

SUPPLEMENTARY INFORMATION

Species-specific length-mass conversion

Conversion of the curved carapace length (CCL in centimetres) to body mass (M in kilograms) was calculated based on the average linear regression relationship for each sea turtle species:

$$Caretta\ caretta\ M = 0.0119 \times CCL^{1.99} \text{ (Hirth, 1982)}$$

$$Chelonia\ mydas\ M = 0.0011 \times CCL^{2.54} \text{ (Balazs \& Chaloupka, 2004; Hirth, 1982)}$$

$$Dermochelys\ coriacea\ M = 0.0000314 \times CCL^{3.24} \text{ (Georges \& Fossette, 2006; Hirth, 1982)}$$

$$Eretmochelys\ imbricata\ M = 0.0025 \times CCL^{2.03} \text{ (Hesni, Tabib, \& Ramaki, 2016; Hirth, 1982; Santos, Freire, Bellini, \& Corso, 2010)}$$

$$Lepidochelys\ kempii\ M = 0.0526 \times CCL^{1.61} \text{ (Hirth, 1982)}$$

$$Lepidochelys\ olivacea\ M = 0.0184 \times CCL^{1.79} \text{ (Hirth, 1982)}$$

$$Natator\ depressus\ M = 0.0038 \times CCL^{2.18} \text{ (Whiting, Thomson, Chaloupka, \& Limpus, 2009)}$$

Egg-volume scaling of egg-energy content

The rate of change in egg-energy content with respect to egg volume (Egg-energy–Egg-volume model) was estimated using a hierarchical linear model:

$$\ln E \sim N(\mu, \sigma)$$

$$\mu = \overline{\ln \beta_0} + \Delta_{\overline{\ln \beta_0}, \zeta} + \overline{\beta_1} \ln V$$

where $\ln E$ represents egg-energy content (kJ) on the natural log scale, $\overline{\ln \beta_0}$ is the between-species mean intercept, $\Delta_{\overline{\ln \beta_0}, \zeta}$ represents the group-level coefficients which account for residual intercept deviations attributable to species uniqueness, β_1 is the between-species mean egg volume slope (i.e., the scaling exponent β_{1M3} in Equation 1 in the main text), $\ln V$ is egg volume (cm^3) on the natural log scale, and σ is the unexplained residual variation. This model was run using individual-level data ($n = 15$) from two species only (4 studies on *Caretta caretta*; 3 studies on *Chelonia mydas*). Bayesian model fitting specifications in *brms* follow those explained in the main text. Model summary output is presented in **Table S10**.

SUPPLEMENTARY TABLES

Table S1. Number of studies that include size and reproductive metric for each turtle species (between population level) from the meta-search. CCL = curved carapace length, M_b = measured body mass.

	<i>C. caretta</i>	<i>C. mydas</i>	<i>D. coriacea</i>	<i>E. imbricata</i>	<i>L. kempii</i>	<i>L. olivacea</i>	<i>N. depressus</i>
CCL	56	55	23	46	6	21	10
M_b	3	6	1	8	1	2	1
Egg diameter	28	30	12	17	2	12	13
Egg mass	23	15	9	11	1	7	8
Hatchling length	23	26	12	16	1	12	8
Hatchling mass	15	17	8	10	1	5	7
Clutch size	52	62	24	47	5	23	13
Clutch mass	3	0	2	2	0	1	0
Clutch frequency	16	27	9	14	2	4	1

Table S2. Raw data descriptors for species and population level analysis.

Column name	Description
author	Surname of the first author of the paper.
study_ID	Unique identifiers for each paper.
species	Binomial nomenclature for species (as Genus_latin).
red_list	Endangered status classification defined by the International Union for Conservation of Nature.
sample_year	Year when the study was conducted.
location	General location of the study site.
pop_ID	Unique identifiers for each population.
population_level	Categorised level of extraction. Either "between population" or "within population".
country	Country of the study.
lat	Latitude decimal georeferenced coordinate in decimals (north–south position).
lon	Longitude decimal georeferenced coordinate in decimals (east–west position).
MPA	Logical binary (YES/NO) whether the coordinates overlay marine protected areas.
MPA2	Logical binary (YES/NO) whether the coordinates overlay marine protected areas +5 km buffer zone.
air_temp	Mean air temperature of the study site during the nesting period (°C).
sand_temp	Mean nest temperature of the study site during the nesting period (°C).
temp	Mean nest temperature or air temperature of the study site (°C).
egg_diameter_mm	Mean diameter of the egg in millimetres (mm).
egg_volume_cm3	Estimated egg volume in cm ³ .
egg_mass_g	Mean egg mass in grams (g).
hatchling_length_mm	Mean hatchling length in millimetre (mm).
hatchling_mass_g	Mean hatchling mass in grams (g).
clutch_size	Mean number of eggs laid per female.
clutch_mass_g	Mean clutch mass laid per female in grams (g).
clutch_freq	Mean number of clutches laid during the breeding season.
pred_freq	Estimated clutch frequency based on linear relationship of species-specific clutch size and female CCL.
total_clutch	Total clutch laid per female during the breeding season.
pred_clutch	Estimated total clutch size (clutch_size x pred_freq).
adult_length_cm	Mean curved carapace length in centimetre (cm).
adult_mass_kg	Mean body mass in kilogram (kg).
pred_mass_kg	Estimated body mass (kg) based on the Mass-CCL relationship in “Species-specific length-mass conversion”.
pub_year	Year of publication.
notes	General comments.
title	Title of the paper.
orig_author	For data extracted from comparative papers, the extracted paper's author names were included.
orig_title	For data extracted from comparative papers, the extracted paper's title was included.
link	Link to extracted paper.

Table S3. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the population-level Fecundity–Mass model, which includes fixed-effect parameters for $\overline{\ln\beta_{0M1}}$, the average across-species intercept; and $\overline{\beta_{1M1}}$, the average across-species mass-scaling exponent of fecundity. Group-level effects include the standard deviations (sd) for phylogenetic variation in the intercept ($\Delta_{\overline{\ln\beta_{0M1}},\phi}$), population-level variation in the intercept ($\Delta_{\overline{\ln\beta_{0M1}},\rho}$), population-level variation in the mass-scaling exponent ($\Delta_{\overline{\beta_{1M1}},\rho}$), species-level variation in the intercept ($\Delta_{\overline{\ln\beta_{0M1}},\zeta}$), species-level variation in the mass-scaling exponent ($\Delta_{\overline{\beta_{1M1}},\zeta}$), as well as correlations (cor) among them. Phylogenetic signal was calculated as $\lambda = \sigma_{\phi}^2 / (\sigma_{\phi}^2 + \sigma^2)$, where σ_{ϕ}^2 is the estimated phylogenetic variance (i.e. $\text{sd}(\Delta_{\overline{\ln\beta_{0M1}},\phi})^2$).

