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

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**Running head:** Early-life telomeres

### 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 as a result of different social and ecological environment 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 telomere dataset, 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 and the slope of the relationship with age varied markedly among cohorts. Telomere length was positively associated with island-wide temporal 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, which leads to adult females having significantly shorter telomeres than males.
5. Our long-term data show that in a natural population, telomere dynamics vary in a highly complex manner over individual lifespans, and across space and time. Variance in telomere dynamics among individuals is the product of 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

**Data archival location:** 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.

### Introduction

A major aim of ecologists and evolutionary biologists is to quantify and understand why individuals vary in their response to different environmental factors. Identifying the costs imposed on populations 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 on the ends of linear chromosomes that protect against DNA damage. Telomeres generally shorten with age (Monaghan and Haussmann 2006), and there is evidence from a range of taxa that the greatest rate of telomere shortening occurs in early life (e.g. Frenck et al. 1998; Haussmann et al. 2003). Telomere shortening is accelerated by oxidative stress, which can be elevated due to many environmental factors (Von Zglinicki 2002). There is evidence from both humans, and 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 et al. 2015). Importantly, the extent of telomere shortening has been directly 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 senescence and telomere length 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 several wild organisms (reviewed in Horn et al. 2010; Haussmann and Marchetto 2010; Simons 2015). As yet there is little direct evidence that the relationship between telomere dynamics and survival is causal (Simons 2015). However, there is mounting evidence that telomeres can act as biomarkers of individual condition and ageing in wild populations, providing a measure of the ecological stress that an individual has been 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 some evidence that telomere length, measured longitudinally from an individual, can increase as well as decrease (Simons et al. 2014; Bateson and Nettle 2016), which has important ramifications for our understanding of how telomeres reflect costs. However, such increases in telomere length are often attributed to measurement error (Steenstrup et al. 2013; but see Bateson and Nettle 2016), and as such its ecological significance is unknown.

Although a considerable amount of effort has been put into studying telomere dynamics in natural populations, our understanding of the forces responsible for explaining variation in telomere length is still limited. Understanding how different factors shape telomere length variation is important, as before we can use telomeres as a measure of the costs experienced by individuals, we need to know how different developmental, genetic and ecological variables interact to affect telomeres. Telomere length and rates of shortening can vary according to parental characteristics (Njajour2007; Heidinger et al. 2016), among sexes (Barrett and Richardson 2011, Watson et al 2017), and with a whole host of environmental conditions experienced at different life-history stages (Monaghan 2014). Recent evidence suggests that telomere dynamics are indeed highly variable over individual lifespans, and that even the relationship between telomeres and age can vary markedly among cohorts (Fairlie et al. 2016). To understand which factors best explain variation in telomere dynamics, more studies are required that incorporate telomere variation over entire lifespans with comprehensive, long-term ecological data.

The longitudinal study (since 1986) of the Seychelles warbler (*Acrocephalus sechellensis*) population on Cousin Island provides an excellent system for studying telomere dynamics and senescence patterns in the wild (reviewed in Hammers et al. 2015). Due to the isolated nature of the study population (Komdeur et al 2004) and intensive field monitoring, we have comprehensive ecological and survival data spanning many years (see Methods, below). Environmental conditions and population density on Cousin Island vary across space and time due to weather-induced changes in foliage cover and insect prey availability availability (Van de Crommenacker et al. 2011). Variation in oxidative stress experienced by individuals is associated with territory quality (Van de Crommenacker et al. 2011). However, the evidence that individual survival and lifespan is associated with spatial variation in early life territory quality or local density is equivocal and confounded by variation in subsequent life-history parameters (Brouwer et al. 2006; Hammers et al. 2013). There is also variation in the social environment that individual Seychelles warblers experience. Facultative cooperative breeding occurs in this species (Komdeur 1994; Richardson et al. 2003b: Richardson et al 2007), and the presence of helpers (but not other resident non-helpers) in the natal territory is associated with increased survival of offspring later in life (Brouwer et al. 2012).

