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Asynchrony of ageing among traits in a wild bird population

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Abstract

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Ageing i.e. age-related changes in a trait, is a highly variable process. Studies have investigated variation in ageing among species and individuals, but little is yet understood about variation between traits. Evolutionary hypotheses argued that traits should age synchronously as selection should improve the trait that first senesces, therefore leading to trait synchrony. However, some past studies have demonstrated that traits do not senesce synchronously. We tested for the (a)synchrony of ageing across 13 reproductive, behavioural, physiological and morphological traits in a population of wild Seychelles warblers (Acrocephalus sechellensis). We modelled ageing trajectories for each trait and quantified synchrony between traits with similar ageing trajectory shapes by comparing the onset and rate of ageing and running bivariate models to quantify covariation between traits. We found that 7 traits exhibited ageing while 6 did not. Upon visual comparison of ageing trajectories, there were 3 groups of traits that shared ageing trajectories of the same shape. There was no support for synchronous ageing among any traits. Our study adds to growing evidence that ageing is asynchronous, and that the theory of synchronous ageing was erroneous. Our finding of senescence in direct fitness indices such as survival and reproductive but not in tarsus length gives weak support to newer evolutionary theories of asynchrony of ageing that traits more strongly associated with fitness age faster.

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Keywords: Ageing, Senescence, Selection pressure, Seychelles Warbler

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Introduction

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Ageing is the age-related change of traits, while senescence is the deterioration of function and fitness associated with advancing age due to the accumulation of cellular damage (Monaghan et al., 2008; Kirkwood & Austad, 2000). Ageing is widespread and highly variable across taxa, among populations and among individuals (Jones et al., 2014; Nussey et al., 2013). Even within individuals, traits can differ in their ageing trajectories – the age of onset and rate of senescence (Hayward et al., 2015). Differing within-individual ageing trajectories between traits is known as asynchronous or mosaic ageing (Walker & Herndon, 2010). The most notable example of asynchronous ageing is menopause (Ricklefs & Finch, 1995; Walker & Herndon, 2010). To date, there is still limited knowledge explaining the evolution of asynchrony of ageing. Further knowledge of patterns of differential ageing across traits is needed to fully understand factors contributing to variation and mechanistic processes underlying senescence. Through studying asynchronous ageing, we can better understand how variation in ageing affects age structures in a population. This is, in turn, important as a population's age structure hugely influences a population's demography, which drives evolution (Charlesworth, 1994; Jones et al., 2014). It was previously proposed that traits within an individual should senesce synchronously i.e., with the same age of senescence onset (Maynard Smith, 1962; Williams, 1957). The logic for this was based on the idea that senescence was caused by generalized deterioration, not from major changes in any one system (Williams, 1957). It was argued that selection should act to improve (delay onset) the first senescing trait that impairs fitness and function, thus synchronizing the onset and rate of senescence (Maynard Smith, 1962; Moorad & Ravindran, 2022; Williams, 1957). There are more recent interpretations of the verbal theory. Hayward (2015) hypothesized that there was a critical threshold for each trait value which if crossed,

will result in death. Thus, selection will be strongest on traits closest to the threshold value (Hayward et al., 2015). In contrast, Gaillard and Lemaître (2017) suggested that selection pressures on traits should differ according to their early life survival, thus aligning ageing trajectories. Regardless of the importance of traits to survival and reproduction, these interpretations of the original idea indicate that since selection does not act on all traits uniformly, ageing should be synchronous. However, selection pressures should be traitspecific (Gaillard & Lemaître, 2017). It, therefore, seems logical that traits more closely linked to fitness should age later and slower. Similarly, weaker selection on traits less important to fitness components would lead to comparatively earlier ageing in those traits, since optimal resource allocation would delegate less resources to repair that trait, leading to asynchronous ageing (Rodríguez-Muñoz et al., 2019). More recent theories on (a)synchrony of ageing have hypothesized that ageing trajectories (rate, onset and shape) are determined by the correlation between the trait and fitness (Boonekamp, Mulder & Verhulst, 2018; Briga & Verhulst, 2021). Traits contributing most to fitness are predicted to be under the strongest selection pressures, and thus have the slowest ageing rates since fitness costs from senescence of these traits will be the highest (Rodríguez-Muñoz et al., 2019). Counterintuitively, a theoretical study found that traits under strongest selection in early life have the fastest rate of decline of age-specific selection, which leads to faster ageing rates for these traits (Moorad & Ravindran, 2022). While the difference in selection pressure has been the most reviewed cause, genetic correlations among traits between and within age classes may also impact asynchrony of ageing, depending on the selection pressures on respective traits (Hayward et al., 2015; Moorad & Ravindran, 2022). Non-evolutionary factors may also contribute to apparent asynchrony of senescence. Traits

