*Supporting information for:*

Accounting for phylogenetic relatedness in cross-species analyses of telomere shortening rates

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**Notes on methods**

*Phylogenetic tree reconstruction*

We compiled species-level phylogenetic trees on mammals from Fritz et al. (2009), birds from Jetzt et al. (2012, birdtree.org) and fish from Rabosky et al. (2012) for time calibration. The nodes of these three orders were time calibrated using estimates from Kumar et al. (2017, timetree.org) and the R code required for reconstructing the full tree in Uyeda et al. (2017) can be found on Github (https://github.com/uyedaj/bmr/tree/master/R). The supertree was pruned using the package ‘ape’ (Paradis & Schliep, 2018). Analyses were performed in R (R Core Team, 2018). We used the package ‘caper’ (Orme et al., 2013) to perform phylogenetic generalized least squares regressions. While power to detect phylogenetic signal in datasets with fewer than 20 species may be low (Garland et al., 2005), Pagel’s λ has been shown to have the smallest type I error, i.e. misidentification of phylogenetic signal in randomly evolving traits (Münkemüller et al., 2012). Although there may not be a strong phylogenetic signal in the traits themselves, the phylogenetic non-independence is evaluated within the residual errors of the trait regression model (e.g. Revell, 2010).

*Species trait data*

Data on species telomere shortening rates (TSR), initial telomere length, body mass, average and maximum life span are available in the online supporting information in Whittemore et al. (2019). In order to replicate their analyses we use these estimates, but note that the average life span (40 years) of the American flamingo (*Phoenicopterus ruber*) may be overestimated: The references provided by Whittemore et al. (2019) suggest a *maximum* life span (in the closely related greater flamingo, *P. roseus*) of 37 years (Perrot et al. 2016), 40 years (Johnson 2000), 18 years (Tavecchia et al. 2001, but cites Johnson for maximum 40 years in the wild and a personal communication for >60 years in captivity), respectively. Fernández-Bellon et al. 2016 claims a longevity in excess of 40 years (*Phoenicopterus spp.*)without data or references. del Hoyo et al. (1991) reports minimum estimates of 33 years in the wild and 44 years in captivity (accessed via Carey & Judge, 2001). Howard (1997) was not accessed. The authors claim to obtain the maximum life span estimate (60 years) from the AnAge database (Tacutu et al. 2018), which states 13 years for *P. ruber* and 44 years for *P. roseus* (with an unconfirmed observation of 83 years). Neither does the maximum life span for *Larus audouinii* (25 years) match the AnAge database (20.9 years). Using the estimates from the AnAge database further attenuates the findings (not shown).

**Notes on results**

Whittemore et al. (2019) write that “there is even a trend for shorter life spans with longer initial telomere lengths”, but the p-values for these trends are all between 0.3-0.7 (Table 1). Statistical significance tests for the correlations in Whittemore et al. (2019) are not presented in their study but included here (Table 1). It is also possible to account for phylogenetic associations in multivariate regressions, but we cannot see how the authors avoid issues with strong multicollinearity (between e.g. heart rate and body mass) in the models presented in the study (their Tables S5 and S6).

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