

1 **Telomere length vary with sex, hatching rank and year of birth in little owls,**

2 ***Athene noctua***

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15

16 **Abstract**

17 Telomeres are non-coding DNA sequences located at the end of linear chromosomes,  
18 protecting genome integrity. In numerous taxa, telomeres shorten with age and telomere  
19 length (TL) is positively correlated with longevity. Moreover, TL is also affected by  
20 environmental stressors and/or resource-demanding situations particularly during early-life.  
21 Thus, TL has been used as a physiological marker of individual quality and also as an indicator  
22 of population trend in conservation physiology. In this study, we investigated the effects of  
23 hatching rank, year of birth (2014 to 2017), sex and nest environment on TL of 137 little owls  
24 nestlings (*Athene noctua*). Little owls' populations in Europe showed a marked decline in the  
25 end of the 20th century. Nowadays, in the studied Alsatian population, the population is  
26 increasing. In this study, our results indicated that telomeres are longer in females and,  
27 independently of sex, in nestlings with the highest body condition. There was also a negative  
28 effect of hatching rank but only for last-hatched nestlings in large clutches of 5 nestlings. We  
29 did not find any effect of the environmental covariates on nestlings' TL. Finally, we found that  
30 nestlings' TL were shorter the last year of the study, while nestlings' body condition stayed  
31 unchanged over the same period. This result is intriguing given the local positive population  
32 dynamics and is further discussed in the context of physiological conservation. Future studies  
33 should investigate the link between reduced TL and survival prospects in this species.

34

## 35 **Introduction**

36 Telomeres are non-coding DNA structures, located at the end of the linear chromosomes,  
37 serving as a safe-keeper for preservation of coding DNA over cell duplication (Blackburn,  
38 1991). Thanks to the formation of a capped structure with specific shelterin proteins,  
39 telomeres help the cell to distinguish real chromosome ends from DNA breaks, thereby  
40 avoiding unappropriated cell emergency responses. Still, this telomere status is degrading  
41 over time, due to the progressive loss of telomere sequences at each cell division, affecting its  
42 functionality and triggering cell senescence (Blackburn, 2000). In addition, telomere  
43 sequences are enriched in GC bases, making them highly sensitive to a well-known ageing  
44 mechanism, the oxidative stress (von Zglinicki, 2002; Reichert & Stier, 2017) (but see  
45 Boonekamp *et al.*, 2017). Such a stress-related property triggered the interest of evolutionary  
46 biologists to study how telomeres (length or dynamics) may vary with age and thus be used  
47 as a proxy to address the question of the existing variance in inter-specific longevity  
48 (Hausmann *et al.*, 2003; Dantzer & Fletcher, 2015; Tricola *et al.*, 2018; Criscuolo *et al.*, 2021)  
49 or inter-individual differences in lifespan and fitness (Beaulieu *et al.*, 2011; Foote *et al.*, 2011;  
50 Boonekamp *et al.*, 2014; Nettle *et al.*, 2017; Bichet *et al.*, 2020; Chatelain *et al.*, 2020;  
51 Fitzpatrick *et al.*, 2021; Sheldon *et al.*, 2021; Salmón & Burraco, 2022).

52         The importance of how early life conditions affect inter-individual telomere length  
53 quickly appears as a key question to understand how somatic growth may shape individual  
54 life trajectories in the context of life history trade-offs (Metcalf & Monaghan, 2003;  
55 Monaghan & Ozanne, 2018). This is based on the observation that growth is a period of high  
56 energy metabolism (2-6 times basal metabolic rate, e.g. Kirkwood, 1991) to fuel intense rate  
57 of cell division, which is likely to be costly in terms of telomere erosion (Vedder *et al.*, 2017;  
58 Spurgin *et al.*, 2018). Studies have shown juveniles exposed to challenging conditions in early

59 life to have shorter telomeres. This could be due to reduced investment in somatic  
60 maintenance as a consequence of low resource availability when conditions are harsh  
61 (Herborn *et al.*, 2014; Nettle *et al.*, 2015, 2017; Reichert *et al.*, 2015; Angelier *et al.*, 2017;  
62 Quque *et al.*, 2021). Interestingly, telomeres may also be affected during the pre-hatching  
63 developmental period. For instance, temperature instability during egg development triggers  
64 shorter telomere length at hatching in Japanese quail (*Coturnix Japonica*, Stier *et al.*, 2020),  
65 and decreasing incubation temperature in the common tern (*Sterna hirundo*) slows down  
66 growth rate and preserve telomere length in matched-body sized hatchlings (Vedder *et al.*,  
67 2018). Yet, telomere dynamics are not only affected by stress effects. Producing eggs is costly  
68 for the female, and depending on maternal characteristics and environmental conditions, we  
69 can expect an adjustment of egg characteristics that will shape consequent embryonic traits  
70 (Williams, 1994; Groothuis & Schwabl, 2008). As such, a large diversity of egg components  
71 (like yolk and hormones), that may be positively or negatively correlated with each other, may  
72 vary and modulate future offspring phenotype (Postma *et al.*, 2014; Williams & Groothuis,  
73 2015). In addition, because an entire clutch is produced over sequential laying of consecutive  
74 eggs, intra-clutch variability in egg traits may be part of a mother strategy of adaptation of the  
75 chick's phenotype, and is then expected to follow the laying order (Groothuis *et al.*, 2005). In  
76 particular, according to the brood reduction hypothesis, it is expected that the probability of  
77 survival of last hatched nestlings (from last laid eggs) will be smaller than that of first hatched  
78 ones in case of harsh conditions (Lack, 1947; Amundsen & Slagsvold, 1996). Thus, we can  
79 expect maternal investment to decrease over the laying sequence. Telomere length is not an  
80 exception, and progressive shortening has been observed within clutch laying order in captive  
81 zebra finches (*Taeniopygia guttata*, Noguera *et al.*, 2016) . In this study, the astonishing result  
82 is that the difference in embryonic telomere lengths between the 1<sup>st</sup> and the last laid eggs

83 represents 60% of the telomere loss an offspring will show over its first year of life. This source  
84 of variation in telomere length may be important to consider since many studies have shown  
85 negative consequences of telomere erosion on future individual fitness, *e.g.* jackdaws (*Corvus*  
86 *monedula*, Boonekamp *et al.*, 2018), king penguins (*Aptenodytes patagonicus*, Geiger *et al.*,  
87 2012) or in wild purple-crowned fairy-wrens (*Malurus coronatus coronatus*, Eastwood *et al.*,  
88 2019), to name a few. Still, we lack data on the effect of laying order in many bird species and  
89 on how laying order effect on telomere length may vary in relation to additional stress sources,  
90 like environmental conditions in the wild (but see Kärkkäinen *et al.*, 2021).

