**Early-life conditions, telomere dynamics and survival: insights from a long-term island bird study**

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**Running head:** Early-life telomeres

### Abstract

1. Understanding the costs individuals and populations face throughout their lifetimes 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. Thus, telomere dynamics may help us quantify individual variation in costs, and enhance our understanding individual variation in natural populations.
2. The Seychelles warbler (*Acrocephalus sechellensis*) is an excellent model system for disentangling the causes and consequences of individual variation in telomere dynamics. Here we study spatiotemporal variation in lifelong telomere dynamics in the Seychelles warbler. We combine long-term ecological data with one the largest longitudinal telomere datasets to date, consisting of 2079 samples from multiple cohorts spanning 19 years. We provide a detailed analysis of how telomere dynamics vary over individual lifespans, and with spatiotemporal variation in the social and ecological environment.
3. We found that telomere length decreases with cross-sectional and longitudinal measures of age, and that telomere length decreases most rapidly early in life. However, both cross-sectional and longitudinal data suggested that telomere length increases occurs in some individuals, and using a large number of repeated measurements we show statistically that this increase is unlikely to be explained by qPCR measurement error.
4. Telomere length and rates of shortening varied markedly both within and among cohorts. Telomere length was positively associated with island-wide temporal variation in food availability. We also found that cohort and age effects led to spurious associations between telomere dynamics and survival.
5. Our comprehensive, long-term data show that in natural populations telomere dynamics vary enormously over both space and time, and that this variation cannot be attributed entirely to measurment error. Ascertaining what explains this variation will require combining long-term ecological and quantitative genetic data.

**Keywords:** 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.

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### Introduction

Telomeres - the protective caps on the ends of chromosomes - may provide a solution to this problem. Telomeres shorten with age (Monaghan and Haussmann 2006), and in response to oxidative stress, which can be elevated due to environmental factors (Von Zglinicki 2002). When telomeres become critically short cells senesce (Campisi 2003), and the accumulation of these cells can result in organismal senescence and death (Wong et al. 2003). This association between senescence and telomere length has inspired a great deal of recent research into telomere evolutionary ecology (reviewed in Horn et al. 2010; Haussmann and Marchetto 2010; Monaghan 2014). While there is little direct evidence that the relationship between telomere dynamics and survival is causal (Simons 2015), there is mounting evidence that telomeres can act as biomarkers of cost in wild populations, providing a signature of the ecological stress that has been experienced and is otherwise difficult to detect (Monaghan 2014; Schultner et al. 2014; Asghar et al. 2015).

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), and that the extent of this shortening is influenced by the conditions experienced during that period (Price et al. 2013; Monaghan 2014; Nettle et al. 2015b; Reichert et al. 2015). Early-life telomere dynamics have been associated with both short-term and late-life survival (Heidinger et al. 2012; Boonekamp et al. 2014), and with other parameters such as cognition (Nettle et al. 2015a). However, few studies have simultaneously analysed how telomere dynamics, early-life conditions and late-life survival are all related in a natural setting. Moreover, how early-life telomere dynamics vary over spatial and temporal scales is poorly understood.

The longitudinal study (since 1986) of the Seychelles warbler (*Acrocephalus sechellensis*) population on Cousin Island provides an excellent system for studying senescence in the wild (reviewed in Hammers et al. 2015). Due to the isolated nature of the study population and intensive field monitoring, we have unusually comprehensive survival data and tissue samples spanning many years (see Methods, below). Ecological conditions and warbler population density on Cousin vary across space and time due to weather-induced changes in foliage cover and food availability (Van de Crommenacker et al. 2011). Seychelles warblers remain on their natal territories for at least six months, and variation in the oxidative stress experienced by individuals is associated with natal territory quality (Van de Crommenacker et al. 2011). However, neither early-life nor adult survival appear to be associated with natal territory quality or natal local density (Brouwer et al. 2006; Hammers et al. 2013). Facultative cooperative breeding occurs in the Seychelles warbler (Komdeur 1994; Richardson et al. 2003b), and the presence of helping subordinates (but not non-helping subordinates) in the natal territory is associated with increased survival later in life (Brouwer et al. 2012). Lastly, we have an established protocol for assessing telomere length in this species (Barrett et al. 2012), and telomere length predicts survival independently of age in adult Seychelles warblers, suggesting that telomeres act as a biomarker of cost (Barrett et al. 2013). Thus, we have an excellent system in which to assess the costs of different social and environmental conditions experienced early in life, and to assess the later-life consequences of early-life conditions.

