1	Variable rate of ageing within species: insights from the Darwin's frog
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## 21 Abstract

Actuarial senescence, the increase in adult mortality risk with increasing age, is a 22 23 widespread phenomenon across the animal kingdom. The onset of senescence, as well as the rate of increase in mortality as organisms age (i.e. ageing rate), varies markedly among 24 species. This variation has been associated with species' life history, body size, and 25 26 phylogeny. At the intraspecific level, occurrence of variation in ageing patterns remains much more debatable. Here, we assess the level of within-species variation in ageing rates 27 of the southern Darwin's frog (Rhinoderma darwinii), a species endemic to the austral 28 29 temperate forest of South America. We quantified ageing rates in four R. darwinii populations distributed in Chile across a latitudinal gradient of 700 km (38° to 45°S). Our 30 results reveal strong among-population variation in ageing rates, and these correlated with 31 population-specific generation time. Thus, a higher ageing rate occurred in populations 32 where individuals exhibited a faster pace of life. Our results, along with recent studies in 33 34 evolutionarily distant amphibian species, indicate that there can be substantial withinspecies variation in the rate of ageing. These findings highlight amphibians as emerging 35 models to study the patterns and mechanisms of intraspecific variation in ageing rate in 36 37 natural populations.

38 Keywords: Amphibians; ageing rate; mortality; senescence

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### 41 Introduction

Actuarial senescence, i.e., the increase in adult mortality risk with increasing age (hereafter 42 43 "ageing"), is a pervasive process across the animal kingdom (Nussey et al. 2013; Jones et al. 2014). While ageing is widespread in the living world, both the onset and the rate of 44 increase in mortality risk with age (i.e. ageing rate) vary markedly across species (Jones et 45 46 al. 2014; Colchero et al. 2019). Studies on terrestrial vertebrates (mostly mammals and birds) have shown that variation in ageing patterns across species are commonly associated 47 with body size (i.e., higher ageing rates in smaller species; Ricklefs 2000, 2010), pace of 48 life (i.e., earlier ageing and steeper ageing rates with faster life histories; Jones et al. 2008; 49 Lemaître & Gaillard 2013), and phylogeny (Ricklefs 2000; Lemaître et al. 2020). 50

51 Although between-species variation in ageing is now well documented, the 52 occurrence of variation in ageing patterns within a given species remains much more debatable (Lemaître et al. 2013). Evidence from humans (Vaupel 2010) and some species 53 54 of non-human primates (Colchero et al. 2021), suggest that the rate of ageing can be relatively constant within a species (i.e. the "invariant rate of ageing hypothesis" sensu 55 56 Colchero et al. 2021). On the contrary, comparisons of senescence patterns between free-57 living and captive mammals have shown that, except for species with a very slow pace of 58 life, ageing rates are generally higher in the wild than in captivity (Lemaître et al. 2013, Tidière et al. 2016). Natural selection can also lead to within-species variation in ageing, 59 both in the laboratory and in the wild (Stearns et al. 2000, Reznick et al. 2004). 60

Until now, our ability to quantify within-species variation in ageing rates has been
limited due to the scarcity of fine-scale demographic data across multiple wild populations
of a given species (Colchero et al. 2021). When available, long-term, individual-based

capture-recapture studies provide the gold standard to reliably assess variation in ageing 64 rates and to identify the eco-evolutionary drivers of such variation. For instance, recently 65 published studies in wild amphibian populations have shown that ageing rate can vary 66 within the same species along environmental gradients (Cayuela et al. 2020, 2021). 67 Here, we assess the level of within-species variation in ageing rates of the southern 68 Darwin's frog (Rhinoderma darwinii), a species endemic to the austral temperate forest of 69 South America. We quantified ageing rates in four disparate *R. darwinii* populations 70 71 distributed in Chile across a latitudinal gradient of 700 km (38° to 45°S) (Fig. 1A). We also 72 explore associations between ageing rate and pace of life (measured by generation time, 73 Gaillard et al. 2005) and environmental factors (i.e. mean environmental temperature, 74 environmental temperature seasonality, and presence of the virulent pathogen 75 Batrachochytrium dendrobatidis [Bd]). These variables are known to influence among- and within-species variation in ageing rates in the wild. A faster pace of life has been associated 76 77 with a steeper ageing rate at the interspecific (Jones et al. 2008) and intraspecific (Cayuela 78 et al. 2020) levels. Cayuela et al. (2021) found that ageing rate was positively associated 79 with mean annual temperature in four amphibian species from North America and Europe. Temperature seasonality explains among-population variation in body size in R. darwinii 80 81 (i.e. a larger body size in more seasonal areas; Valenzuela-Sánchez et al. 2015) and body size is positively associated with ageing rate at the interspecific scale (Jones et al. 2008, 82 Lemaître & Gaillard 2013). Also, there is evidence that infection with Mycobacterium bovis 83 can accelerate ageing in badgers (McDonald et al., 2014; Hudson et al., 2019). We end by 84 85 discussing why among-population variation in ageing rates might occur, and the available empirical evidence of within-species variation in ageing rates. 86

