* Collection/generation methods

Detailed in (Sparks et al., 2021): “The Seychelles warbler is a small passerine endemic to the Seychelles archipelago (Komdeur et al., 1991). The entire population (~320 adult individuals in 115 territories) on Cousin island (29 ha; 04°20′S, 55°40′E) has been monitored intensively since 1985 (Hammers et al., 2019; Komdeur, 1992; Raj Pant et al., 2019; Richardson et al., 2007).”, “Since 1990, blood samples (~25 μl) have been taken and stored at room temperature in absolute ethanol, thus allowing …. telomere length measurement (Barrett et al., 2013).” “We used the telomere data set generated in Spurgin et al. (2018), which included birds caught and blood sampled between 1995 and 2014, when the data were most complete. RTL was estimated using qPCR (quantitative polymerase chain reaction; Barrett et al., 2013; Bebbington et al., 2016; Spurgin et al., 2018). DNA integrity (agarose gel) and 260/280 ratios were checked in all samples before running any qPCR, and any samples with signs of degradation were removed, reextracted and checked again.”

* Nature and Units of recorded values

relative telomere length (RTL)

* Quality control

Detailed in (Sparks et al., 2021): “Within-plate repeatability was 0.74 (95% confidence intervals [CI] =0.74–0.75) and 0.73 (95% CI =0.71– 0.74) for the GAPDH and telomere cq values, respectively (Spurgin et al., 2018). Between-plate repeatability of RTL, based on 422 samples measured at least twice at different time points (the different time points being a key point to replicate the actual technical error across normal samples), was 0.68 (95% CI =0.65–0.70) (Spurgin et al., 2018). All repeatability estimates were calculated on RTL measurements from the same DNA extraction and may be lower if DNA extractions were also repeated. There were no storage time effects (of the blood samples) on telomere length (Spurgin et al., 2018). Our cleaned data set included 2,664 samples from 1,318 individuals that passed quality control (Bebbington et al., 2016) and filtering steps (sample removal criteria: telomere cq ≥25 or cq replicate difference ≥0.5; GADPH cq ≤21 or ≥26 or cq replicate difference ≥0.5; RTL values ≥3). To investigate plate variance (by including qPCR plate as a random effect in our statistical models), where samples had replicates across plates (*n* = 388), an RTL value for a given blood sample was taken at random.”

From(Spurgin et al., 2018): “The following thresholds were applied before samples were included for further analysis: (1) DNA concentration must be at least 15 ng/μl (based on a mean of three measurements), (2) the 260/280 absorbance ratio has to be between 1.8 and 2.0 for acceptable DNA purity, and (3) the 260/230 absorbance ratio must be higher than 1.8. DNA integrity was further validated by visualisation 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 older samples (Figure S1). All DNA extractions that passed the above criteria were diluted to 3.3 ng/μl before telomere measure”; “Prior to qPCR, we used a random number generator to assign samples to qPCR plates, to ensure that no systematic bias could occur with regard to age, sex, cohort or ecological environment. Based on the distribution of observed cq values, we excluded outlier samples with extremely large cq values (cq values >25 and 26 were excluded for the telomere and GAPDH reactions respectively), which were assumed to be failed reactions.”

* Details of data structure

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| --- | --- |
| **Column descriptions** | |
| BirdID | Individual bird identifier |
| Sex | Sex of the individual where 0 is female and 1 is male |
| AgeY | Age of bird at catch in years |
| AgeClass | Age class of the bird (A - adult, CH - chick, FL - fledgling, J - juvenile, OFL - old fledgling, SA - subadult) |
| BirthFPID | Birth fieldwork period ID (where fieldwork periods are usually in the minor and major breeding season each year) |
| U\_PlateID | qPCR plate ID for RTL measurements |
| RTL | Relative telomere length |
| Technician | Technician who carried out the qPCR (2 levels) |
| Terr | Territory in which the bird was living during the catch FPID |
| FPID | Fieldwork period ID when the bird was caught |
| mum | Mum ID from genetic pedigree |
| dad | Dad ID from genetic pedigree |
| MAC | Maternal age at conception (years) |
| PAC | Paternal age at conception (years) |
| BrF | Dominant female in the natal territory |
| BrM | Dominant male in the natal territory |

* Experimental design/Sampling regime

Detailed in (Sparks et al., 2021): “The major breeding season runs from June to September, although some pairs also breed in the minor breeding season between January and March (Komdeur et al., 1991; Komdeur & Daan, 2005).” “Each breeding season as many birds as possible are caught using mist nets”

* Fieldwork and laboratory instrumentation

Detailed in (Bebbington et al., 2016): “DNA was extracted using a DNeasy blood and tissue kit (Qiagen) according to the manufacturer’s instructions with modiﬁcation of overnight lysis at 37 °C and a ﬁnal DNA elution volume of 80 micro-L. DNA integrity was veriﬁed visually using electrophoresis on a 1.2% agarose gel, and the concentration was quantiﬁed using a NanoDrop 8000 Spectrophotometer (ThermoScientiﬁc)”

**References**

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