Conservation of genetic diversity using life history predictors of adaptive potential

by
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Abstract

Biodiversity loss is reducing population sizes globally, leading to a decline in genetic diversity. This is concerning, as genetic diversity is vital for species' survival and adaptation to future environmental change. Conservation frameworks, such as the International Union for Conservation of Nature (IUCN) Red List, assess extinction risk but overlook genetic diversity and adaptive potential. This is primarily because genetic data is not available for most species. My project directly addresses the lack of consideration of genetic diversity conservation framework by examining the relationship between adaptive potential and easy-to-measure life history traits. If easy-to-measure traits reflect adaptive potential, they can be used to guide conservation where direct estimates of adaptive potential are lacking. Adaptive potential reflects the additive genetic variance (V_A) underlying fitness. V_A reflects genetic diversity and capacity for adaptation and is used in calculating heritability. I hypothesized that life history traits (e.g., body mass, longevity, fecundity, and age of maturity) predict adaptive potential, measured by heritability. The data for heritability were derived from studies by Mittel et al. (2015), Holstad et al. (2024), and life history trait data from Myhrvold et al. (2016). Data inclusion consisted of heritability measured for morphological, life history, behavioural, and physiological traits, for terrestrial vertebrate species and from wild populations. The relationship between heritability and life history traits was measured using generalized linear mixed models. My results revealed significant relationships between heritability and life history traits. Larger body mass and longer lifespan were associated with low heritability, while larger litter/clutch sizes and earlier ages of maturity were associated with high adaptive potential. Morphological heritability estimates exhibited stronger correlations with life history traits compared to other heritability estimates, suggesting they may be a more reliable proxy for predicting adaptive potential. These findings

highlight the potential of using life history traits to infer species' genetic diversity and adaptive potential, offering a valuable tool to improve conservation prioritization.

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Table of Contents

List of Tables

List of Figures

Introduction:

The biggest threat to the world's ecosystems is the loss of biodiversity. To preserve biodiversity, we must conserve species' adaptive potential so that they can persist in changing ecosystems. Genetic diversity is an important part of biodiversity because it provides the genetic variation necessary for adaptation, which supports the persistence of species facing environmental changes (DeWoody et al 2021). Thus, adaptive potential and genetic diversity are important metrics for informing conservation policy (Van Oosterhout et al. 2022; Schmidt et al. 2023). However, the International Union for Conservation of Nature (IUCN) Red List uses species range, population size, habitat quality and fragmentation criteria to assess species extinction risk (IUCN 2012). The current IUCN criteria does not directly consider genetic diversity, and a species' IUCN Red List status does not accurately predict its genetic diversity (Schmidt et al. 2023). Suggesting that the current criteria does not act as an appropriate proxy of species genetic diversity. Therefore, finding easy-to-measure proxies that are directly related to a species' adaptive potential and genetic diversity will be key to future conservation assessment and is the focus of this project.

Adaptive potential is important for understanding a species' ability to adapt to rapidly changing environmental conditions. The genetic diversity and variation associated with adaptive potential are reflected in measurements of the additive genetic variance (V_A) underlying fitness (Mittell et al. 2015; Falconer and Mackay 1996). In general, additive genetic variance represents the combined additive effect of multiple alleles across many genes that contribute to the expression of a particular trait (Singh and Singh 2018). The additive genetic variance underlying fitness itself, the quantitative genetic definition of adaptive potential, is hard to estimate because fitness is hard to estimate (Wadgymar et al. 2024). Fitness is a difficult concept to define and

challenging to accurately measure (Wadgymar et al. 2024). However, theory predicts that the additive genetic variance underlying traits should be correlated with the additive genetic variance underlying fitness (Falconer and Mackay 1996), and thus, the additive genetic variance underlying traits could predict adaptive potential (Mittell et al. 2015). Low additive genetic variance is expected to be associated with reduced genetic diversity and adaptive potential (Wood et al. 2016). If this is true, species traits could serve as a straightforward proxy for adaptive potential where there is insufficient data to estimate adaptive potential directly.

