Supporting information

Tables S1 – S11

Figures S1 – S15

Table S1. Loadings of four beak traits on principal components axes 1 and 2. Larger values of beak traits load positively on PC1. We therefore consider PC1 to be a measure of beak size. Beak length loads negatively on PC2 while beak width and depth load positively on PC2. We therefore consider PC2 to be a measure of beak shape. Loadings were identical for resident/breeding and resident/non-breeding datasets.

Trait	PC1	PC2
Log beak length total culmen	0.45	-0.49
Log beak length from nares	0.51	-0.55
Log beak width	0.48	0.46
Log beak depth	0.56	0.50

Table S2. Models that included intercepts (power function with an intercept and Brownian motion model with an intercept) were better fits than models forced through the origin (power function, Ornstein Uhlenbeck and Brownian motion models) for the resident/non-breeding dataset; results are similar for the resident/breeding dataset (Table 1).

response variable	model	Δ AIC
beak size	power function intercept	0
	Brownian motion intercept	-12.24
	power function	-21.67
	Ornstein Uhlenbeck	-40.26
	Brownian motion	-42.71
beak shape	power function intercept	0
	Brownian motion intercept	-4.20
	power function	-14.19
	Ornstein Uhlenbeck	-42.87
	Brownian motion	-70.95

Table S3. For the resident/breeding dataset, latitudinal zone is a predictor of beak shape evolution but not beak size evolution. *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + latzone (intercept)	0.42
	power intercept + latzone (intercept)	power intercept + latzone (intercept and slope)	0.67
	Brownian motion intercept	Brownian motion intercept + latzone (intercept)	0.33
	Brownian motion intercept + latzone (intercept)	Brownian motion intercept + latzone (intercept and slope)	0.33
	power	power + latzone	0.93
	Ornstein Uhlenbeck	Ornstein Uhlenbeck + latzone	0.46
	Brownian motion	Brownian motion + latzone	0.42
beak shape	power intercept	power intercept + latzone (intercept)	0.0022
	power intercept + latzone (intercept)	power intercept + latzone (intercept and slope)	0.029
	Brownian motion intercept	Brownian motion intercept + latzone (intercept)	0.0017
	Brownian motion intercept + latzone	Brownian motion intercept + latzone (intercept and slope)	0.79
	power	power + latzone	0.031
	Ornstein Uhlenbeck	Ornstein Uhlenbeck + latzone	0.0045
	Brownian motion	Brownian motion + latzone	0.00077

Table S4. For the resident/breeding dataset, range overlap (“patry”) is a predictor of beak shape evolution but not beak size evolution. *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + patry (intercept)	0.19
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.12
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.53
	power intercept + patry (intercept) + lat zone (intercept)	power intercept + patry (intercept) + lat zone (intercept and slope)	0.67
beak shape	power intercept	power intercept + patry (intercept)	0.0023
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.10
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.0075
	power intercept + patry (intercept) + lat zone (slope & intercept)	power intercept + patry (intercept) + lat zone (intercept intercept and slope)	0.020

Table S5. For the resident/breeding dataset, range overlap (“patry”) is a predictor of beak shape evolution but not beak size evolution when defining sister pairs as sympatric when they have any range overlap at all (> 0 % range overlap; 579 sympatric versus 562 allopatric sister pairs). *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + patry (intercept)	0.40
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.33
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.59
	power intercept + patry (intercept) + lat zone (intercept)	power intercept + patry (intercept) + lat zone (intercept and slope)	0.80
beak shape	power intercept	power intercept + patry (intercept)	0.012
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.23
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.0090
	power intercept + patry (intercept) + lat zone (slope & intercept)	power intercept + patry (intercept) + lat zone (intercept intercept and slope)	0.0028

Table S6. For the resident/breeding dataset, range overlap (“patry”) is a predictor of beak shape evolution but not beak size evolution when defining sister pairs as sympatric when they have range overlap of 50% or greater (254 sympatric versus 887 allopatric sister pairs). *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + patry (intercept)	0.096
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.54
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.57
	power intercept + patry (intercept) + lat zone (intercept)	power intercept + patry (intercept) + lat zone (intercept and slope)	0.74
beak shape	power intercept	power intercept + patry (intercept)	0.0065
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.18
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.0074
	power intercept + patry (intercept) + lat zone (slope & intercept)	power intercept + patry (intercept) + lat zone (intercept intercept and slope)	0.0032