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept, $\overline{\ln\beta_{0M1}}$	0.49	1.39	-2.41	2.92
Mass scaling, $\overline{\beta_{1M1}}$	1.14	0.24	0.73	1.66
Group-level effects (species level)				
$\text{sd}(\Delta_{\overline{\ln\beta_{0M1}},\phi})$	1.22	1.29	0.06	4.52
$\text{sd}(\Delta_{\overline{\ln\beta_{0M1}},\zeta})$	1.56	1.33	0.07	4.79
$\text{sd}(\Delta_{\overline{\beta_{1M1}},\zeta})$	0.43	0.31	0.04	1.19
$\text{cor}(\Delta_{\overline{\ln\beta_{0M1}},\zeta}, \Delta_{\overline{\beta_{1M1}},\zeta})$	-0.56	0.48	-1.00	0.74
$\text{sd}(\Delta_{\overline{\ln\beta_{0M1}},\rho})$	0.54	0.42	0.03	1.51
$\text{sd}(\Delta_{\overline{\beta_{1M1}},\rho})$	0.13	0.1	0.01	0.36
$\text{cor}(\Delta_{\overline{\ln\beta_{0M1}},\rho}, \Delta_{\overline{\beta_{1M1}},\rho})$	-0.61	0.52	-0.99	0.81
Phylogenetic signal				
λ	0.78	0.26	0.04	1

Table S4. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the population-level Egg-volume–Mass model, which includes fixed-effect parameters for $\overline{\ln\beta_{0M2}}$, the average across-species intercept; and $\overline{\beta_{1M2}}$, the average across-species mass-scaling exponent of fecundity. Group-level effects include the standard deviations (sd) for population-level variation in the intercept ($\Delta_{\overline{\ln\beta_{0M2},\rho}}$), population-level variation in the mass-scaling exponent ($\Delta_{\overline{\beta_{1M2},\rho}}$), species-level variation in the intercept ($\Delta_{\overline{\ln\beta_{0M2},\zeta}}$), species-level variation in the mass-scaling exponent ($\Delta_{\overline{\beta_{1M2},\zeta}}$), as well as correlations (cor) among them.

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept, $\overline{\ln\beta_{0M2}}$	3.06	1.70	-0.64	6.53
Mass scaling, $\overline{\beta_{1M2}}$	0.14	0.30	-0.47	0.67
Group-level effects (species level)				
sd($\Delta_{\overline{\ln\beta_{0M2},\zeta}}$)	2.17	3.24	0.05	10.79
sd($\Delta_{\overline{\beta_{1M2},\zeta}}$)	0.35	0.64	0.01	1.92
cor($\Delta_{\overline{\ln\beta_{0M2},\zeta}}$, $\Delta_{\overline{\beta_{1M2},\zeta}}$)	-0.25	0.59	-0.99	0.92
sd($\Delta_{\overline{\ln\beta_{0M1},\rho}}$)	0.38	0.32	0.02	1.21
sd($\Delta_{\overline{\beta_{1M1},\rho}}$)	0.08	0.07	0.00	0.25
cor($\Delta_{\overline{\ln\beta_{0M1},\zeta}}$, $\Delta_{\overline{\beta_{1M1},\zeta}}$)	-0.45	0.55	-0.99	0.85

Table S5. Point estimates (as determined using Bayesian methods) of population differences in fecundity, egg volume, and clutch volume scaling exponent [\pm 95% CI]. Clutch volume was calculated from population-level Fecundity–Mass and Egg-volume–Mass model. n = number of observations.

Species	Population	Fecundity		Egg volume		Clutch volume
		n	Exponent (95% CI)	n	Exponent (95% CI)	Exponent (95% CI)
<i>C. caretta</i>	South Africa	176	1.18 [0.96–1.46]	171	0.15 [0.04–0.33]	1.33 [1.22–1.51]
<i>C. caretta</i>	USA	123	1.01 [0.63–1.19]	44	0.13 [-0.07–0.27]	1.13 [0.94–1.28]
<i>C. caretta</i>	Tunisia	8	1.14 [0.79–1.47]			
<i>C. caretta</i>	Cyprus	84	1.19 [0.96–1.46]			
<i>C. caretta</i>	Brazil	26	1.18 [0.90–1.53]	27	0.14 [-0.06–0.31]	1.32 [1.12–1.49]
<i>C. caretta</i>	Greece	54	1.18 [0.90–1.49]	12	0.14 [-0.04–0.31]	1.3 [1.14–1.49]
<i>C. caretta</i>	Japan	108	1.18 [0.94–1.46]	51	0.17 [0.06–0.41]	1.34 [1.21–1.58]
<i>C. mydas</i>	Ascension Island			44	0.18 [0.05–0.39]	
<i>C. mydas</i>	Malaysia	286	1.03 [0.69–1.20]	72	0.08 [-0.16–0.19]	1.11 [0.87–1.22]
<i>C. mydas</i>	Mexico	96	1.08 [0.74–1.27]			
<i>C. mydas</i>	Cyprus	126	1.18 [0.95–1.41]			
<i>C. mydas</i>	Sri Lanka	132	1.09 [0.81–1.30]	120	0.14 [0.01–0.27]	1.25 [1.10–1.37]
<i>C. mydas</i>	Costa Rica	65	1.21 [0.94–1.53]			
<i>D. coriacea</i>	South Africa	24	1.18 [0.97–1.47]	24	0.11 [-0.13–0.25]	1.29 [1.05–1.43]
<i>D. coriacea</i>	Costa Rica	173	1.14 [0.91–1.40]			
<i>E. imbricata</i>	Mexico	153	0.99 [0.54–1.19]			
<i>E. imbricata</i>	Oman	9	1.11 [0.74–1.39]			
<i>E. imbricata</i>	Qatar	143	1.16 [0.90–1.48]			
<i>E. imbricata</i>	Sudan	26	1.2 [0.98–1.58]			
<i>E. imbricata</i>	Brazil	38	1.1 [0.73–1.34]			
<i>E. imbricata</i>	Iran	38	1.11 [0.76–1.43]			
<i>E. imbricata</i>	Malaysia	33	1.21 [0.81–1.62]			
<i>L. kempii</i>	Mexico	48	1.16 [0.85–1.51]			
<i>L. olivacea</i>	Brazil	106	1.25 [1.00–1.80]			

Table S6 Raw data descriptors for the Terengganu population analysis.

Column name	Description
year	Year of the nesting survey.
ID	Unique Identifier assigned to each nesting turtle.
recruit	Logical binary (First time/Recurring) of whether the turtle surveyed is a first time nester on the island, or a recurring nester from the previous years.
count_year	Number of a times the female arrived on the island.
sum_eggs	Total number of eggs laid during the nesting season.
mean_eggs	Mean number of eggs laid per nesting event (clutch size).
SD_eggs	Variation in clutch size as standard deviation.
mean_length_cm	Mean curved carapace length in centimetre (cm).
SD_length	Variation in curved carapace length as standard deviation.
mean_width_cm	Mean curved carapace width in centimetre (cm).
SD_width	Variation in curved carapace width as standard deviation.
mass_kg	Estimated body mass in kilogram (kg) from the length-mass conversion in Ganyai (2017).

Table S7. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the species-level Egg-Volume–Mass model, which includes fixed-effect parameters for $\overline{\ln\beta_{0M2}}$, the average across-species intercept; and $\overline{\beta_{1M2}}$, the average across-species mass-scaling exponent of fecundity. Group-level effects include the standard deviations (sd) for phylogenetic variation in the intercept ($\Delta_{\overline{\ln\beta_{0M2}},\phi}$), species-level variation in the intercept ($\Delta_{\overline{\ln\beta_{0M2}},\zeta}$), species-level variation in the mass-scaling exponent ($\Delta_{\overline{\beta_{1M2}},\zeta}$), as well as correlations (cor) among the latter two. Phylogenetic signal was calculated as $\lambda = \sigma_{\phi}^2 / (\sigma_{\phi}^2 + \sigma^2)$, where σ_{ϕ}^2 is the estimated phylogenetic variance (i.e. $\text{sd}(\Delta_{\overline{\ln\beta_{0M2}},\phi})^2$).