Heritability plays a role in determining the predicted evolutionary response to selection (R) in the following generation. Heritability is calculated by dividing the additive genetic variance by the phenotypic variance (V_P) among individuals of the observed values of a trait, eq. (1). Narrow sense heritability captures the proportion of genetic variation due to additive genetic variance that can be transmitted to the next generation (Houle 1992) and populations with substantial genetic diversity generally exhibit greater additive genetic variation and higher adaptive potential (Van Oosterhout et al. 2022). By quantitative theory, the adaptive potential is proportional to heritability and can be treated similarly (Falconer and Mackay 1996).

$$h^2 = \frac{V_A}{V_P} \quad (1)$$

According to classic population genetic theory, life history traits are closely related to fitness (Falconer and Mackay 1996). To add to this neutral genetic theory tells us that genetic diversity is predicted by population size and the effects of genetic drift (i.e., greater genetic diversity is found in larger populations with reduced effects of genetic drift) (Hague and Routman 2016). Furthermore, a significant relationship was found between diversity and life history traits, such as body mass, that is potentially correlated with population size, highlighting

how life history traits can influence population size and, in turn, explain differences in genetic diversity (Romiguier et al., 2014). Therefore, life history traits being closely related to fitness and a predictor of genetic diversity make life history traits good candidate predictors of adaptive potential. The important life history traits to consider for higher fitness and genetic diversity include body mass, fecundity, lifespan and age of maturity. Body mass captures the long-term, multi-generation changes in population size, as body mass is negatively correlated with population size and the strength of genetic drift and genetic variation (Frankham 1996; Romiguier et al., 2014). Species with long lifespans, low fecundity, and late maturity often have smaller effective population sizes (Ne), as they produce fewer offspring and take longer to reproduce (Romiguier et al. 2014; Hague and Routman 2016). This reduces the rate of gene flow and limits the introduction of new genetic variants into the population (Hague and Routman 2016). Additionally, these traits increase the impact of genetic drift, which can more easily eliminate genetic variation in smaller populations over time (Hague and Routman 2016). Consequently, these life-history traits lead to lower genetic diversity compared to species with shorter lifespans, higher fecundity, and earlier maturity (Romiguier et al. 2014; Hague and Routman 2016). Despite the established links between life history traits and genetic diversity, no studies have compared these traits to adaptive potential.

Research Objectives and Hypotheses

The relationship between life history traits, genetic variation, and adaptive potential remains poorly understood. I hypothesize that fitness-related traits, such as life history traits, predict the adaptive potential of species as measured by heritability. To examine this hypothesis, I synthesized datasets of terrestrial vertebrate species globally (Table 1.). Predictions are summarized in Table 2. My predictions assume population size predicts genetic drift (i.e., the smaller the population, the higher the genetic drift) and that genetic drift affects fitness related to

life history traits. In the scenario where population size is small and genetic drift is high, species with a large body mass, I predict will have low heritability and adaptive potential. Similarly, I predict species with longer lifespans, high fecundity, and early age of maturity will all have low heritability and adaptive potential. I also hypothesize that the traits used to measure heritability (i.e. morphological, life history, behavioural and physiological) will affect the relationship between heritability and life history traits. I predict that heritability measured from morphological traits will have a stronger relationship with the life history traits (body size, lifespan, fecundity, and age of maturity) than heritability measured by life history, behavioural, or physiological traits. Heritability measured from morphological traits are the most accurate as morphological traits are the easiest to measure, are consistently measured using similar tools of measurement, resulting in them being the most abundantly reported in the literature. My objectives are to 1) evaluate the relationship between heritability and life history traits, and 2) identify life history traits associated with low or high adaptive potential. The results from this project will help inform general patterns of adaptive potential based on life history attributes. Informing a potential proxy for genetic diversity not currently used in conservation.

Table 1. Vertebrate terrestrial species included in this study, the regions and populations they belong to.

