Additional information on literature review and statistical analyses

This supplement includes a list of databases used to identify sea turtle growth studies (Table S1), the results of the Fabens method estimation of L_∞ and K for data from Hart et al. (2013) for hawksbill sea turtles and Snover et al. (2007a) for loggerhead sea turtle (Table S2), a list of studies that were excluded from the meta-analysis and justification for their exclusion (Table S3), equations used to convert curved carapace length (CCL) to straight carapace length (SCL) along with the values of L_∞ that were converted (Table S4), the geographic definitions for regional management unit (RMU) utilized herein (Table S5), and the Pareto k diagnostic parameters for each meta-analysis model (Table S6). Figure S1 includes the residuals for the Fabens method fits, Figures S2 and S3 are the residual plots and qqnormal plots for the meta-analysis models, Figure S4 shows the predicted mean parameter values from the model including latitude as a predictor variable, and Figure S5 shows the mean von Bertalanffy fit for each species from model D. The JAGS code for models D and E are also provided. Code and data for all models are available at https://github.com/matthewdramirez/SeaTurtleGrowthMeta-analysis

Table S1. Resources scanned for literature review of growth studies on sea turtles. Additional resources not listed here include governmental status assessments and reports.

Resource Type	Source	Website or Citation
Online database	Web of Science	
	ProQuest Biological Science Database	
	Archie Carr Center for Sea Turtle Research Online Bibliography	https://accstr.ufl.edu/resources/online-bibliography/
	Sea Turtles of India Bibliography	https://www.seaturtlesofindia.org
	Proceedings of the International Sea Turtle Symposium	https://internationalseaturtlesociety.org
Journals	Chelonian Conservation and Biology	
	Herpetological Conservation and Biology	
	Marine Ecology Progress Series	
	Endangered Species Research	
	Fishery Bulletin	
	Scientia marina	
	Zoology in the Middle East	
	Revista de Biología Tropical	
	Marine Turtle Newsletter	https://www.seaturtle.org/mtn
	Indian Ocean Turtle Newsletter	https://www.iotn.org
Books	The Biology of Sea Turtles v1 (Ch. 9)	Lutz & Musick (1997)
	The Biology of Sea Turtles v2 (Ch. 5 and 11)	Lutz et al. (2002)
	Sea Turtles: A Complete Guide to Their Biology, Behavior, and Conservation	Spotila (2004)
	Marine Turtles of the Indian Subcontinent	Shanker & Choudhury (2007)
	Biology and Conservation of Sea Turtles	Bjorndal (1995)

Table S2. Parameter estimates for Fabens method fits to data from Hart et al. (2013) for hawksbill sea turtles and Snover et al. (2007a) for loggerhead sea turtles.

Parameter	Estimate	Standard error	t value	Pr(>|t|)
Hart et al. (2013), hawksbill				
L_∞	81.560	6.212	13.129	0.000
K	0.137	0.027	4.996	0.000
Snover et al. (2007a), loggerhead				
L_∞	90.292	20.758	4.350	0.001
K	0.093	0.075	1.249	0.240

Table S3. Studies with published von Bertalanffy growth parameters that were excluded from the meta-analysis. See Table S5 for RMU definitions.

Species	RMU	Study	Reason for exclusion
G	ANW	Bjorndal et al. (1995)	Same data as Bjorndal & Bolten (1995)
G	Med	Omeyer et al. (2018)	K not reported
G	PNW	Kameda et al. (2017)	L_∞ fixed to 102.4 cm (1995–2003) and 96.5 cm (2004–2016)
G	PE	Eguchi et al. (2012)	Unnatural setting—power plant waters
G	ASC	Le Toquin et al. (1980)	Unusual method—scale growth
G	PNC	Van Houtan (2015)	L_∞ fixed to 89.7 cm, t_0 fixed at –0.181
L	ANW	Frazer & Schwartz (1984)	Data for captive turtles
L	ANW	Frazer & Ehrhart (1985)	Data expanded upon in Frazer (1987)
L	ANW	Snover (2008)	K from Bjorndal et al. (2000, 2001)
L	ANW	Braun-McNeill et al. in NMFS SEFSC (2001)	Data expanded upon in NMFS SEFSC (2001)
L	ANW	Vaughan (2009)	Same data as Snover (2002)
L	ANW	Marn et al. (2017)	Simulation model; do not report L_∞ and K
L	Med	Piovano et al. (2011)	L_∞ fixed at 124 cm (Atlantic origin) and 99 cm (Mediterranean origin)
L	Med	Casale et al. (2011b)	L_∞ fixed at 99 cm
L	Med	Casale et al. (2009b)	Data only fit to small turtles < 4 yrs old
H	PNC	Van Houtan et al. (2016)	L_∞ fixed to 81 cm, t_0 fixed at –0.17
H	PSC	Witzell (1980)	Data for captive turtles
KR	ANW	Zug (1990)	Data expanded upon in Zug et al. (1997)
KR	ANW	Snover (2002)	Data updated in Snover et al. (2007b)
KR	ANW	Avens et al. (2017)	Atlantic data; from Snover et al. (2007b)
KR	ANW	Schmid (1995)	Data expanded upon in Turtle Expert Working Group (2000)
KR	ANW	Schmid (1998)	Data expanded upon in Turtle Expert Working Group (2000)
KR	ANW	Schmid & Witzell (1997)	Combines data from Schmid (1995, 1998); Data expanded upon in Turtle Expert Working Group (2000)
KR	ANW	Gallaway et al. (2016)	L_∞ not reported