Table S7. For the resident/non-breeding dataset, latitudinal zone is not a predictor of beak size or beak shape evolution. *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + latzone (intercept)	0.26
	power intercept + latzone (intercept)	power intercept + latzone (intercept and slope)	0.64
	Brownian motion intercept	Brownian motion intercept + latzone (intercept)	0.30
	Brownian motion intercept + latzone (intercept)	Brownian motion intercept + latzone (intercept and slope)	0.37
	power	power + latzone	0.11
	Ornstein Uhlenbeck	Ornstein Uhlenbeck + latzone	0.27
	Brownian motion	Brownian motion + latzone	0.36
beak shape	power intercept	power intercept + latzone (intercept)	0.88
	power intercept + latzone (intercept)	power intercept + latzone (intercept and slope)	0.52
	Brownian motion intercept	Brownian motion intercept + latzone (intercept)	0.85
	Brownian motion intercept + latzone	Brownian motion intercept + latzone (intercept and slope)	0.41
	power	power + latzone	0.47
	Ornstein Uhlenbeck	Ornstein Uhlenbeck + latzone	0.99
	Brownian motion	Brownian motion + latzone	0.70

Table S8. For the resident/non-breeding dataset, range overlap (“patry”) is a predictor of beak size and beak shape evolution. *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + patry (intercept)	0.11
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.013
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.21
	power intercept + patry (intercept) + lat zone (intercept)	power intercept + patry (intercept) + lat zone (intercept and slope)	0.60
beak shape	power intercept	power intercept + patry (intercept)	0.0078
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.69
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.96
	power intercept + patry (intercept) + lat zone (slope & intercept)	power intercept + patry (intercept) + lat zone (intercept intercept and slope)	0.80

Table S9. For the resident/non-breeding dataset, range overlap (“patry”) is a predictor of beak size and beak shape evolution when defining sister pairs as sympatric when they have any range overlap at all (> 0 % range overlap; 497 sympatric versus 652 allopatric sister pairs). *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + patry (intercept)	0.61
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.033
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.23
	power intercept + patry (intercept) + lat zone (intercept)	power intercept + patry (intercept) + lat zone (intercept and slope)	0.62

response variable	reduced model	full model	*p*-value
beak shape	power intercept	power intercept + patry (intercept)	0.041
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.12
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.95
	power intercept + patry (intercept) + lat zone (slope & intercept)	power intercept + patry (intercept) + lat zone (intercept intercept and slope)	0.82

Table S10. For the resident/non-breeding dataset, range overlap (“patry”) is a predictor of beak size evolution but not beak shape evolution when defining sister pairs as sympatric when they have range overlap of 50% or greater (275 sympatric versus 874 allopatric sister pairs). *P*-values are from *F* tests comparing model fit between full and reduced models.

response variable	reduced model	full model	*p*-value
beak size	power intercept	power intercept + patry (intercept)	0.020
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.019
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.18
	power intercept + patry (intercept) + lat zone (intercept)	power intercept + patry (intercept) + lat zone (intercept and slope)	0.56
beak shape	power intercept	power intercept + patry (intercept)	0.11
	power intercept + patry (intercept)	power intercept + patry (intercept and slope)	0.96
	power intercept + patry (intercept)	power intercept + patry (intercept) + lat zone (intercept)	0.99
	power intercept + patry (intercept) + lat zone (slope & intercept)	power intercept + patry (intercept) + lat zone (intercept intercept and slope)	0.81

Table S11. Studies included in meta-analysis of evolutionary rates in tropics versus temperate zone, with information on rate type, sample size, ratio of evolutionary rates in temperate zone versus tropics, and notes on calculating ratios.