Region	Species common name	Population
Europe	Long-tailed Tit	Rivelin Valley Sheffield, UK
	European Roe	Chize, France
	European Roe	Bogesund, Sweden
	Red Deer	Isle of Rum, UK
	Eurasian Blue Tit	Pirio, French Island of Corsica
	Eurasian Blue Tit	South of France Rouviere
	Eurasian Blue Tit	Downy Oak Muro, French Island of Corsica
	Eurasian Blue Tit	E Muro, French Island of Corsica
	Collared Flycatcher	Swedish Island, Gotland
	Collared Flycatcher	Hungary
	European Pied Flycatcher	Sweden

	European Pied Flycatcher	Central Spain
	European Pied Flycatcher	Sorkedalen. Norway
	Great Tit	Wytham Woods, UK
	Great Tit	Hoge Veluwe, Netherlands
	Great Tit	Konnevesi, Finland
	Great Tit	Vlieland, Netherlands
	House Sparrow	Northern, Norway
	House Sparrow	Lundy, UK
	Eurasian Blackcap	Radolfzell, Germany
	Barn Swallow	Denmark
	Barn Swallow	Kraghede, Denmark
	Barn Swallow	Milano, Italy
	Red Sheep	St.Kilda, Scotland
	Western Barn Owl	Western, Switzerland
New Zealand	Common Starling	Belmont, New Zealand
North America	Yellow-bellied Marmot	East River Valley Gunnison County, US
	Song Sparrow	Mandarte Island, BC, Canada
	Bighorn Sheep	Ram Mountain, Alberta, Canada
	North American Deermouse	Rocky Mountains, USA
	Western fence lizard	Klickitat County, WA, USA
	Eastern fence lizard	Arkansas
	Eastern fence lizard	Alabama
	Eastern fence lizard	Mississippi
	Red Squirrel	Yukon, Canada
	Western Terrestrial Garter Snake	California, US
	Western Terrestrial Garter Snake	Coastal Western, North America
	Western Terrestrial Garter Snake	Inland Western, North America
	Common side-blotched lizard	Los Banos Grandes, California, US
South America	Medium Ground Finch	Galapagos Islands, Ecuador
	Common Cactus Finch	Galapagos Islands, Ecuador
	Brown-mantled Tamarin	Amazon Basin, South America
	Cottontop Tamarin	Northwestern, Colombia

Table 2. Predictions on how life history parameters are associated with population size, genetic drift, the extreme of each trait, heritability, and adaptive potential.

Life history parameter	Trait	Population Size	Genetic Drift	Heritability	Adaptive potential
Adult body mass	Large mass	↓	↑	↓	↓
Lifespan (longevity)	Long lifespan	↓	↑	↓	↓
Fecundity (litter/clutch size)	Large litter/clutch size	↑	↓	↑	↑
Development (female and male age of maturity)	Early development	↑	↓	↑	↑

Materials and Methods:

Databases

Data is derived from studies by Mittel et al. (2015), Holstad et al. (2024), and Myhrvold et al. (2016). Detailed information on databases used in these studies is provided below.

Mittell et al. (2015) compiled a comprehensive database guided by the criteria and initial sources established by Hansen et al. (2011) for synthetic analyses of heritability estimates for plants and animals. This database includes estimates derived from behavioural, life history, morphological, and physiological traits, obtained through various methods such as cloning, full/half-sibling analyses, mid or single-parent-offspring regressions, and animal models. The database also contains mean trait values from laboratory/controlled and wild populations. Mittell et al. (2015) used these heritability estimates to compare quantitative genetic variation with molecular markers of genetic diversity.

Holstad et al. (2024) collected similar data to Mittell et al. (2015), with the distinction that Holstad et al. (2024) focused exclusively on populations that diverged in the wild, excluding

populations subject to artificial selection. The traits considered are consistent with those in the Mittell et al. (2015) database (i.e. morphological, life history, behavioural, and physiological traits). Holstad et al. (2024) used heritability estimates and mean-scaled variance of traits in fossil records to illustrate evolutionary divergence among populations.

The Amniote Life History database by Myhrvold et al. (2015) contains 29 life history parameters from 21,322 species of birds, mammals, and reptiles. The data was compiled from peer-reviewed studies on individual species, macroecological studies of multiple species, existing life history databases, published books, and other compilations. The Amniote Life History database is open source, and its intended use is to perform comparative analyses with birds, mammals, and reptiles.