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept, $\overline{\ln\beta_{0M2}}$	2.38	0.63	1.17	3.74
Mass scaling, $\overline{\beta_{1M2}}$	0.31	0.13	0.04	0.56
Group-level effects				
$\text{sd}(\Delta_{\overline{\ln\beta_{0M2}},\phi})$	0.41	0.42	0.01	1.52
$\text{sd}(\Delta_{\overline{\ln\beta_{0M2}},\zeta})$	0.62	0.59	0.02	2.17
$\text{sd}(\Delta_{\overline{\beta_{1M2}},\zeta})$	0.16	0.15	0.01	0.54
$\text{cor}(\Delta_{\overline{\ln\beta_{0M2}},\zeta}, \Delta_{\overline{\beta_{1M2}},\zeta})$	-0.47	0.54	-1	0.84
Phylogenetic signal				
λ	0.68	0.3	0.01	0.99

Table S8. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the Malaysia *Chelonia mydas* Fecundity-Mass model (10th, 50th, 90th, and 50th isometric), and Egg-energy–Volume model, which includes fixed-effect parameters for the average intercept $\ln\beta_0$ (natural log-transformed) or β_0 ; and the mass-scaling exponent (β_1) or slope (α) for isometric model of fecundity and egg-energy content.

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects (10th quantile)				
Intercept, $\ln\beta_{0M1}$	1.59	0.43	0.68	2.39
Mass scaling, β_{1M1}	0.61	0.09	0.44	0.81
Fixed effects (50th quantile)				
Intercept, $\ln\beta_{0M1}$	-1.09	0.65	-2.31	0.23
Mass scaling, β_{1M1}	1.45	0.14	1.17	1.71
Fixed effects (90th quantile)				
Intercept, $\ln\beta_{0M1}$	1.59	0.3	1.01	2.19
Mass scaling, β_{1M1}	1.04	0.06	0.91	1.16
Fixed effects (10th quantile isometric)				
Intercept, β_{0M1}	34.73	11.68	10.92	56.75
Mass slope, α_{M1}	0.47	0.11	0.26	0.69
Fixed effects (50th quantile isometric)				
Intercept, β_{0M1}	-120.32	33.84	-186.18	-52.98
Mass slope, α_{M1}	3.46	0.32	2.82	4.09
Fixed effects (90th quantile isometric)				
Intercept, β_{0M1}	-66.74	36.79	-137.65	4.36
Mass slope, α_{M1}	5.68	0.35	5.01	6.36
Fixed effects (Egg-energy-Volume model)				
Intercept, $\ln\beta_{0M3}$	1.94	0.99	-0.05	3.94
Mass scaling, β_{1M3}	1.04	0.27	0.5	1.58

Table S9. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the species-level Fecundity–Mass model, which includes fixed-effect parameters for $\overline{\ln\beta_{0M1}}$, the average across-species intercept; and $\overline{\beta_{1M1}}$, the average across-species mass-scaling exponent of fecundity. Group-level effects include the standard deviations (sd) for phylogenetic variation in the intercept ($\Delta_{\overline{\ln\beta_{0M1}},\phi}$), species-level variation in the intercept ($\Delta_{\overline{\ln\beta_{0M1}},\zeta}$), species-level variation in the mass-scaling exponent ($\Delta_{\overline{\beta_{1M1}},\zeta}$), as well as correlations (cor) among the latter two. Phylogenetic signal was calculated as $\lambda = \sigma_{\phi}^2 / (\sigma_{\phi}^2 + \sigma^2)$, where σ_{ϕ}^2 is the estimated phylogenetic variance (i.e. $\text{sd}(\Delta_{\overline{\ln\beta_{0M1}},\phi})^2$).

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept, $\overline{\ln\beta_{0M1}}$	1.40	0.75	-0.25	2.78
Mass scaling, $\overline{\beta_{1M1}}$	0.92	0.13	0.68	1.17
Group-level effects				
$\text{sd}(\Delta_{\overline{\ln\beta_{0M1}},\phi})$	0.63	0.55	0.03	2.02
$\text{sd}(\Delta_{\overline{\ln\beta_{0M1}},\zeta})$	0.68	0.64	0.02	2.37
$\text{sd}(\Delta_{\overline{\beta_{1M1}},\zeta})$	0.15	0.14	0.00	0.51
$\text{cor}(\Delta_{\overline{\ln\beta_{0M1}},\zeta}, \Delta_{\overline{\beta_{1M1}},\zeta})$	-0.38	0.56	-0.99	0.88
Phylogenetic signal				
λ	0.71	0.28	0.01	0.99

Table S10. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the Egg-energy–Egg-volume model. which includes fixed-effect parameters for $\overline{\ln\beta_{0M3}}$, the average between-species intercept; and $\overline{\beta_{1M3}}$, the average between-species mass-scaling exponent of fecundity. Group-level effects include the standard deviation (sd) for species-level variation in the intercept ($\Delta_{\overline{\ln\beta_{0M3}},\zeta}$).

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept, $\overline{\ln\beta_{0M3}}$	1.54	3.57	-1.31	4.40
Mass scaling, $\overline{\beta_{1M3}}$	1.07	0.17	0.73	1.41
Group-level effects				
sd($\Delta_{\overline{\ln\beta_{0M3}},\zeta}$)	1.41	1.41	0.21	5.12

Table S11. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the species-level Hatchling–Mass model, which includes fixed-effect parameters for $\overline{\ln\beta_0}$, the average across-species intercept; and $\overline{\beta_1}$, the average across-species mass-scaling exponent of fecundity. Group-level effects include the standard deviations (sd) for phylogenetic variation in the intercept ($\Delta_{\overline{\ln\beta_0},\phi}$), species-level variation in the intercept ($\Delta_{\overline{\ln\beta_0},\zeta}$), species-level variation in the mass-scaling exponent ($\Delta_{\overline{\beta_1},\zeta}$), as well as correlations (cor) among the latter two. Phylogenetic signal was calculated as $\lambda = \sigma_\phi^2 / (\sigma_\phi^2 + \sigma^2)$, where σ_ϕ^2 is the estimated phylogenetic variance (i.e. $\text{sd}(\Delta_{\overline{\ln\beta_0},\phi})^2$).

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept, $\overline{\ln\beta_0}$	3.37	0.24	2.88	3.82
Mass scaling, $\overline{\beta_1}$	0.11	0.04	0.03	0.21
Group-level effects				
sd($\Delta_{\overline{\ln\beta_0},\phi}$)	0.18	0.17	0.01	0.60
sd($\Delta_{\overline{\ln\beta_0},\zeta}$)	0.23	0.21	0.01	0.77
sd($\Delta_{\overline{\beta_1},\zeta}$)	0.06	0.05	0	0.19
cor($\Delta_{\overline{\ln\beta_0},\zeta}, \Delta_{\overline{\beta_1},\zeta}$)	-0.50	0.53	-0.99	0.84
Phylogenetic signal				
λ	0.79	0.26	0.04	0.99

Table S12. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the species-level Protected-beach–Mass model, which includes fixed-effect parameters for the average intercept, slope of body mass, and nesting temperature as a covariate. Group-level effects include the standard deviations (sd) for species-level variation in the intercept, the slope, as well as correlations (cor) among them.

