Spatio-temporal variation in lifelong telomere dynamics in a long-term ecological study

Lewis G. Spurgin[1], Kat Bebbington[1], Eleanor A. Fairfield[1], Martijn Hammers[2], Jan Komdeur[2], Terry Burke[3], Hannah L. Dugdale[2,4] and David S. Richardson[1,5,].

1. School of Biological Sciences, University of East Anglia, Norwich Research Park, NR4 7TJ, United Kingdom

2. Groningen Institute for Evolutionary Life Sciences, University of Groningen, Groningen, The Netherlands

3. Department of Animal and Plant Sciences, University of Sheffield, Sheffield, UK

4. School of Biology, The Faculty of Biological Sciences, University of Leeds, Leeds LS2 9JT, UK

5. Nature Seychelles, Roche Caiman, Mahé, Republic of Seychelles

Correspondence: Lewis Spurgin: l.spurgin@uea.ac.uk; David Richardson: david.richardson@uea.ac.uk

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Abstract

1. Understanding individual-level variation in response to the environment is fundamental to understanding life-history evolution and population dynamics. Telomeres, the protective caps at the ends of chromosomes, shorten in response to oxidative stress, and telomere shortening is correlated with reduced survival and lifespan. Investigating telomere dynamics may help us quantify individual variation in the costs experienced from social and ecological factors, and enhance our understanding of the dynamics of natural populations.

2. Here we study spatio-temporal variation in lifelong telomere dynamics in the Seychelles warbler, *Acrocephalus sechellensis.* We combine long-term life-history and ecological data with a large longitudinal dataset of mean telomere lengths, consisting of 1808 samples from 22 cohorts born between 1993 and 2014. We provide a detailed analysis of how telomere dynamics vary over individual lifespans and cohorts, and with spatio-temporal variation in the social and ecological environment.

3. We found that telomere length decreases with cross-sectional and longitudinal measures of age, and most rapidly very early in life. However, both cross-sectional and longitudinal data suggested that against this overall pattern of shortening, bouts of telomere length increase occur in some individuals. Using a large number of repeated measurements we show statistically that these increases are unlikely to be explained solely by qPCR measurement error.

4. Telomere length varied markedly among cohorts. Telomere length was positively associated with temporal variation in island-wide insect abundance - a key resource for the insectivorous Seychelles warbler - suggesting that the costs associated with living in harsher environments can be studied by investigating telomere dynamics. We also found evidence for sex-specific relationships between telomeres and tarsus length, potentially reflecting differential costs of growth.

5. Our long-term data show that in a natural population, telomere dynamics vary in a complex manner over individual lifespans, and across space and time. Variance in telomere dynamics among individuals is the product of a wide array of genetic, parental and environmental factors. Explaining this variation more fully will require the integration of comprehensive long-term ecological and genetic data from multiple populations and species.

Keywords: Biomarkers; Intra- and inter-individual variation; Life history; Telomere; Seychelles warbler; Senescence

Introduction

A major aim of ecologists and evolutionary biologists is to understand why individuals vary in their response to different environmental factors. Identifying this variation in individual responses to the environment is central to understanding variation in fitness (Lindström 1999), and thus for understanding population and community dynamics (Bolnick et al. 2011). Furthermore, knowledge of the relative impact that different environmental factors exert on individuals, and why individuals may differ in mitigating these costs, is important to understanding evolutionary trade-offs and life-history strategies (Stearns 1992). However, fully quantifying individual-level variation in costs is impossible in wild systems, and thus effective biomarkers that reflect the physiological consequences of individual-level experiences are required.

Telomeres have been proposed to be a potential biomarker of such costs (Monaghan 2014). Telomeres are repetitive DNA sequences at the ends of linear chromosomes that protect against DNA damage. Telomeres generally shorten with age (Müezzinler, Zaineddin, and Brenner 2013; Barrett et al. 2013), and there is evidence from a range of taxa that telomere shortening is fastest in early life (e.g. Frenck, Blackburn, and Shannon 1998; Heidinger et al. 2012). *In vitro* research has shown that telomere shortening can be accelerated by oxidative stress (Von Zglinicki 2002), which can be elevated due to many environmental factors. There is evidence from humans, and from captive and wild animal populations, that telomere shortening is influenced by the conditions experienced during both early life and adulthood (Price et al. 2013; Monaghan 2014; Nettle et al. 2015; Reichert, Criscuolo, and Zahn 2015). Importantly, the extent of telomere shortening is linked to senescence and survival. When telomeres become critically short, cells senesce (Campisi 2003), and the accumulation of these cells has been suggested to result in organismal senescence and death (Wong et al. 2003). The association between telomere length and senescence has inspired a great deal of recent research into telomere evolutionary ecology, and relationships between telomere dynamics and survival or lifespan have been documented in wild populations of several species (Barrett et al. 2013; Stier et al. 2015). As yet, however, there is little direct evidence that the relationship between telomere dynamics and survival is causal (Simons 2015).

Although the causal role of telomeres in senescence and survival is not yet clear, there is mounting evidence that telomeres can act as biomarkers of individual condition and ageing in wild populations. Specifically, telomeres may be able to provide a measure of the ecological stress that an individual has experienced - a signature that can otherwise be difficult to detect (e.g. Schultner et al. 2014; Asghar et al. 2015; Bebbington et al. 2016). There is also evidence that telomere length, measured longitudinally in individuals, can increase as well as decrease (Simons, Stulp, and Nakagawa 2014; Bateson and Nettle 2016), which has important

73 ramifications for our understanding of how telomeres reflect costs. However, such increases in telomere length

74 are often attributed to measurement error (Steenstrup et al. 2013; but see Bateson and Nettle 2016), and as

75 such their ecological significance is unknown.

76 Although a considerable amount of effort has been put into studying telomere dynamics in natural populations,

77 our understanding of the forces responsible for explaining variation in telomere length is still limited.

78 Understanding how different factors shape telomere length variation is important, as before we can use

79 telomeres as a measure of the costs experienced by individuals, we need to know how different developmental,

80 genetic and ecological variables interact to affect telomeres. Telomere length and rates of shortening can vary

81 according to parental characteristics (Njajou et al. 2007; Heidinger et al. 2016), among sexes (Barrett and

82 Richardson 2011; Watson et al. 2017), and with a whole host of environmental conditions, including altitude

83 (Stier et al. 2016), heat stress (Simide et al. 2016) or infection (Asghar et al. 2015). Recent evidence suggests

84 that telomere dynamics are indeed highly variable over individual lifespans, and that even the relationship

85 between telomeres and age can vary markedly among cohorts (Fairlie et al. 2016). To understand which

86 factors best explain variation in telomere dynamics, more studies are required that incorporate telomere

87 variation over entire lifespans with comprehensive, long-term ecological data.