Importantly, we have an established protocol for assessing telomere length in the Seychelles warbler (Barrett et al. 2012; Bebbington et al. 2016). Furthermore, telomere dynamics predict survival independently of age (Barrett et al. 2013) and are negatively associated with inbreeding (Bebbington et al. 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 (years). 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 across longitudinal samples are larger than expected based on measurement error. Finally, we test how a wide range of social and environmental variables are related to telomere length and shortening in order 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 et al. 2003a; Spurgin et al. 2014). This species' main breeding season runs from June-September (though a small number of territories do sometimes try to 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 et al. 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). The 22 birth year cohorts used in this study cover 1993 to 2014 – the time period during which our data and sampling is most complete.

The majority 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 et al. 2003a). As Seychelles warblers are non-migratory endemics naturally confined to the island (Komdeur et al. 2004), an 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 et al. 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 of foraging and territorial defence behaviour (Richardson et al. 2003a). Territory quality was assessed for each territory – estimated 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). Cousin is subject to considerable intra- and inter-annual variation in rainfall and, consequently, insect availability and 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 l) 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 mm2 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 l. 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 l-1 (based on a mean of three measurements), ii) the 260/280 absorbance ratio has to be between 1.8 and 2 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. All DNA extractions that passed the above criteria were diluted to 3.3 ng l-1 before telomere measurement. We measured relative telomere length (RTL) for all samples using a quantitative PCR (qPCR) assay of telomeres and a GAPDH control gene, following Bebbington *et al.* (2016).

For a large subset of birds we had longitudinal data, with two or more samples taken at different ages (n = 1057 measurements from 402 birds). For these individuals we calculated the within-individual change in RTL by subtracting RTL at time point *t* from RTL at time point *t* + 1 (hereafter RTL, n = 655 measurements). Negative values of RTL reflect decreases in telomere length with age, while positive values reflect increases.

##### Statistical analyses

We performed all statistical analyses using R version 3.2.2 (R Development Core Team 2011). RTL was square root transformed to improve linear model fits, and we assessed repeatability of RTL using the rptR package.

We explored the cross-sectional relationship between RTL and age among cohorts using linear mixed models (LMMs) carried out in the lme4 package (Bates et al. 2014). Following a similar approach to Fairlie *et al.* (2016), we compared a selection of models fitting different relationships between RTL and age. We created models where the relationship between RTL and age was linear, quadratic, log-linear, and where age was fitted as a factor. For each age term, we fitted additional models including birth year (cohort) as a factor, and an interactions between cohort age. All fitted models are included in Table 1. Note that we do not carry out full model selection or model averaging here, as our aim was to compare a set of specifically defined models. For random effects we included individual ID, and catch year. Models were compared using AIC with correction for finite sample size (AICc).

Using the longitudinal data, we then tested how telomeres change with age in individuals, using LMMs of RTL as a response and age (a longitudinal measure based on within-subject centring; Pol and Wright 2009) as an explanatory variable. We calculated age using log and polynomial transformed age data, and carried out model selection as above, with the exception that we did not model age as a factor (due to a lack of discreet groupings), and mean age was also included in models to partition within-individual vs cross-sectional effects (Pol and Wright 2009).

We also used longitudinal data to determine individual-level consistency in RTL. We constructed a LMM with RTL at time *t* + 1 as the response variable, RTL at time *t* and age at time *t* as fixed effects, and individual ID and cohort as random effects. To obtain an estimate of explanatory power of the fixed effects, we calculated marginal R2 following Nakagawa & Schielzeth (2013).

When examining the distribution of longitudinal telomere changes we observed some increases in telomere length with age in individuals. We then used repeat measurements to test whether these increases could be explained by measurement error. We calculated the change in RTL between pairs of repeat measurements within the same samples (hereafter RTL*sample*; N = 422 measurements from 293 samples) in exactly the same way as for across samples (hereafter RTL*individual*), using completely separate reactions run on separate plates. To test whether greater changes in RTL were observed among individuals compared to among repeat samples, we compared the variance in RTL*sample* and RTL*individual* using a Levene's test. Then, to separately test whether the extent of telomere increases and decreases within individuals was greater than expected by measurement error, we split RTL measurements into groups in which RTL decreased (RTL < 0) and increased RTL (RTL > 0), and tested whether RTL*individual* values were significantly different from RTL*sample* values, using Wilcoxon tests.