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept	65.41	50.86	-32.54	167.54
Protected beaches	0.06	0.17	-0.31	0.34
Nest temperature	-2.21	1.64	-5.48	0.96
Random effects				
sd(Δ Intercept)	167.45	50.47	99.21	291.82
sd(Δ Protected beaches)	0.17	0.18	0.01	0.62
cor(Δ Intercept, Δ Protected beaches)	0.22	0.54	-0.87	0.97

Table S13. Summary of the number of *Chelonia mydas* individuals, mean body size, and fecundity across sampling years in the Terengganu population.

Year	Number of unique individuals		Mean body mass (kg)		Mean fecundity (sum of eggs)	
	First time	Recruit	First time	Recruit	First time	Recruit
1993	89		107.2		246	
1994	53		108.68		327	
1995	101	2	107.91	110.78	350	514
1996	51	22	108.82	113.61	341	428
1997	60	20	105.31	112.13	403	593
1998	49	29	105.56	113.26	399	550
1999	59	48	109.39	109.71	417	487
2000	23	21	106.99	113.73	309	527
2001	45	34	108.86	108.11	419	507
2002	36	38	104.28	112.69	365	631
2003	19	23	107.84	111.83	316	340
2004	52	39	107.73	110.78	303	382
2005	18	22	110.65	111.02	297	412
2006	16	15	118.72	99.52	185	219
2007	38	28	112.79	110.59	407	522
2009	57	28	104.57	107.36	342	433
2010	115	30	113.89	94.92	315	396
2011	96	36	109.63	107.8	318	403
2012	97	30	104.54	111.2	317	470
2013	170	62	105.31	110.32	329	451
2014	102	33	102.14	109.88	251	380
2015	48	25	104.71	113.06	149	207
2016	307	89	102.69	109.81	288	402
2017	107	47	102.66	108.51	215	190
2018	145	38	100.64	108.35	276	371
2019	179	54	101.71	107.05	197	199

Table S14. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the Malaysia *Chelonia mydas* generalised additive Mass–Year model, which includes fixed-effect parameters for the average intercept, group (First time and recurring nesters), and the smoothing parameters. Group-level effects include the standard deviations (sd) for individual-level variation in the intercept.

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept	104.42	0.26	103.91	104.93
Group	7.12	0.47	6.18	8.05
Year x First time	-21.37	13.76	-47.68	6.88
Year x Recurring	-6.85	19.44	-49.9	33.76
Group-level effects				
sd(Intercept)	8.51	0.27	7.96	9.03

Table S15. Point estimates and 95% credible intervals (as determined using Bayesian methods) for fitted parameters estimated for the Malaysia *Chelonia mydas* generalised additive Fecundity–Year model, which includes fixed-effect parameters for the average intercept, group (First time and recurring nesters), and the smoothing parameters. Group-level effects include the standard deviations (sd) for individual-level variation in the intercept.

Parameter	Estimate	Est.Error	Q2.5	Q97.5
Fixed effects				
Intercept	298.65	4.6	289.78	307.65
Group	75.21	10.4	54.82	95.37
Year x First time	408.02	315.35	-175.78	1059.82
Year x Recurring	165.5	1017.24	-1534.7	2426.52
Group-level effects				
sd(Intercept)	91.74	6.44	78.6	103.79

SUPPLEMENTARY FIGURES

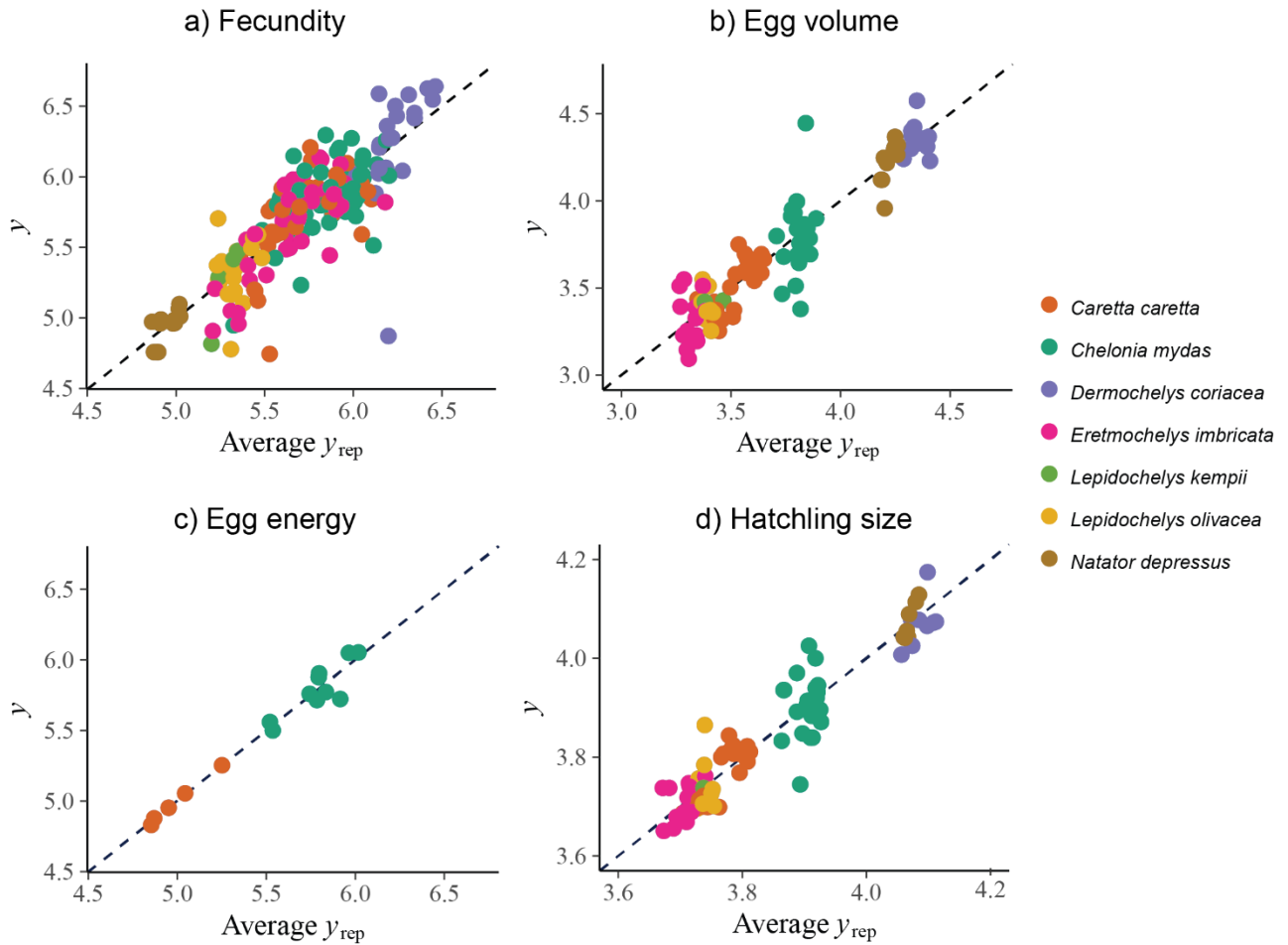


Fig. S1 | Scatterplots of the observed data (y) vs the average simulated data (y_{rep}) from the posterior predictive distribution for the species-level a) Fecundity–Mass b) Egg–Volume–Mass, c) Egg–energy–Volume, and d) Hatchling–Mass model. Dashed line represents a slope of 1.