88 The longitudinal study (since 1986) of the Seychelles warbler (*Acrocephalus sechellensis*) population on Cousin

89 Island provides an excellent system for studying telomere dynamics and senescence patterns in the wild

90 (reviewed in Hammers et al. 2015). Due to the isolated nature of the study population (Komdeur et al. 2004)

91 and intensive field monitoring, we have comprehensive ecological and survival data spanning many years (see

92 Methods, below). Environmental conditions and population density on Cousin Island vary across space and

93 time due to weather-induced changes in foliage cover and insect prey availability (Van de Crommenacker et

94 al. 2011). Variation in oxidative stress experienced by individuals is associated with territory quality (Van de

95 Crommenacker et al. 2011). However, the evidence that individual survival and lifespan is associated with

96 spatial variation in early-life territory quality or local density is equivocal and confounded by variation in

97 subsequent life-history parameters (Brouwer et al. 2006; Hammers et al. 2013). There is also variation in the

98 social environment that individual Seychelles warblers experience. Facultative cooperative breeding occurs

99 in this species (Komdeur 1994; Richardson, Komdeur, and Burke 2003; Richardson, Burke, and Komdeur

100 2007), and the presence of helpers (but not other resident non-helpers) in the natal territory is associated

101 with increased survival of offspring later in life (Brouwer, Richardson, and Komdeur 2012).

102 Importantly, we have an established protocol for assessing telomere length in the Seychelles warbler (Barrett

103 et al. 2012; Bebbington et al. 2016). Furthermore, telomere dynamics predict survival independently of

104 age (Barrett et al. 2013) and telomere length is negatively associated with inbreeding (Bebbington et al.

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2016), suggesting that individual variation in telomere length is ecologically relevant in this species. Thus, we have an excellent system in which to determine the impact of different social and environmental conditions experienced by individuals, and to assess how these costs vary over space and time.

In this study, we test how lifelong telomere dynamics are related to environmental variation across 22 Seychelles warbler cohorts. We first study how telomere length and rates of shortening are related to age and sex across all life stages, and how this relationship varies among cohorts, in order to gain an in-depth understanding of the temporal dynamics of telomere changes. We then examine, within individuals, how telomere length changes with age, and statistically test whether observed increases in telomere length over individual lifespans are larger than can be accounted for by measurement error. Finally, we test how telomere length and shortening are related to a wide range of social and environmental variables in order to gain a fuller understanding of the forces driving telomere dynamics in natural populations.

Methods

Study species and sampling

The Seychelles warbler is a small (~15 g), insectivorous passerine bird with a mean life expectancy of 5.5 years at fledging (Hammers et al. 2013). The population of *ca* 320 adult birds on Cousin Island (04'20'S, 55'40'E) has been intensively studied since 1986 (Komdeur 1992; Richardson, Burke, and Komdeur 2003; Spurgin et al. 2014). This species' main breeding season runs from June-September (though a small proportion of pairs also breed between January–March), when the breeding females on many of the *ca* 110 territories will attempt to breed, laying one or, rarely, two or three eggs (Komdeur, Bullock, and Rands 1991). Breeding attempts are often unsuccessful, and as a result of this low reproductive output, and higher mortality in first-year birds (39% in first-year birds versus 16% in adults; Brouwer et al. 2006), cohort sizes in the Seychelles warbler are typically small (< 50; Table S1). The 22 hatch year cohorts used in this study cover 1993 to 2014 – the time period during which our data and sampling are most complete.

The majority (96%) of individuals are ringed (with an individually numbered metal ring and unique combination of colour rings) within the first year of life, and so are of known age. We aged all birds using information on eye colour at first capture (Komdeur 1991) and previous capture history (Richardson, Burke, and Komdeur 2003). Within the first year of life, birds are classified as nestlings less than one month old (rounded to one month for analyses), fledglings less than six months old (rounded to six months) or subadults up to one year old (rounded to 10 months). Ages for adult birds were rounded to the nearest year. As Seychelles warblers are non-migratory endemics naturally confined to the island (Komdeur et al. 2004), an

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extensive biannual census of birds on Cousin during each breeding season gives accurate measures of local density, social status (e.g. breeder, helper, non-helper) and individual survival (Crommenacker, Komdeur, and Richardson 2011; Barrett et al. 2013). Full details of monitoring methods can be found in Brouwer *et al.* (2012).

Seychelles warblers are highly territorial and all territories were mapped during each main breeding season using detailed observational data on foraging and territorial defence behaviour (Richardson, Burke, and Komdeur 2003). Territory quality is calculated based on territory size, foliage cover and insect abundance (Komdeur 1992). Where territory quality estimates were not available for a specific year we used the average value for that territory across years (Hammers et al. 2013; see Komdeur et al. 2016 for an explanation of how territory quality varies on Cousin Island). Cousin is subject to considerable intra- and inter-annual variation in rainfall and, consequently, insect availability (Komdeur et al. 2016). Such island-wide temporal variation may override the effects of variation in individual territory quality across the island. As an estimate of seasonal variation in food availability, we calculated an index of the abundance of insects across the entire island during each main breeding season (referred to hereafter as 'insect abundance'). This index is calculated as the mean number of insects found per unit leaf area over all monthly surveys carried out on the island in a main breeding season.

Each time a bird is caught on Cousin a range of morphometric measurements are taken, including body mass and tarsus length (to the nearest 0.1g and 0.1mm, respectively). A blood sample (*ca* 25 μl) is taken via brachial venipuncture, and stored at room temperature in 1 ml of absolute ethanol in a 1.5 ml screw-cap microfuge tube.

Molecular methods

For each sample, genomic DNA was extracted from a ~2 mm^2 flake of preserved blood using the DNeasy Blood and Tissue Kit (Qiagen), following the manufacturer's protocol, with the modification of overnight lysis at 37ºC and a final DNA elution volume of 80 μl. Sex was determined using the PCR-based method outlined by Griffiths *et al.* (1998). Prior to telomere analysis, DNA concentration and purity were quantified using a NanoDrop 8000 Spectrophotometer (ThermoScientific). The following thresholds were applied before samples were included for further analysis: i) DNA concentration must be at least 15 ng μl^{-1} (based on a mean of three measurements), ii) the 260/280 absorbance ratio has to be between 1.8 and 2.0 for acceptable DNA purity, and iii) the 260/230 absorbance ratio must be higher than 1.8. DNA integrity was further validated by visualization with ethidium bromide after electrophoresis on a 1.2% agarose gel, and all samples with evidence of DNA degradation were re-extracted or excluded. We found no evidence of DNA degradation in

166 older samples (Fig. S1). All DNA extractions that passed the above criteria were diluted to 3.3 ng μl^{-1} before

167 telomere measurement. We measured relative telomere length (RTL) for all samples using a quantitative

168 PCR (qPCR) assay of telomeres and a GAPDH control gene, following Bebbington *et al.* (2016). Prior to

169 qPCR, we used a random number generator to assign samples to qPCR plates, to ensure that no systematic

170 bias could occur with regards to age, sex, cohort or ecological environment. Based on the distribution of

171 observed cq values, we excluded outlier samples with extremely large cq values (cq values > 25 and 26 were

172 excluded for the telomere and GAPDH reactions, respectively), which were assumed to be failed reactions.