91         Our study is based on 4 years of data from a wild population of Little Owl (*Athene*  
92 *noctua*) reproducing in artificial nestboxes. All nestlings are ringed and measured before  
93 fledging. After checking for hatching rank and environmental effects on chick phenotype, we  
94 used telomere length measurements made on individual feather sampling to test how nestling  
95 telomere length varied with hatching rank and with the local characteristics of nest  
96 environment. To do so, we controlled for nestling sex, age, body condition, clutch size and  
97 year of birth. To estimate nest environment characteristics, we calculated the proportion of  
98 orchards, meadows, crops, buildings, water and forests around each nest box from land use  
99 maps. In central Europe, the Little Owl is a bird species associated with traditional farmlands  
100 and its optimal habitat should provide cavities, perches for hunting and short herbage with  
101 invertebrates and small rodents (herbage size is linked to prey accessibility and availability,  
102 van Nieuwenhuysen *et al.*, 2008). In particular, meadows and orchards are supposed to be food-  
103 rich habitats (Michel *et al.*, 2017).

104         We predicted last hatched nestlings to be in worse condition (body mass, telomere  
105 length) than first hatched nestlings according to the brood size reduction hypothesis. We also

106 predicted shorter telomeres in broods raised in unfavourable environments, *i.e.* more  
107 proportion of buildings, water and forests around the nest box.

108

## 109 **Material and Methods**

### 110 *Model species and data collection*

111 The Little Owl is a small nocturnal raptor living in open or semi-open areas, such as farmland  
112 or orchards (van Nieuwenhuysse *et al.*, 2008). The Little Owl is territorial and breeds in cavity,  
113 including artificial nestboxes. In Alsace (France), numerous ringers and volunteers from the  
114 French league for the protection of birds (LPO) installed and maintained more than 1,500 nest  
115 boxes since 2006, thereby monitoring the yearly reproductive success of the local population.  
116 Females lay 2-6 eggs in April, hatching occurs *ca.* 1 month later and nestlings are ringed  
117 between 15-35 days of age. At ringing, nestlings' body mass was measured with an electronic  
118 balance to the nearest 0.1 g, as well as tarsus length with a calliper to the nearest 0.1 mm, and  
119 the length of the third primary feather with a ruler to the nearest mm. The measure of the  
120 feather allows us to approximate the age of the nestling with the formula:  $\text{age} = (\text{length of the}$   
121  $\text{feather} + 36) / 3.3$ , where the age is in days and the length of the feather is in mm (Juillard, 1984;  
122 Hameau *et al.*, 2015). This formula is valid between age 15 and 35 when there is a linear  
123 growth of the feather. Using the age of each nestling in a nest, the hatching rank was deduced.  
124 When two nestling had the same estimated age, we assigned them the same hatching rank.  
125 We also collected 3-6 ventral feathers that are stored in ethanol 70% at ambient temperature  
126 during fieldwork and then at 4°C in the lab.

127 For this study, we used data collected on 142 nestlings from 39 broods from 2014 to 2017. All  
128 those broods had more than 1 chick. We included in our study only broods with more than 1

129 chick in order to estimate the effect of hatching rank (n=3, n=14, n=16, n=6 for broods with  
130 respectively 2, 3, 4 and 5 chicks).

### 131 *Land use around the nestbox*

132 To determine the land use around the nest boxes, we used a land cover database for Alsace  
133 (Source: BdOCS CIGAL v2 2011/2012, [www.geograndest.fr](http://www.geograndest.fr)) which categorizes all the habitats  
134 found in our study area. We used the software QGIS version 3.4.14 (QGIS Development Team,  
135 2020) to map the active nest boxes and create a circular buffer zone of a 150 m radius around  
136 each one of them. This radius was established thanks to data on home range size (Exo, 1992;  
137 Génot, 2005) and the field observations made during the breeding season. Due to the high  
138 number of habitats, we made groupings based on the environmental characteristics of each  
139 variable to calculate the area (m<sup>2</sup>) covered by each land type within the buffer zones. Our final  
140 nest environment included six categories: (1) buildings, (2) meadows, (3) crops (crop fields,  
141 hedges, and vineyard), (4) orchards, (5) forest and (6) water. Because of the rarity of the last  
142 two categories, forest and water were pooled together. The surface of habitat of the different  
143 categories were correlated with each other and thus we used in the model only the proportion  
144 of surface of favorable habitat defined as the proportion of meadows and orchards in the  
145 buffer.

### 146 *Relative telomere length (RTL) measurement and sexing*

147 Genomic DNA was extracted from feathers using an adapted protocol of the NucleoSpin Tissue  
148 kit (Macherey Nagel, Düren, Germany). RTL was measured in the 142 nestlings in one 384-  
149 wells plate, using the quantitative PCR (qPCR) methodology (see Electronic Supplementary  
150 Material, ESM). Intra-plate repeatability of RTL (ICC, see (Eisenberg *et al.*, 2020)) was of 0.769.  
151 Molecular sexing of nestlings was determined using the same extracted DNA (following  
152 Griffiths *et al.*, 1998). Briefly, the technique is based on the existence of two conserved CHD

153 (chromo-helicase-DNA-binding) genes that are located on the sex chromosomes. The CHD-W  
154 gene is located on the W chromosome (only in females) and the CHD-Z gene is located on the  
155 Z chromosome (both in males and females). For technical reasons, sex could not be  
156 determined in 5 nestlings. All the statistical analyses were performed on the remaining 137  
157 nestlings with known sex.