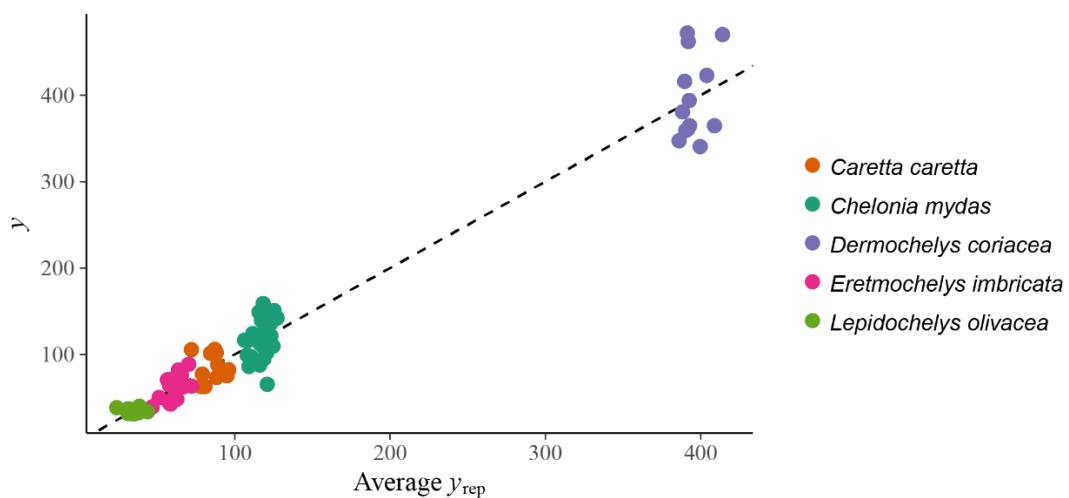


Fig. S2 | Scatterplots of the observed data (y) vs the average simulated data (y_{rep}) from the posterior predictive distribution for the species-level Mass-Protected area model. Dashed line represents a slope of 1.

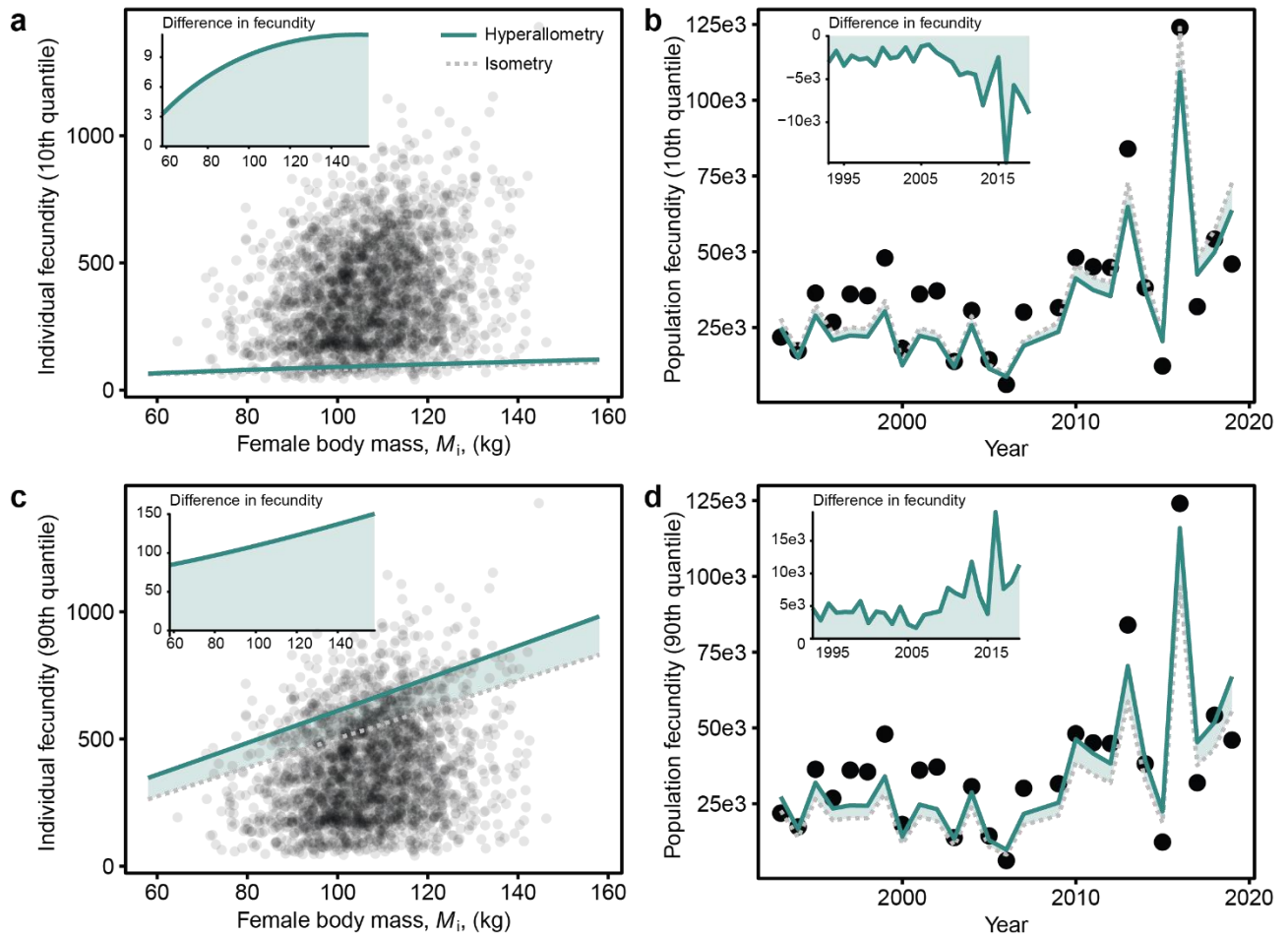


Fig. S3 | Difference in hyperallometric (solid green line) and isometric relationship (grey dashed line) of individual fecundity (a, c) and population fecundity by year (b, d). Top figures (a, b) represent the 10th quantile models, and bottom figures (c, d) represent the 90th quantile models. Inset plots on the top-left shows differences in predicted fecundity between the hyperallometric relationship and isometric relationship.