173 For a large subset of birds we had longitudinal data, with two or more samples taken at different ages (n =

174 1057 measurements from 402 birds). For these individuals we calculated the within-individual change in RTL

175 by subtracting RTL at time point t from RTL at time point $t + 1$ (hereafter ΔRTL, n = 655 measurements).

176 Negative values of RTL reflect decreases in telomere length with age, while positive values reflect increases.

177 Individuals were not always caught in the same month, but were generally caught within a 3 month breeding

178 season window.

179 *Statistical analyses*

180 We performed all statistical analyses using R version 3.2.2 (R Development Core Team 2011). RTL was

181 square root transformed to improve linear model fits, and we calculated mean values for samples with repeat

182 measurements. We assessed repeatability of RTL using the rptR package.

183 We explored the cross-sectional relationship between RTL and age among cohorts using linear mixed models

184 (LMMs) carried out in the lme4 package (Bates et al. 2014). Following a similar approach to Fairlie *et al.*

185 (2016), we compared a selection of models fitting different relationships between RTL and age. We created

186 models where the relationship between RTL and age was linear, quadratic, log-linear, and where age was

187 fitted as a factor. For each age term, we fitted additional models including hatch year (cohort) as a factor.

188 All fitted models are included in Table 1. Note that we do not carry out full model selection or model

189 averaging here, as our aim was to compare a set of specifically defined models. For random effects we included

190 individual ID, catch year and qPCR plate ID. Models were compared using AIC with correction for finite

191 sample size (AICc; Hurvich and Tsai 1989).

192 Using the longitudinal data, we then tested how telomeres change with age in individuals, using LMMs of

193 RTL as a response and Δage (a longitudinal measure based on within-subject centring; Pol and Wright

194 2009) as an explanatory variable. We calculated Δage using log and polynomial transformed age data, and

195 carried out model selection as above, with the exception that we did not model Δage as a factor (due to

196 a lack of discreet groupings), and mean age was also included in models to partition within-individual *vs*

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₁₉₇ cross-sectional effects (Pol and Wright 2009). We also excluded the qPCR plate ID random effect from the

₁₉₈ longitudinal analyses, as each longitudinal measurement was obtained from reactions run on separate plates.

₁₉₉ We used two approaches to determine individual-level consistency in RTL. We first calculated individual-level

₂₀₀ repeatability in RTL by dividing the random variance explained by individual ID by the total random

₂₀₁ variance, in a model of that accounted for age and cohort effects. Second, we constructed a LMM with RTL

₂₀₂ at time $t + 1$ as the response variable, RTL at time t and age at time t as fixed effects, and individual ID

₂₀₃ and cohort as random effects. We estimated the slope of the relationship between within-individual telomere

₂₀₄ measurements, as well as the variance explained, by calculating the marginal R^2 (Nakagawa and Schielzeth

₂₀₅ 2013) of the model.

₂₀₆ When examining the distribution of longitudinal telomere changes we observed some increases in telomere

₂₀₇ length with age in individuals. We therefore repeated the qPCR on a large number of samples, using

₂₀₈ completely separate reactions run on separate plates. We used these repeat measurements to test whether

₂₀₉ these increases could be explained by measurement error. We calculated the change in RTL between pairs

₂₁₀ of repeat measurements within the same samples (hereafter ΔRTL_{sample}; N = 422 pairs of measurements

₂₁₁ from 293 birds) in exactly the same way as for across samples (hereafter $\Delta RTL_{individual}$). To test whether

₂₁₂ greater changes in RTL were observed among individuals compared to among repeat samples, we compared

₂₁₃ the variance in ΔRTL_{sample} and $\Delta RTL_{individual}$ using a Levene's test. Then, to separately test whether the

₂₁₄ extent of telomere increases and decreases within individuals were greater than expected by measurement

₂₁₅ error, we split ΔRTL measurements into groups in which RTL decreased ($\Delta RTL < 0$) and increased ΔRTL

₂₁₆ ($\Delta RTL > 0$), and tested whether $\Delta RTL_{individual}$ values were significantly different from ΔRTL_{sample} values,

₂₁₇ using Wilcoxon tests.

₂₁₈ We also tested whether consistent telomere lengthening occurred across our dataset using a modified version

₂₁₉ of the approach developed by Simons *et al.* (2014). Briefly, this approach utilises samples with at least three

₂₂₀ telomere measurements to compare residual variance in telomere change over time with the overall change

₂₂₁ in telomere length between the first and last telomere measurements (Simons, Stulp, and Nakagawa 2014).

₂₂₂ If, in samples that increase in length, the overall increase in telomere length exceeds the residual variance,

₂₂₃ then telomere lengthening cannot be explained by error (Simons, Stulp, and Nakagawa 2014). If, on the

₂₂₄ other hand, increases in telomere length are due to measurement error, within-individual residual variance in

₂₂₅ telomere length is expected to be similar to overall observed increases in telomere length.

₂₂₆ We used LMMs to explore how variation in environmental and social conditions influenced telomere length

₂₂₇ and dynamics within cohorts. We first created a full model with RTL as a response variable, alongside the

₂₂₈ following explanatory variables: log age (based on the RTL and age analysis; see results), tarsus length at

₂₂₉ capture, body mass at capture, sex, insect abundance in sampling season, territory quality in sampling season,

₂₃₀ island-wide population density in sampling season (an annual measure estimated from the summer breeding

₂₃₁ census), territory group size in sampling season, and the number of helping subordinate birds present in the

₂₃₂ territory in the sampling season. The random effects structure was informed by the analysis of telomere

₂₃₃ dynamics and age (see results): we included individual ID, qPCR plate ID, cohort ID, and a random slope

₂₃₄ of log age among cohorts (to allow the effect of age on RTL to vary among cohorts). We report model

₂₃₅ estimates and confidence intervals for all effects included in the full model. We also calculated marginal R^2

₂₃₆ (incorporating only fixed effects; Nakagawa and Schielzeth 2013) and conditional R^2 (incorporating fixed

₂₃₇ and random effects; Johnson 2014) to assess the explanatory power of these models. As a complementary

₂₃₈ approach, we also performed model averaging, using the MuMIn package in R (Bartoń 2012). Model selection

₂₃₉ was performed using the full model described above. A top model set was then defined, containing all models

₂₄₀ with AICc $\leq$ 6 compared to the best supported model (Burnham, Anderson, and Huyvaert 2011). We report

₂₄₁ model-averaged coefficients, confidence intervals and 'relative importance', which reflects the relative weights

₂₄₂ of each predictor variable across the top model set.