We then used LMMs to test how variation in environmental and social conditions influenced telomere length within cohorts. We created a full model with RTL as a response variable, alongside the following explanatory variables: log age (based on the RTL and age analysis; see results), tarsus length, body mass, sex, insect abundance, territory quality, island-wide population density (an annual measure estimated from the summer breeding census), territory group size, and the number of helping subordinate birds present in the territory. The random effects structure was informed by the analysis of telomere dynamics and age (see results): we included individual ID, cohort ID, and a random slope of log age among cohorts. We report model estimates and confidence intervals for all effects included in the full model. We also calculated marginal R2 and conditional R2 (incorporating fixed and random effects, respectively; Johnson 2014) to assess the explanatory power of these models. As a complementary approach, we also performed model averaging, using the MuMIn package in R (Bartoń 2012). Model selection was performed using the full model described above and a top model set defined, containing all models with AICc 6 compared to the best supported model (Burnham et al. 2011). We report model-averaged coefficients, confidence intervals and 'relative importance', which reflects the relative weights of each predictor variable across the top model set.

For individuals with longitudinal data we repeated the above analyses of telomere dynamics, replacing telomere length with RTL*individual* as the response variable, and including the environmental/social explanatory variables from the first of the two sampling points. We excluded the cohort ID random effect from this analysis, as longitudinal telomere dynamics did not differ among cohorts; see results.

### Results

We measured telomere lengths using a total of 1808 unique samples from juvenile and adult Seychelles warblers from 22 cohorts born between 1993 and 2014. Efficiencies (mean s.d.) for our telomere and GAPDH reactions were (1.78 0.05) and (1.92 0.04) respectively. Inter-plate repeatability of RTL, based on 422 samples measured at least twice was 0.68 (CI = 0.65, 0.70).

##### Telomere dynamics and age among cohorts

We first tested how RTL was related to age among cohorts using a model selection approach. The top model contained a loglinear relationship between RTL and age, as well as a log age x cohort interaction (Table 1A). The second-best model contained log age and cohort ID, with no interaction term, although this model was substantially poorer in terms of model fit (AICc > 10). All other models fitted the data much less well (AICc > 35; Table 1). The log-linear relationship between RTL and age could be seen clearly in the raw data; RTL decreased with age (estimate = -0.050, CIs = -0.064, -0.036), 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 age in 21 of the 22 cohorts, but the slope of the relationship between log age and RTL varied substantially among cohorts (Fig.1C). 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 artifact of the sampling in this season rather than a real relationship.

A within-individual analysis of RTL and age revealed that the top model explaining RTL contained log age, which reflects within-individual changes in log-transformed age (Table 1B). Models including cohort ID and cohort x age interactions were substantially poorer fits than models only containing age (Table 1B). RTL decreased with log age (estimate = -0.052, CIs = -0.085, -0.018), confirming that within-individual telomere shortening occurs across the Seychelles warbler dataset.

There was 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 R2 = 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 within two samples taken from the same individuals over time - increased with age in 44% of our 655 RTL*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. RTL < 0) and increasing (i.e. RTL > 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).

##### Telomere dynamics and the environment

In addition to age, RTL was associated with tarsus length, sex and insect abundance (Fig. 3A). Tarsus length was negatively related to RTL 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 R2 = 0.07), although including the random effect terms increased this substantially (conditional R2 = 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 S1; Fig. S1). One interesting finding from the model selection was that sex only appeared in top models where tarsus length was also present (Table S1). In accordance with this, when tarsus length was removed from the full model sex was no longer significant (estimate = 0.009, CIs = -0.012, 0.031), and a sex x tarsus interaction was significant when included (estimate = 0.020, CIs = 0.002, 0.039); 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 RTL using the full model approach (Table S2). Using model selection, we found that the top model explaining RTL contained age and population density (Table S3). RTL 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. S2).