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may vary in the extent of damage they accumulate from environmental factors over time, causing differing rates of senescence (Moorad & Ravindran, 2022). There is considerable empirical work providing evidence for the asynchrony of ageing across traits (Moullec, Reichert & Bize, 2023) but, to the best of our knowledge, none supporting William's theory of synchronous senescence. Health and lifespan are commonly found uncoupled in humans and laboratory model organisms (Bansal et al., 2015; Christensen et al., 2009). Studies have also demonstrated that traits differ in onset and rate of ageing in various taxa under both wild and captive conditions, such as plants, Caenorhabditis elegans, mammals, birds and snakes (Briga & Verhulst, 2021; Boonekamp, Mulder & Verhulst, 2018; Cayuela et al., 2020; Cooper et al., 2021; Herndon et al., 2002; Hayward et al., 2015; Moullec, Reichert & Bize, 2023; Rodríguez et al., 2017). Most studies showed asynchrony of senescence in reproductive and survival traits (e.g. Cayuela et al., 2020; Cooper et al., 2021; Fay et al., 2021), while two found asynchrony in physiological traits (Briga & Verhulst, 2021; Boonekamp, Mulder & Verhulst, 2018). Additionally, Hayward et al (2015) studied whether traits within a functional grouping (e.g., reproductive, survival, behavioural) senesced more similarly in Soay Sheep (Ovis aries), but did not detect any synchrony of ageing. However, only a few studies have investigated the synchrony of senescence across a broad range of traits. Here we address this gap by testing asynchrony of senescence across a wide range of traits in a longitudinal wild bird population. The Seychelles warbler (Acrocephalus sechellensis) (here after SW) population on Cousin Island provides an exceptional longitudinal study system. Owing to bi-annual sampling for c.a. 30 years, the lack of (im)migration (<0.1%) (Komdeur et al., 2004) and high mean resighting probability (Brouwer et al., 2010), we have comprehensive life history data for individuals from birth to death, accurate survival data, and longitudinal measures of numerous traits

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(Sparks et al., 2022). Importantly, these repeated individual measures allow us to account for selective disappearance by statistically separating within- and between-individual trait variation (van de Pol & Verhulst, 2006). Given the lack of predators of adults on the island, there are low levels of adult extrinsic mortality contributing to annual mortality (van de Crommenacker et al., 2017). Consequently, the SW is relatively long-lived with a mean lifespan of ca. 4.4 years post fledgling (Figure s1), and a maximum of 19 years (Hammers & Brouwer, 2017). The warblers exhibit actuarial, reproductive and telomere length senescence (Barrett et al., 2013; Hammers et al., 2013, 2015), and ageing in provisioning rate (Hammers et al., 2021). Reproductive senescence begins at 6 years for females without helpers (Hammers et al., 2012) and 7.8 years for males (Raj Pant et al., 2020) respectively. These features make this population an excellent study system for investigating (a)synchronous ageing. In this study, we aim to 1) quantify the ageing trajectories of 13 traits in the SW including morphological, physiological behavioural and fitness related traits, and 2) test for their (a)synchrony of ageing. This study will help us identify wider patterns in variation in ageing between traits, and enable us to further understand the drivers of evolution of asynchronous ageing.

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Study system

Seychelles warblers are small (13-14cm) passerine birds endemic to the Seychelles. On Cousin island (4.3315° S, 55.6620° E) the population of this facultatively cooperative breeder is structured into ca. 115 territories each containing 1 breed group that consists of a dominant breeding pair, offspring, and may include helper or non-helper subordinates (Richardson, Burke & Komdeur, 2002). The Cousin population of c.a. 320 individuals has been monitored more intensively since 1985 (Komdeur, 1992, Komdeur & Daan 2005). Since 1997, ~ 96% of the individuals have been ringed with a unique British Trust for Ornithology (BTO) ring and colour ring combination (Richardson et al., 2001; Sparks et al., 2022). Fieldwork occurs twice a year, in the minor (Jan-Mar) and major (Jun-Oct) breeding seasons. Individuals were captured using mistnets and playback. Unringed birds were ringed with a British Trust for Ornithology metal ring and a unique colour ring combination. Ca 70 µl of blood was collected via brachial venipuncture (Brown et al., 2021b). These blood samples have previously been used for molecular sexing and genetic parentage assignment (Sparks et al., 2022; Richardson et al., 2001), measuring malaria presence (Hammers et al., 2016), buffy coat (Brouwer, 2007), telomere length (Barrett et al., 2013; Brown et al., 2022), haematocrit (Brown et al., 2021b), oxidative stress and antioxidant capacity (van de Crommenacker et al., 2011). Unringed individuals were aged according to eye colour (Komdeur, Bullock & Rands, 1991). Morphological traits were measured including body mass (± 0.1g), wing length (± 0.1mm), right tarsus length (± 0.1mm) and fat score (0-5).

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Individual territories were visited every two weeks to carry out a population census. Survival and social status were determined by observing colour-ringed birds and following the

dominant female of each territory for 15 minutes (Crommenacker, Komdeur & Richardson, 2011; van Boheemen et al., 2019). The dominant breeders were defined as the pair-bonded male and female in a territory according to interactions and nesting behaviour, while subordinates were defined as helpers or non-helpers depending on whether they displayed brooding or offspring provisioning (Richardson, Burke & Komdeur, 2002). If a nest was found in the territory, the nest was checked every week to determine nest stage (Komdeur & Daan, 2005). 60-90 min nest watches were carried out during the incubation and provisioning stage of nesting (van Boheemen et al., 2019). Provisioning rates of individuals were calculated as the total number of provisioning events per bird over the duration of the watch. Watches where more than 10% of provisions were by unidentified birds were excluded (van Boheemen et al., 2019). Food (insect prey) abundance was measured according to Komdeur (1996), and mean insect availability was calculated from averaging insect abundance across the island in a year or season. Territory quality was defined as the insect availability within a territory (Hammers et al., 2015), and was calculated as $\alpha \cdot \sum (c_x i_x)$, where α is the territory size (hectares), c_x is the foliage cover for broad-leafed tree species x, and ix is the mean monthly insect count for tree species x per unit leaf area dm² (Komdeur, 1992, 1996).