₂₄₃ For individuals with longitudinal data we repeated the above analyses of telomere dynamics, replacing telomere

₂₄₄ length with $\Delta\text{RTL}_{individual}$ as the response variable, and including the environmental/social explanatory

₂₄₅ variables from the first of the two sampling points. We excluded the qPCR plate ID random effect from this

₂₄₆ analysis (see above), and excluded the cohort ID random effect, as longitudinal telomere dynamics did not

₂₄₇ differ among cohorts; see results.

Results

₂₄₉ We measured telomere lengths using a total of 1808 unique samples from juvenile and adult Seychelles

₂₅₀ warblers from 22 cohorts born between 1993 and 2014 (Table S1). Efficiencies (mean $\pm$ s.d.) for our telomere

₂₅₁ and GAPDH reactions were 1.78 $\pm$ 0.05 and 1.92 $\pm$ 0.04 respectively. Intra-plate repeatability was 0.74 (CI

₂₅₂ = 0.74,0.75) and 0.73 (CI = 0.71,0.74) for the GAPDH and Telomere Cq values, respectively. Inter-plate

₂₅₃ repeatability of RTL, based on 422 samples measured at least twice at different time points, was 0.68 (CI =

₂₅₄ 0.65, 0.71). Using samples taken from adults greater than one year old, we checked whether RTL was related

₂₅₅ to sample storage time, and found no evidence of such a relationship (estimate = -0.002, CIs = -0.007, 0.002).

₂₅₆ *Telomere dynamics and age among cohorts*

₂₅₇ We first tested how RTL was related to age among cohorts using a model selection approach. The top model

contained cohort ID and a log-linear relationship between RTL and age (Table 1A). All other models fitted the data much less well (ΔAICc > 20; Table 1A). The log-linear relationship between RTL and age could be seen clearly in the raw data; RTL decreased with age (estimate = -0.070, CIs = -0.085, -0.054), with the greatest decrease occurring in the first year of life (Fig. 1A). There was substantial variation in RTL among cohorts, with no obvious trend over time (Fig. 1B). There was a negative relationship between RTL and log age in 21 of the 22 cohorts, but the slope the relationship varied substantially among cohorts (Fig. 1C). To test whether this variation was significant we fitted a model including the log age x cohort interaction term, and found that this was a marginally better fit than a model including only main effects (ΔAICc = 11.32). In the one year in which RTL increased with age (2013), 17 of the 18 birds sampled were fledglings or subadults, suggesting that the observed pattern was an artefact of the sampling in this season (i.e. a lack of variation in age among sampled birds), rather than a real relationship.

A within-individual analysis of RTL and age revealed that the top model explaining RTL contained Δlog age, which reflects within-individual changes in log-transformed age (Table 1B). Models including cohort ID were substantially poorer fits than a model only containing age (Table 1B). RTL decreased with Δlog age (estimate = -0.052, CIs = -0.085, -0.018), confirming that within-individual telomere shortening occurs across the Seychelles warbler dataset. Further, we found no evidence that within and between individual slopes of telomere shortening varied (estimate = -0.003, CIs = -0.008, 0.003), suggesting that there was no difference between cross-sectional and longitudinal telomere shortening with age (see Pol and Wright 2009).

Individual repeatability in RTL was 0.068, meaning that 7% of variance in RTL could be explained by within-individual consistency. Accordingly, there was a positive correlation between RTL measured from different samples taken at different time points during an individual's life (Fig. 2A), but this was very weak (marginal R^2 = 0.01), and not significant (estimate = 0.066, CIs = -0.006, 0.137).

Although both cross-sectional and longitudinal data indicated a general trend of telomere shortening with age, we found that RTL - measured across two samples taken from the same individuals over time - increased with age in 44% of our 655 ΔRTL$_{individual}$ measurements (Fig. 2A). To test whether increases in telomere length in our dataset could be explained by measurement error, we compared variance in telomere length among repeat measurements of the same samples to the variance observed among different samples of the same individual. We found significantly higher variance in telomere length over individual lifetimes compared to among sample replicates (Levene's test: F = 43.63; P < 0.001; Fig. 2B). Splitting the longitudinal data into instances of decreasing (i.e. ΔRTL < 0) and increasing (i.e. ΔRTL > 0) telomere length revealed that not only did we observe significantly greater decrease in RTL within individuals compared to within samples (Wilcoxon test: P < 0.001), but also a significantly greater increase (P < 0.001; Fig. 2B).

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To better understand how longitudinal telomere dynamics vary with age, we examined patterns of short-term telomere change, including only pairs of samples taken within two years of each other. We found that the likelihood of telomere lengthening increased with log age (GLMM with lengthened yes/no as binomial response; estimate = 0.296, CIs = 0.005, 0.588). Increases in telomere length were most likely to be observed shortly after the juvenile period, at around four years of age, and later in life (although sample sizes for older birds are much smaller; Fig. 2C,D).

Using the approach outlined by Simons *et al.* we tested whether overall increases in RTL over lifespans could be detected statistically in our dataset. We found no evidence that this was the case: overall increases in RTL within individuals did not exceed residual variance; in fact, residual variance in RTL was significantly greater than observed RTL increases over lifespans (P = 0.02). This suggests that increases in RTL within individuals are sporadic, and not consistent over individual lifespans.

Telomere dynamics and the environment

In addition to age, RTL was associated with tarsus length, sex and insect abundance (Fig. 3A). RTL was negatively related to tarsus length and males had longer telomeres than females (Fig. 3B), while insect abundance was positively related to RTL (Fig. 3C). The full model was weak in terms of explanatory power of fixed effects (marginal $R^2 = 0.07$), although including the random effect terms increased this substantially (conditional $R^2 = 0.22$). The model averaging approach yielded qualitatively identical results to the full LMM, with the same explanatory variables 'significant' in terms of being retained in top models, and having model-averaged confidence intervals not overlapping zero (Table S2; Fig. S2). One interesting finding from the model selection was that sex only appeared in top models where tarsus length was also present (Table S2). In accordance with this, when tarsus length was removed from the full model sex was no longer significant (estimate = 0.008, CIs = -0.014, 0.030), and a sex x tarsus interaction was significant when included (estimate = 0.021, CIs = 0.002, 0.040); RTL decreased with tarsus length in both sexes, but this decrease was stronger in females (Fig. 3B). No social or ecological environmental variables were significant predictors of ΔRTL using the full model approach (Table S3). Using model selection, we found that the top model explaining ΔRTL contained age and population density (Table S4). ΔRTL was positively related to age, consistent with telomere shortening being highest in early life, and negatively related to population density; however, in both instances model averaged confidence intervals overlapped zero (Fig. S3).

