



**Fig. 3. Fossil-calibrated nuclear time tree.** Concentric background circles mark 10-million-year intervals; solid gray circles in internal nodes show fossil calibration points (36); species marked with solid circles at tips show paraphyly or polyphyly when including additional individuals to estimate the topology.

dispersal mode (60–62). To account for potential phylogenetic inertia in trait evolution, we generated PGLS models using either genetic diversity or mutation rate as the response variable and individual traits as the predictors. We find traits within mating systems, activity budget, climatic niche, ranging patterns, and life history to be significant predictors of diversity ( $p < 0.05$ ), and traits within the former three categories remaining so after accounting for multiple testing (Benjamini-Hochberg correction, false discovery rate = 0.05). Species organized in

single-male polygynous mating systems show lower diversity than the background ( $r^2_{\text{pred}} = 0.11$ ,  $p_{\text{corr}} = 1.53 \times 10^{-2}$ ), consistent with expectations of reduced contribution of allelic diversity from males (63). Within the climatic niche, we observe a gradient of diversity declining from south to north ( $r^2_{\text{pred}} = 0.28$ ,  $p_{\text{corr}} = 1.45 \times 10^{-5}$ ), which is driven by highly diverse lemur species in the Southern Hemisphere. We also find a significant correlation with mean temperature and amount of precipitation ( $r^2_{\text{pred}} = 0.33$ ,  $p_{\text{corr}} = 1.97 \times 10^{-4}$ ). It is worth noting that these

measurements are not highly correlated with each other (Pearson's  $r$  –0.27 to 0.17), and the relationships are thus at least partly independent. Lastly, within the activity budget, we find the amount of time spent socializing to be correlated with diversity ( $r^2_{\text{pred}} = 0.11$ ,  $p_{\text{corr}} = 5.56 \times 10^{-3}$ ). However, we caution that the measurement of activity budget is difficult to standardize across species, and interpreting this relationship is thus challenging. We find no significant impact of life-history traits such as body mass or longevity on genetic diversity