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Trait	Rationale for inclusion	Predicted
Body mass	Body mass is the most simple and common	(direction) Declines
body mass	indicator of body condition (Labocha & Hayes,	Decimes
	2012). Many studies attributed body mass ageing	
	to senescence in function and condition (Nussey et	
	al., 2011).	
Wing length	Indicator of flight ability and feather quality, may	Declines
	affect a bird's foraging ability and	
	thermoregulation (Kiat & Sapir, 2018).	
Right tarsus	Treated as a control of ageing trajectory as tarsus	No change
	length is developmentally determined and not	
	known to senesce (Tjørve & Tjørve, 2010).	
Fat score	Fat score indicates energy reserves and condition in birds (Labocha & Hayes, 2012).	Declines
Oxidative stress	Damages biological macromolecules which may	Increases
(ROMs)	cause accelerated ageing and degenerative	
	diseases (Beckman & Ames, 1999; Finkel &	
	Holbrook, 2000).	
Antioxidant	Buffers against oxidative stress which may help	Declines
capacity (OXYs)	individuals avoid the harmful consequences of	
	oxidative stress (Felton & Summers, 1995).	
Haematocrit	Reflects haemoglobin concentration. An indicator	Declines
	of aerobic capacity, which is important in	
	endurance and performance in SW(Brown et al.,	
	2021b).	
Buffy coat	Refers to the white blood cell layer after	Declines
	centrifugation. Measure of leucocyte content in	
	blood, which may be indicator of immune function	
	and survival (Mondragão-Rodrigues & Macedo,	
	2023; Møller & Saino, 2004).	
Malaria presence	Potential indicator of immune response against	Decreases then
- 1 1 1	infection in SW (Hammers et al., 2016).	increases
Telomere length	Biomarker of senescence that declines with age	Declines
Due delenine vete	and predicts survival in SW(Barrett et al., 2013)	La successión de la cons
Provisioning rate	Declines in female, but not male SWs, with age and	Increases then
	offspring first year survival declines with parent age (Hammers et al., 2021)	decreases
Annual	Senesces in SW (Hammers et al., 2012; Raj Pant et	Increases then
reproductive	al., 2020).	declines
success (ARS)		
Annual survival	Senesces in the SW (Hammers et al., 2013).	Declines after age
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Measurement of physiological and fitness traits:

Oxidative stress (ROMs) and Antioxidant capacity (OXYs): Undertaken as part of a previous study (Brown et al., 2021b; van de Crommenacker et al., 2011). Plasma from each blood sample was separated by centrifugation (9889 g for 8 minutes) and frozen. The oxidative damage and antioxidant compounds were quantified using d-ROMs test kit (Diacron, Grosseto, Italy) and OXY-Adsorbent test kits (Diacron) respectively (van de Crommenacker et al., 2011). Full assay details can be found in van de Crommenacker et al., (2011b). ROMs were calculated as the sum of oxidative damage compounds while OXYs were calculated as the sum of antioxidant compounds.

Haematocrit and Buffy coat: Within ca. 3 hours of bleeding, the heparinized capillary tube was centrifuged for 8 minutes at 6000 g (Brown et al., 2021b). Haematocrit was measured as the proportion of erythrocytes to the whole blood volume in the capillary tube with calipers to the nearest 0.01mm. Buffy coat was measured under a 10x magnifying glass as the proportion of leukocytes and platelets to the whole blood volume.

Malaria: Blood samples were tested for the presence or absence of haemosporidian parasite infection using a nested PCR technique (Hellgren, Waldenström & Bensch, 2004; Hammers et al., 2016) run twice per sample. Individuals with conflicting test results from the test consensus were removed from the dataset. 87% of samples had consistent test results across both PCR runs (Fairfield et al., 2016).

Telomere length: We used the telomere dataset from Spurgin et al (2018) for samples collected between 1995-2014. A qPCR method was used to estimate Relative Telomere Length (RTL; Barrett et al., 2013). Within and between plate repeatability for all samples screened over different years was 0.74 (95% CI = 0.74 - 0.75) and 0.68 (95% CI = 0.65 - 0.70)

respectively (Sparks et al., 2022). There were no detected blood sample storage time effects on telomere length (Spurgin et al., 2018).

Annual reproductive success (ARS): Blood samples were genotyped and parentage was assigned using package MasterBayes 2.52, from which a pedigree was constructed (Hadfield, Richardson & Burke, 2006). Details of the parentage analysis and pedigree construction can be found in Sparks et al (2022). ARS was quantified as the number of offspring in the genetic pedigree assigned to a parent with >=80% genetic confidence in a year (Sparks et al., 2022). Survival: Given the high resighting probabilities in this population (of 0.92 \pm 0.02 for individuals \leq 2 years and 0.98 \pm 0.01 for older individuals) (Brouwer et al., 2010), birds not seen for two consecutive field seasons were assumed dead unless resighted thereafter.