### 88 Methods

#### 89 Study design

- 90 From 2014 to 2020, we carried out a capture-recapture study of four *R. darwinii*
- 91 populations in Chile (Fig. 1A): Monumento Natural Contulmo ('CON'), Reserva Biológica
- 92 Huilo Huilo ('HUI'), Parque Tantauco ('TAN') and Reserva Natural Melimoyu ('MER').
- 93 The populations are within native old-growth forests sharing similar characteristics, such as
- 94 the absence of anthropogenic stressors besides the emerging chytrid fungus Bd
- 95 (Valenzuela-Sánchez et al. 2022). Each year, we carried out one survey period in early
- summer during the peak of the reproductive season (January-February; see Valenzuela-
- 97 Sánchez et al. 2014). Briefly, all captured frogs were measured (snout-to-vent length, SVL)
- and photographed for individual recognition (see Valenzuela-Sánchez et al. 2014, 2017,
- 99 2022 for further details).

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### 101 Assessing ageing patterns

We used the "Bayesian survival trajectory analysis" (BaSTA) package in R (Colchero et al. 2012) to assess interpopulation variation in trajectories of age-specific mortality during adulthood. This model allows to estimate the apparent mortality rate at a given age, while accounting for imperfect detection, left-truncated (i.e., unknown birth date) and for rightcensored (i.e., unknown death date) from capture-recapture data. Birth dates were estimated for a variable proportion of adult frogs that were first captured as juveniles (Table S1) while death dates were unknown for all adults (and estimated as a latent variable using BaSTA). Since we previously detected time variation in recapture probability across primary capture periods (Valenzuela-Sánchez et al. 2017, 2022), we allowed this parameter to vary among primary capture periods. In BaSTA, we fitted a Siler model on age-specific mortality data (Siler 1979) to obtain comparable metrics for each population (for a justification of the use of this model, see Lemaître et al. [2020]). The Siler model is given by:

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$$\mu(x) = a_0 \exp(-a_1 x) + c + b_0 \exp(b_1 x)$$

where  $a_0, a_1, b_0, b_1$  and c are the parameters of the mortality function, x the age in years, 115 and  $\mu(x)$  the age-specific rate of mortality. The exponential function with parameters a 116 117 describes the changes in mortality in the early adult stage, whereas c gives the lower limit of mortality during the adult stage. The exponential function with b parameters corresponds 118 to the mortality increase during the senescent stage. The parameter  $b_1$  measures the 119 120 exponential increase in mortality rate with increasing age during the senescent stage and corresponds to the ageing rate in vertebrates (Lemaître et al. 2020). We ran four MCMC 121 122 chains with 40,000 iterations, a burn-in of 10,000, and no thinning. Chain convergence was evaluated using the potential scale reduction factor (Colchero et al. 2012). 123

We conducted a pairwise comparison to evaluate differences in ageing rate between populations. For each pair of populations, we evaluated the proportion of the posterior distributions of  $b_1$  that did not overlap using the R package "overlapping" (Pastore 2018). This value can range from 0 to 1, where zero indicates perfect overlap between the two distributions and a value of 1 indicates the total absence of overlap. Therefore, this value can be interpreted as the probability that the ageing rate differs between a given pair of populations.