Table S4. Conversions of L_∞ values from curved carapace length (CCL) to straight carapace length (SCL) for three species of sea turtles: green (G, *Chelonia mydas*), loggerhead (L, *Caretta caretta*), and hawksbill (H, *Eretmochelys imbricate*).

Species	Study	CCL L_∞	SCL L_∞	Conversion Equation	Conversion Equation Reference
G	Frazer & Ladner (1986)	121.64	114.76	$SCL = \frac{CCL + 0.4579}{1.064}$	Lenz et al. (2017)
G	Watson (2006)	117.40	110.77		
G	Hof et al. (2017)	108.90	103.77	$SCL = 0.9533 \text{ x } CCL - 0.043$	Tanaka (2009)
L	Parham & Zug (1997)	104.03	97.18	$SCL = 0.948 \text{ x } CCL - 1.442$	Teas (1993)
L	Bjorndal et al. (2000)	105.50	98.57		
L	Bjorndal et al. (2000), Atlantic	118.50	110.90		
L	Bjorndal et al. (2001), GoM	113.00	105.68		
L	Casale et al. (2009a)	95.63	89.22		
L	Casale et al. (2011a)	111.6	104.35		
H	Hart et al. (2013)	81.56	74.05	$SCL = \frac{CCL - 0.1}{1.1}$	Hawkes et al. (2014)

Table S5. Regional management unit (RMU) abbreviations and descriptions for sea turtle populations included in this study. All were from Wallace et al. (2010) with the exception that we separated Kemp's ridley from the Gulf of Mexico from the rest of the NW Atlantic because of known regional variability in growth rates for this species.

Species	RMU	Abbrev.	Geographic Boundaries
Green	Atlantic Northwest	ANW	Central American and the Gulf of Mexico, the Caribbean (excluding the Antilles), out to Bermuda and back into the US at the mid-Atlantic coast (includes Aves Island)
	Indian Southwest	ISW	Southern Somalia out to Chagos Archipelago, coming down around St. Brendan, wrapping around South Africa to middle of the coast of Namibia; southern extent is 42° S
	Pacific East	PE	Los Angeles south, sweeping down the coast of Chile and the Eastern Tropical Pacific out to 145° W
	Pacific Northwest	PNW	Midway along the largest Japanese island down to include the southern Japanese islands, Taiwan and China from 30° N south
	Pacific Southwest	PSW	South of the eastern extent of Indonesia to midway through New South Wales Australia, wraps around Papua New Guinea and out to New Caledonia but excludes the Solomon Islands and Vanuatu, includes overlap in the Banda, Celebes and Sulu Seas

Species	RMU	Abbrev.	Geographic Boundaries
Loggerhead	Atlantic Northwest	ANW	Cape Cod, Grand Banks, Azores, Madeira, In the Mediterranean west of southern Italy and Tunisia, Gulf Stream, Sargasso Sea, Gulf of Mexico, Bahamas, Cuba, US, up to 50° N and down to French Guinea
	Mediterranean	Med	Entire Mediterranean, through the Strait of Gibraltar and up the Portugal coastline.
Hawksbill	Atlantic West Caribbean/USA	AWCar	Mid-Atlantic US out to 35° W, south through the Caribbean, to midway down the coast of Guyana
	Pacific North Central	PNC	Waters surrounding Hawaii, including the Northern Hawaiian Islands
Olive ridley	Atlantic West	AW	Margherita and Barbados south to Sergipe Brazil, northwest across to mid-Atlantic out to 15° W
Kemp's ridley	Atlantic Northwest, Atlantic	ANW_{Atl}	East Coast of Florida and up the US east coast to Cape Cod
	Atlantic Northwest, Gulf of Mexico	ANW_{GoM}	Gulf of Mexico