Statistical analysis

Statistical analyses were conducted in R 4.2.2 (R development Core Team 2022). We analysed ageing trajectories of 13 traits (Table 1) with data collected between the years 1981-2022, using mixed Generalised Additive Models (GAMs) using the package *mgcv* 1.9 (Wood, 2017). GAMs allowed us to fit non-parametric smoothing terms between a trait and age, which were more suitable as it allowed for combined testing of gradual and threshold changes with age due to its flexible nature, as observed e.g. in body mass and metabolism (Nussey et al., 2011, Douhard et al., 2017, Briga et al., 2019, Briga et al., 2021). All models were fitted with a smoothing term for age (main effect). Selective appearance and/or disappearance can obscure apparent senescence patterns if the relationship between trait values in older age and lifespan are stronger in certain traits, and the between- and within-individual differences are not distinguished (van de Pol & Verhulst, 2006). We controlled for selective disappearance by fitting lifespan as fixed effect and bird identity as random effect (van de Pol & Verhulst,

2006). Age of first and last reproduction was fitted in the ARS trait model to account for selective disappearance. Lifespan was not fitted in the survival model as individuals only die once. We fitted annual insect abundance, social status (dominant or subordinate) and sex as control variables for all models. Food abundance is an indicator of available resources on the island and energy acquisition in the warblers (Hammers et al., 2012), and social status may affect a bird's energy allocation and usage. Individual differences in the availability and allocation of these resources may influence senescence trajectories (Kirkwood, 1977). Sex was included to account for possible sex differences in ageing (Brouwer et al., 2006). We compared model fit for each trait using Akaike's Information Criterion (AIC) to determine whether an age by sex interaction should be fitted. The model with the lowest AIC was considered as the best fit (ΔAIC<4) (Burnham, Anderson & Huyvaert, 2011). Tarsus length was fitted in the body mass and wing length trait models to control for body size. Birth cohort was fitted as a random effect in all models. For all morphological traits, haematocrit, buffy coat, and provisioning rate models, observer identity was fitted as a random effect. Technician identity was fitted as a random effect for RTL. All response variables with a Gaussian distribution were z-transformed. All models were checked for convergence and tested for concurvity with the mgcv package. The full results of the ageing models, including all fixed and random effects for each trait can be found in the supplementary material (Tables S1-S13). As GAMs do not produce interpretable or meaningful effect sizes or p values for smooth terms, we calculated the first order derivatives of the age smooth term to determine which traits demonstrated ageing. Positive derivative values indicate a positive slope, suggesting improvements with age, vice versa for negative derivative values, while value of 0 indicates maxima or minima. Traits reach maximum values when their first-order derivative is zero.

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Hence, we defined a trait's ageing as statistically significant when the upper 95% confidence of the derivative crossed zero.

There are currently three main approaches to quantifying asynchrony of ageing. Hayward et al's (2015) quantitative method works well to quantify features of ageing trajectories. However, by normalizing age-specific means, this approach may miss variation in ageing rates. Cooper et al's (2021) quantitative approach also identifies whether ageing onset and ageing rates are determined by biologically meaningful trait values. However, this method may find asynchrony of senescence in traits with differing age-specific variances that have the same age-specific means. Results may therefore differ according to the methodology used to detect asynchrony of senescence or compare ageing rates (Moorad & Ravindran, 2022). The two methods outlined above both make indirect comparisons of ageing trajectories which do not estimate synchrony of ageing. Differently, Briga and Verhulst (2021) directly quantifies synchrony of ageing by estimating within-individual correlation of ageing rates between traits.

We tested for asynchrony of ageing according to the methods outlined in Briga and Verhulst (2021). Trait ageing trajectories were visually compared first. If trait GAMs showed different ageing trajectory shapes between traits, they were considered to have asynchronous ageing. If ageing traits showed visually similar ageing trajectory shapes, a bivariate model was run between the traits to estimate the covariance between the two traits to compare within individual ageing rates (Briga & Verhulst, 2021).

Visual comparison produced three groups of traits with similar ageing trajectories. We restricted the bivariate models to traits with age-related declines, which resulted in two groups. Bivariate models were run on traits in group 1 (traits ageing quadratically) and group

2 (traits ageing linearly). The package *mcgv* was used for models with only Gaussian responses, while *MCMCglmm* 2.36 was used for the models including non-Gaussian responses. Bivariate models were not run between survival and the other two traits in group 1 as comparing a within-individual ageing trajectory (body mass and provisioning rate) and a between-individual ageing trajectory (survival) is not biologically meaningful. Bivariate models from group 2 containing buffy coat (F) as one of the responses can only be compared among female warblers since the males showed a non-linear ageing trajectory and bivariate models require data from the same individual at the same age for both traits to estimate a covariance. We used uninformative priors with an Inverse Wishart distribution in the *MCMCglmm* bivariate models. For each *MCMCglmm* model, we checked convergence by ensuring autocorrelation was lower than 0.1, visual inspection of posterior trace plots and effective sample size being greater than 1000. The table of the full model and variables included can be found in the supplementary material (Tables S14-17).