In this study we examine how telomeres are related to early-life environmental variation and short and long-term survival in the Seychelles warbler. Because telomere dynamics are expected to reflect individual-level variation in the costs of early-life experiences, they may allow a more sensitive analysis of the effects of early-life environmental variation than would be possible with a direct comparison of how survival is affected by the early-life environment. With this in mind, we first conduct an exploratory analysis of how the environmental and social factors experienced in early life affect telomere dynamics. We then test the hypothesis that longer telomeres and lower rates of telomere shortening in early life are associated with greater survival.

### 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 birds on Cousin Island (04'20'S, 55'40'E) has been intensively studied since 1986 (Richardson et al. 2003a; Spurgin et al. 2014). This species' main breeding season runs from June-August, when the breeding females on each of the *ca*. 115 territories lay one or, rarely, two or three eggs (Komdeur et al. 1991). As a result of this low reproductive output, combined with higher mortality in first-year birds (39%; Brouwer et al. 2006), cohort sizes in the Seychelles warbler are small (<50).

Individuals are usually ringed in their first year of life, and so are of known age. They are then followed throughout their lives, and as they are non-migratory endemics naturally confined to the island (Komdeur et al. 2004), a biannual census of birds on Cousin during each breeding season gives accurate measures of local density, social status (e.g. breeding male/female, helping subordinate, non-helping subordinate) and individual survival (Crommenacker et al. 2011; Barrett et al. 2013). The isolated nature of the Cousin population is a key advantage of the system for analyses involving survival, which in other systems are often confounded by emigration (see Ergon and Gardner 2014 for a recent discussion). Full details of catching and monitoring methods can be found in Brouwer *et al.* (2012).

Seychelles warblers are highly territorial and all territories are mapped during the breeding seasons using detailed observational data of foraging and territorial defence behaviour, and surveyed for territory quality (Richardson et al. 2003a). Territory quality is calculated based on territory size, foliage cover and insect abundance (Komdeur 1992), and 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 intra- and inter-annual variation in rainfall and food availability, and such island-wide temporal variation may override the effects of individual territory quality. As an estimate of seasonal variation in food availability, we calculated an index of the number of insects across the entire island during each breeding season. This index is calculated as the mean number of insects found per unit leaf area over all surveys carried out on the island in a breeding season.

Each time a bird is caught on Cousin body mass and tarsus length are measured (to the nearest 0.1g and 0.1mm, respectively). Using information on eye colour (Komdeur 1991) and previous captures (Richardson et al. 2003a), we grouped birds into three age categories: one month old (birds still in the nest), 6 months old (fledglings with light grey eyes) and 10 months old (subadults with light brown eyes). A blood sample (*ca* 25 l) is taken from each bird captured 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), and 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 ratio has to be between 1.8 and 2 and, iii) the 260/230 ratio should 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, using the molecular methods outlined by Bebbington *et al.* (In Press).

For a subset of first-year birds we had longitudinal data, with an additional sample taken as an adult. For these individuals we calculated the within-individual change in RTL by subtracting early-life RTL from adult RTL (hereafter RTL). Negative values of RTL reflect telomere shortening, while positive values reflect telomere lengthening.

##### Statistical analyses

We performed all analyses using R version 3.0.1 (R Development Core Team 2011). Our dataset differs from slightly from that of Barrett *et al.* (2013) in that we are using RTL calculated directly from the qPCR data rather than converting into an absolute measure, and we are including many additional samples. We therefore first re-tested, using all available samples, whether telomere length decreases with age and age (a longitudinal measure based on within-subject centring; Pol and Wright 2009) in the Seychelles warbler, using linear mixed models with individual ID as a random effect. For the analysis of age we we only included birds who had been sampled at least twice. We then, using the juvenile samples, explored how telomere length varied within the first year of life (telomere length vs age in months) and among cohorts (telomere length vs cohort ID), again using linear mixed models with individual ID as a random effect. We tested how temporal variation in telomere length varied with temporal variation in population density (measured as the number of adult birds on the island at the end of each breeding season) and food availability, using linear mixed models with cohort ID as a random effect.