Citation	Rate type	Sample size and taxa	Ratio	Notes
(Bromham & Cardillo 2003)	molecular evolution	45 lineage pairs of birds	0.90	I used branch lengths for both cyt b (N = 33; 15 longer in tropics) and ND2 (N = 22; 14 longer in tropics).
(Wright *et al.* 2006)	molecular evolution	45 lineage pairs of plants	0.48	
(Gillman *et al.* 2009)	molecular evolution	130 lineage pairs of mammals	0.68	
(Wright *et al.* 2010)	molecular evolution	94 lineage pairs of amphibians	0.85	
(Wright *et al.* 2011)	molecular evolution	68 lineage pairs of fishes	0.62	
(Gillman *et al.* 2012)	molecular evolution	30 lineage pairs of birds	0.74	
(Lourenço *et al.* 2013)	molecular evolution	224 species of turtles	0.86	I estimated the rate at latitude 0 as -4.66 and the substitution rate at latitude 40 as -5.40 using WebPlotDigitizer.
(Rolland *et al.* 2016)	molecular evolution	141 sister pairs of squamates	0.91	
(Orton *et al.* 2019)	molecular evolution	8037 lineage pairs from six animal phyla	0.94	
(Martin *et al.* 2010)	trait evolution (color)	78 sister pairs of birds	1.56	I downloaded data from Appendix S4 and fit a linear model to estimate slopes of color divergence as a function of genetic distance and latitudinal zone (tropical/temperate). The slope of color divergence in tropics was 0.32; the slope of color divergence in

				temperate zone was 0.50
(Weir & Wheatcroft 2011)	trait evolution (song)	116 sister pairs of birds	11	I took the average of reported ratios of trait evolution for syllable diversity and song length.
(Weir & Price 2019)	trait evolution (song)	109 sister pairs of birds	6	
(Lawson & Weir 2014)	trait evolution (climatic niche)	111 sister pairs of birds	5.74	I estimated evolutionary rates in the tropics (at the equator) and temperate zone (at latitude = 40) for PC1 (269 and 1069), PC2 (identical), and PC3 (0.42 and 5.14) using WebPlotDigitizer and took the average of these three ratios.
this study	trait evolution (beak)	1,141 sister pairs of birds	1.03	I calculated estimated divergences in beak size and shape for tropics vs. temperate zone at evolutionary age = 5 million years from best-fit models. The estimated divergences for the breeding season analysis are: beak shape: 0.063 in tropics, 0.076 in temperate zone; beak size: 0.060 in tropics, 0.064 in temperate zone. And for the non-breeding season analysis are: beak shape: 0.069 in tropics, 0.068 in temperate zone; beak size: 0.14 in temperate zone, 0.12 in tropics. I considered this study to be a single data point and hence took the ratio of each of the four comparisons above, then took the average of these four ratios.
(Weir & Schluter 2007)	speciation rate	309 sister pairs of birds and mammals	3.35	I estimated evolutionary rates in the tropics (at the equator) and temperate zone (at latitude = 40) for speciation rates (0.17 and 0.57) using WebPlotDigitizer.
(Rabosky *et al.* 2015)	speciation rate	2,571 species of birds	1.10	
(Rabosky *et al.* 2018)	speciation rate	31,526 species of ray-finned fishes	2.22	I used estimates reported for BAMM (nearly identical to estimates using the DR statistic)
(Igea & Tanentzap 2020)	speciation rate	60,000 species	1.12	

of angiosperms;

References for Table S11

Bromham, L. & Cardillo, M. (2003). Testing the link between the latitudinal gradient in species richness and rates of molecular evolution. *J. Evol. Biol.*, 16, 200–207.

Gillman, L.N., Keeling, D.J., Ross, H.A. & Wright, S.D. (2009). Latitude, elevation and the tempo of molecular evolution in mammals. *Proc. R. Soc. B Biol. Sci.*, 276, 3353–3359.

Gillman, L.N., Mccowan, L.S.C. & Wright, S.D. (2012). The tempo of genetic evolution in birds: Body mass and climate effects. *J. Biogeogr.*, 39, 1567–1572.

Igea, J. & Tanentzap, A.J. (2020). Angiosperm speciation cools down in the tropics. *Ecol. Lett.*, 23, 692–700.

Lawson, A.M. & Weir, J.T. (2014). Latitudinal gradients in climatic-niche evolution accelerate trait evolution at high latitudes. *Ecol. Lett.*, 17, 1427–1436.

Lourenço, J.M., Glémin, S., Chiari, Y. & Galtier, N. (2013). The determinants of the molecular substitution process in turtles. *J. Evol. Biol.*, 26, 38–50.

Martin, P.R., Montgomerie, R. & Lougheed, S.C. (2010). Rapid sympatry explains greater color pattern divergence in high latitude birds. *Evolution*, 64, 336–347.

Orton, M.G., May, J.A., Ly, W., Lee, D.J. & Adamowicz, S.J. (2019). Is molecular evolution faster in the tropics? *Heredity*, 122, 513–524.