Results

Ageing trajectories

Seven out of thirteen traits, one of which was sex-specific, showed age-related declines: Body mass, fat score, telomere length, buffy coat in females, provisioning rate, annual reproductive success (ARS) and annual survival probability (Figure 1 & 2 a, d, h, j, l, m, n respectively; Tables S1,S4, S8, S10, S11, S12 & S13 respectively). Body mass and provisioning rate showed a quadratic relationship with age, initially increasing then decreasing post-peak from c.a. 8.5 and 6 years, respectively (Fig. 1 & 2 a, l; Table 2). Similarly, annual survival probability displayed an increase until the age of significant decline – 8.5 years (Fig 1 & 2 n; Table 2). Fat score and telomere length for both sexes, and buffy coat in females decreased linearly with

age (Figures 1 & 2 d, h, j, respectively; Table 2). ARS increased until age 3 then remains roughly constant from age 3 to 11, except displaying a small significant decrease at age 7, followed by a plateau, then a larger significant decrease after age 11 (Fig 1 & 2 m; Table 2).

Wing length and oxidative stress did not show statistically significant ageing, but showed a slight quadratic relationship (Figures 1 & 2b,e). Antioxidant capacity and haematocrit also did not show significant ageing, and had a linear relationship. As expected, tarsus length is developmentally determined, thus was constant throughout life (Fig 1 & 2 c). Buffy coat in males, and malaria presence showed an initial decrease (until ages 3 and 5, respectively) and then levelled out (Fig 1 & 2 i and j), thus there was no age-related decline as both traits remained steady with age after the initial decline.

Table 2. Age of onset of decline for seven phenotypic traits in the Seychelles warbler population on Cousin island (dates differ per dataset, minimum date 1981, maximum date 2022) based on the derivatives of the curves obtained from the Generalized Additive Models for each trait with significant ageing trajectories (Fig 2 a, d, h, k, l, m & n). The mean of the derivative of the slope indicates the estimated population mean age of ageing. The upper and lower 95% confidence intervals where the derivative of the slope crosses 0 estimates the variation around the mean age of ageing. NA indicates instances where the onset of ageing is not a biologically meaningful age, as the trait declines from early-life, thus onset will be negative. F= female. RTL = relative telomere length.

Trait	Body	Fat score	RTL	Provisionin	Buffy	Surviva	Annual
mean &	mass			g rate	coat F	1	Reproductiv
95% CI							e Success
Upper	8.5	0	0	6	0	8.5	7 and 11
Mean	4.7	NA	NA	NA	NA	6.2	6 and 10
Lower	1	NA	NA	NA	NA	3.8	2.8

Of the traits that showed significant age-related changes, three different age-specific trajectories were observed. Group 1: Body mass, provisioning rate and annual survival had a quadratic ageing trajectory (Fig 2a, I and n). Group 2: Buffy coat (Female), fat score and relative telomere length showed a linear decline (Fig 2d, h, and k). Group 3: Male buffy coat, and malaria prevalence decreased in early life and then stabilized in later life (Fig 2i & j). Annual reproductive success (ARS) did not show a similar age-trajectory with any other traits (i.e. ages asynchronously to other traits, Fig 2m). The traits within these 'similar trajectory' groups do not belong to the same functional grouping (e.g., morphological, physiological, fitness traits) except for group 3 being immune traits.

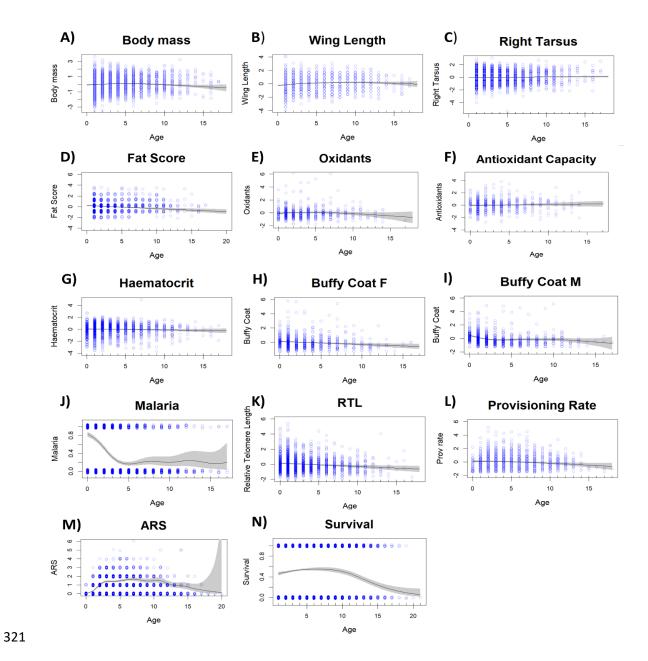


Figure 1. The age-specific trajectories of 13 phenotypic traits in individuals the Seychelles warbler population of Cousin Island (dates differ per dataset, minimum date 1981, maximum date 2022) identified through Generalized Additive Models. The x-axis is age in years, and the y-axis is the trait value; all traits, except for annual reproductive success, survival and malaria, are z-transformed. The solid black line depicts the model-predicted curve and the grey shaded areas depict the standard error. Blue points are raw data points. RTL = relative telomere length. ARS = Annual Reproductive Success. For buffy coat (Fig 1h & i), F indicates female, M indicates male.