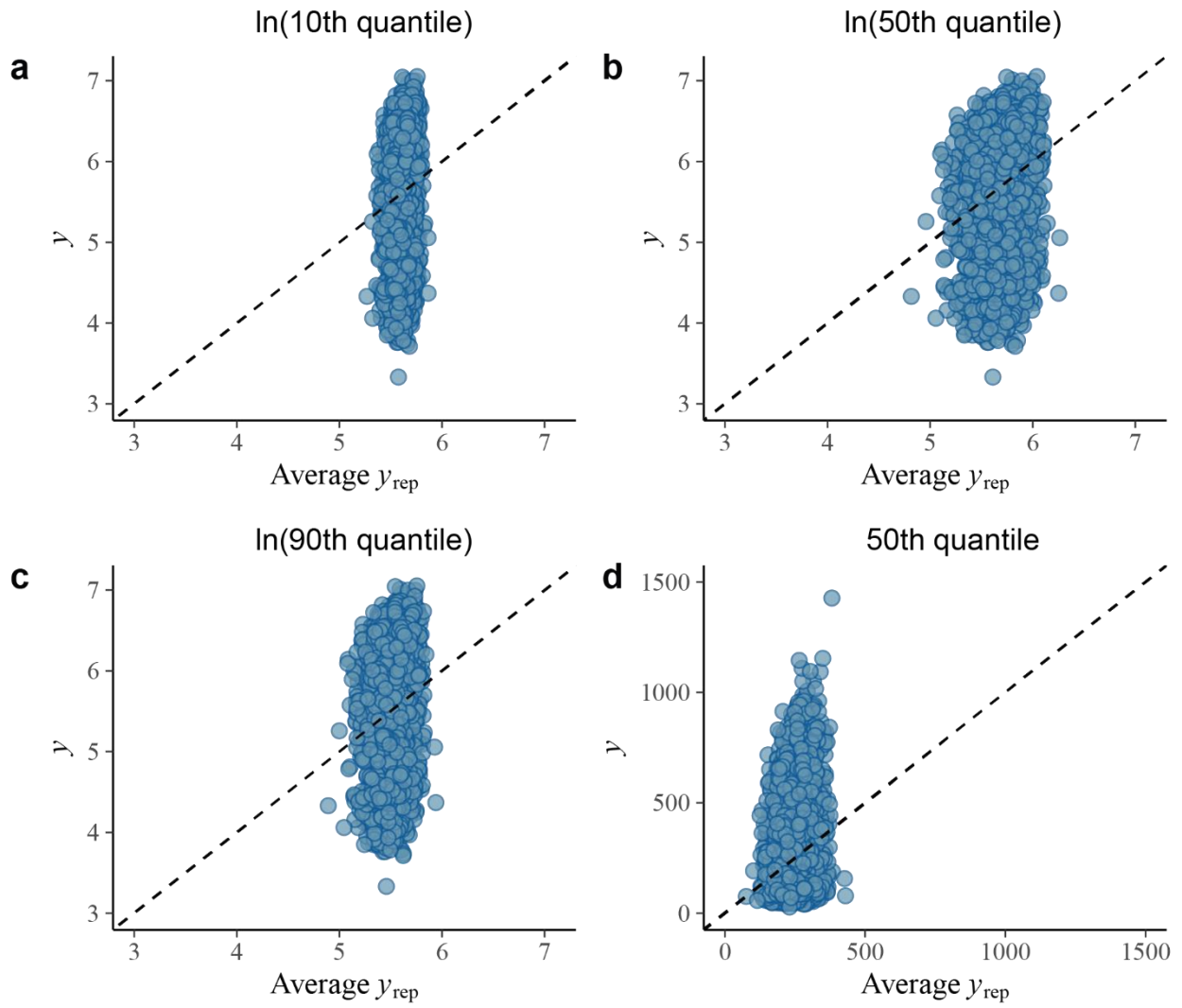


Fig. S4 | Scatterplots of the observed data (y) vs the average simulated data (y_{rep}) from the posterior predictive distribution for the Terengganu *Chelonia mydas* a) ln(10th quantile, b) ln(50th quantile), c) ln(90th quantile), and 50th quantile Fecundity–Mass model. Dashed line represents a slope of 1.

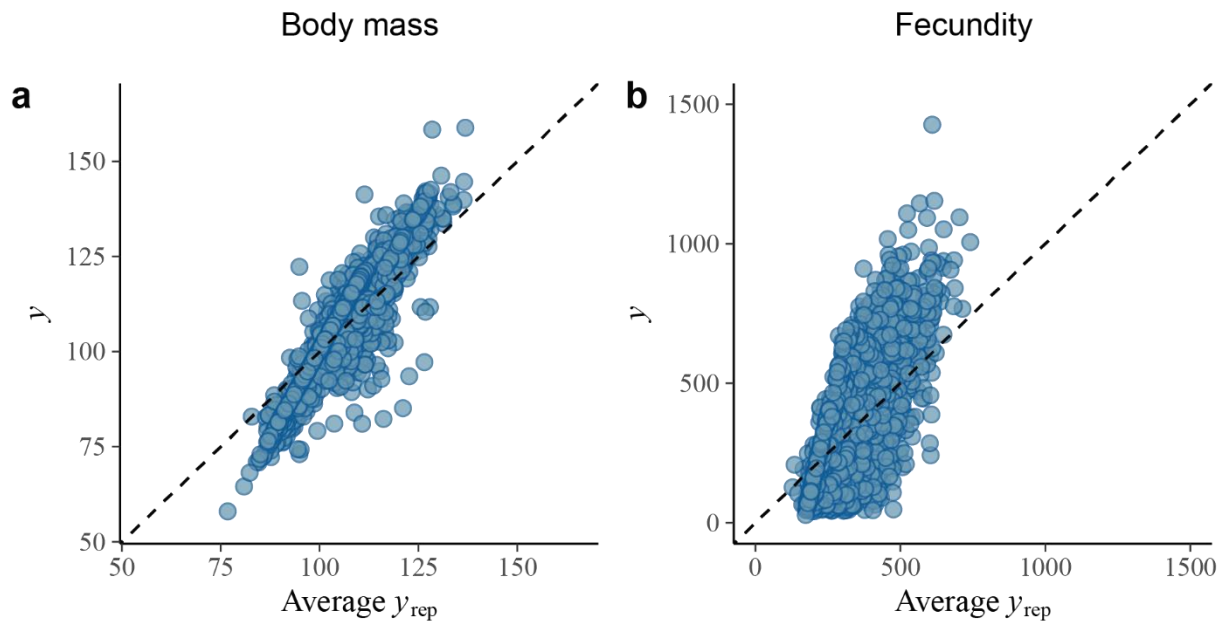


Fig. S5 | Scatterplots of the observed data (y) vs the average simulated data (y_{rep}) from the posterior predictive distribution for the Terengganu *Chelonia mydas* a) Mass–Year and Fecundity–Year model. Dashed line represents a slope of 1.