131	Finally, we conducted an exploratory visual analysis to identify factors that might
132	explain among-population variation in ageing rate. We plotted ageing rate estimated for
133	each of the four studied populations against population-specific generation time (extracted
134	from Valenzuela-Sánchez et al. 2022), mean annual temperature (extracted from
135	Valenzuela-Sánchez et al. 2015), temperature seasonality (extracted from Valenzuela-
136	Sánchez et al. 2015), and Bd infection presence (extracted from Valenzuela-Sánchez et al.
137	2022) at these populations.
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# 139 **Results**

140 The number of captures, adults found, and percentage of adults with known birth date are141 presented as Table S1.

We found two different patterns of ageing, which did not follow a latitudinal cline 142 (Fig. 1B, C). Ageing rates were higher (more than a twofold difference) in CON ( $b_1 =$ 143 144 1.010, 95% Bayesian credible interval [CRI]= 0.654 - 1.366) and TAN ( $b_1 = 0.998, 95\%$ CRI = 0.793 - 1.207) than in HUI ( $b_1 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_1 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_2 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_3 = 0.423, 95\%$  CRI = 0.253 - 0.649) or MER ( $b_4 = 0.$ 145 146 0.481, 95% CRI = 0.097 - 0.820). The pairwise analysis of overlap between the posterior distributions of ageing rates provided strong evidence of a difference between populations 147 148 with fast and slow ageing (i.e. the probability that  $b_1$  was different between a pair of 149 populations with high vs. low ageing rate was consistently higher than 0.9) (Fig. 1C). A negative association occurred between ageing rate and generation time: the two 150 151 populations with higher ageing rates had a shorter generation time (i.e. 2.7 and 3.2 years in CON and TAN, respectively) than the two population with the lower ageing rates (4.8 and 152

3.7 years in HUI and MER, respectively; Fig. 1D). None of the environmental factors we
analysed accounted for population differences in ageing rate (Fig. 1D), although small
sample size might have prevented a proper quantitative assessment of these putative
associations.

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## 158 Discussion

Our findings in *R. darwinii* provide clear evidence of large among-population variation inageing rates within this species (Fig. 1).

161 Among-population variation in ageing rate are expected to occur due to at least through 162 two intertwined mechanisms. (1) As ageing rate increases in organisms with fast life-163 history strategies (Jones et al. 2008), population-specific variation in biological times, such as generation time, are expected to be associated with variation in ageing rate. Our results 164 165 support the existence of a positive association between ageing rate and pace of life among populations of *R. darwinii*: the two populations with the highest ageing rates were the two 166 with the shortest generation times (Fig. 1D). These results are similar to those reported for 167 168 the amphibian, Bombina variegata (Cayuela et al. 2020). (2) As ageing rate increases with increasing mean mortality rate during adulthood (i.e., Williams' (1957) second prediction 169 170 of ageing evolution, reviewed in Gaillard & Lemaître 2017), population-specific patterns of 171 environmentally driven adult mortality are expected to cause variation in ageing rate. This could explain the acceleration in ageing rate observed in badgers infected with 172 Mycobacterium bovis (McDonald et al. 2014, Hudson et al. 2019). Due to lethal effect of 173 Bd infection, adults from CON have the highest mortality rate among the four studied R. 174

175	darwinii populations (see Valenzuela-Sánchez et al. 2017, 2022). In agreement with
176	William's second prediction, this population also exhibited the highest ageing rate. The
177	HUI and TAN populations, however, had dissimilar ageing patterns despite having similar
178	mean mortality rates (Fig. S1).
179	Among-population variation in ageing rates in amphibians and other organisms has been
180	attributed to local environmental conditions such as environmental temperature (Ganetzky
181	and Flanagan 1978, Valenzano et al. 2006, Lee and Kenyon 2009, Cayuela et al. 2020,
182	2021). For example, Cayuela et al. (2021) found that among-population variation in ageing
183	rate was positively associated with mean annual temperature across four amphibian species.
184	We did not find any clear association between ageing rate and environmental temperature
185	in our study system. The link between ageing rate and environmental temperature could be
186	caused by several behavioural, physiological, and genetic mechanisms. For instance,
187	Cayuela et al. (2021) argued that metabolic depression during hibernation could slowdown
188	the ageing process leading to the slow ageing rate they observed in populations of $R$ .
189	luteiventris, A. boreas, and R. temporaria inhabiting cold areas. In R. darwinii, hibernation
190	duration is most likely driven by temperature seasonality as more seasonal areas exhibit
191	colder and longer winters (Valenzuela-Sánchez et al. 2015). In addition, as seasonality is
192	positively associated with body size in R. darwinii (Valenzuela-Sánchez et al. 2015),
193	allometric constraints on ageing rate (Ricklefs 2000, 2010) could lead to a faster ageing in
194	populations within less seasonal areas. In our study, TAN and HUI populations inhabit,
195	respectively, the least and most seasonal areas known for populations of this species
196	(Valenzuela-Sánchez et al. 2015). Among these populations the observed pattern of ageing
197	was as expected, with TAN exhibiting a faster ageing than HUI (Fig. 1D). Individuals from