Table S6. Pareto k values for the fitted meta-analysis models (A–I).

k range	Category	A	B	C	D	E	F	G	H	I
(-Inf, 0.5]	(good)	0.81	0.95	0.81	0.97	0.84	0.81	0.95	0.86	0.95
(0.5, 0.7]	(ok)	0.16	0.03	0.16	0.03	0.14	0.14	0.03	0.11	0.03
(0.7, 1]	(bad)	0.03	0.03	0.03	0	0.03	0.05	0.03	0.03	0.03
(1, Inf)	(very bad)	0	0	0	0	0	0	0	0	0

Table S7. Nesting female maximum straight carapace length data (L_{max}) summarized in Table 3.

Species	Study	Country	N	L_{max} (cm SCL)
Green	Weber et al. (2014)	Ascension Island	80	116.97[a]
	Whiting et al. (2014)	Australia	16	109.36[a]
	Almeida et al. (2011)	Brazil	3010	135.30[a]
	Ng et al. (2014)	China	5	102.87[a]
	Innocenzi et al. (2010)	Comoros	742	121.67[a]
	Azanza Ricardo et al. (2013)	Cuba	607	128.00
	Broderick et al. (2003)	Cyprus	92	100.05[a]
	Hanafy (2012)	Egypt	76	113.21[a]
	Livesey (2013)	Mexico	64	109.92[a]
	Summers et al. (2018)	Northern Mariana Islands	38	105.04[a]
	Phillips et al. (2017)	Seychelles	292	115.94[a]
	Ekanayake et al. (2016)	Sri Lanka	74	113.40[a]
	West et al. (2013)	Tanzania	18	111.33[a]

Species	Study	Country	N	L_{max} (cm SCL)
	Balazs et al. (2015)	United States (Hawaii)	3414	106.00
	Prieto-Torres et al. (2013)	Venezuela	48	118.29[a]
Loggerhead	Limpus et al. (1984)	Australia	380	100.94[a]
	Limpus et al. (1992)	Australia	24	96.20[a]
	Lima et al. (2012)	Brazil	217	107.10[a]
	Soares et al. (2017)	Brazil	79	114.00
	Loureiro (2008)	Cape Verde	21	80.09[a]
	Broderick et al. (2003)	Cyprus	159	81.03[a]
	Patel et al. (2015)	Greece	18	87.00
	Hatase et al. (2018)	Japan	49	94.20
	Sato et al. (1997)	Japan	398	103.10
	Rees et al. (2010)	Oman	10	101.42[a]
	Tucker et al. (2018)	Oman	34	103.79[a]
	Hughes (1975)	South Africa	254	99.52[a]
	Türkozan and Yilmaz (2008)	Turkey	103	86.50
	Phillips et al. (2014)	United States (Florida)	841	112.10
	Flower et al. (2018)	United States (Georgia)	37	106.63[a]
Hawksbill	Limpus and Miller (2008)	Australia	1500	86.27[a]
	Beggs et al. (2007)	Barbados	1310	93.00[a]
	Soares et al. (2017)	Brazil	30	90.82[a]
	Moncada et al. (2010)	Cuba	87	84.45[a]
	Gaos et al. (2017)	Ecuador	158	99.91[a]
	Liles et al. (2011)	El Salvador	26	79.91[a]
	Tomás et al. (2010)	Equatorial Guinea	13	82.64[a]
	Askari Hesni et al. (2016)	Iran	50	68.64[a]
	Pilcher and Ali (1999)	Malaysia	431	89.00[a]
	Xavier et al. (2006)	Mexico	81	108.09[a]
	Lagueux et al. (2003)	Nicaragua	22	85.30
	Al-Merghani et al. (2000)	Saudi Arabia	499	84.45[a]
	Hitchins et al. (2004)	Seychelles	117	86.82[a]
	McKeown (1977)	Solomon Islands	40	89.00
	Seitz et al. (2012)	United States (Hawaii)	685	90.00
Olive ridley	Whiting et al. (2007)	Australia	85	70.76[a]
	Islam et al. (1999)	Bangladesh	22	70.59[a]
	Cornelius (1976)	Costa Rica	53	72.50
	Viejobueno Muñoz and Arauz (2015)	Costa Rica	1000	65.79[a]
	James and Melero (2015)	Costa Rica	7	73.05[a]
	Brenes Arias et al. (2015)	Costa Rica	100	73.87[a]
	Tomás et al. (2010)	Equatorial Guinea	30	76.32[a]
	Catry et al. (2009)	Guinea-Bissau	24	77.96[a]
	James et al. (1991)	India	100	73.00
	Giri and Chaturvedi (2003)	India	8	73.00
	Tripathy et al. (2006)	India	6	72.23[a]
	Marquez et al. (1976)	Mexico	1203	73.00
	Frazier (1983)	Mexico	81	67.00
	Hart et al. (2014)	Mexico	57	68.14[a]
	Schulz (1975)	Suriname	500	75.00