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Discussion

Here we use a long-term, multi-cohort dataset to assess lifelong telomere dynamics and the relationship between these and spatio-temporal variation in the ecological environment in a contained population of Seychelles warblers. We found that telomere length decreases with age, and that this decrease is greatest very early in life. Telomere length decreased with age in almost all of the 22 cohorts studied, but telomere length varied substantially among cohorts. Despite an overall pattern of telomere shortening with age in the Seychelles warbler, we found evidence of within-individual increases in telomere length, and that the extent of these increases could not be explained solely by qPCR measurement error. Finally, we found that telomeres are related to tarsus length in a sex-specific manner, and that telomere length is positively associated with temporal fluctuations in food availability.

Our study adds to the substantial body of literature from humans and wild animals showing that telomere length decreases with age, and that this decrease is most rapid in early life. Rapid telomere shortening in early life occurs as a consequence of the much more rapid rate of cellular division that occurs during the growth phase, but also perhaps higher levels of cellular stress during development (e.g. Frenck, Blackburn, and Shannon 1998; Haussmann, Vleck, and Nisbet 2003; Heidinger et al. 2012). Because we are rarely able to sample Seychelles warblers more than once in the nest, our system is not the best suited for looking in detail at the reasons behind telomere shortening during the growth phase. In contrast, we have good longitudinal and cross-sectional sampling from across individual lifespans, and using this data we have shown that, despite an overall trend for shortening, telomere length both increased and decreased, especially after the juvenile period. Importantly, these increases were observed in longitudinal as well as cross-sectional data, indicating that selective disappearance of individuals with shorter telomeres is not sufficient to explain this pattern. Longitudinal increases in measured telomere length have been observed in humans and wild animals (Steenstrup et al. 2013; Kotrschal, Ilmonen, and Penn 2007; Fairlie et al. 2016; Hoelzl, Cornils, et al. 2016; Hoelzl, Smith, et al. 2016). The most commonly invoked explanation for increases in telomere length is measurement error, which can be a particular problem in qPCR-based telomere studies (Nussey et al. 2014; Steenstrup et al. 2013; Verhulst et al. 2015). However, recent modelling work suggests that longitudinal telomere dynamics in humans are indeed consistent with instances of lengthening, and that dismissing apparent telomere lengthening as solely measurement error is "too strong" without additional data (Bateson and Nettle 2016). Here, we explicitly compare intra-individual variation among samples to variation among sample replicates, on a large scale. Our results suggest that despite the substantial levels of qPCR measurement error in our study, error alone cannot explain observed increases in RTL observed within individuals.

Increases in telomere length were not consistent over individual lifespans, but occurred in bouts, against a backdrop of overall lifelong telomere shortening. This is consistent with recent findings in edible dormice *Glis glis*, in which telomere elongation was observed only later in life (Hoelzl, Smith, et al. 2016). Consistent with a pattern of sporadic changes in telomere length with age, we found that within-individual telomere measurements were only weakly correlated. Although some of this low within-individual repeatability will occur due to measurement error, our within-sample repeatability was still much higher than our within-individual repeatability. Such a low value of within-individual repeatability in telomere length is in contrast to other avian studies in which within-individual telomere length measurements were highly consistent, and individual-level telomere shortening occurred throughout the juvenile period and into adulthood (Heidinger et al. 2012; Boonekamp et al. 2014). However, the lifelong telomere dynamics found in Seychelles warblers are strikingly similar to those found in Soay sheep (Fairlie et al. 2016). This discrepancy in results may be because in our study, and that of Fairlie et al. (2016), individuals were born and reared in the wild, as opposed to in nestbox or laboratory conditions. Alternatively it may be because our longitudinal telomere measurements have been taken over longer time periods.

The finding that increases in telomere length may be sporadic and overlaid on an overall pattern of shortening with age is an important point when assessing the occurrence of telomere lengthening. Previously described approaches to distinguish telomere elongation from measurement error, based on assumptions about follow-up time between measurements (Steenstrup et al. 2013), or based on measuring variance among measurements (Simons, Stulp, and Nakagawa 2014), assume that telomere elongation within individuals is consistent over time. Our data, and that of others (Fairlie et al. 2016; Hoelzl, Cornils, et al. 2016; Hoelzl, Smith, et al. 2016) suggest that this is not the case. Such inconsistent changes in telomere length over lifespans could occur due to changes in the cellular composition of of the blood within individual samples, due to variation in the presence of interstitial telomeric sequence, or due to the actual elongation of telomeres (Blackburn et al. 1989). Determining the mechanism of these changes is essential for how we view telomeres as biomarkers of costs. For example, if telomeres can be lengthened in response to improvements in environmental conditions, this would suggest that they reflect short- to medium-term costs, rather than the cumulative costs that an individual has faced over its lifespan (Bateson 2016). It is clear that telomeres can be a marker of long-term as well as short-term costs, as telomere length has been associated with both survival and lifespan in wild populations (Barrett et al. 2013; Stier et al. 2015), but we do not yet know how biologically meaningful within-individual fluctuations in telomere length are. New research is therefore required to determine when and why telomere length increases within individuals, so that biologically informed hypotheses about the nature of telomeres as biomarkers in wild populations.

Measurement of cohorts across seasons or years is required if we are to understand how the environment impacts telomere dynamics. Although a few studies have shown that temporal variation in telomere dynamics occurs in natural populations, these have been limited in the number of seasons they cover (Mizutani et al. 2013; Watson, Bolton, and Monaghan 2015; Fairlie et al. 2016). Other studies have found cohort effects but not discussed them in an ecological context (Stier et al. 2014; Becker et al. 2015). One problem with studying cohort effects is that it can be difficult to tease apart true cohort effects from effects that may arise if samples degrade with storage time, and/or batch effects in telomere assays, although neither of these factors were a problem in our study. Indeed, the long-term Seychelles warbler dataset has allowed us to show that temporal variation in telomere dynamics can occur over substantial time periods. Our data suggest that conditions during the hatch year are a very important factor in shaping telomere dynamics throughout lifespan. Thus, our findings suggest that the telomere dynamics of a population at a given point in time represent a snapshot of a temporally varying process. Research of telomere dynamics within and across multiple cohorts and populations will enable us to better understand how and why population-level telomere dynamics vary over space and time.