Rabosky, D.L., Chang, J., Title, P.O., Cowman, P.F., Sallan, L., Friedman, M., *et al.* (2018). An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, 559, 392–395.

Rabosky, D.L., Title, P.O. & Huang, H. (2015). Minimal effects of latitude on present-day speciation rates in New World birds. *Proc. R. Soc. B Biol. Sci.*, 282.

Rolland, J., Loiseau, O., Romiguier, J. & Salamin, N. (2016). Molecular evolutionary rates are not correlated with temperature and latitude in Squamata: An exception to the metabolic theory of ecology? *BMC Evol. Biol.*, 16, 1–6.

Weir, J.T. & Price, T.D. (2019). Song playbacks demonstrate slower evolution of song discrimination in birds from Amazonia than from temperate North America. *PLoS Biol.*, 17, e3000478.

Weir, J.T. & Schluter, D. (2007). The latitudinal gradient in recent speciation and extinction rates of birds and mammals. *Science*, 315, 1574.

Weir, J.T. & Wheatcroft, D. (2011). A latitudinal gradient in rates of evolution of avian syllable diversity and song length. *Proc. R. Soc. B-Biological Sci.*, 278, 1713–1720.

Wright, S., Keeling, J. & Gillman, L. (2006). The road from Santa Rosalia: A faster tempo of evolution in tropical climates. *Proc. Natl. Acad. Sci. U. S. A.*, 103, 7718–7722.

Wright, S.D., Gillman, L.N., Ross, H.A. & Keeling, D.J. (2010). Energy and the tempo of evolution in amphibians. *Glob. Ecol. Biogeogr.*, 19, 733–740.

Wright, S.D., Ross, H.A., Keeling, D.J., McBride, P. & Gillman, L.N. (2011). Thermal energy and the rate of genetic evolution in marine fishes. *Evol. Ecol.*, 25, 525–530.

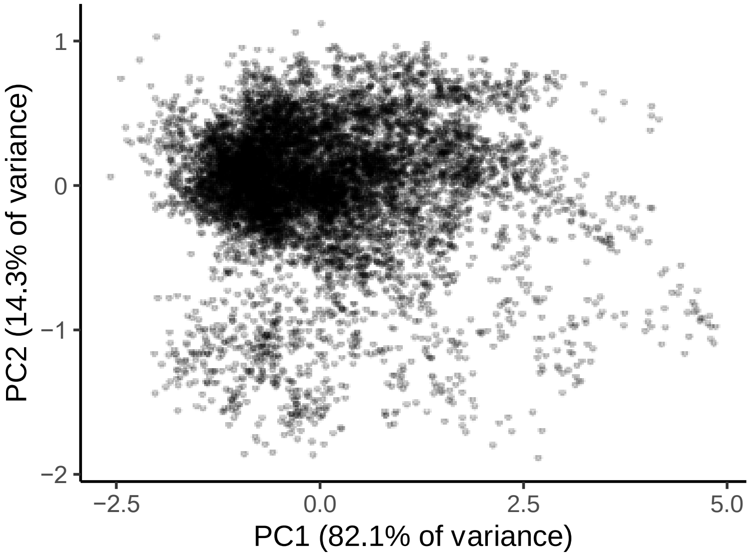

Figure S1. The two-dimensional beak morphospace analyzed in this study. Pictured is the beak morphospace for the resident/breeding dataset; the beak morphospace for the resident/non-breeding dataset was nearly identical. Dots represent the position in morphospace of 9,966 individuals from the 1,141 sister pairs (2,282 total species) included in this analysis. PC scores for each species are calculated from raw averages for 4 beak traits generated from measurements of multiple specimens (mean of 4.4 specimens measured per species).