### 158 *Statistical analyses*

159 We used R version 4.3.1 (R Core Team, 2023) to compute mixed models (package lme4 version  
160 1.1-33 and lmerTest version 3.1-3). In all statistical models, brood identity was included as a  
161 random factor to account for the non-independence of nestlings of the same brood. We  
162 checked models' assumptions (homoscedasticity, normal distribution of residuals) graphically  
163 using the package DHARMA (version 0.4.6). We assessed multicollinearity among predictors  
164 by calculating variance inflation factor, VIF (package car, version 3.1-2).

### 165 Individual phenotypic characteristics

166 To test for inter-individual variation in body condition, we first calculated the Scale Mass Index  
167 (SMI) following the formula of Peig & Green (2009):  $SMI = M_i [L_0/L_i]^b$  where  $M_i$  and  $L_i$  are the  
168 body mass and size measurements of individual  $i$ ,  $b$  is the slope of the standardised major axis  
169 (SMA) regression of log-transformed  $M$  on log-transformed  $L$  and  $L_0$  is the arithmetic mean of  
170  $L$  for the study population. We then computed a linear mixed model with SMI as a dependent  
171 variable and hatching rank, sex, nestling number, nestling age, cohort, the proportion of  
172 meadows and orchards, the interaction between hatching rank and sex, and the interaction  
173 between hatching rank and the proportion of meadows and orchards as fixed effects. From  
174 this global model, we fitted every possible model and then selected a set of top models (AICc  
175 threshold of 2). Then, if the null model was not the best model, we averaged the models from  
176 these top models set (conditional average, package MuMIn, version 1.47.5).



177 Inter-individual variation in Relative Telomere Length

178 RTL were log-transformed before analyses. We computed a linear mixed model with individual  
179 covariates (hatching rank, sex, the interaction between hatching rank and sex, nestling  
180 number, nestling age, SMI and cohort) and environmental covariates (the proportion of  
181 meadows and orchards, the interaction between hatching rank and this proportion) as fixed  
182 effects. The model selection procedure was the same as described above.

183

184 **Results**

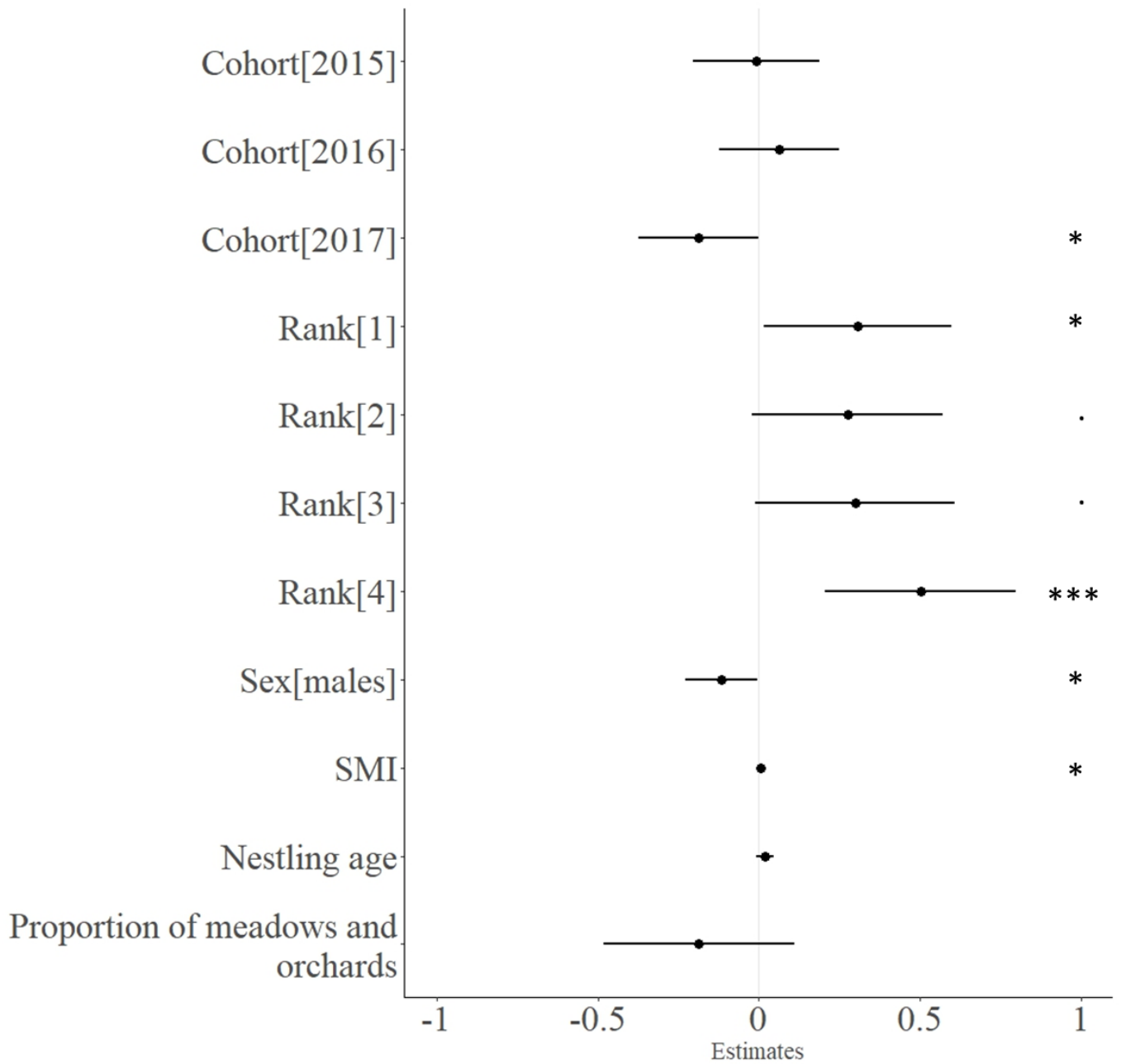
185 Individual phenotypic characteristics

186 Concerning individual covariates, there were no significant variables that explained variation  
187 in SMI in our models. The fixed effects retained in the top models set (5 models) were the  
188 proportion of meadows and orchards, nestling number and sex (see Table S1) but their effects  
189 were not significantly different from 0 (see Figure S1). This is consistent with the fact that the  
190 null model was in the top models set (see Table S1).