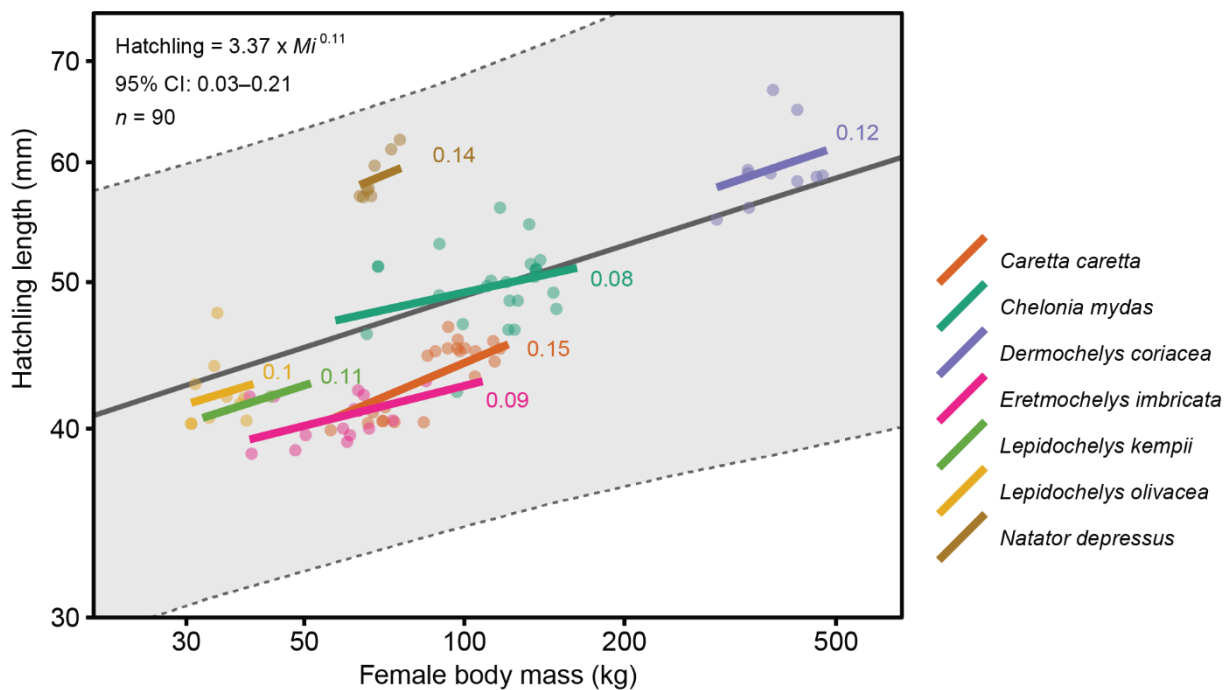


Fig. S6 | Scaling relationships of the hatchling body length (mm) upon emergence with female body mass (M_i , kg). Data points represent mean values from each study. Black solid and dashed regression line represents the overall mean estimate \pm 95% CI (all species combined). Equations in the top-left corners depict the phylogenetic-corrected model fit when all seven species were combined. Coloured regression lines represent mean posterior fits of the scaling exponent (from 4000 posterior samples) with exponent values presented for each turtle species.

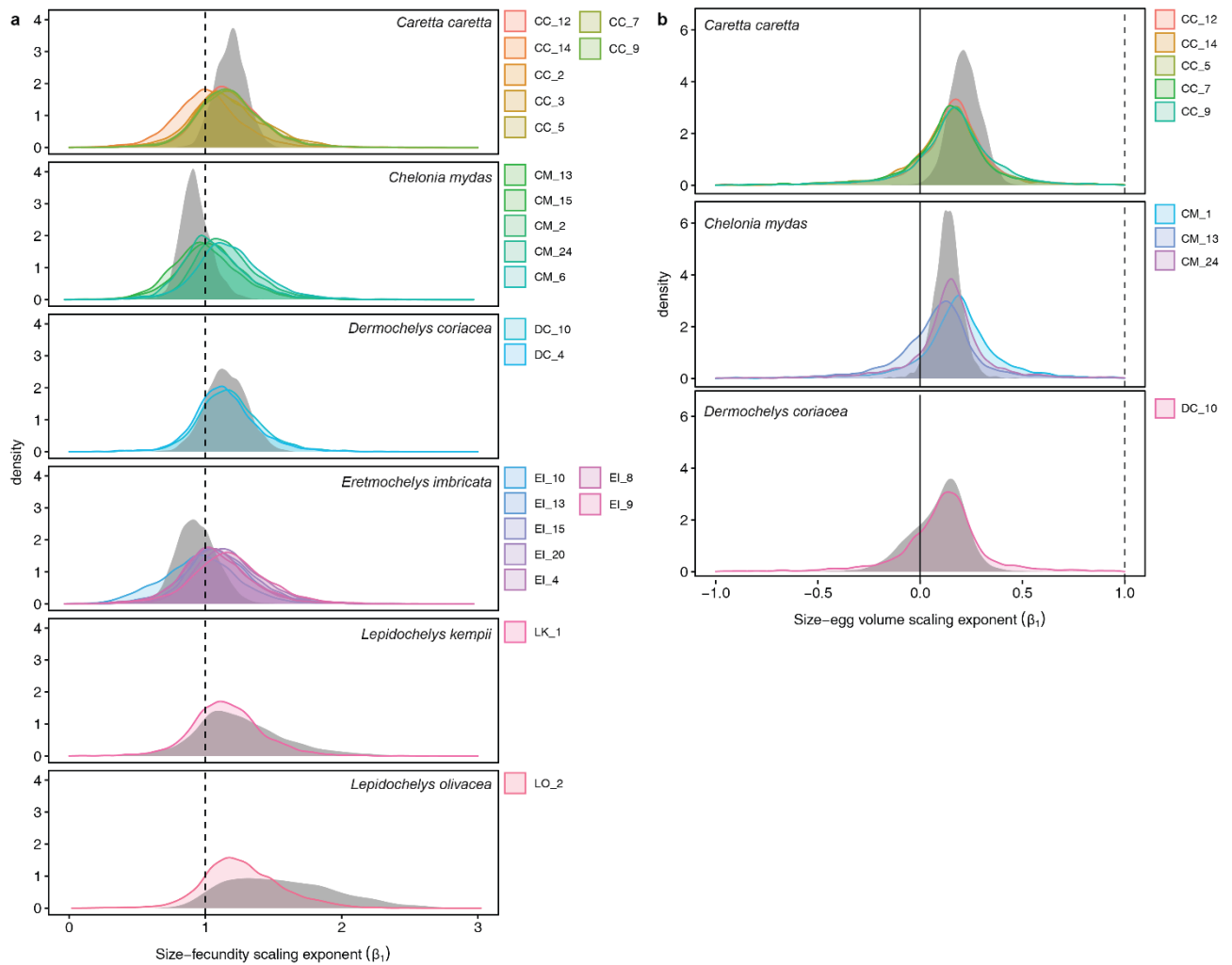


Fig. S7 | Posterior distribution density (4,000 subset iterations) of a) size-fecundity scaling exponent (β_1) and b) size-egg volume scaling exponent (β_1) of sea turtle populations. Grey density represents the species-level scaling exponent. Coloured densities represent within-population scaling exponent where population labels were labelled as unique identifier code for each population examined. Vertical dashed lines represent one (in plot a and b), and values above indicates a hyperallometric scaling relationship with body mass. Vertical solid lines represent zero (in plot b), and values above this line indicates a positive relationship with body mass.

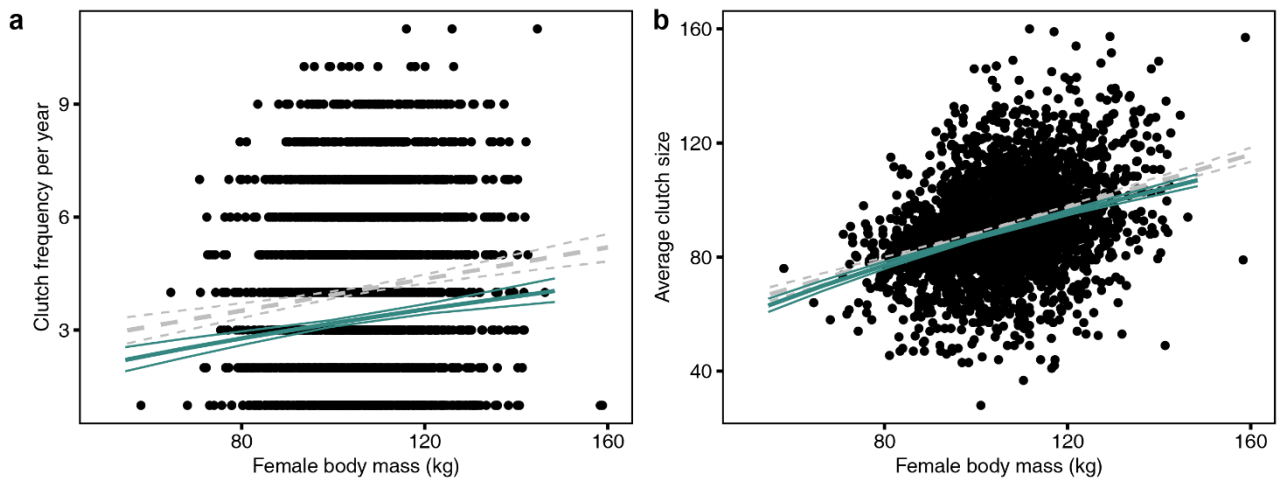


Fig. S8 | Relationship between *Chelonia mydas* body mass (kg) with (a) clutch frequency and (b) average clutch size of 2,211 individuals from the Redang Island population (1993–2019). Grey line represents isometric relationship \pm 95% credible interval (95% CI), and the green line represents hyperallometric relationship \pm 95% CI. The Bayesian R^2 estimate \pm 95% CI presented in the figure. Clutch frequency isometric $R^2 = 0.01$ [0.006–0.02], Clutch frequency hyperallometric $R^2 = 0.01$ [0.004–0.18], Clutch size isometric $R^2 = 0.11$ [0.097–0.14], Clutch size hyperallometric $R^2 = 0.1$ [0.08–0.13].