We found that temporal variation in insect prey availability was positively related to telomere length. This is consistent with the strong cohort effects we found, and suggests that temporal variation in environmental conditions may be a key driver of costs in the Seychelles warbler. Although the environmental conditions on Cousin Island are relatively benign in comparison to other island systems (e.g. Coulson et al. 2001), substantial annual variation in rainfall does occur, with associated changes in insect abundance (Komdeur 1996), and it appears that this confers a cost - in terms of intrinsic biological condition - to Seychelles warblers. Our results concur with other studies which show that early life conditions / food availability can have a very significant and long term impacts on telomere length (and intrinsic biological condition) in captive and wild animals (e.g. Stier et al. 2014; Nettle et al. 2015; Watson, Bolton, and Monaghan 2015).

We also found evidence for sex-specific telomere dynamics: males had longer telomeres than females. Interestingly this sex difference interacts with tarsus length: telomere length was negatively correlated with tarsus length in both sexes, but this effect was stronger in females than males. If the sex-dependent relationship between telomere and tarsus length was due to differential growth alone then we would expect the opposite pattern to that observed, as male Seychelles warblers are larger than females (Fig. 3B). One possibility is that the environment imposes differential costs on males and females: a recent study in captive zebra finches found that manipulation of dietary nutrients had sex-dependent effects on telomere dynamics (Noguera et al. 2015). Also worth noting is that the effect of telomere length on survival is strongest in male Seychelles warblers (Barrett et al. 2013), although comparative research suggests that the nature of the

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relationship between sex, telomeres and survival is not yet clear (Barrett and Richardson 2011).

It is worth considering the fact that the social and ecological variables we tested here explained only a small proportion of the variance in RTL. Furthermore, some factors such as territory quality and social group size were not related to telomere dynamics when we may have expected them to be (Van de Crommenacker et al. 2011; Brouwer, Richardson, and Komdeur 2012). Measurement error is clearly an issue in our study, and has almost certainly decreased the explanatory power of our models, and elevated levels of Type II error. The low repeatability we observed is the product of i) lower levels of efficiency in the telomere qPCR reaction than we would have liked, ii) the long-term nature of the study. Samples for this study were run aver a period of up to six years, during which reagents, consumables and personnel all change. Our repeatability estimate includes samples that were run several years apart, and reflect all the sources of error that accumulated over that time. Compared to a set-up where a small amount of samples are all run at the same time, it is unsurprising that we have a higher error rate - indeed, in our own studies where we have run all the samples within a short timeframe we have observed higher repeatability [Barrett2012;@Bebbington2016]. Techniques for measuring telomere length with a greater degree of precision are likely to prove helpful in future long-term ecological studies of telomere dynamics (Nussey et al. 2014), and discussions are now required on how to best optimise measuring telomere length for long-term studies. A central issue to resolve is how best to balance the trade-off between obtaining precise telomere measurements, and utilising the large sample sizes necessary for ecological study.

While sampling error is a problem in our study, we are confident that because of our study design, and plate randomisation in particular, sampling error is highly unlikely to have resulted in a high false positive rate. This is clearly a problem that needs to be considered, however, when designing long-term studies of telomere dynamics. And, clearly, sampling error is not the only factor contributing to the unexplained variance in telomere length in our study. It should always be borne in mind that, in any system, unmeasured environmental and genetic variables will contribute to unexplained variance in telomere dynamics. A key question to be addressed is the extent to which RTL, especially in early life, reflects inheritance and parental effects (e.g. Becker et al. 2015; Asghar et al. 2014; Heidinger et al. 2016). For example, parental age and quality may key variables that impact the telomere dynamics of offspring in the Seychelles warbler, and will be addressed in future studies. Long-term ecological study systems are uniquely suited to addressing such questions in natural systems (Clutton-Brock and Sheldon 2010). To gain a full understanding of telomere dynamics in natural systems, long-term studies combining ecological and genetic data will be required from a range of species.

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Data accessibility

This manuscript was written in R Markdown (http://rmarkdown.rstudio.com/). All data and scripts required to reproduce the manuscript, figures and analyses will be made available on GitHub.

Author contributions

DSR, HLD, JK and TB manage the long-term Seychelles warbler project. DSR conceived and obtained funding for the telomere research. EAF and KB performed the molecular work. LGS processed the telomere data, with input from EAF, KB, MH, HLD and DSR. LGS analysed the data and wrote the manuscript, with input from DSR and all authors.

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Table 1 Cross-sectional (**A**) and longitudinal (**B**) telomere dynamics and age in Seychelles warbler cohorts.

664 Linear mixed models were created with RTL (**A**) or ΔRTL (**B**) as the response variable, and different

665 measures of age, along with cohort ID, were included as explanatory variables (see methods for details).