191

192

193 **Figure 1. Forest-plot of estimates for the average model of relative telomere length and**  
 194 **individual covariates (see Table S3).** Reference level for sex is females, for cohort is 2014  
 195 (the first year of the study) and for rank is 5 (last hatched chicks). Significance levels are  
 196 annotated with asterisks: \*\*\*  $p < 0.001$ , \*\*  $p < 0.01$ , \*  $p < 0.05$ , .  $p < 0.10$



197  
 198

199

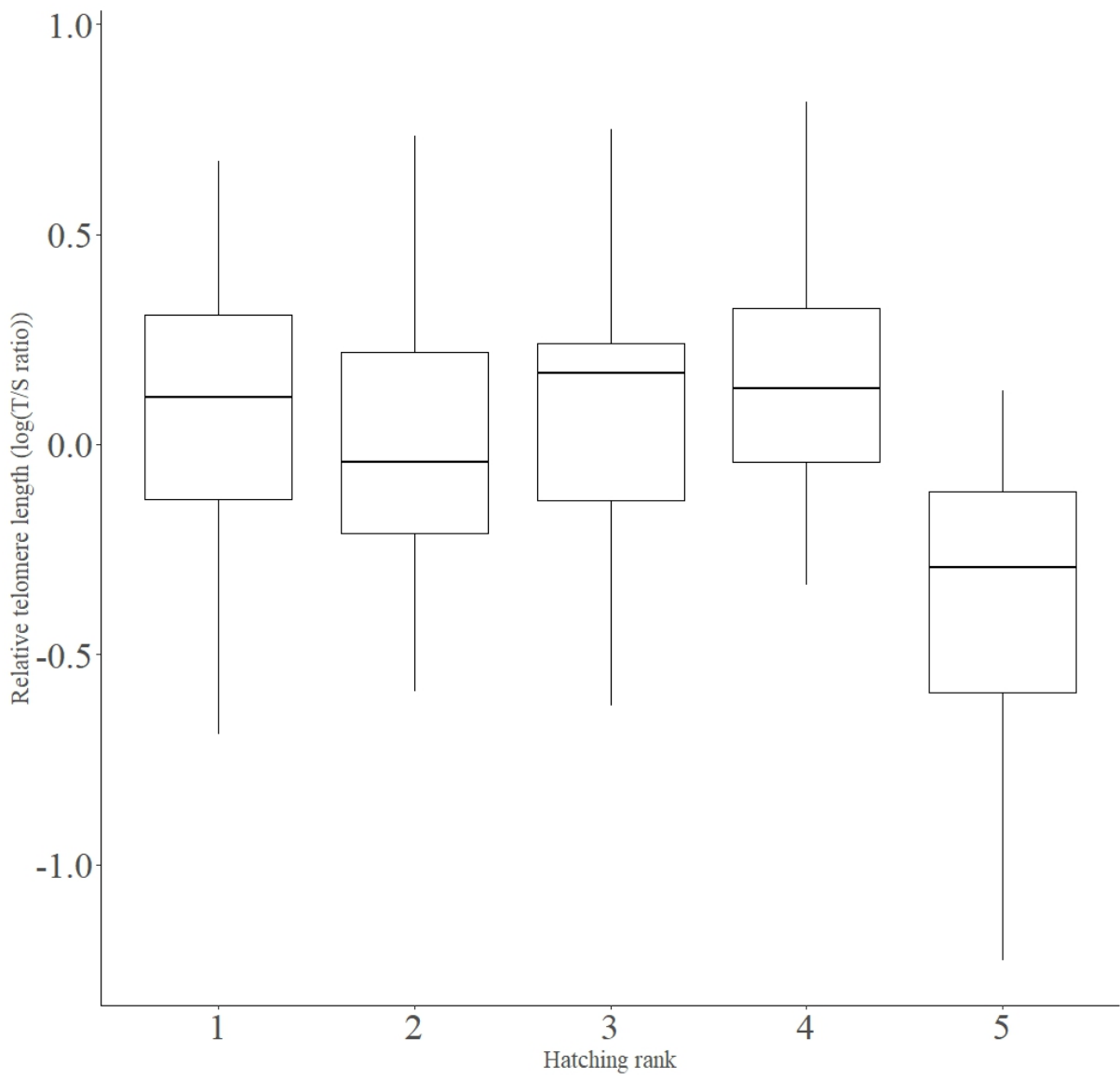
200

201 Inter-individual variation in Relative Telomere Length (RTL)

202 Concerning individual covariates, RTL was not dependent on nestling number and there was  
203 no interaction between rank and sex, or between rank and the proportion of meadows and  
204 orchards. The variables in the top models set (6 models) were rank, sex, SMI, cohort, nestling  
205 age and the proportion of meadows and orchards (Table S3, Figure 1). Males have significantly  
206 shorter telomeres than females and there is a small significant positive effect of SMI on RTL  
207 (Figure 1). In addition, last hatched nestlings have shorter telomeres but only in the largest  
208 brood of 5 nestlings (Figures 1 and 2). The effect of the year of birth is significant for the last  
209 year of study, meaning that individuals born in 2017 have shorter telomeres than individuals  
210 born earlier (Figures 1 and 3). Concerning environmental covariates, the proportion of  
211 meadows and orchards was kept in the best model but has no significant effect on RTL (Figure  
212 1).