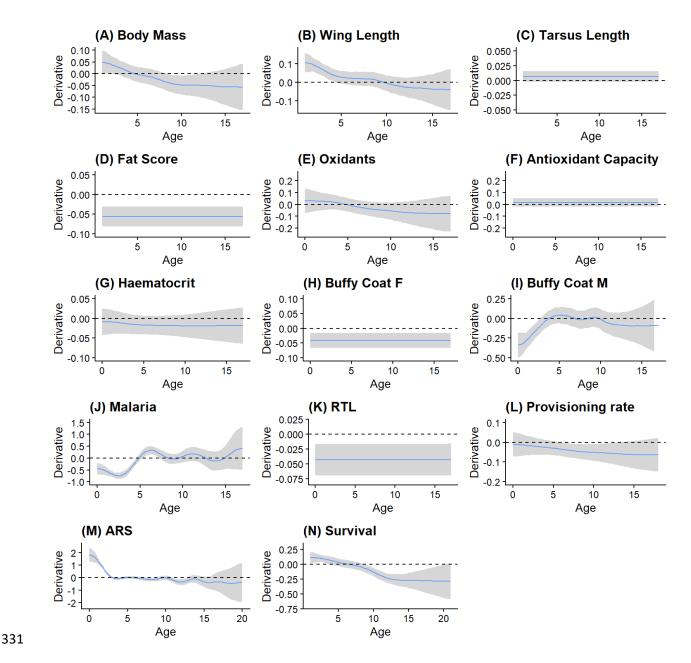


Figure 2. The ageing rates of the 13 phenotypic traits in individuals of the Seychelles warbler population of Cousin Island (dates differ per dataset, minimum date 1981, maximum date 2022). The rate of ageing of each trait was calculated by obtaining first-order derivatives (solid blue line) of the model-predicted curve of the age term in each Generalized Additive Model. On the y-axis is the derivative of the curve, with age (years) on the x-axis. The solid blue line depicts the ageing rate and the grey shaded areas around the blue line depict the 95% confidence intervals. A derivative value above 0 indicates the slope is positive, and vice versa.

Traits with 95% upper confidence intervals that cross the dotted zero line demonstrate significant trait ageing. This includes A) body mass, D) fat score, H) female buffy coat, K) RTL (relative telomere length), L) Provisioning rate, M) ARS (annual reproductive success) and N) survival.

Within individual covariance of senescence rate between traits

Only traits in group 1 and group 2 showed age-related declines. Thus bivariate models were run on pairs of traits within groups 1 and 2. Survival was not included as a response variable in any of the group 1 bivariate models as survival ageing is a between individual estimate. The degree of synchrony of ageing between traits was low (<|0.13|). Most trait pairs show a negative covariance with the exception of RTL and buffy coat F (Table 3 a & b). The full model output for the bivariate models are in the supplementary material (S14-17)

Table 3. Covariances between pairs of SW traits that visually had similar ageing trajectories estimated from bivariate Generalized Additive Models and bivariate MCMCglmm models.

Table 3a contains covariances of traits ageing with a negative quadratic pattern (Group 1).

Table 3b contains covariances of traits that showed a linear decline with age (Group 2).

Results for bivariate models containing buffy coat are only pairwise comparisons between female SW individuals, as buffy coat only declined in later-life for females. The covariances are reported on the latent scale. RTL = relative telomere length

3a 3b

Trait	Body Mass	Provisioning
	iviass	rate
Body mass		-0.03178245
Provisioning		
rate		

Trait	Fat	Buffy	RTL
	Score	Coat F	
Fat Score		-0.1283	-0.016682
Buffy Coat F			0.01222042
RTL			

Discussion

We quantified ageing trajectories, and tested for asynchrony of ageing, across 13 phenotypic traits in the Seychelles warbler. We found age-related declines in seven traits: body mass, fat score, buffy coat (female), relative telomere length, provisioning rate, ARS and annual survival probability. There were three groups of traits sharing similar ageing trajectories; 1) Quadratic with age: Body mass, provisioning rate and survival, 2) Linear decline with age: Buffy coat (female), fat score and telomere length, 3) Improves in early life and stabilizes in late life: Buffy coat (male) and malaria infection. However, the onset of ageing often differed between those traits that aged (Table 2), and the degree of synchrony of ageing was low between traits that shared similar trajectories (Tables 3a & b). Additionally, there were sex differences in asynchrony of ageing due to sex differences in ageing of buffy coat (white blood cell abundance). Among the groupings of traits that shared similar trajectories, there was no pattern of similarities in ageing in functional grouping (morphological, physiological, immune, behavioural, fitness traits) aside from group 3 where both traits were immune traits. Overall, our study showed asynchrony of ageing in the SW.

- Phenotypic trait ageing in the Seychelles Warbler
 - i. Morphological trait ageing (Body mass, wing length, Right tarsus length, fat score)

Ageing of morphological traits has not been previously studied in the SW, but the present study revealed key patterns. First, the observed decline of both body mass (accounting for tarsus length) and fat score indicated body condition ageing in the SW. Most studies on body mass senescence in other species support our findings (Beirne, Delahay & Young, 2015; Douhard et al., 2017; Nussey et al., 2011; Kroeger et al., 2018), while a couple do not (Hämäläinen et al., 2014; Moullec, Reichert & Bize, 2023). In contrast, the only study (to our knowledge) using fat score did not report ageing (Milenkaya et al., 2013). Wing length did not show significant ageing in SW, unlike previous findings in other species (Piliczewski & and Wysocki, 2018; Moullec, Reichert & Bize, 2023; Śliż, 2022). SW often prefer to hop or do short flights for foraging and do not disperse across islands (Komdeur et al., 2004), thus rely less on flight ability. This potentially results in negligible trade-offs between feather quality and other traits if the cost to maintain feather quality is lower than expected (Buttemer, Addison & Klasing, 2020; Kiat & Sapir, 2018), explaining the lack of ageing. Overall, our findings suggested body condition ageing in the warblers, but not ageing in other morphological traits.

ii. Physiological trait ageing (Oxidative stress, antioxidant capacity, telomere length, haematocrit)

Telomere length was the only physiological trait that showed ageing, which aligns with previous studies in the SW (Barrett et al., 2013; Brown et al., 2022), and many other species (Le Clercq et al., 2023; Remot et al., 2022). Additionally, telomere length senesces in the SW as short telomere length and higher telomere attrition rates predicted survival in the SW (Barrett et al., 2013; Brown et al., 2022).