### 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 (except .), but the rate of decrease of telomere length with age, and consequently the mean telomere length of adults, varied substantially among cohorts. Despite an overall pattern of telomere shortening with age in the Seychelles warbler, we found that our measure of telomere length increased within some individuals over two consecutive age points, and that the extent of these increases could not be explained solely by qPCR measurement error. We also found that telomere shortening was related to tarsus length in a sex-specific manner and this interaction resulted in males having significantly longer telomeres than females. Finally, telomere length (rate of shortening) was 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 (e.g. Frenck et al. 1998; Haussmann et al. 2003; Heidinger et al. 2012). However, we also found 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 does not explain this pattern. Longitudinal increases in measured telomere length have been observed in humans and wild animals (reviewed in Steenstrup et al. 2013) (Kotrschal et al. 2007; Fairlie et al. 2016; Hoelzl et al 2016a,b). The most commonly invoked explanation for increases in telomere length is measurement error, which can be a particular problem in qPCR-based telomere studies (Steenstrup et al. 2013; Nussey et al. 2014; Verhulst et al. 2015). However, recent modelling work suggests that longitudinal telomere dynamics in humans are indeed consistent with apparent lengthening, and that dismissing apparent telomere lengthening as solely due to measurement error is "too strong" without additional data (Bateson and Nettle 2016). Furthermore, it is hard to see how a pattern where within-individual telomere lengthening is associated with specific individual characteristics can be explained by measurement error. For example, in the edible dormice, *Glis glis*, measured telomere length increases with age in older (> 5 years) but not younger individuals (Hoelzl et al 2016b). Here, we explicitly compare intra-individual variation among samples to variation among sample replicates, on a large scale. Our results suggest that qPCR measurement error alone cannot explain the increases in RTL we observed within individuals.

Increases in telomere length were not consistent over individual lifespans, but occurred during specific, periods, against a backdrop of overall lifelong telomere shortening. Consistent with a pattern of sporadic changes in telomere length with age, we found that within-individual telomere measurements were only weakly correlated. These findings are in contrast to other avian studies where birds were reared in laboratory (Heidinger et al. 2012) or nest-box (Boonekamp et al. 2014) conditions, in which within-individual telomere length measurements were highly consistent, and individual-level telomere shortening occurred throughout the juvenile period and into adulthood. However, the lifelong telomere dynamics found in Seychelles warblers are strikingly similar to those found in Soay sheep (Fairlie et al. 2016), and we anticipate that a similar pattern may be found in other wild populations.

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 et al. 2014), assume that telomere elongation within individuals is consistent over time. Our data, and that of Fairlie et al (2016) and Hoelzl et al (2016a,b) suggest that this is not the case. Such inconsistent changes in telomere length over lifespans could occur due to changes in the composition of cell types within individual samples, 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). New statistical and technical approaches are therefore required to determine the mechanisms behind increases in telomere length within individuals, so that biologically informed hypotheses about the ecological causes and consequences of these increases can be generated and tested.

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 et al. 2015; Fairlie et al. 2016). 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, and that age-related declines in telomere length vary among cohorts. The rate of early-life telomere loss for a cohort was highly variable and had a persistent effect of the mean adult telomere length of the cohort. This effect is consistent with telomere length being strongly influenced by environmental, as well as genetic, factors - something that is becoming apparent from the, as yet, limited number of quantitative genetic studies of telomere dynamics in wild populations (e.g. Olsson et al 2011, Atema et al 2015, Becker et al 2015) . Moreover, 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 during the hatch year 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. ({Nettle, 2015 #2308}{Heidinger, 2012 #2403}{Watson, 2015 #2398}

We also found evidence for sex-specific telomere dynamics: males had longer-telomeres than females apparently due to greater very early life telomere attrition in females than males. 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 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 in strongest in male Seychelles warblers (Barrett et al. 2013), although the nature of the relationship between sex, telomeres and survival is not yet clear (Barrett and Richardson 2011)