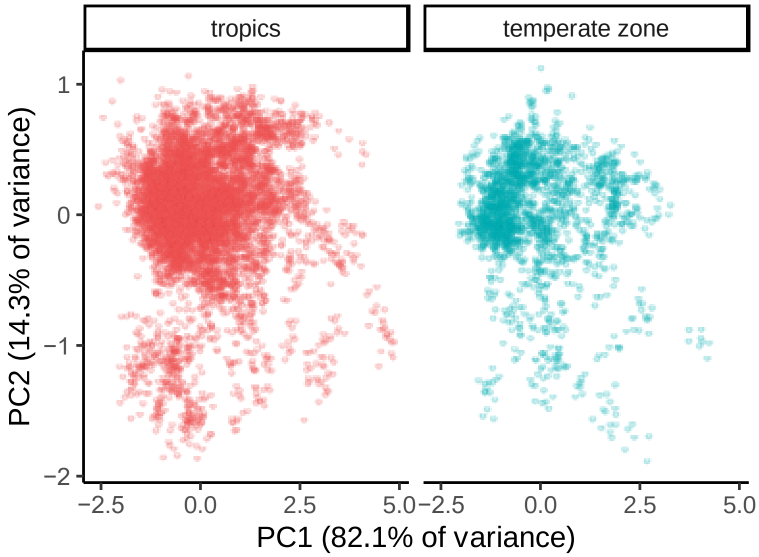

Figure S2. The two-dimensional beak morphospace analyzed in this study, shown separately for tropical and temperate species. Pictured is the beak morphospace for the resident/breeding dataset; the beak morphospace for the resident/non-breeding dataset was nearly identical. Dots represent the position in morphospace of tropical (N = 7872 individuals measured for 800 sister pairs [1600 species]) and temperate (N = 2,282 individuals for 341 sister pairs [682 species]) species included in this analysis. PC scores for each species are calculated from raw averages for 4 beak traits generated from measurements of multiple specimens (mean of 4.4 specimens measured per species).

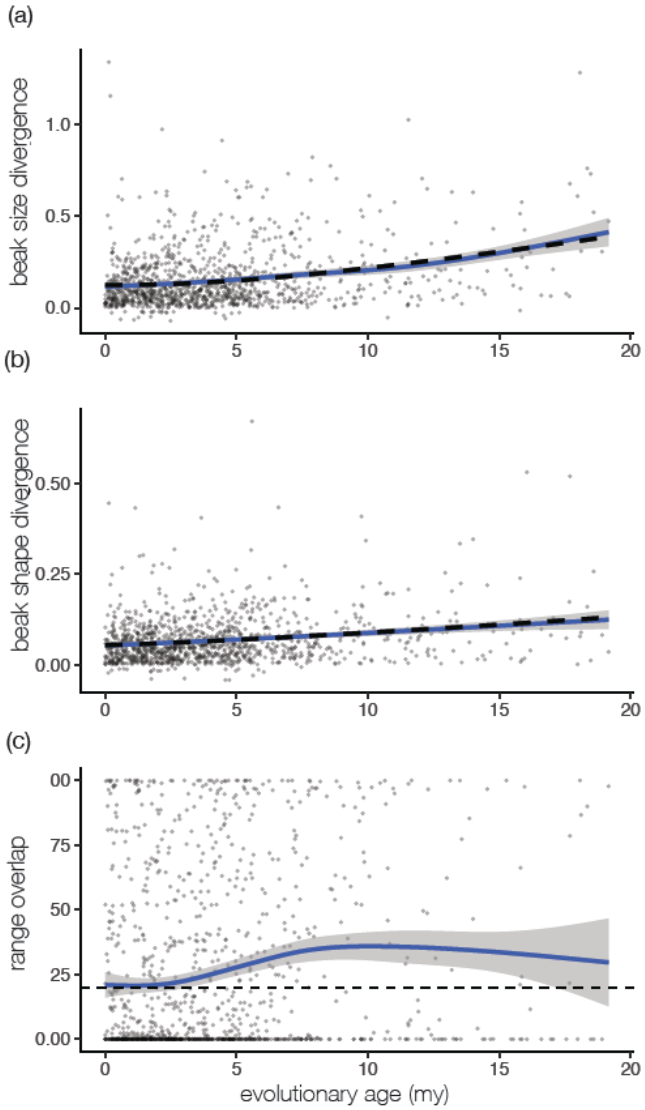

Figure S3. Patterns of divergence in beak size (a), beak shape (b) and range overlap (c) for the 1149 sister pairs of birds in the resident/non-breeding dataset. Raw data are plotted. Loess regressions are shown in blue; predictions from the best-fit models (power functions with intercepts) are shown as dashed black lines. Beak size and shape divergence values are corrected for bias arising from sampling error. Range overlap is the proportion of the smaller-ranged species that falls within the range of the larger-ranged species. Sister pairs were coded as sympatric if they had range overlaps > 0.20 (the dashed line). Results are similar for the resident/breeding dataset (see Figure 1).