[a]Curved carapace length (CCL) converted to SCL using species-specific conversion equations from Lenz et al. (2017), Teas (1993), Hawkes et al. (2014), and Whiting et al. (2007)

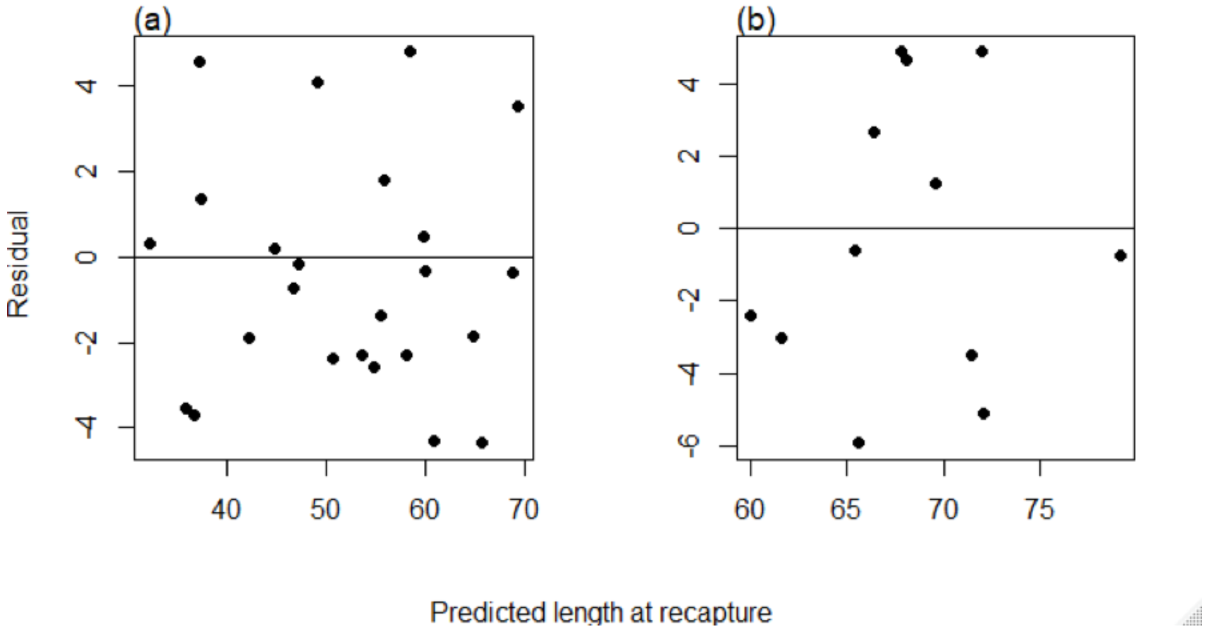

Figure S1. Residuals for Fabens method fits to data from (a) Hart et al. (2013) for hawksbill sea turtles (n = 24) and (b) Snover et al. (2007a) for loggerhead sea turtles (n = 12).