Although we found clear associations between the environment and telomere dynamics, we should bear in mind that the social and ecological variables we tested here explained only a small proportion of the variance in RTL. A poor social and ecological environment is known to be detrimental to Seychelles warblers, both in terms of oxidative stress and survival (Van de Crommenacker et al. 2011; Brouwer et al. 2012), and it is therefore perhaps surprising that these variables do not explain more variance in RTL. While telomere measurement error will account for some of this lack of explanatory power, it is also likely that early-life RTL in the Seychelles warbler is explained by a set of environmental and genetic variables not considered here (e.g. Bebbington et al. 2016). A key question to be addressed is the extent to which RTL, especially in early life, reflects inheritance and parental effects (Asghar et al. 2014; e.g. Becker et al. 2015; 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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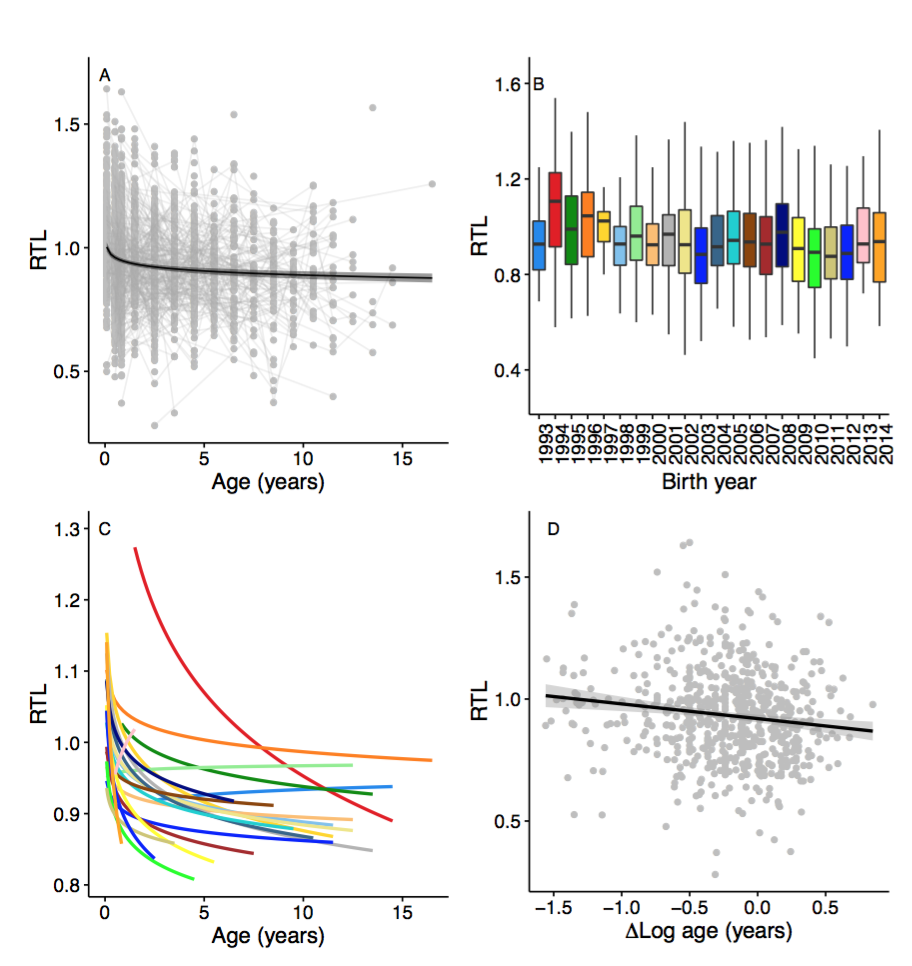
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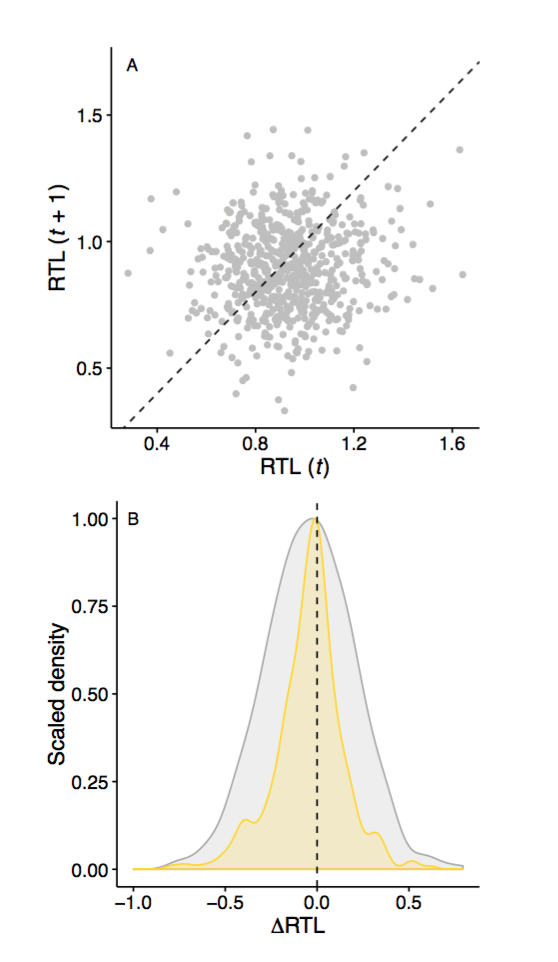
**Table 1** Telomere dynamics and individual age in Seychelles warbler cohorts. Linear mixed models were created with RTL as the response variable, and different measures of age, cohort ID, and cohort x age interactions as explanatory variables (see methods for details). Models are ranked by AICc, with best models at the top of the table.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | df | AICc | Delta AICc | Weight |
| A | - | - | - | - |
| Cohort + Age (log) + Age (log)\*cohort | 48 | -1074.102 | 0 | 0.997 |
| Cohort + Age (log) | 27 | -1062.782 | 11.32 | 0.003 |
| Age (quadratic) + Cohort + Age (quadratic)\*cohort | 48 | -1039.028 | 35.073 | 0 |
| Age (linear) + Cohort + Age (continuous)\*cohort | 48 | -1036.929 | 37.173 | 0 |
| Age (linear) + Cohort + Age (factor) + Age (continuous)\*cohort | 63 | -1035.722 | 38.379 | 0 |
| Age (linear) + Cohort | 27 | -1035.072 | 39.03 | 0 |
| Age (log) | 6 | -1034.942 | 39.16 | 0 |
| Age (linear) + Cohort + Age (factor) | 42 | -1032.966 | 41.135 | 0 |