Because we observed apparent telomere lengthening in our data, we used the entire Seychelles warbler dataset to test whether this lengthening could be explained by measurement error. We used all birds (adults and juveniles) with at least two telomere measurements (N = 811 samples from 474 birds). We then calculated RTL for each pair of samples (for example, for a bird with three longitudinal measurements throughout their life we calculated the change in RTL between the first and second sample and between the second and third sample). We then compared these longitudinal changes in telomere length to sampling error, using all samples where we had at least two repeat telomere measurements for the same sample (i.e. completely seperate reactions run on separate plates: N = 596 measurements from 386 samples). We calculated RTL between pairs of repeat measurements within samples in exactly the same way as for across samples, except that repeat measurements were ordered by the date at the qPCR was run rather than by age. Secondly, if telomere lengthening is an artifact of measurement error, it is likely to occur more frequently when there is a short follow up time between samples (Steenstrup et al. 2013). We therefore tested whether telomere lengthening was more likely to occur at short sampling intervals by relating the sample follow up time to both the probability of telomere lengthening (GLM with a binomial error structure, telomere lengthening yes/no as response), and to the dgree of lengthening (LM using only samples where RTL increased over time, RTL as response).

We used linear mixed models with model averaging to explore how spatial variation in early-life environmental and social conditions influenced telomere length within cohorts. Model averaging was carried out using the MuMIn package (version 1.10.5) in R (Bartoń 2012). We first created a full model containing the following explanatory variables: age (in months), tarsus length, sex, territory quality and the number of helping and non-helping subordinate birds present in the natal territory. We also included interaction terms between age and all the other variables as telomere dynamics are expected to vary within the first year of life (Heidinger et al. 2012). As random effects we included cohort, territory ID and qPCR plate ID. Model selection was then performed 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 (*n* = 811) we repeated the above analyses of telomere dynamics, replacing telomere length with telomere loss as the response variable, and excluding the plate ID random effect (as each measurement of telomere loss was based on two or more measurements, and so run on multiple plates). For both sets of models, we first ran the model averaging procedure including all interaction terms, then re-ran the pipeline excluding non-significant interactions in order to obtain more accurate model averaged parameter estimates and confidence intervals.

We used generalised linear mixed models to test whether telomere length/loss were related to survival to adulthood. Models were set up with a binomial error structure, and included RTL or RTL and juvenile age as explanatory variables, along with the same random effects as for the model averaging (see above). We then used Cox regression, implemented in the survival package in R (**???**), to test whether long-term survival was related to individual-level telomere dynamics. For the cross-sectional data we used lifespan (in years) as survival time, while for the longitudinal data we used remaining lifespan from the second sampling event. We ran these models with cohort as a frailty term to exclude cohort effects, and only included cohorts in which at least 70 percent of individuals had died (all years up to and including 2008).

### Results

We measured telomere lengths using a total of 2079 unique samples from juvenile and adult Seychelles warblers. Efficiencies (mean s.d.) for our telomere and GAPDH reactions were (1.78 0.05) and (1.92 0.05) respectively. Inter-plate repeatability of RTL, based on 596 samples measured at least twice, was 0.78 (CI = 0.73-0.82).

##### Telomere dynamics and age

Using the cross-sectional data RTL decreased with age across the entire lifespan of the Seychelles warbler (LMM: t = -5.69; P < 0.001). We found that modelling a non-linear effect age explained almost double the variation in telomere length (R2 of linear regression of telomere length and log age = 0.016 than a linear model 0.012. Also worth noting is that while the overall trend was for decreasing telomere length, there were clear increases in cross-sectional telomere length after one year of age and at several points later in life (Fig. 1A).

Longitudinal data showed that early-life RTL was not related to adult RTL (R2 = 0.02; t = 3.94; P = 0.00; Fig. 4A). Running this analysis separately for juvenile age classes revealed that this relationship was not significant for nestlings (R2 = 0.00; t = 0.33; P = 0.74), fledglings (R2 = 0.01; t = 0.90; P = 0.37) or subadults (R2 = 0.03; t = 2.05; P = 0.04). RTL was significantly lower than zero in nestlings (t = -3.80; P < 0.001), but not in fledglings (t = -0.31; P = 0.76) or subadults (t = -1.27; P = 0.21), suggesting that telomere shortening was highest shortly after the nestling phase, after which both telomere shortening and telomere lengthening were observed (Fig. 4B).

To test whether the apparent telomere lengthening in our dataset could be explained by measurement error, we compared variance in telomere length among repeat measurements of samples to the variance observed among different samples of the same individual (see methods for details). We found significantly higher variance in telomere length over individual lifetimes compared to among sample replicates (Levene's test: F = 60.77; P < 0.001; Fig. 4C). Importantly, splitting the longitudinal data into instances of shortening (RTL < 0) and lenghtning (RTL > 0) revealed that not only did we observe significantly more shortening within individuals compared to within samples (Wilcoxon test: W = 5.834810^{4}; P < 0.001), but also significantly more lengthening (W = 53815; P < 0.001). We found no evidence that the likelihood of telomere lengthening was related to the follow up time between sampling events (GLM: t = -2.25; P = 0.02), and considering those samples that did show increases in RTL, the degree of increase was not related to follow up time (LM: t = 0.50; P = 0.62).