Data Inclusion

I extracted heritability estimates for Holstad et al. (2024) and Mittell et al. (2015) measured for morphological, life history, behavioural, and physiological traits, calculated by any model, a terrestrial vertebrate species from class Aves, Mammalia, and Reptilia and from wild populations only. I therefore excluded heritability estimates from artificial selection or laboratory-controlled populations. From the Amniote Life History database, I used measurements for body mass, lifespan, fecundity, and age of maturity that are adult body mass (grams), longevity (years), litter/clutch size (N), and female and male age of maturity (days), respectively. After combining the datasets, there are 521 data points from 26 species (Table 1). The number of heritability estimates by terrestrial species class (Aves, Mammalia, and Reptilia) and the density distribution of life history traits data are shown in Figure 1.

The bar plot on the left of Figure 1. shows that morphological traits are the most frequently used to calculate heritability across Aves, Mammalia, and Reptilia classes, with

Mammalia exhibiting the highest counts. Life history traits are the second most represented, particularly in Mammalia and Aves, while behavioural and physiological traits are less prevalent overall. The density plots on the right of Figure 1. display the scaled distributions of traits. Traits such as female age at maturity, litter or clutch size, and longevity exhibit relatively even density distributions. In contrast, male age at maturity shows a bimodal distribution with peaks at early and late maturity, while adult body mass demonstrates a skewed distribution, with the majority of data concentrated at smaller body sizes.