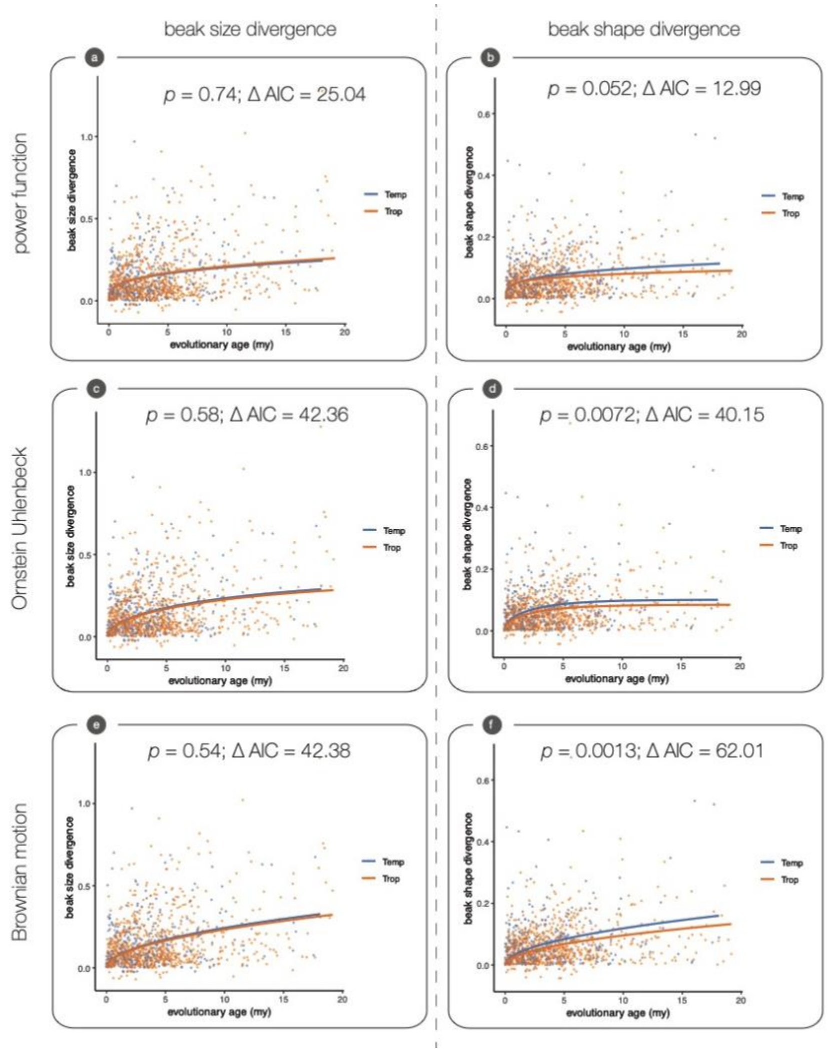

Figure S4. For the resident/breeding dataset, rates of beak size evolution are similar between tropics and temperate zone (left panels), but beak shape evolution is faster in the temperate zone (right panels). Model predictions are plotted for power functions forced through the origin (a, b), Ornstein Uhlenbeck models (c, d), and Brownian motion models (e, f). *P*-values are from *F* tests testing whether the inclusion of a tropical/temperate term improved model fit. Δ AIC values compare different model fits for beak size and beak shape relative to the best-fit model, a power function with an intercept (see Figure 2 in main text).