| Cohort + Age (factor) | 41 | -1027.498 | 46.604 | 0 |
| Age (linear) + Age (factor) | 21 | -1009.351 | 64.751 | 0 |
| Age (quadratic) + Cohort | 27 | -1007.366 | 66.736 | 0 |
| Age (linear) | 6 | -1006.873 | 67.229 | 0 |
| Age (factor) | 20 | -1004.885 | 69.217 | 0 |
| Cohort | 26 | -1000.037 | 74.065 | 0 |
| Age (quadratic) | 6 | -996.559 | 77.543 | 0 |
| Null model | 5 | -989.909 | 84.193 | 0 |
| Age (linear) + Cohort + Age (factor) + Age (factor)\*cohort | 189 | -936.877 | 137.225 | 0 |
| Age (linear) + Cohort + Age (factor) + Age (continuous)*cohort + Age (factor)*cohort | 208 | -931.359 | 142.743 | 0 |
| Cohort + Age (factor) + Age (factor)\*cohort | 188 | -926.127 | 147.975 | 0 |
| B | - | - | - | - |
| Delta age (log) | 6 | -371.11 | 0 | 0.41 |
| Delta age (log) + MeanAge | 7 | -370.124 | 0.986 | 0.25 |
| Delta age (linear) + MeanAge | 7 | -368.331 | 2.779 | 0.102 |
| Cohort + Delta age (log) + MeanAge | 28 | -367.567 | 3.543 | 0.07 |
| Delta age (linear) | 6 | -366.596 | 4.513 | 0.043 |
| Cohort + Delta age (linear) + MeanAge | 28 | -366.467 | 4.643 | 0.04 |
| Delta age (quadratic) | 6 | -365.591 | 5.519 | 0.026 |
| MeanAge | 6 | -365.397 | 5.712 | 0.024 |
| Delta age (quadratic) + MeanAge | 7 | -364.439 | 6.67 | 0.015 |
| Null model | 5 | -364.379 | 6.731 | 0.014 |
| Cohort + MeanAge | 27 | -360.94 | 10.17 | 0.003 |
| Cohort + Delta age (quadratic) + MeanAge | 28 | -360.043 | 11.066 | 0.002 |
| Cohort + Delta age (log) | 27 | -359.688 | 11.422 | 0.001 |
| Cohort + Delta age (linear) + MeanAge + Delta age (continuous)\*cohort | 48 | -354.619 | 16.491 | 0 |
| Cohort + Delta age (quadratic) | 27 | -354.605 | 16.505 | 0 |
| Cohort + Delta age (log) + MeanAge | 48 | -354.366 | 16.744 | 0 |
| Cohort + Delta age (linear) | 27 | -352.972 | 18.138 | 0 |
| Cohort | 26 | -350.968 | 20.142 | 0 |
| Cohort + Delta age (log) | 47 | -347.557 | 23.553 | 0 |
| Cohort + Delta age (linear) + Delta age (continuous)\*cohort | 47 | -343.587 | 27.523 | 0 |
| Cohort + Delta age (quadratic) + MeanAge + Delta age (quadratic)\*cohort | 48 | -336.136 | 34.974 | 0 |
| Cohort + Delta age (quadratic) + Delta age (quadratic)\*cohort | 47 | -330.365 | 40.745 | 0 |

