**The influence of phylogeny and life history on telomere lengths and telomere rate of change among bird species: a meta-analysis**

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**Electronic Supplementary Material 2: Life history and telomere length data collection**

**Life history traits**

Life history variables were selected as follows: the observed *maximal lifespan* (AnAge database, [[1](#_ENREF_1)], <http://genomics.senescence.info/species/>), the *post-hatching and embryonic growth rates*, *female adult body mass and mean adult body size* [[2](#_ENREF_2), [3](#_ENREF_3)], *egg mass* and *hatching mass* [[4-9](#_ENREF_4)], *mean age at sexual maturity* (age at which an individual is physiologically able to reproduce), *clutch size, incubation duration* and *age at fledging* (when chicks leave the nest) [[10](#_ENREF_10), [11](#_ENREF_11)], and *post-fledging parental care* (as the number of days fledged chicks stay with their parents) [[12](#_ENREF_12)]. All those data were crossed-checked with sources of general information on the species’ biology [[1](#_ENREF_1), [12](#_ENREF_12), [13](#_ENREF_13)]. We also examined previous reviews using a meta-analysis approach on bird growth rate, longevity or telomere length to build our dataset [[14-16](#_ENREF_14)]. When records differed between sources, we choose to take the mean value for all variables, except the *observed maximal lifespan* for which we took the highest recorded value. *Observed maximal lifespan* was previously shown to be strongly related to telomere biology in birds [[15](#_ENREF_15)] and is likely to be more representative of endogenous ageing processes than mean lifespan, being independent of exogenous causes of mortality (*e.g.* predation). Available data for adult female body mass was missing for 6 species, for which we relied on mean adult body mass (*Chrysolophus pictus*, *Amazona amazonica*, *Aphelocoma ultramarina*, *Cepphus grylle*, *Tachymarptis melba*, *Uria lomvia*).

**Bird telomere length**

When data were only available in the form of figures, we extracted the values using GetData Graph Digitizer 2.26 (<http://www.getdata-graph-digitizer.com>). In addition, unpublished data were requested from researchers for two species, the Alpine swift (*Apus melba*, P. Bize pers.com.) and the Barnacle goose (*Branta leucopsis*, A. Pauliny pers.com.). Sample size for *Adult TL* varied from 1 to 104 (mean value ± SE, 20.9 ± 2.9, ESM 1). Telomere length data collected consisted of average value *per* species within adult life stage, but we did not include age-class because this would have reduced the sample size drastically. Therefore, we did not include age in our analysis of telomere length – life history / growth patterns, which may reduce (but not increase) our chances of detecting biological patterns. However, we conducted a separate analysis on *Chick TL* for those species were the data were available, and an additional one on telomere length rate of change (TROC). Avian telomeres have the peculiarity of being distributed over three classes of sizes, from kb to Mb [[17](#_ENREF_17)], but TRF measurements on which we relied do not use Mb sizes. However, ultra-long telomeres may generally shorten more during the nestling stage than the adult stage [[18](#_ENREF_18)], thereby being of less interest in our study. This methodological limit must be kept in mind, with the global idea that the rate of telomere shortening, which leads to the shortest telomeres, has been previously shown to be related both to embryonic growth rate in common terns (*Sterna hirundo*) [[19](#_ENREF_19)] and to maximum lifespan in birds [[15](#_ENREF_15)]. Dunlin and Sand martin TRF are from [[20](#_ENREF_20)], for which the method of TRF measurement was since then criticized [[21](#_ENREF_21)]. However, running our analysis without those two species did not change the significant results, and we chose to keep them in our study. We also check that data from old studies using traditional Southern blot technique (*e.g.* [[17](#_ENREF_17)]) instead of the more recent in-gel hybridization did not alter the significance of the presented results.

**Figure ESM 2**

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**Flow diagram describing the different phases of selection of studies and dataset of telomere length values determined by telomere restriction fragment (TRF) method (n = number of studies).**

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