198 CON and MER, however, experience a moderate and similar seasonality but contrasting
199 ageing patterns (Fig. 1D). Altogether, our results from this small set of populations suggest
200 that ageing patterns in *R. darwinii* are unlikely to be driven by a single major structuring
201 factor. Instead, ageing rate might be determined by the interactions of multiple factors, such
202 as seasonality and Bd infection.

203 Among-population variation in ageing rate is available for a range of amphibian species 204 (Fig. 2). These studies show that ample variation in ageing rates can exist within species of 205 amphibians. For example, the magnitude of variation in ageing rates across populations of 206 Rana luteiventris and Anaxyrus boreas was larger than the overall variation estimated 207 across 101 mammalian species (Lemaître et al. 2020, Cayuela et al. 2021). These findings, 208 along with those in the current study, highlight amphibians as emerging models to study the 209 patterns and mechanisms of intraspecific variation in ageing rates in natural populations. 210 We encourage researchers to take advantage of the increasing number of long-term, 211 individually based studies in amphibians and other poorly studied taxonomic groups in 212 terms of ageing patterns to conduct comparative analyses to explore within-species 213 variation in ageing. Such analyses are likely to provide important insights into the forces 214 driving the evolution, maintenance, and variation of ageing across natural populations.

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#### 217 **Data availability statement**

218 Data and code will be available at Zenodo.

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Figure 1. Actuarial senescence patterns in adults from four Southern Darwin's frog 338 (Rhinoderma darwinii) populations located in Southern Chile. (A) Study area showing the 339 studied populations: 1= Contulmo ('CON'), 2= Reserva Biológica Huilo Huilo ('HUI'), 3= 340 Parque Tantauco ('TAN'), 4=Reserva Elemental Melimoyu ('MER'). (B) Age-specific 341 342 mortality rate at each population. Note that this is a hazard rate, not a probability (i.e., it is not 1 -survival). The shaded areas represent the Bayesian 95% credible intervals. (C) 343 344 Density plots for the posterior distributions of the ageing rate parameter,  $b_1$ , from the Siler 345 model. This parameter represents the magnitude of the exponential increase in mortality 346 rate with age during the ageing stage. (D) Relationship between ageing rate and generation 347 time (extracted from Valenzuela-Sánchez et al. [2022]), mean annual temperature (extracted from Valenzuela-Sánchez et al. [2015]), temperature seasonality (extracted from 348

- 349 Valenzuela-Sánchez et al. [2015]), and *Batrachochytrium dendrobatidis* (Bd) infection
- presence (extracted from Valenzuela-Sánchez et al. [2022]) at each population.





**Figure 2.** Among-population variation in ageing rate (i.e.,  $b_1$  parameter from Siler model) in 354 amphibians. The range of minimum and maximum values (line), median (dot; only species 355 with more than two studied populations), and number of populations studied (numbers) are 356 displayed. In the inset we show the geographical location of the studied populations. Data 357 358 obtained from: Anaxyrus boreas (Cayuela et al. 2021), Bombina variegata (Cayuela et al. 359 2020), Bufo bufo (Cayuela et al. 2021), Rana luteiventris (Cayuela et al. 2021), Rana temporaria (Cayuela et al. 2021), Rhinoderma darwinii (this study), Salamandra salamandra 360 361 (Cayuela et al. 2019).

**Table S1.** Details of the 7-year capture-recapture study (2014-2020) at four populations of

Site	CON	HUI	TAN	MER
No. frogs	77	228	306	23
No. captures	101	352	426	38
Percentage of frogs	36.4	21.5	29.7	73.9
with known birth date				

the Southern Darwin's frog (*Rhinoderma darwinii*) in southern Chile.

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**Figure S1.** Relationship between ageing rate and annual adult survival probability



370 Darwin's frog (*Rhinoderma darwinii*) in southern Chile.