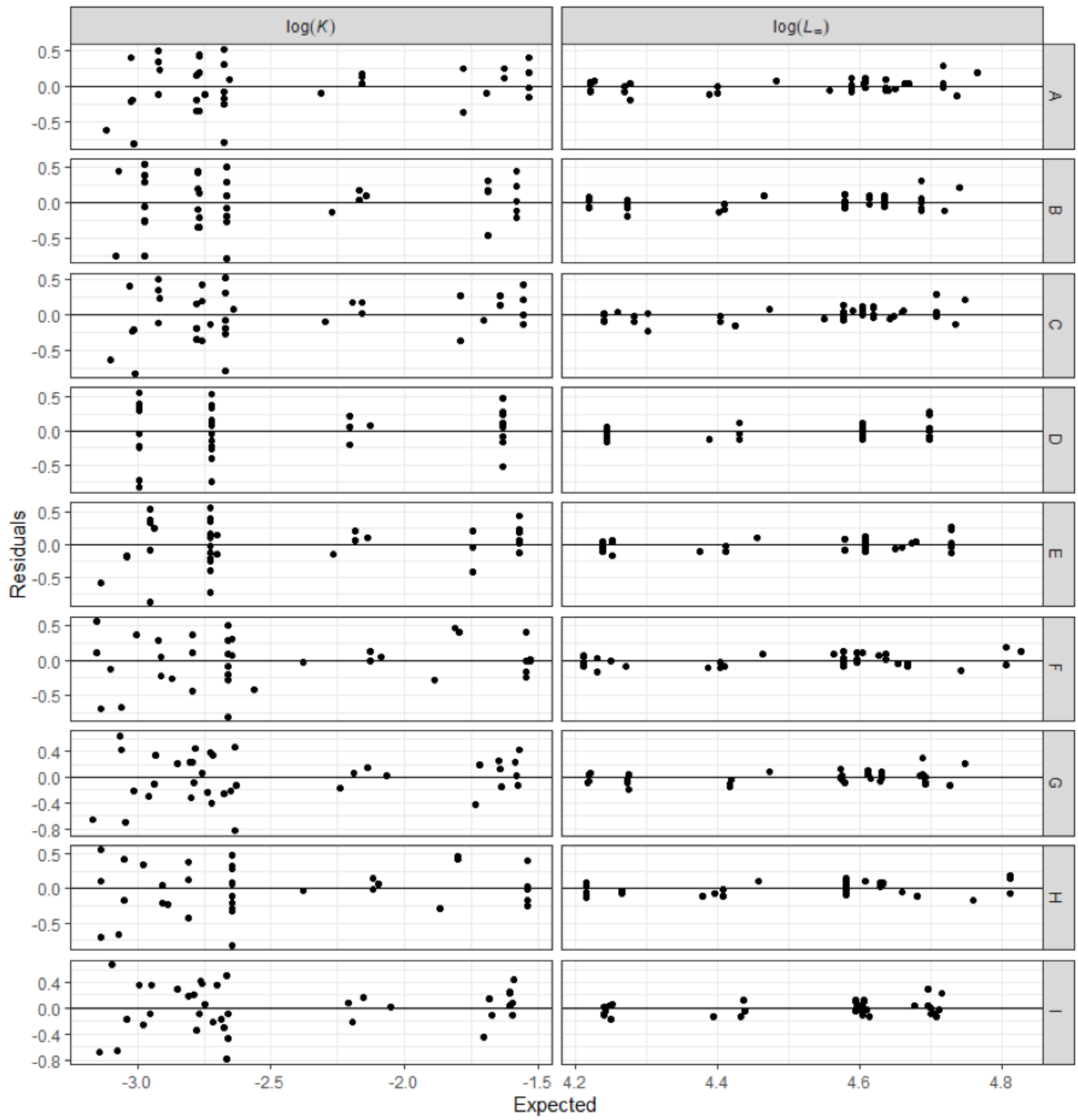

Figure S2. Posterior means of the residuals plotted against posterior means of the expected values for models A–I (columns) for K and L_∞ (rows).