213

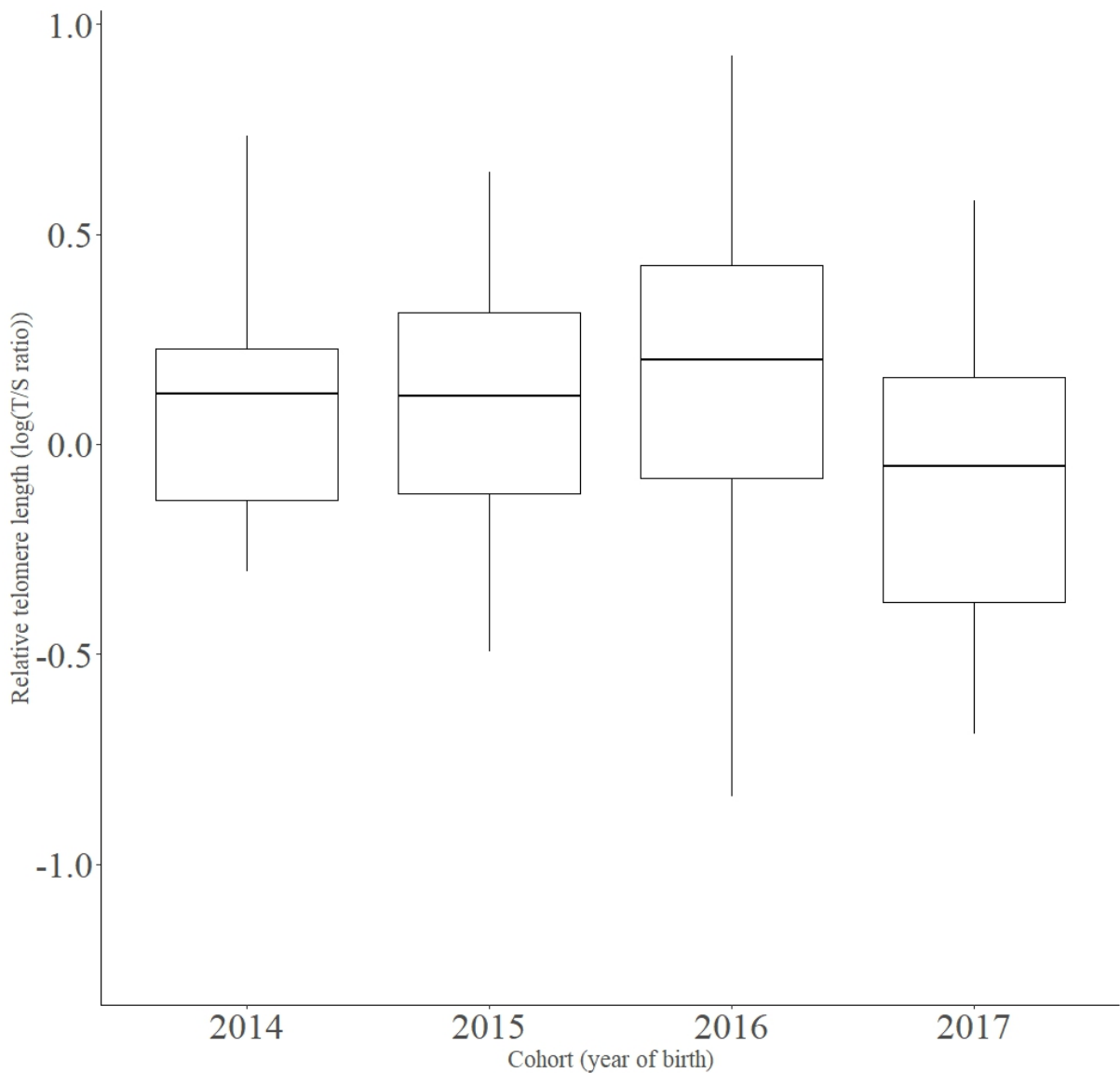
214 **Figure 2. The effect of hatching rank on the relative telomere length before fledging.**



215

216

217 **Figure 3. The effect of the cohort on the relative telomere length before fledging.**



218

219 **Discussion**

220 Based on the current knowledge on growth and telomeres in bird nestlings, we initially  
221 predicted that RTL of little owl nestlings will be: (i) negatively related to the hatching rank and  
222 (ii) negatively affected by the unfavourable nature of the nest surroundings. Our results  
223 indicated that RTL are longer in females and, independently of sex, in nestlings with the  
224 highest body condition. They also supported a mixed negative effect of hatching rank and  
225 intra-brood competition on little owl nestlings' RTL, i.e. detectable only in the largest brood  
226 size, suggesting that the effect of hatching rank on telomeres is dependent on a threshold

227 effect in this species. We did not find an effect of the environmental covariates on nestlings'  
228 RTL. Finally, our scan of nestlings' RTL over years surprisingly underlined a possible progressive  
229 shortening, independent of any changes in body condition.

230 Little owl nestlings' RTL were shorter in the last year of the study (2017) in comparison  
231 to previous years (2014 onwards). Both telomere data and such year effect are of great  
232 interest in the context of conservation physiology aiming at developing physiological markers  
233 of individual quality to infer consequences at the population level (Beaulieu & Costantini,  
234 2014; Lea *et al.*, 2018). Telomeres are good candidate to be such marker because telomere  
235 length at a given age is not reflecting only the negative effects of time on the cells (i.e.  
236 chronological age), it also points out the cumulative effects of stressors encountered over time  
237 that may accelerate the rate of loss of telomere ends over the expected rate at a given age for  
238 a given species (Asghar *et al.*, 2015; Louzon *et al.*, 2019; Chatelain *et al.*, 2020; Salmón &  
239 Burraco, 2022). Thus, the use of telomere assay is potentially providing data that are useful to  
240 establish survival rates at specific age stages, like the nestling period. Since deleterious  
241 environmental conditions can affect negatively telomere length, the period of growth is  
242 supposed to be the life stage where telomere sequences can be the most impacted (Salomons  
243 *et al.*, 2009; Young *et al.*, 2013; Monaghan & Ozanne, 2018). Beside the classical explanation  
244 that the growing period is particularly sensitive to environmental stressors because the rate  
245 of cell division and/or the oxidative metabolism are higher in a growing organism, it is likely  
246 that chicks can just hardly escape the trade-off between growth and survival. As such,  
247 sustaining a fast (but not too fast, see below) rate of growth to shorten as much as possible  
248 the nestling period may be done at a cost for telomere length. Thus, depending on the  
249 harshness of early life environment, erosion of telomeres can be accelerated for a given age  
250 (e.g. Boonekamp *et al.*, 2014; Stier *et al.*, 2015), leading the fledglings to be grown