The non-significant ageing of oxidative stress traits, i.e. ROMs and OXYs is consistent with past studies finding oxidative stress markers to be stable with age (Hindle et al., 2010; Hübner-Woźniak et al., 2011; Nussey et al., 2009), although another study found the opposite

(Williams, Roberts & Elekonich, 2008). As oxidative stress had the shortest timeframe of data collection (2006-2013), a lack of older individuals (age > 6, N=114) may have led to a reduced power to detect ageing.

Although non-significant, the trend of haematocrit decreasing with age found in the present study aligned with previous research on this species, which found a significant decline with age (Brown et al., 2021). Studies in other species also found age-related declines in haematocrit content (Elliott et al., 2015; Hickmott et al., 2024; Goldberg et al., 2023). Since haematocrit does not predict survival in later life in the SW (Brown et al., 2021b), it likely does

not senesce in this species. Overall, there was therefore little evidence of ageing in

iii. Immune trait ageing (Malaria presence, Buffy coat)

physiological traits in SW aside from RTL.

There was no evidence for age-related declines in immune traits in male SW. Although previously thought to be attributed to selective disappearance (van Oers et al., 2010), the results from the present study and Hammers et al (2016) refuted this. This suggests SW maintain immune function in late life (Hammers et al., 2015). The lack of ageing in male buffy coat that our results showed further supports the lack of immune trait ageing in male warblers, which differed to that found in the Soay sheep (Froy et al., 2019). We observed sex differences in ageing of buffy coat (Figure 2h & I). SW are hypothesized to show no differences in energy expenditure between sexes since they exhibit biparental care and share costs of breeding (Williams, 1957; Hammers et al., 2013; Komdeur, 1994, van Boheemen et al., 2021), which should suggest no sex differences in ageing. Coupled with no sex differences in lifespan in the SW, our results were not expected. Nonetheless, studies in other species often found sex differences in the ageing of immune parameters (Hickmott et al., 2024; Klein & Flanagan, 2016; van Lieshout et al., 2020). More generally, the evidence for immunosenescence / ageing

is mixed; with some finding ageing in immune traits (Cheynel et al., 2017; Peters et al., 2019) and others not (Bichet et al., 2022; Peters et al., 2019; Roast et al., 2022). This may be due to studies failing to quantify within-individual change (Peters et al., 2019). Although there is currently no consensus in wider immune trait ageing research, potential differences in selection pressure between sexes (Metcalf, Roth & Graham, 2020) may explain the observed sex differences in immune function senescence in SW, leading to sex differences in asynchrony of senescence.

iv. Behavioural trait ageing (Provisioning rate)

The ageing trajectory of provisioning rate identified in the current study was similar to previous results in the SW, showing a decline in provisioning rate with age (Hammers et al., 2021). This aligns with results in another bird species (Krist et al., 2024), but contrasted other studies (Cansse et al., 2024; Wilcoxen, Boughton & Schoech, 2010). In terms of implications for senescence of provisioning rate in the SW, although offspring first-year survival declines with breeder age in the SW (Hammers et al., 2021), it remains unclear whether this results specifically from age-related declines in provisioning rate, as breeder age may also affect offspring survival through factors like egg quality (Beamonte-Barrientos et al., 2010).

v. Fitness related trait ageing (ARS and survival).

Finding senescence in annual reproductive success (ARS) and survival in the SW was expected based on previous results in SW(Hammers et al 2015) and studies across a range of taxa (Jones et al., 2014; Lemaître & Gaillard, 2017; Tidière et al., 2018; Torres, Drummond & Velando, 2011; Vágási et al., 2021; Vrtílek, Žák & Reichard, 2022). The stability in ARS may partially be due to SW producing single-egg clutches in 91% of breeding attempts (Komdeur, 1996). Only 3% of SW had an ARS larger than two in our data, resulting in little variation in the cost of reproduction between breeders. Differences in estimated onset of reproductive senescence

Pant et al., 2020), likely stem from dataset differences, as prior work excluded significant amounts of reproductive data gained in minor seasons and subordinates (Hammers et al 2012).

Survival probability ageing in our study shared the same trajectory shape with a previous SW study (Hammers et al., 2015), and is consistent with previous research across various taxa (Cooper et al., 2021; Hammers et al., 2015; Gaillard & Lemaître, 2020; Jones et al., 2014; Nussey et al., 2013). Unfortunately, survival senescence is a cross-sectional measure, since it is not possible to separate within and between individual heterogeneity in survival probability with a linear mixed model or GAM. To quantify survival senescence accurately, different approaches such as capture-mark-recapture models are required to account for individual variation in survival probability (Gimenez, Cam & Gaillard, 2018). Nonetheless, survival senescence is very well documented across taxa (Jones et al., 2014; Nussey et al., 2013). Overall, the ageing trajectories studied in the warbler largely aligned with past findings, demonstrating that the SW represents an excellent system to study ageing in the wild.

