVS
Copulate	100	3.30	25
Feed	1460	48.15	43
Groom	218	7.19	38
Move	215	7.09	40
Rest	1039	34.27	43
TOTAL	3032		43

Supplementary Table 2: Plant species in the Fabaceae (Leguminosae) family consumed by red colobus at intervals when individuals were negative or positive for whipworm eggs in feces. Bolded values indicate statistically significant differences in plant species consumption between infection statuses, assessed using binomial tests.

Plant Species	% Consumed	
	Negative	Positive
Acacia bravespica	7.27	4.17
Acacia hockii	3.64	1.67
Acrocarpus sp.	0.91	0.42
Albizia grandbracteata	**19.54**	**37.08**
Albizia gummifera	**4.09**	**7.92**
Erythrina abyssinica	1.36	0.83
Millettia dura	15.00	9.17
Newtonia bucchanani	48.18	38.75
TOTAL *N* Fabaceae	220	240
TOTAL *N* (All Plant Families)	945	760

Supplementary Figure Captions

Supplementary Figure 1. The relationship between whipworm egg presence and activity of red colobus monkeys. Generalized linear mixed models (GLMMs) were used to test how the proportion of observations spent on each of five behaviours (A-E) was affected by (i) sex and (ii) infection status (positive or negative for whipworm eggs in feces). Individual identity was included as a random effect. Individuals (thin lines) and GLMM model fit (thick lines) are color coded by sex (males = orange, females = green). Details of GLMM results are given in Table 1.

Supplementary Figure 2. Phylogenetic relationships of plant families consumed by red colobus monkeys. Plants consumed by red colobus were classed into plant families whose phylogenetic relationships were reconstructed in Phylomatic using the R20120829 backbone tree for plants. Branch lengths were dated in Phylocom. Plant families consumed in $\geq$ 5% of all feeding events are bolded irrespective of infection status, since red colobus did not change the phylogenetic structure of their feeding choices between whipworm-positive and negative intervals.

Supplementary Figure 3. Individual variation in mean behaviour duration (mean switching time) at whipworm positive and negative intervals. Data from eight adult female (F1-8) and six adult male (M1-6) red colobus.

Supplementary References

1. Webb C.O., Ackerly D.D., Kembel S.W. 2008 Phylocom: software for the analysis of phylogenetic community structure and trait evolution. *Bioinformatics* **24**(18), 2098-2100. (doi:10.1093/bioinformatics/btn358).

2. Kembel S.W., Cowan, P.D., Helmus, M.R., Cornwell, W.K., Morlon, H., Ackerly, D.D., Blomberg, S.P., and Webb, C.O. 2010 Picante: R tools for integrating phylogenies and ecology. *Bioinformatics* **26**, 1463 - 1464. (doi:10.1093/bioinformatics/btq166).

3. Webb C.O., Ackerly D.D., McPeek M.A., Donoghue M.J. 2002 Phylogenies and community ecology. *Annu Rev Ecol Syst* **33**, 475-505. (doi:10.2307/3069271).