251 physiologically old. In addition, variation in growth rate, due to changes in food availability,  
252 may affect telomere length and not body mass or body condition. As an example, growth rate  
253 may accelerate after a stunt when optimal feeding conditions are re-established, which are  
254 known to trigger transient over-optimal compensatory growth rate and faster telomere  
255 erosion (Metcalf & Monaghan, 2001; Geiger *et al.*, 2012). This has, theoretically, obvious  
256 consequences for the individuals in terms of survival prospects and recruitments as adult  
257 breeders in the population, as early life telomere length or rate of telomere loss have been  
258 shown to predict future individuals' survival (Boonekamp *et al.*, 2014; Watson *et al.*, 2015;  
259 Wood & Young, 2019). Consequently, it also has the potential to affect the population  
260 dynamics. First conceptualized few years ago (Stindl, 2004), such a hypothesis was recently  
261 supported by studies conducted on ectotherms' populations (Dupoué *et al.*, 2017, 2022). In  
262 the common lizard populations studied, analysis of telomere length in yearlings of populations  
263 showing different risks of collapsing due to local global warming pointed out reduced mean  
264 telomere length in the most endangered populations (Dupoué *et al.*, 2017). Thereafter, the  
265 same group showed that short telomeres were already inherited in neonates of declining  
266 populations, thereby suggesting (epi)genetic roots, i.e. progressive telomere shortening being  
267 not only the result of bad early life conditions (Dupoué *et al.*, 2022). We cannot draw the same  
268 conclusions in our case, particularly because (i) our data indicate that 2017 was the only year  
269 with shorter telomeres and (ii) we lack data on inter-generational variation of telomere length.  
270 It can be noted that in vertebrates, heritability estimates are moderate (Chik *et al.*, 2022), but  
271 this recent meta-analysis has no data on raptors (Chik *et al.*, 2022). In addition, as low rates of  
272 recruitments of juveniles as first-breeders is an important determinant of population decline  
273 in the little owl (Le Gouar *et al.*, 2011), the link between reduced telomere length and survival  
274 prospects of nestlings needs to be established. Finally, this result is counter-intuitive in our

275 study population of little owl since the population is expanding and not decreasing (Bersuder  
276 & Wassmer, 2020), contrary to other populations (Andersen *et al.*, 2017). Whether 2017 is a  
277 transient year with unknown bad conditions for chicks or is actually the start of a longer  
278 adverse period for our population is currently unknown. Thus, the effects of yearly variations  
279 in food availability, intra-nest competition or density on telomere length need to be addressed  
280 in future studies.

281 Little owl female nestlings had longer telomeres than male ones. This has several  
282 implications for our understanding of sex-differences in telomere dynamics and of its meaning  
283 in terms of sex-biased life history. Differences in telomere length in relation to sex has been  
284 previously illustrated in several taxa (reviewed in Barrett & Richardson, 2011), and particularly  
285 in birds with sex-biased body size or investment in reproduction, producing no consistent  
286 male-female differences (e.g. Caprioli *et al.*, 2013; Remot *et al.*, 2020; Saulnier *et al.*, 2022 for  
287 no sex differences) (e.g. Bauch *et al.*, 2020 for sex differences). In our study, sex-differences  
288 in RTL were observed at the nestling stage, with longer telomeres in the females. A previous  
289 study showed that females were slightly but consistently of bigger size (Tschumi *et al.*, 2019),  
290 however it is not the case in our population. Yet, we did not investigate nestlings growth rates,  
291 which can be different even if the final size and/or body mass is similar (e.g. Criscuolo *et al.*,  
292 2008). Higher growth rates are usually associated with shorter telomeres (Geiger *et al.*, 2012;  
293 Monaghan & Ozanne, 2018) and generally the larger sex is growing at a slower rate in sexually  
294 dimorphic bird species (e.g. Teather & Weatherhead, 1994). This may potentially account for  
295 our sex-difference in telomere length as females may dilute the growth-body maintenance  
296 trade-off over a longer period. However, we also found that, independently of sex, nestlings  
297 in better body condition had in general longer telomeres. Thus, it is either unlikely that little  
298 owl nestlings had to face such a growth-body maintenance trade-off, or that our result is



299 driven by high quality individuals that can sustain growth without showing any associated cost  
300 in terms of telomere loss. Given that body mass is a determinant of survival from hatching to  
301 fledging in little owl (Tschumi *et al.*, 2019), nestling telomeres rather acts as a proxy of  
302 individual quality (Angelier *et al.*, 2019). In addition, our results do not match with the idea  
303 that the heterogametic sex (*i.e.* females) would be more prone to telomere erosion than the  
304 homogametic one (*i.e.* males) due to the unguarded expression of deleterious alleles of sex  
305 chromosomes for telomere maintenance (see Barrett & Richardson, 2011; Remot *et al.*, 2020  
306 for a deep discussion related to telomere dynamics). One alternative explanation lies on  
307 optimal parental care towards the offspring sex with the highest chance of survival  
308 (Hasselquist & Kempenaers, 2002). It has been shown previously that females have a higher  
309 survival probability from hatching to fledging, independent of any variation in body mass  
310 (Tschumi *et al.*, 2019). However, it is not known whether this sex-difference persists in older  
311 individuals. In that context, the parents would favour female individuals, meaning that within  
312 little owl broods females may, on average, benefit from better access to food resources due  
313 to specific parental investment. This may lead to an attenuated body maintenance (*i.e.*  
314 telomere length) and growth rate trade-off. Still, further study in our case is needed to  
315 determine whether adaptive brood sex ratio actually occurs, since it may result from non-  
316 adaptive additional effects (e.g. sex specific mortality, see Bortolotti, 1986; Hasselquist &  
317 Kempenaers, 2002).