666 Models are ranked by AICc, with best models at the top of the table.

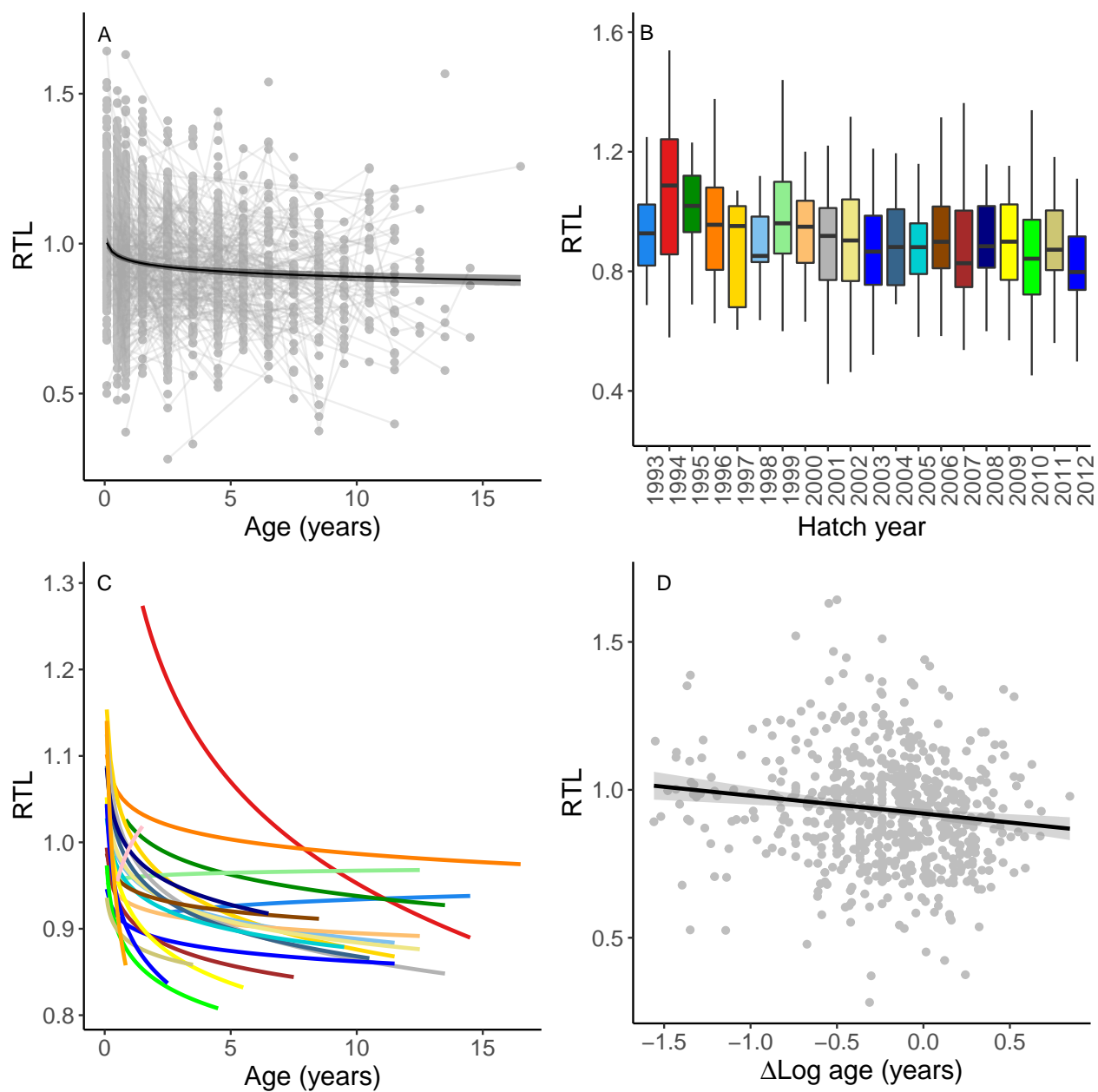| Model	df	AICc	Delta AICc	Weight
A	-	-	-	-
Cohort + Age (log)	27	-1062.782	0	1
Age (quadratic) + Age (linear) + Cohort	28	-1039.504	23.278	0
Age (linear) + Cohort	27	-1035.072	27.71	0
Age (log)	6	-1034.942	27.84	0
Cohort + Age (factor)	41	-1027.498	35.284	0
Age (quadratic) + Age (linear)	7	-1013.793	48.989	0
Age (linear)	6	-1006.873	55.909	0
Age (factor)	20	-1004.885	57.897	0
Cohort	26	-1000.037	62.745	0
Null model	5	-989.909	72.873	0
B	-	-	-	-
Delta age (log) + Mean age	7	-370.124	0	0.459
Delta age (linear) + Mean age	7	-368.331	1.792	0.187
Cohort + Delta age (log) + Mean age	28	-367.567	2.556	0.128
Delta age (linear) + Delta age (quadratic) + Mean age	8	-366.53	3.594	0.076
Cohort + Delta age (linear) + Mean age	28	-366.467	3.657	0.074
Mean age	6	-365.397	4.726	0.043
Cohort + Delta age (linear) + Delta age (quadratic) + Mean age	29	-364.538	5.586	0.028
Cohort + Mean age	27	-360.94	9.184	0.005

24

Figure Legends

Figure 1 Telomere dynamics in relation to age in Seychelles warbler cohorts. **A** RTL and age across all individuals. Points and connecting thin grey lines represent individual samples and birds, respectively. The thick line and shaded area represent the fitted values and 95% confidence limits of a linear regression of RTL and log-transformed age. **B** Boxplot of variation in RTL among juvenile individuals from all cohorts. **C** RTL and age among cohorts. Lines represent fitted values from a linear regression of RTL and log-transformed age, and colours correspond to **B**. **D** RTL in relation to and ΔLog age (i.e. within individual variation in log age).