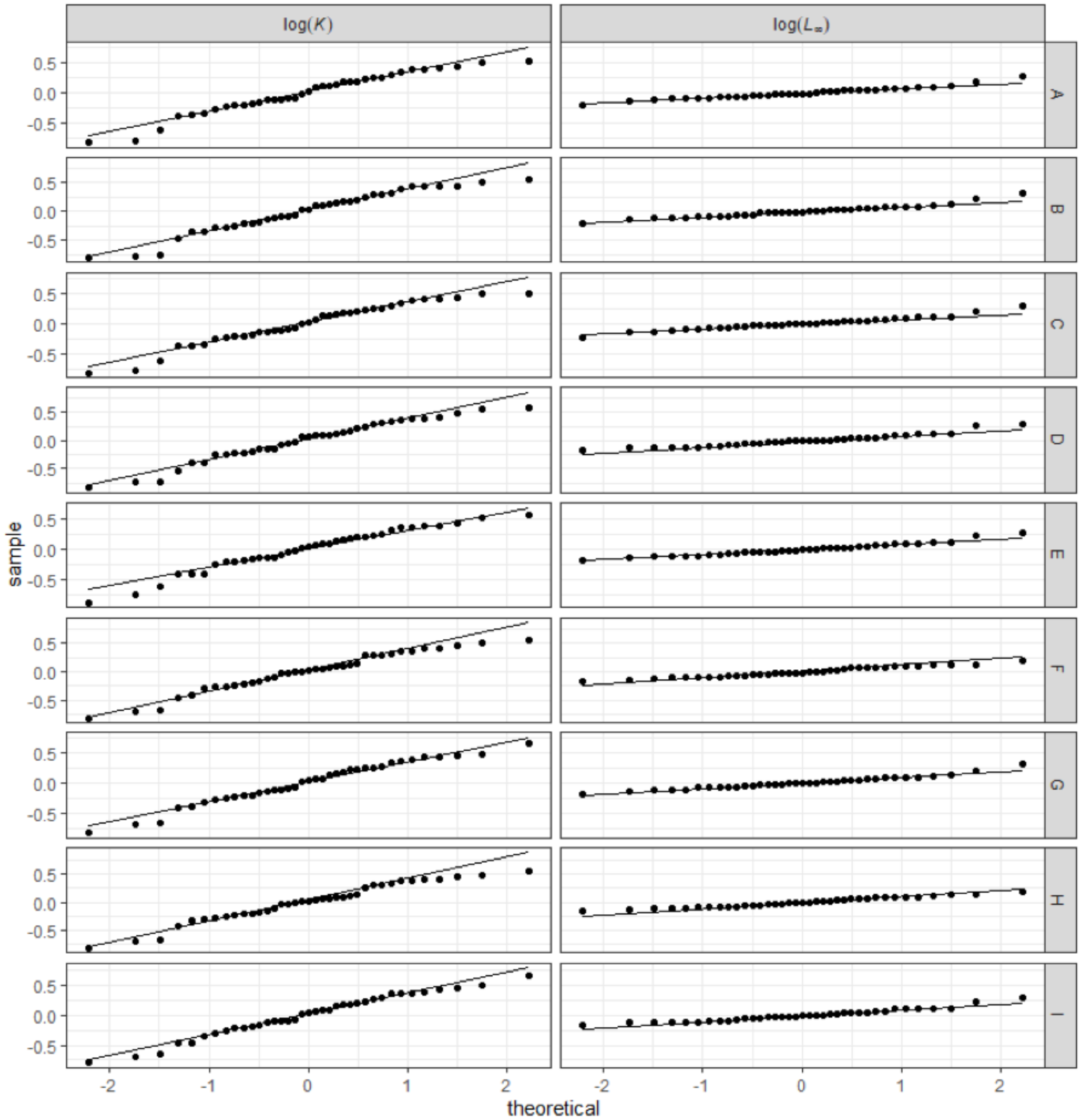

Figure S3. QQ normal plots of the posterior mean residuals for models A–I (columns) for K and L_∞ (rows).