318         The hypothesis that RTL is an indicator of quality is further supported by the fact that,  
319 in the largest clutches, the last hatchling of little owl presented the shortest telomeres. Even  
320 if our sample size is small (*i.e.*, 6 clutches with 5 eggs), our data are in accordance with the  
321 brood size reduction hypothesis that predicts a lower investment with laying order. Still, our  
322 data would restrict such an effect to the last laid egg. We cannot distinguish between effects

323 of the laying order *per se* on RTL (see introduction) and postnatal effects. Postnatal effects  
324 may arise from selective parental care as discussed above. Last-hatched nestling may also  
325 suffer from intra-brood competition. Indeed, in a brood, larger nestlings have a competitive  
326 advantage compared to smaller nestlings for feeding (“Competitive advantage hypothesis”,  
327 Anderson *et al.*, 1993). A previous experiment testing the effect of competitive disadvantage  
328 within a brood, based on the size of the nestlings cross-fostered among clutches, highlighted  
329 an interesting increased telomere attrition of less competitive nestlings without affecting  
330 body mass growth (in European starlings, Nettle *et al.*, 2015).

331 Finally, our study only suggested non-significant effects of nest surroundings. In other  
332 studies, local habitat types around nests and also the heterogeneity of habitats available have  
333 been shown to affect reproductive output in our species (Thorup *et al.*, 2010; Michel *et al.*,  
334 2017). Moreover, it has been shown that the home range size is dependent on the  
335 environment around the nest and also is different between males and females (Michel *et al.*,  
336 2017). Thus, it may be important to consider the habitat at a fine scale. Future studies should  
337 explore how environmental quality, food resources, parental care, chick growth, intra-brood  
338 competition and sex-specific susceptibility to stressors are intertwined factors that determine  
339 offspring telomere length and how all these factors affect population dynamics of little owls.

340

341 **Ethics statement.** This work is in accordance with the French legislation concerning the  
342 capture and the biological sampling of wildlife. All the ringers of the project had received  
343 ringing licenses and authorizations for feather sampling from the CRBPO (National Museum  
344 of Natural History, Paris, France) as part of a program led by Bertrand Scaar (PP N°454).

345 **Data accessibility.** Datasets used in this study are openly available on zenodo (doi:  
346 10.5281/zenodo.7701530).

347 **Authors' contributions.** JB and FC conceived the study. BS and volunteers collected the data.  
348 SZ developed and performed the sexing and qPCR measurements. IF sorted the samples and  
349 calculated the land use around nest boxes. JB and FC ran the statistical analyses and, with SZ  
350 for the ESM, wrote the first draft of the manuscript. All authors provided comments on the  
351 manuscript and agreed on the final version of the manuscript to be submitted for publication.

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592 **Amplification of telomere repeats using q-PCR methodology**

593 The protocol for DNA extraction from feathers provided us with sufficient amount of DNA to  
594 run both sexing and telomere determinations. One to three feathers per individual were selected  
595 and a 0.5-1 cm piece from each feather were cut in small pieces with a sterilized scissor. After  
596 digestion, feather quills will remain unlysed. For samples containing unlysed quills, we  
597 centrifuge briefly and we transfer the supernatant to another tube before proceeding with step  
598 4 of the standard protocol.