Figure 2 Longitudinal telomere dynamics in the Seychelles warbler. **A** Variation in RTL within individuals sampled at different time points. The dotted line represents parity, and thus points above and below the line represent increases and decreases in RTL, respectively. **B** Scaled density plots of repeated RTL measurements among individual samples, and among different samples taken from the same individual. Areas of the density plot to the left of the dotted line represent decreases in RTL, while areas to the right represent increases. **C** ΔRTL in relation to age in pairs of samples taken within two years. Black line and shaded area represent fitted values and 95% confidence limits from a linear regression of RTL and log-transformed age. **D** Probability of telomere lengthening occurring in relation to age. Points at zero and one represent pairs of samples where RTL has decreased and increased, respectively, with point size scaled by the number of overlapping values. The black line represents the proportion of samples in which increases in RTL where observed at each age category.
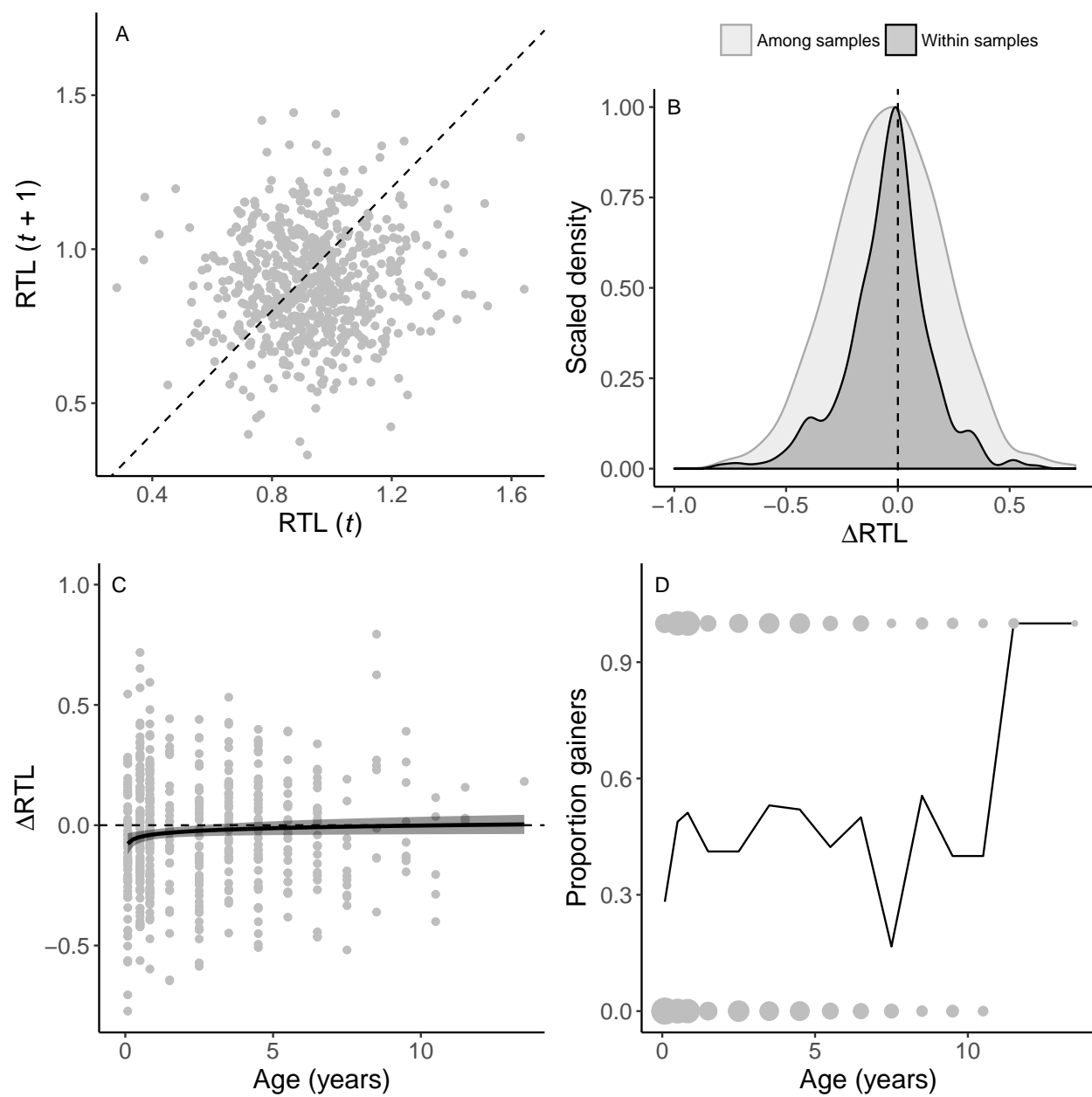
Figure 3 Telomere length in relation to the social and ecological environment in the Seychelles warbler. **A** Estimates and 95% confidence intervals for all explanatory variables fitted in a linear mixed model (see methods for details). **B** RTL in relation to tarsus length and sex. **C** RTL in relation to variation in annual food availability. Lines and shaded areas represent the fitted values and 95% confidence limits from linear regressions.
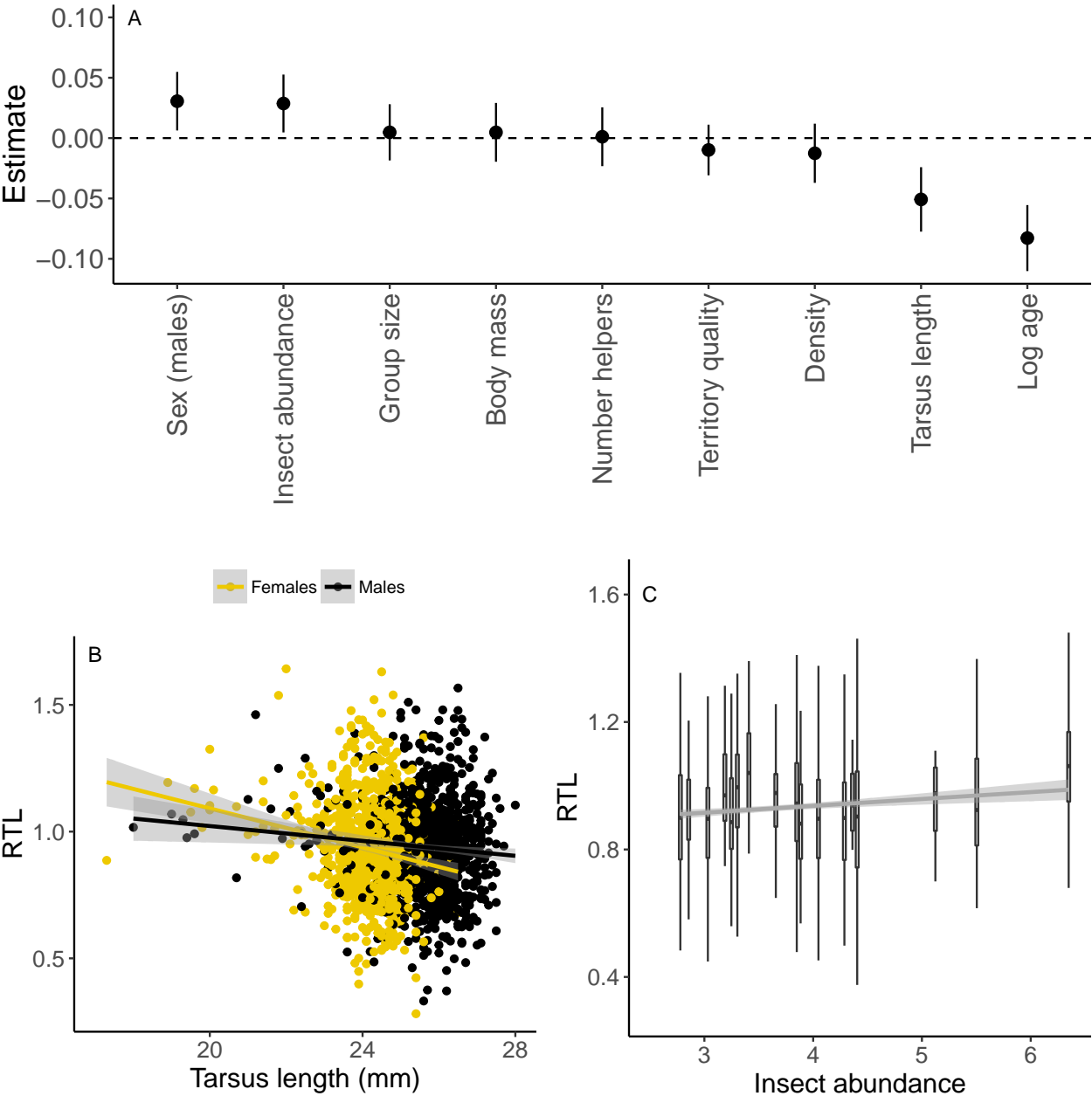
Figure 1

Figure 2

Figure 3