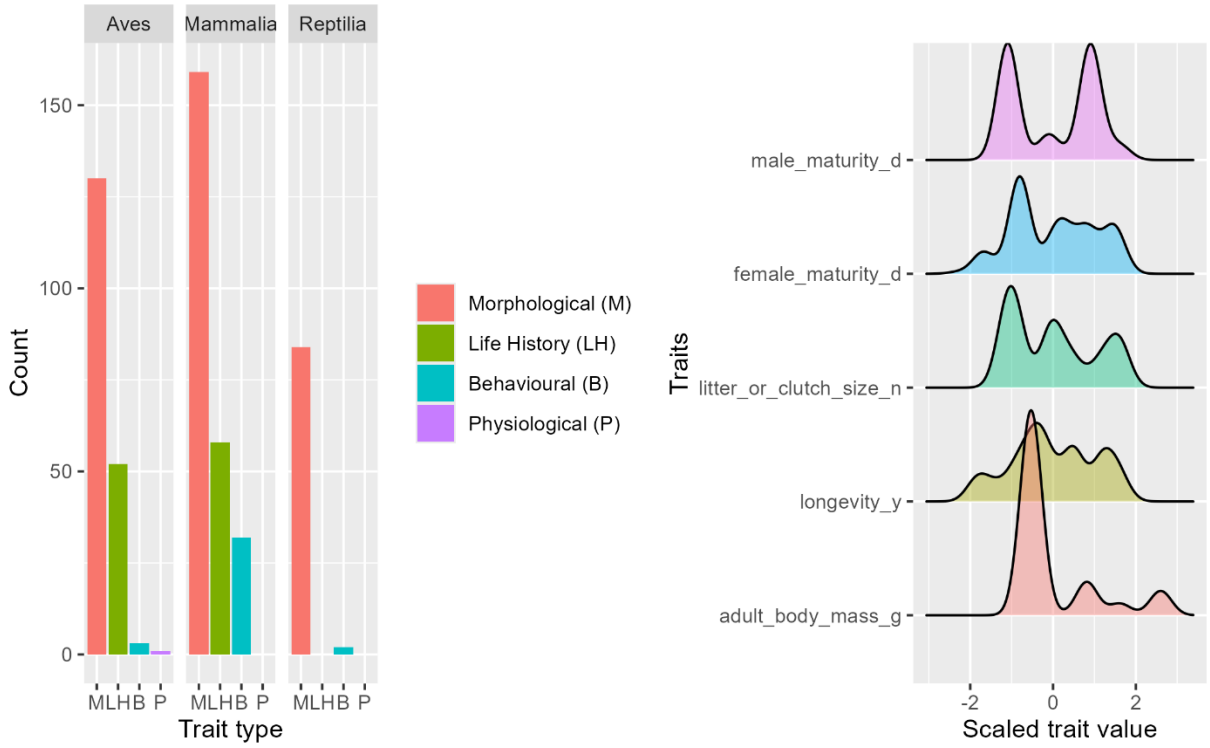

Figure 1. The number of heritability estimates by class and trait type (M- morphological trait, LH- life history trait, B- behavioural traits, P- physiological trait) (left graph). Also, the density distribution of life history predictors data, scaled to show all on one graph (right graph).

Data analysis

The data analysis was conducted using R (v 4.4.1) (R Core Team 2024), to model the relationship between life history traits (independent variable X) and heritability estimates (dependent variable Y). I separated the data into morphological heritability estimates (373 data points), life history (110 data points), behavioural traits (37 data points), and physiological characteristics (1 data point). I used generalized linear mixed models to test relationships between life history traits and heritability estimates. I produced models for all heritability estimates (combined model), as well as for morphological, life history, and behavioural heritability estimates (Table 3). There was not sufficient data to build models with physiological heritability estimates. I used the random effect of reference, which refers to the study from which the heritability estimates were sourced. Clustered by species but also population, as each paper was for different species but also different populations, controlling for variability within and between species. I used a log transformation for body mass to help with the normality and scale the wide range of value. I used the R package 'brms' to build mixed models allowing random intercepts and slopes (Bürkner 2017). The brms package uses Stan, which is a Bayesian statistical modelling program software that fits models with MCMC (Markov Chain Monte Carlo) sampling (Bürkner 2017). The model fitting is complicated; however, the models can be interpreted as any other linear model. I reported the marginal r-squared, conditional r-squared, estimate (mean), 95% confidence interval (CI) and p-value. Marginal r-squared represents the variance explained by fixed effects, while the conditional r-squared includes both fixed and random effects. The estimate indicates the effect size and direction of the predictor on the outcome, with negative values showing a negative relationship and positive values a positive relationship. The 95% confidence interval (CI) provides a range where the true effect is likely to fall. Lastly, the p-value assesses the probability of observing the direction of effect (i.e.,

observing the estimate calculated by the model), with values below 0.05 suggesting strong evidence that the predictor influences the outcome.

Results:

All results are summarized in Table 3. The marginal r-squared ranged from 0.082 to 0.201 for all models, indicating that the fixed effects alone explained 8-20% of the variance in the data. Conditional r-squared ranges from 0.260-0.452 across all models, meaning life history traits and the random effect reference predict 26-42% of the variance seen in heritability. The results indicate consistent patterns across data categories. Morphological models show that body mass (-0.031; 95% CI 0.045 – -0.017; $p < 0.001$) has a significant negative effect on the outcome, while longevity (-0.016; 95% CI -0.029 - -0.002; $p = 0.009$) also has a slight but statistically significant negative association. Litter/clutch size (0.042; 95% CI 0.082 – 0.046; $p = 0.046$) has a significant positive effect, whereas female (-0.0005; 95% CI -0.0008 - 0.000; $p = 0.010$) and male age of maturity (-0.0006; 95% CI -0.0009 - -0.0003; $p = <0.001$) have estimates close to zero but remain statistically significant. Life history models follow similar patterns, where body mass (-0.028; 95% CI -0.028 - -0.0399; $p < 0.001$) and longevity (-0.013; 95% CI -0.013 – -0.023; $p = 0.011$) have negative effects, and litter/clutch size (0.030; 95% CI -0.00006 – 0.061; $p = 0.025$) is positive but weaker. Female (-0.0003; 95% CI -0.0003 - -0.0006; $p = 0.020$) and male maturity (-0.0004; 95% CI -0.0004 - -0.0007; $p = 0.019$) again show near-zero estimates but statistical significance. Combined heritability models (All Heritability Data) indicate that longevity (-0.018; 95% CI -0.028 - -0.008; $p < 0.001$) and body mass (-0.028; 95% CI -0.040 - -0.017; $p = <0.001$) has a strong negative effect, while litter/clutch size (0.025, $p = 0.086$, -0.010 – 0.062) is positive but not statistically significant. Female (-0.0005; 95% CI -0.0007 - -0.0003; $p < 0.001$) and male maturity (-0.0005; 95% CI -0.0008 - -0.0002; $p < 0.001$) remain small but statistically