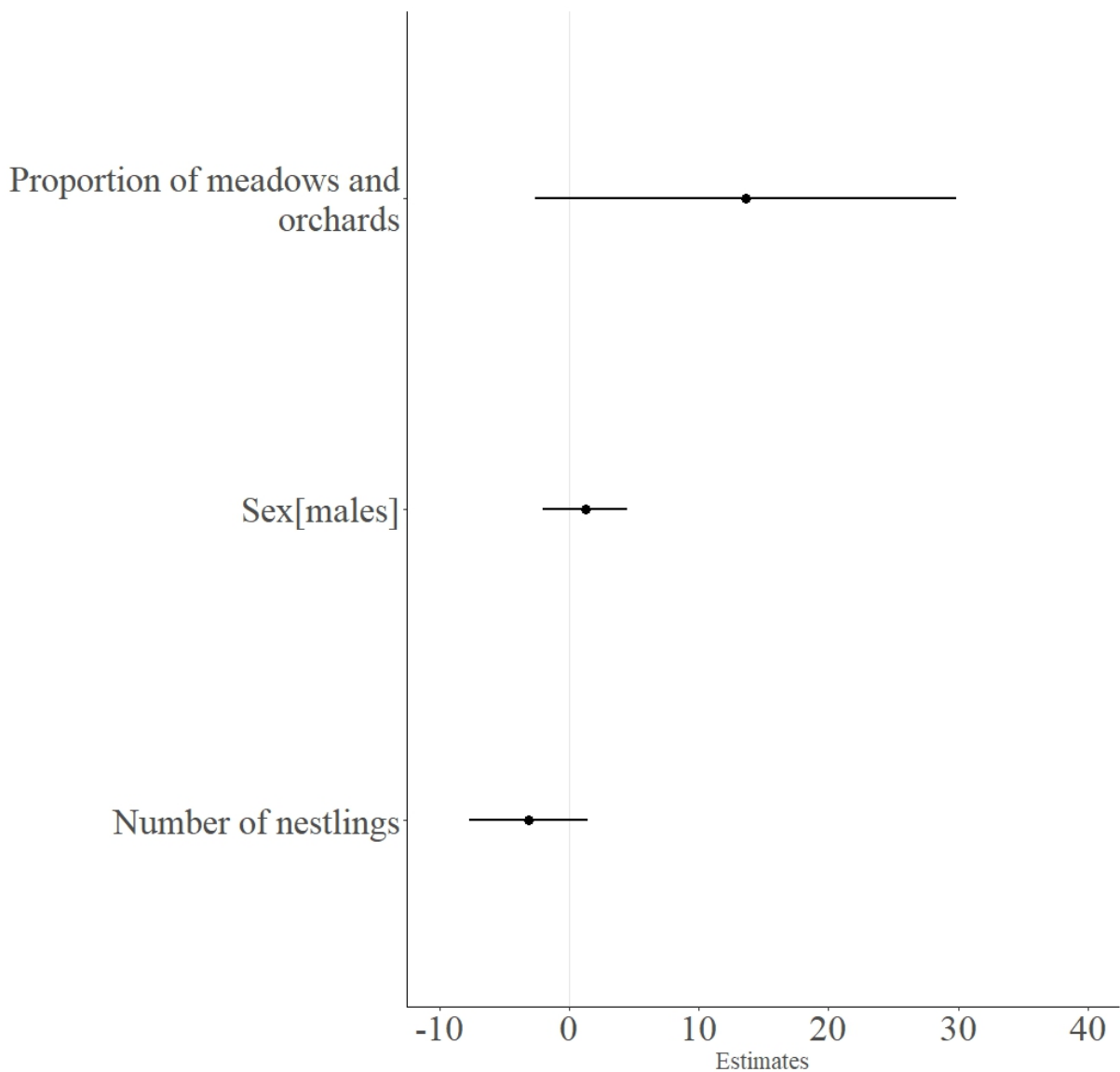
599 Individual relative telomere length (RTL) were obtained following the qPCR methodology  
600 previously used in several bird species by our group (*e.g.* Criscuolo et al. 2009, Bize et al. 2009,  
601 Criscuolo et al. 2020, Chatelain et al. 2021). DNA quantity and quality were assessed based on  
602 spectrophotometer absorbance (Nano-Drop 1000, Thermo Fisher Scientific, Waltham, MA,  
603 USA, ratios A260/280 and A260/230) and gel migration. Individual DNA were all diluted to a  
604 concentration of 5.0 ng/ $\mu$ L, and further used for RTL determination by qPCR. To control for  
605 variation in DNA concentrations among diluted samples (due to potential pipetting errors),  
606 which may induce a methodological bias to the final RTL values, we amplified, for each  
607 individual, a genomic DNA sequence, defined so far as non-variable in copy numbers. The gene  
608 used in our species was RAG-1 gene (recombination activating protein 1 gene, NCBI number  
609 EU348872.1). Amplifications were conducted in two 384 wells-plates filled by a calibrated  
610 automated liquid handling workstation (Epmotion, Eppendorf, Montesson, France), using one  
611 distinct plate for control gene and telomere amplifications, due to the different qPCR conditions  
612 due to primers sequences properties. Conditions of amplification were 2 min at 95°C followed  
613 by 40 cycles of 15 s at 95°C, 30 s at 56°C and 1 min at 72°C (control gene) and of 2 min at  
614 95°C followed by 30 cycles of 15 s at 95°C, 30 s at 56°C and 30 sec at 72°C, (telomere  
615 sequence). Reactions were done in a master mix prepared for each primer set, with 5  $\mu$ L GoTaq  
616 QPCR Mix (Promega, Madison, WI, USA). We used 10 ng of DNA (in a volume of 2  $\mu$ L), to  
617 which we added the telomere primers at a concentration of 200 nM or the control gene primers  
618 at 400 nM (for a final reaction volume of 10  $\mu$ L in each well, completed with ultra-pure water).  
619 In both plates (control gene and telomere sequences) we amplified individuals' DNA samples  
620 plus three quality control references. A DNA golden sample (as a mix of 22 individual samples  
621 randomly chosen) that was used as the reference value of 1 for RTL calculations. A dilution  
622 curve obtained from the amplification of a randomly chosen reference sample that was serially  
623 diluted (from 10 to 0.625 ng/mL). Dilution curves enable us to assess quality of control gene  
624 and telomere sequences qPCR amplifications (*i.e.* efficiency values (control gene 0.999;  
625 telomere sequences 0.993) and  $r^2$  (0.993 and 0.995, respectively) of the dilution curves). A  
626 negative control sample (ultra-pure water) to control for putative contaminations of non-bird  
627 DNA. All runs ended by a fusion curve to verify the absence of non-specific amplifications.  
628 RTL values were calculated following Pfaffl (2001), shortly as the ratio between Telomere (T)  
629 and Control gene (S) Cq values, controlled for their respective amplification efficiencies and  
630 expressed relatively to the golden sample T/S value of 1. All samples were run in duplicates  
631 and intra-individual repeatability of RTL, evaluated using the Intra Class Coefficient  
632 (Eisenberg *et al.*, 2020), was of 0.769.

633

634 **Table S1. Top models set for models of SMI.** For continuous variables, each value  
 635 represents the estimate of the effect; for categorical variables, there is a “+” when the variable  
 636 is retained in a model.  
 637 df = degree of freedom. delta = difference of AICc with the model with the lowest AICc.  
 638

Intercept	Nestling number	Proportion of meadows and orchards	Sex	df	AICc	delta
125.8		14.44		4	1057.3	0.00
145.3	-3.52			4	1058.0	0.70
136.7	-2.66	11.93		5	1058.1	0.82
132.3				3	1058.3	0.93
125.3		14.32	+	5	1058.9	1.59

639 **Figure S1. Forest-plot of estimates for the average model from Table S1.** Reference level  
 640 for sex is females.  
 641



642  
 643  
 644

645 **Table S3. Top models set for models of RTL.** For continuous variables, each value  
 646 represents the estimate of the effect; for categorical variables, there is a “+” when the variable  
 647 is retained in a model.  
 648 df = degree of freedom. delta = difference of AICc with the model with the lowest AICc.  
 649

Intercept	Proportion of meadows and orchards	Nestling age	Cohort	Rank	Sex	SMI	df	AICc	delta
-0.82			+	+	+	0.0049	12	103.8	0.00
-0.86				+	+	0.0046	9	104.6	0.81
-1.16		0.019	+	+	+	0.0047	13	104.6	0.83
-0.84	-0.17		+	+	+	0.0055	13	104.9	1.12
-0.86			+	+		0.0046	11	105.3	1.46
-1.23	-0.20	0.021	+	+	+	0.0054	14	105.3	1.48

650  
 651

652 **Supplementary references**

653

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