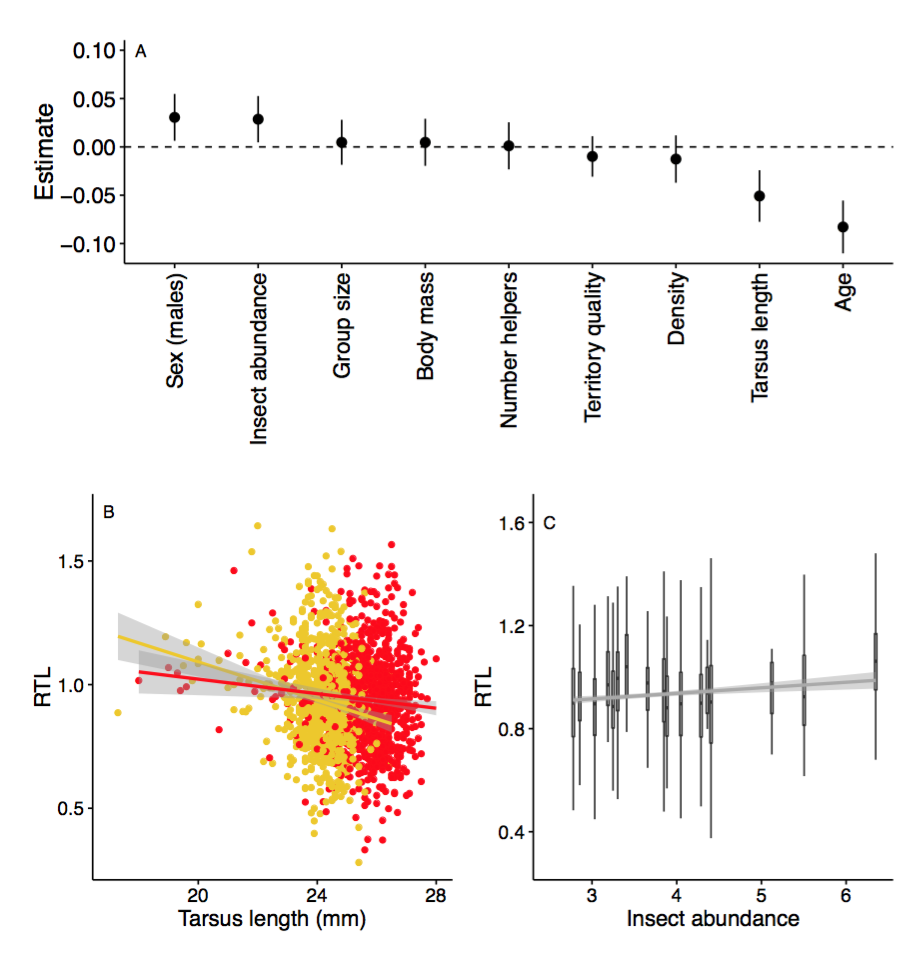
**Figures**



**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 cohorts. **C** RTL and age among cohorts. Lines represent fitted values from a linear regression and log-transformed age, and colours correspond to **B**. **D** RTL in relation to and Log age (i.e. within indiviual 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 (grey), and among different samples taken from the same individual (yellow). Areas of the density plot to the left of the dotted line represent decreases in RTL, while areas to the right represent increases.



**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.