significant. Behavioural models differ in that body mass (-0.029; 95% CI -0.103 - -0.048; p = 0.135) and longevity (-0.007; 95% CI 0.066 – 0.060; p = 0.329) have weak estimates, with p-values suggesting no strong effect. Litter size (0.043; 95% CI -0.041 – 0.118; p = 0.116) is positive but not statistically significant. Female (-0.0004;95% CI -0.0004 - -0.0026 p = 0.254) and male maturity (-0.0004; 95% CI -0.003 - 0.002; p = 0.253) have estimates near zero and high p-values, indicating no strong evidence of an effect.

All model results are visualized in Figure 2. Each point represents the estimate, and the tails extending from each point represent the 95% confidence interval (CI). Overall, across the models body mass, longevity, and female and male maturity all have a negative relationship with heritability and litter/clutch size has a positive relationship. For combined, morphological, and life history models, the life history traits of body mass, longevity, and female and male maturity have a narrow CI that does not cross zero, suggesting substantial relationships. For all models litter/clutch size and behavioural models, the CI crosses zero (Figure 3.) suggesting uncertainty or variability in these relationships. Behavioural models have wider CI intervals indicating less precision in estimates, likely due to smaller sample sizes or higher variability (Figure 3.). Of all models, morphological models have relatively larger effect sizes compared to other panels. This suggests that traits might have a more noticeable relationship with morphological heritability.

Table 3. The model outputs of general linear mixed models with a random effect of study reference. Output includes marginal r-squared, conditional r-squared, p-value, parameter estimate, and 95% confidence interval (CI).

Predictor	Marginal R^2	Conditional R^2	Estimate	Lower 95% CI	Upper 95% CI	P-Value
All Heritability Data						
log_adult_body_mass_g	0.14134	0.39746	−0.02829	−0.03952	−0.01717	0.00000*
longevity_y	0.14217	0.36096	−0.01806	−0.02804	−0.00836	0.00000*
litter_or_clutch_size_n	0.08250	0.39401	0.02549	−0.01023	0.06187	0.08567
female_maturity_d	0.16268	0.41984	−0.00052	−0.00076	−0.00027	0.00013
male_maturity_d	0.12758	0.41454	−0.00050	−0.00077	−0.00024	0.00013
Morphological Data						
log_adult_body_mass_g	0.14934	0.36831	−0.03098	−0.04548	−0.01699	0.00000*
longevity_y	0.10820	0.32383	−0.01571	−0.02893	−0.00249	0.00875
litter_or_clutch_size_n	0.19751	0.36911	0.04152	−0.00889	0.08192	0.04600
female_maturity_d	0.09949	0.39214	−0.00045	−0.00084	−0.00007	0.01087
male_maturity_d	0.17759	0.38863	−0.00058	−0.00087	−0.00030	0.00013
Life History Data						
log_adult_body_mass_g	0.14235	0.39822	−0.02837	−0.03992	−0.01624	0.00000*
longevity_y	0.15047	0.30675	−0.01272	−0.02272	−0.00242	0.01078
litter_or_clutch_size_n	0.14776	0.31789	0.02967	−0.00006	0.06105	0.02544
female_maturity_d	0.12361	0.30797	−0.00032	−0.00061	−0.00001	0.02087
male_maturity_d	0.11818	0.26025	−0.00037	−0.00069	−0.00002	0.01925
Behavioural Data						
log_adult_body_mass_g	0.17319	0.43852	−0.02903	−0.10269	0.04820	0.13500
longevity_y	0.10670	0.42483	−0.00725	−0.06603	0.06011	0.32867
litter_or_clutch_size_n	0.20075	0.45183	0.04343	−0.04147	0.11818	0.11600
female_maturity_d	0.15533	0.42353	−0.00040	−0.00261	0.00186	0.25450
male_maturity_d	0.14221	0.42437	−0.00045	−0.00253	0.00186	0.24250