##### Early life environment and telomere dynamics

Early-life RTL varied significantly among cohorts (Likelihood ratio test: F = 3.70; P < 0.001). Cohort-level variation in juvenile RTL was not related to adult population density (LMM controlling for age and cohort: t = 0.40; P = 0.071), or to temporal variation in food availability (t = 7.55; P = < 0.001).

RTL did not differ significantly among cohorts (F = 1.57; P = 0), although power for this analysis was limited as longitudinal sample sizes within cohorts were low. Model selection revealed that the top model explaining RTL was the null model (Table S2).

Within cohorts, the top model explaining variation in early-life RTL contained age, territory quality, tarsus length, and the interaction between age and tarsus length (Table S1). Model-averaged confidence intervals of the age and tarsus x age effects did not overlap zero, but the tarsus and territory quality effects were not significant (Fig. 3A). Tarsus length was negatively related to RTL in nestlings, unrelated to RTL in fledglings, and positively related to RTL in subadults (Fig. 3B). Territory quality was negatively related to RTL, particularly in nestlings, although this effect was weak (Fig. 3C).

##### Early-life telomere dynamics and survival

Early-life RTL was not related to survival to adulthood (estimate = -0.29; P = 0.00), with no interaction effect between RTL and juvenile age (estimate = 0.01; P = 0.22), suggesting that there were no age-specific effects of juvenile RTL on survival to adulthood. To test whether cohort-level effects on RTL influenced survival we calculated cohort-level RTL (i.e. the median RTL for each cohort) and added this term to a GLMM, and found that cohort-level RTL was not related to survival to adulthood (estimate = 1.21; P = 0.14).

### Discussion

Here we use one of the largest datasets to date to assess the relationships between early-life conditions, telomere dynamics and survival in a closed population of Seychelles warblers. We found that, as in other studies, telomeres are lost at the greatest rate early in life. We found that telomere dynamics are subject to strong cohort effects. Within cohorts, we found little evidence that the ecological or social environment influenced telomere dynamics, and we found no evidence that early-life telomere length is related to juvenile or later-life survival.

Our study adds the the now substantial body of literature 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). Our finding that tarsus length was related to juvenile RTL in an age-dependent manner (Fig. 3) most likely represents an additional age effect - in passerine birds tarsus length is correlated with age during the nestling stage, but not after fledging (Ricklefs 1976). Telomere loss is most rapid early in life due to ongoing growth (Frenck et al. 1998), and a negative correlation between RTL and body size in early life is therefore expected (see also Ringsby et al. 2015). We also found weak evidence for sex-specific telomere dynamics in Seychelles warblers, with males having longer-telomeres and higher loss of telomeres (Fig. 3C, Fig. 5B). We do not wish to speculate too much on this effect as confidence intervals for both sex effects overlapped zero. However, it is worth noting while we found no evidence that juvenile RTL has a sex-specific effect on survival, in adults the effect of telomere length on survival is strongest for males (Barrett et al. 2013). Together, these results suggest that sex effects should at least be considered when studying any aspect of telomere dynamics (see also Barrett and Richardson 2011).

We found that at the individual-level, juvenile and adult telomere were not correlated, and that consistent telomere shortening only occurs very early in life (Fig. 4). This is 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 juvenile and adult telomere length were highly correlated, and individual-level telomere shortening clearly occurs throughout the juvenile period, and into adulthood. However, in accordance with our study, a recent study on Soay sheep (*Ovis aries*) found only a very weak correlation between juvenile and adult RTL, and a highly complex pattern of telomere dynamics across the lifespan (**???**). It is too soon to speculate as to what may be generating this variation among species, but one possibility is that environmental variability itself affects the resolution with which we can observe telomere shortening in natural populations (see also **???**). Regardless, our data suggest the efficacy of telomeres as individual biomarkers of cost in wild populations will depend on the age structure of the study population, as well as the sampling resolution.