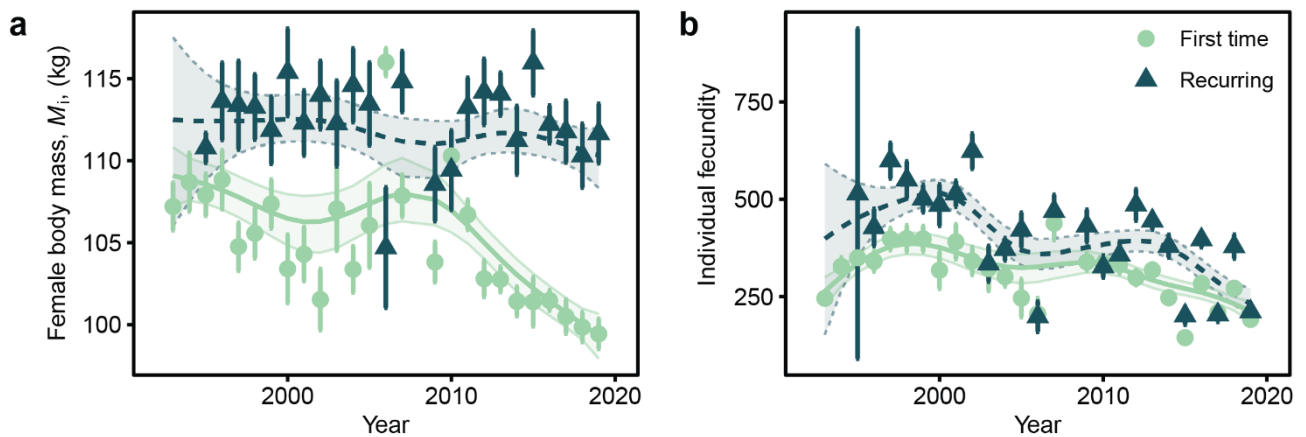


Fig. S9 | Changes in (a) nesting female body mass and (b) clutch size from 1993–2019 for first-time (smaller, light-green silhouette: circles) and recurring (larger, dark-green silhouette: triangles). Data presented as mean \pm s.e. for each year, and solid lines and shade represent the estimate (\pm 95% CI) of the Bayesian hierarchical general additive model. Model summary presented in Tables S14–15.

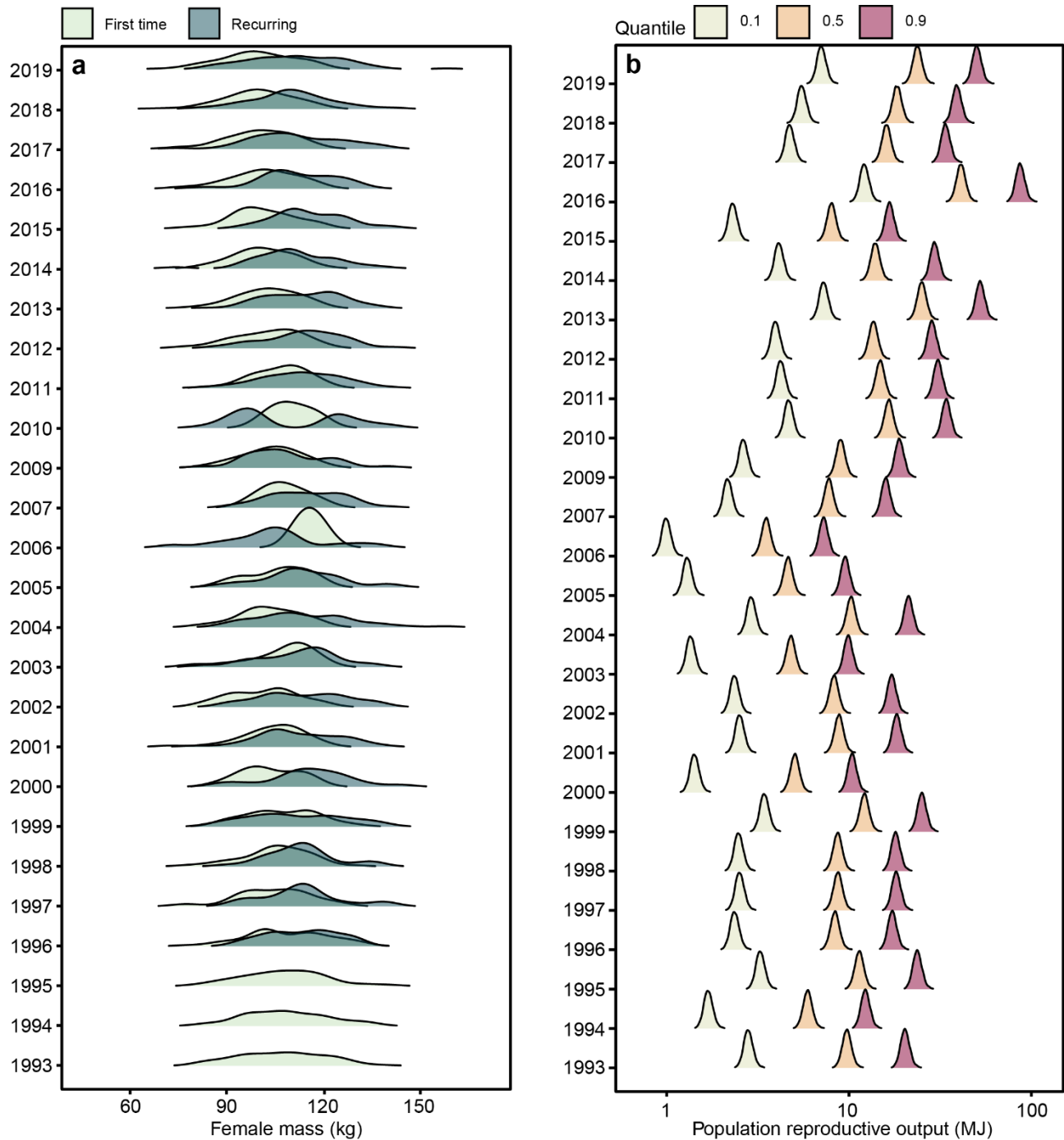


Fig. S10 | Temporal shifts size and reproduction in nesting *Chelonia mydas* from the Terengganu population

(1993–2019). **(a)** changes in body mass distribution across the sampling period. Data were grouped into newly recruited females (first time nesters; light green), and recurring nesters (dark green). **(b)** The population reproductive output across the sampling period. Data shows the posterior distribution of the 10th (light yellow), 50th (orange), and 90th (red) quantile regression model.

SUPPLEMENTARY REFERENCES

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