* value is <0.00001

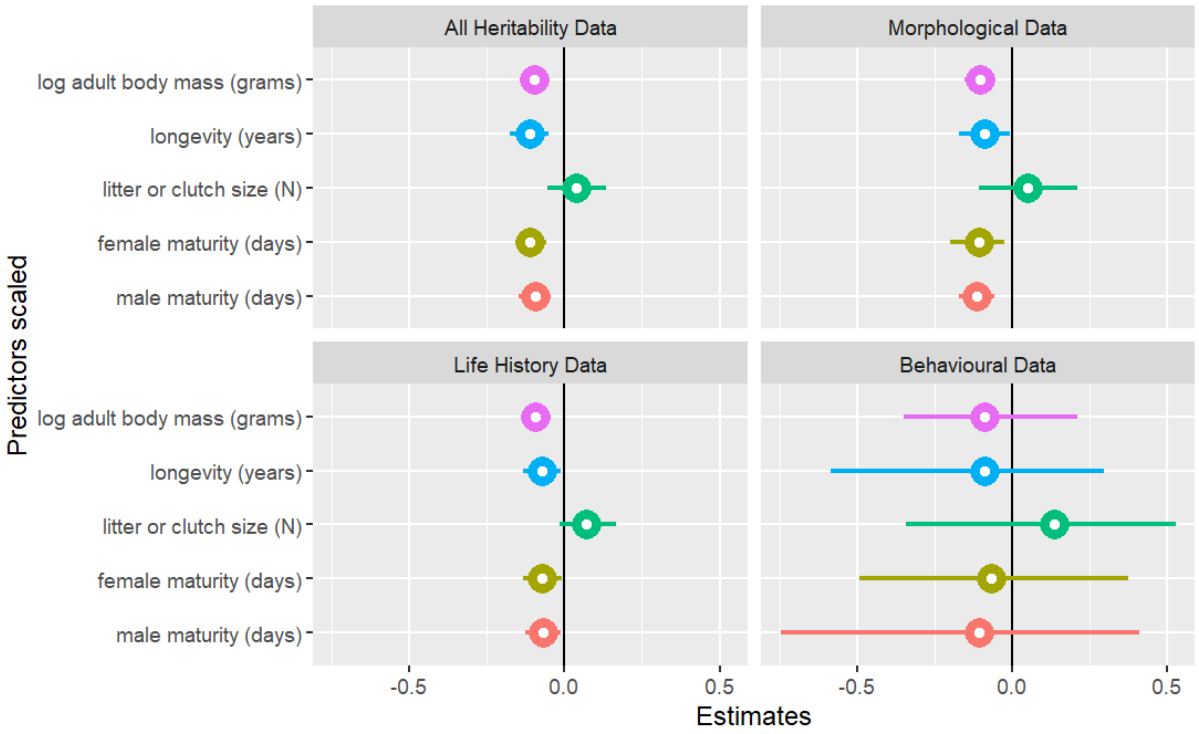

Figure 2. Orchard plot. The points are the estimate and show its proximity to zero, with tails on either end, which is the upper and lower 95% confidence interval (CI). CI that overlaps zero indicates uncertainty in the model. Predictors are scaled for easier interpretation between predictors.

Discussion:

Through environmental impacts, biodiversity has declined globally. Therefore, genetic diversity must be preserved to prevent species extinction. However, the IUCN Red List's current extinction criteria does not have an appropriate proxy for species' genetic diversity. I investigated the relationship between adaptive potential, as measured by heritability, and life history to identify species with particular life history traits that demonstrate low or high adaptive potential and thereby low or high genetic diversity.