Perhaps the clearest result from our study is that RTL varies among cohorts. A few studies have now shown that temporal variation in telomere dynamics occurs in natural populations, although these have been limited in the number of seasons (**???**; Mizutani et al. 2013; Watson et al. 2015). The long-term Seychelles warbler dataset has allowed us to show that temporal variation in telomere dynamics can occur over substantial time periods. Moreover, because of the large number of cohorts we have been able to show statistically that that temporal variation in RTL is related to variation in the environment (Fig. 1C). In some systems a negative relationship between population density and RTL may be expected, as increased competition for resources is known to effect juvenile telomere length. However, in the Seychelles warbler it is likely that population density acts as an indicator of overall island 'quality' for Seychelles warblers. This can clearly be seen from data from the 1980s and 1990s, when adult population size on Cousin increased as habitat quality improved (Komdeur and Pels 2005). Population size has fluctuated around 300 since the late 1990s (Fig. 2B), and we suggest that this variation captures this island-wide conditions more accurately than measures of insect abundance or territory quality. If cohort-level variation in telomere dynamics continues to be found in other systems, this has potential consequences for our understanding of telomere dynamics in natural populations. In particular, our findings suggest that the telomere dynamics of a population at a given point in time represent a snapshot of a temporally varying process. More research is now needed within and across multiple cohorts and populations to better understand how how and why population-level telomere dynamics vary over space and time.

Despite substantial cohort-level variation in juvenile RTL, within cohorts we found no evidence that any of the social or environmental variables we measured affect juvenile RTL. This is surprising, as a poor social and ecological environment is known to be detrimental to juvenile Seychelles warblers, both in terms of oxidative stress and later life survival (Van de Crommenacker et al. 2011; Brouwer et al. 2012). A possible explanation for this could be that temporal variation in RTL in our data masks our ability to detect spatial trends. However, this is unlikely we controlled for cohort ID, and within-cohort variation in RTL greatly exceeds among-cohort variation (Fig. 1C). A second possibility is that effects are generally weak and levels of noise in our telomere measurements and/or ecological data preclude detection of significant effects. While noise in telomere measurements and problems with power are a problem in any study using qPCR to measure telomere length (Nussey et al. 2014), our sample sizes and levels of repeatability compare favourably with other studies of natural populations that have found significant effects of the early-life environment on telomere length (e.g. **???**). More likely is that early-life RTL in the Seychelles warbler is explained by a set of variables that we have not measured. A key question to be addressed is the extent to which early-life RTL reflects inheritance (Asghar et al. 2014; e.g. Becker et al. 2015). This is important, as inheritance may capture a large amount of unexplained variation in early-life RTL within our dataset. Future research on the Seychelles warbler will examine, in a quantitative genetic framework, how genetic and environmental components, and their interactions, affect telomere dynamics and senescence.

While the relationship between mortality and telomeres in adults has been established for some time (Cawthon et al. 2003), only recently has the link between later-life survival and early-life telomere dynamics been studied. In captive zebra finches, juvenile telomere length predicts late-life survival (Heidinger et al. 2012), and in wild bird populations survival to the nestling phase (Watson et al. 2015), and survival to adulthood (Boonekamp et al. 2014), have been linked with early-life telomere dynamics. It is worth noting that here we have considered survival, but telomere length and shortening in early life may also be linked to other components of fitness (reviewed in Monaghan 2014). Reproductive senescence occurs in the Seychelles warbler (reviewed in Hammers et al. 2015), making this system well suited to examining how telomere length predicts lifetime reproductive success. We expect that by gaining a fuller understanding of telomere dynamics in natural populations, the fields of life-history evolution and evolutionary ecology will be greatly enhanced.

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m1 <- lmer(RTL~LogAge+(1|BirdID),data=dd) m2 <- lmer(RTL~LogAge+(1|BirdID) + (1|LayYear),data=dd) m3 <- lmer(RTL~LogAge+(1|BirdID) + (LogAge|LayYear),data=dd)

anova(m1,m2,m3)

m1 <- lmer(RTL~Agemonths+(1|BirdID) + (1|LayYear),data=dd) m2 <- lmer(RTL~LogAge+(1|BirdID) + (1|LayYear),data=dd) m3 <- lmer(RTL~factor(Agemonths)+(1|BirdID) + (1|LayYear),data=dd)

anova(m1,m2,m3)

dd14 <- subset(dd,DeathYear<2015) dd14$RowID <- c(1:nrow(dd14))

summary(glmer(SurvivedNext~RTL \* LogAge + Tarsus + Sex + (1|BirdID)+(1|LayYear),data=dd14,family = 'binomial'))

ggplot(dd14,aes(x = Agemonths, col = factor(SurvivedNext),y = RTL))+ geom\_smooth(method = 'lm',formula = y~log(x))

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