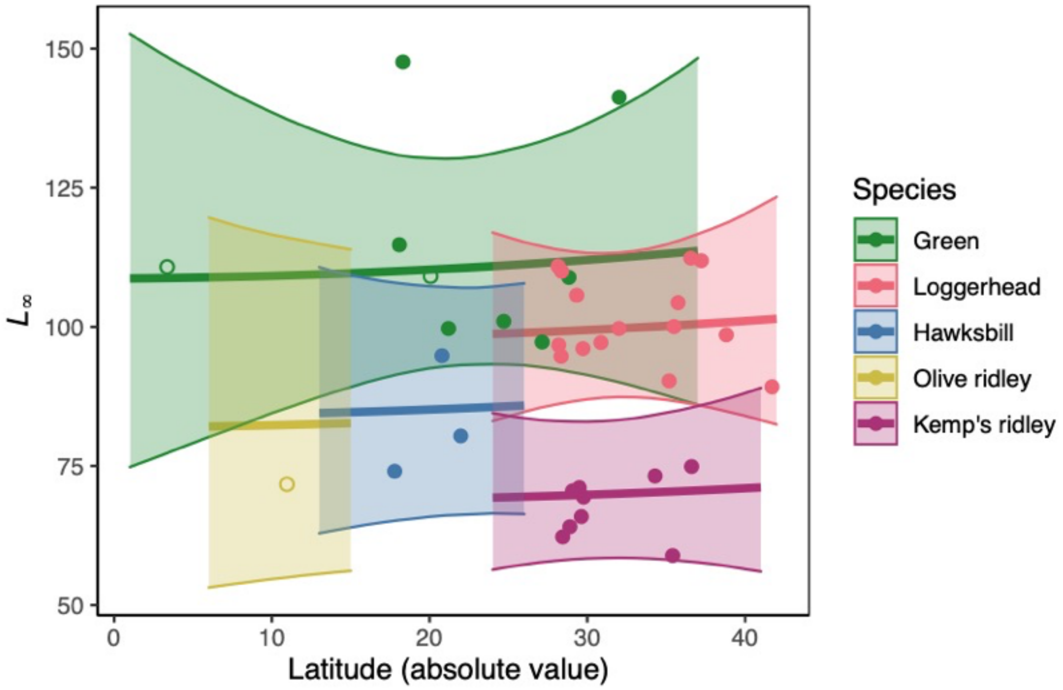

Figure S4. Predicted mean values of L_∞ with 95% credible intervals by species and latitude (Model I). Filled points denote data from the Northern Hemisphere, whereas open points denote data from the Southern Hemisphere.

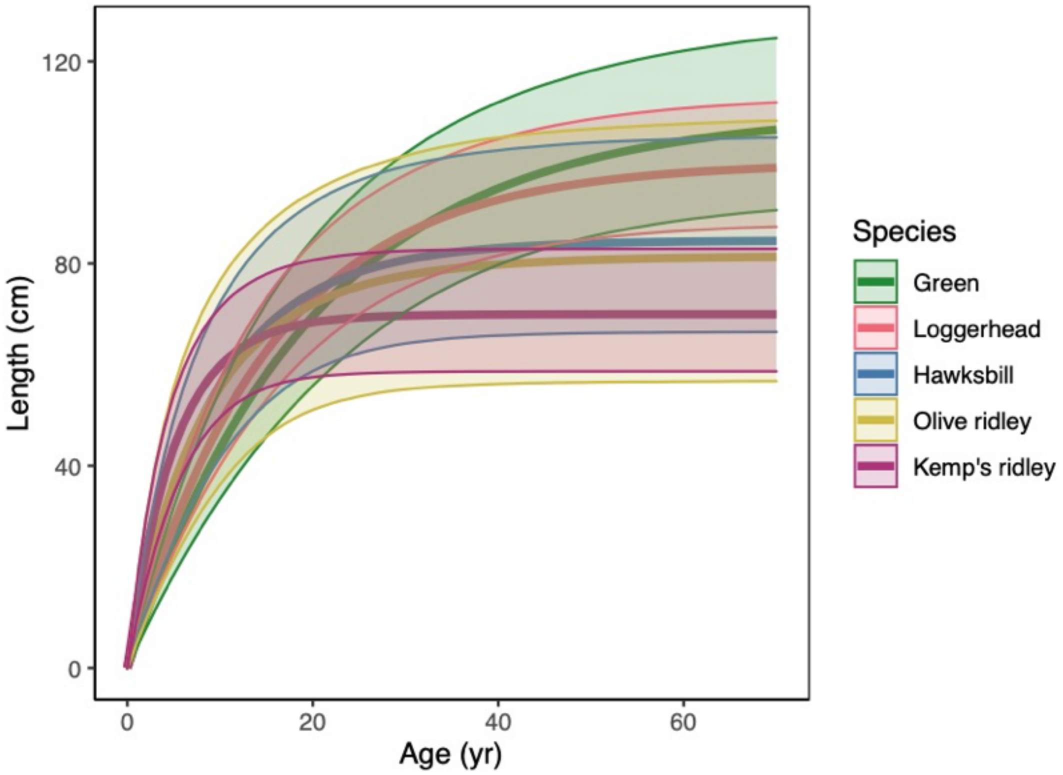

Figure S5. Average growth curve with 95% credible intervals by species from the model with species effects only (Model D). t_0 was fixed to zero.