Larger body mass and longer lifespan were negatively associated with heritability and therefore larger and longer-lived species may have low adaptive potential, while larger

litter/clutch sizes showed a positive relationship and high adaptive potential. Additionally, earlier male and female maturity ages were linked to greater heritability and high adaptive potential. The results support the hypothesis that the traits used to measure heritability influence the relationship between heritability and life history traits. Specifically, as predicted, heritability measured from morphological traits exhibits a stronger relationship with life history traits. Larger effect sizes (estimates) for morphological data suggest an increased accuracy of morphological estimates. My finding of a negative relationship between lifespan and heritability reflects the role of longer generation times in slowing genetic recovery following genetic drift, further complicated by small population size. A study by Hague and Routman (2016) outlined the lifespan dynamic by showing that sympatric lizard species with shorter lifespans, such as *C. draconoides* and *C. variegatus*, have higher genetic diversity, likely due to their faster generation turnover and larger effective population sizes. For the same species. Hague and Routman (2016) observed high reproductive output and high genetic diversity. This follows my finding of a positive association between fecundity (larger litter/clutch size) and heritability. Further, a study from Romiguier et al. (2014) found a strong correlation between fecundity and increased genetic diversity. Romiguier et al. (2014) found this correlation across 31 families of 8 major animal phyla, including Arthropoda, Echinodermata, Chordata, Cnidaria, Mollusca, Nemerta, and Annelida.

The negative association I found between body mass and heritability aligns with Hague and Routman's (2016) observation of lower genetic diversity in large-bodied lizard species such as *S. ater* and *D. dorsalis*. Larger body size is often associated with longer generation times and smaller population sizes. Finally, the negative relationship we observed between maturity age and heritability is consistent with the findings that lizard species with earlier sexual maturity,

such as *U. stansburiana*, exhibit higher genetic diversity (Hague and Routman 2016). Earlier maturity contributes to faster generation turnover, which can facilitate the accumulation of mutations and maintain higher genetic variability within populations (Hague and Routman 2016). This study relies on the assumptions that population size predicts genetic diversity and genetic drift. Although a relationship between genetic diversity and population size has been observed, many studies have found no such correlation (Nabholz et al., 2008; Leffler et al., 2012). This suggests that population size is not always a reliable predictor of genetic diversity, and small populations do not necessarily exhibit low genetic diversity. For example, research on Chilean blue whales (*Balaenoptera musculus*) showed that, despite significant population declines due to whaling, these whales maintain considerable genetic diversity (Torres-Florez et al., 2014). However, the study also suggested that insufficient time has passed since the end of whaling to observe clear effects on genetic diversity. Additionally, species with long generation times, like blue whales, take longer to show declines in genetic diversity.

While low genetic diversity is often associated with reduced adaptability and an increased risk of extinction, some species defy this expectation. For instance, a study on wandering and Amsterdam albatrosses (*Diomedea exulans* and *D. amsterdamensis*) found that, despite having genetic diversity levels approximately one-third of the minimum reported in other vertebrates, these birds maintain high breeding success and stable populations (Milot et al., 2007). This challenges the assumption that low genetic diversity always has negative consequences for species survival. However, it is important to recognize that such cases of small population size with high genetic diversity, and low genetic diversity with high breeding success, are exceptions rather than the rule. These examples challenge the assumption underlying this project that small populations inevitably experience low genetic diversity and its associated negative

consequences, highlighting the need to consider species-specific factors such as life history traits and ecological resilience.

This study accomplished its objectives by evaluating the relationship between heritability and life history traits and identifying key traits associated with high or low adaptive potential. By synthesizing datasets across terrestrial vertebrate species, the analysis demonstrated how life history traits, such as body mass, lifespan, fecundity, and age of maturity, can effectively predict heritability and adaptive potential. Calculating heritability directly may be impractical for some species due to the lack of generational data. My results suggest that species' traits can help predict adaptive potential for species that have no estimates of genetic diversity or heritability. Importantly, heritability provides a unique advantage as it integrates multi-generational data, capturing the next generation's genetic variation to project future adaptive potential more accurately. As a future direction, testing the predictive accuracy of heritability based on life history traits could offer a valuable alternative, enabling conservationists to estimate adaptive potential in species where heritability is difficult to measure. Such models would enhance conservation efforts by providing accessible proxies for adaptive potential, ultimately supporting biodiversity preservation, and improving conservation assessments, such as the IUCN Red List.

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