(age 11 here vs. 6 for females and 7.7 for males in earlier studies: Hammers et al., 2012; Raj

Asynchrony of senescence

The asynchronous ageing of traits in the SW demonstrate that the original verbal theories on synchronous ageing by Williams (1957) and Maynard Smith (1962) are erroneous, and add to growing evidence of asynchrony of senescence in a wide range of taxa e.g. (Briga & Verhulst, 2021; Cayuela et al., 2020; Cooper et al., 2021; Hayward et al., 2015; Herndon et al., 2002; Tully, Le Galliard & Baron, 2020; Tully, 2023). Apart from the similar ageing trajectory of immune related traits in male SW (Group 3), there is little evidence for functional grouping

patterns in ageing across traits in the Seychelles warbler. This is consistent with the findings of Hayward et al (2015) in the Soay sheep. In terms of the evolutionary theory behind the asynchrony of senescence, this study provides weak evidence for the theoretical study that traits more associated with fitness undergo more rapid ageing (Briga & Verhulst, 2021; Moorad & Ravindran, 2022). We found age-related declines in direct fitness indices—i.e. survival and reproduction but not in traits less important to fitness such as wing length, tarsus length, antioxidant, and oxidant capacity. However, the role of selection pressure as a driver of patterns of senescence in traits less consequential to fitness still remains unknown. Considering the ageing trajectory of body mass and immune traits (e.g. malaria presence) as examples, ageing was significant in the first trait but not in the latter. Two predictions can arise according to the newer theories suggesting trait-specific selection pressure explains ageing trajectories: 1) body mass ages faster because body mass is under stronger selection than immune traits, 2) immune traits don't age because they are under stronger selection than body mass. We can envision prediction one to be plausible; Body mass as important indicator of condition (Gaillard et al., 2000; Nussey et al., 2011), may experience strong selection pressure both in early life and late life (Jebb et al., 2021; Merilä, Kruuk & Sheldon, 2001; Ronget et al., 2018). In SW, juvenile body mass predicts survival till adulthood (Brown et al., 2021a), i.e. strong selection on body mass. Thus, body mass is hypothesised to experience a more rapid waning of selection pressure and ageing rate according to Moorad and Ravindran (2022). Yet, prediction two is equally plausible. We can expect immune traits to experience strong selection, as the benefit of an optimized immune function for survival and fitness is extremely apparent (Sheldon & Verhulst, 1996; McKean & Lazzaro, 2011; Seppälä, 2015).

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Nevertheless, the strength of selection pressure on traits in specific populations can be difficult to predict. Although most studies suggest that body mass is under strong selection, there is also evidence suggesting low association between fitness and body mass (Boratyński & Koteja, 2010; Cox & Calsbeek, 2015; Warkentin et al., 2016). Likewise, the strength of selection on immune traits may depend on the environment and the strength of the immune challenge (Seppälä, 2015; Langeloh et al., 2023, Roast et al., 2020). In the SW, there was no evidence that avian malaria presence affected adult warbler survival (Hammers et al., 2016), which may indicate low strength of immune challenge, hence low covariation between immunity and fitness in warblers. Widely speaking, selection on a trait can be dependent on population dynamics and environment (Wright et al., 2019), making it difficult to draw broader conclusions. We currently lack understanding of trait-specific selection to definitively predict how selection determines the rate and onset of senescence or ageing patterns across traits. Nonetheless, we can predict that the trait with similar ageing trajectories may share age-specific selection pressure patterns and vice versa.

Caveats and future directions

Senescence refers to a decline in a function in an organism that results in a decline in survival and reproductive success (Ricklefs, 2008). Therefore, inference of trait senescence is limited in our present study as for 4 out of the 7 traits that showed ageing, we have no evidence of a causative link between trait ageing and survival/reproduction decreases.

Further studies are needed to test how age-specific selection pressure on traits explains the asynchrony of ageing (Moorad & Ravindran, 2022). Additionally, genetic correlations within and between age classes, differential energy allocation and trade-offs may affect the evolution of asynchrony of senescence (Charlesworth, 2001; Hayward et al., 2015; Moorad & Ravindran, 2022). Testing for presence of genetic correlations between traits may elucidate

the genetic architecture of asynchrony of senescence. Understanding potential non-evolutionary causes of asynchrony of senescence is also instrumental in providing insight to asynchronous ageing (Moorad & Ravindran, 2022). For example, since telomere senescence rates in the SW are affected by the environment (Brown et al., 2022), this study could be extended to test the environmental effects on senescence rates across various traits to examine whether environmental damage leads to differences in trait ageing. Additionally, a path analysis or structural equation modelling how individual trait ageing contributes to the timing of actuarial senescence would provide insight on the mechanistic explanation of individual senescence (Lemaître & Gaillard, 2017).

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- 553 Declaration of Interest
- 554 The authors declare no conflicts of interest.

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- 556 Data Availability
- 557 The data and code are available on github: https://github.com/Clairetls/Asynchrony-of-
- 558 <u>ageing-code.git</u>

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