JAGS code for Model D

```
model {
for (i in 1:N) {
Y[i, 1:2] ~ dmnorm(mu[i,], Sigma.inv[,])
LL[i]<-logdensity.mnorm(Y[i,], mu[i,],Sigma.inv[,])
for (j in 1:2) {
mu[i,j]<-alpha[j]+species[sp[i],j]
resid[i,j]<-Y[i,j]-mu[i,j]
}
}
#Prior for intercept for Linf and K
for(j in 1:2) {
alpha[j]~dnorm(0,1.0E-6) #loop over Linf and K
}
# Random effect priors for species
sp.cor~dunif(-1,1)
for(j in 1:2) {
sp.tau[j]~dgamma(0.01,0.01)
sp.sd[j]<-1/sqrt(sp.tau[j])
sp.cov[j,j]<-1/sp.tau[j]
sp.mean[j]<-0
}
sp.cov[1,2]<-sp.cor*sp.sd[1]*sp.sd[2]
sp.cov[2,1]<-sp.cor*sp.sd[1]*sp.sd[2]
sp.prec[1: 2, 1: 2] <- inverse(sp.cov[, ])
for(i in 1:n.sp) {
species[i,1:2]~dmnorm(sp.mean[],sp.prec[,])
}
Sigma.inv[1:2, 1:2] ~ dwish(R[,], 2)
Sigma[1:2, 1:2]<- inverse(Sigma.inv[,])
# predicted values for each species
for(i in 1:n.sp) {
for(j in 1:2) {
mean.mu[i,j]<-alpha[j]+species[i,j]
exp.mean[i,j]<-exp(mean.mu[i,j])
```

```
}}
# population intercept without log
for(j in 1:2) {intercept[j]<-exp(alpha[j])}
}
```

JAGS code for Model E

```
model {
for (i in 1:N) {
Y[i, 1:2] ~ dmnorm(mu[i,], Sigma.inv[,])
LL[i]<-logdensity.mnorm(Y[i,], mu[i,],Sigma.inv[,])
for (j in 1:2) {
mu[i,j]<-alpha[j]+population[pop[i],j]
resid[i,j]<-Y[i,j]-mu[i,j]
}
}
#Prior for intercept for Linf and K
for(j in 1:2) {
alpha[j]~dnorm(0,1.0E-6) #loop over Linf and K
}
# Random effect priors for species and population
sp.cor~dunif(-1,1)
pop.cor~dunif(-1,1)
for(j in 1:2) {
sp.tau[j]~dgamma(0.01,0.01)
sp.sd[j]<-1/sqrt(sp.tau[j])
pop.tau[j]~dgamma(0.01,0.01) # assumes variance among pops same for all species
pop.sd[j]<-1/sqrt(pop.tau[j])
sp.cov[j,j]<-1/sp.tau[j]
pop.cov[j,j]<-1/pop.tau[j]
sp.mean[j]<-0
}
sp.cov[1,2]<-sp.cor*sp.sd[1]*sp.sd[2]
sp.cov[2,1]<-sp.cor*sp.sd[1]*sp.sd[2]
pop.cov[1,2]<-pop.cor*pop.sd[1]*pop.sd[2]
pop.cov[2,1]<-pop.cor*pop.sd[1]*pop.sd[2]
sp.prec[1: 2, 1: 2] <- inverse(sp.cov[, ])
pop.prec[1: 2, 1: 2] <- inverse(pop.cov[, ])
for(i in 1:n.sp) {
species[i,1:2]~dmnorm(sp.mean[],sp.prec[,])
}
```

```
for(i in 1:n.pop) {
population[i,1:2]~dmnorm(species[sp.pop[i],],pop.prec[,])
}
Sigma.inv[1:2, 1:2] ~ dwish(R[,], 2)
Sigma[1:2, 1:2]<- inverse(Sigma.inv[,])
# predicted values for each species
for(i in 1:n.sp) {
for(j in 1:2) {
mean.mu[i,j]<-alpha[j]+species[i,j]
exp.mean[i,j]<-exp(mean.mu[i,j])
}}
# predicted values for each population
for(i in 1:n.pop) {
for(j in 1:2) {
mean.mupop[i,j]<-alpha[j]+population[i,j]
exp.meanpop[i,j]<-exp(mean.mupop[i,j])
}}
# population intercept without log
for(j in 1:2) {intercept[j]<-exp(alpha[j])}
}
```

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