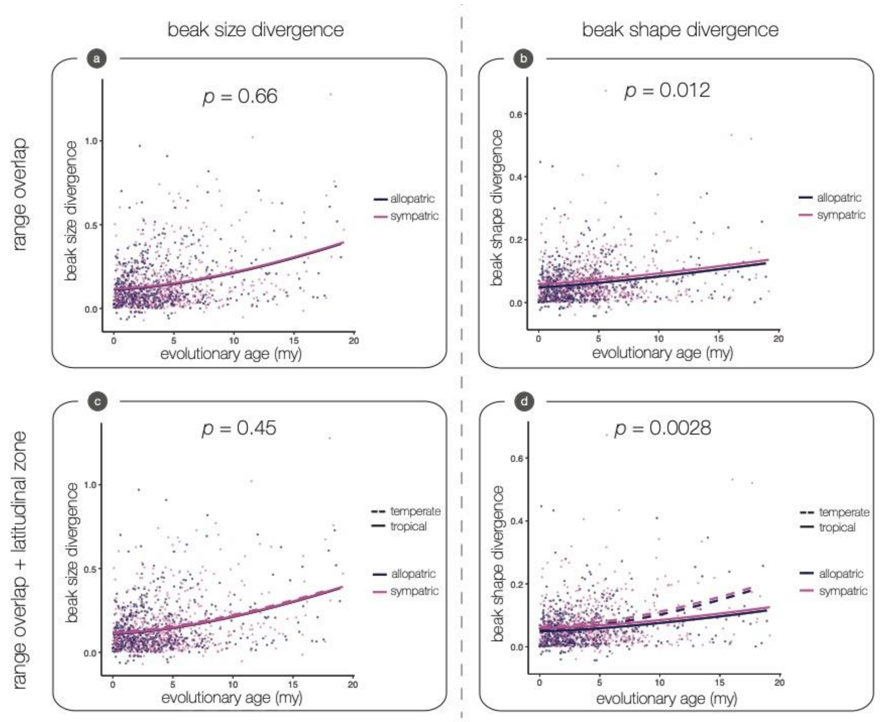

Figure S5. For the resident/breeding dataset, rates of beak size evolution are similar between allopatric (n = 562) and sympatric (n = 579) sister pairs (left panels), but beak shape evolution is faster in sympatry (right panels), when defining sister pairs as sympatric when they have any range overlap at all (> 0 % range overlap). *P*-values are from *F* tests testing whether the inclusion of an allopatric/sympatric term to a power function with an intercept improved model fit (a, b), or whether the inclusion of a tropical/temperate term to a power function with an intercept and an allopatric/sympatric term improved model fit (c, d). The *p*-value for beak shape (d) is from a *F* test comparing a reduced model with an allopatric/sympatric term to a full model with terms allowing both the intercept and slope to differ between tropics and temperate zone. Beak shape evolution is faster in the temperate zone in both allopatry and sympatry compared to the tropics.

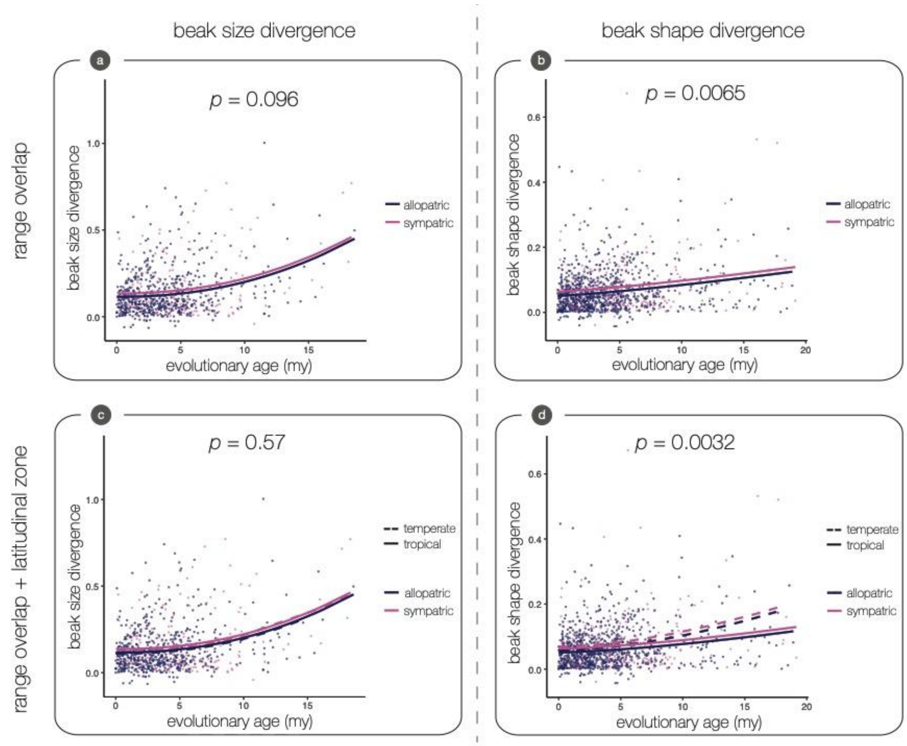

Figure S6. For the resident/breeding dataset, rates of beak size evolution are similar between allopatric (n = 887) and sympatric (n = 254) sister pairs (left panels), but beak shape evolution is faster in sympatry (right panels), when defining sister pairs as sympatric when they have 50% or greater range overlap. *P*-values are from *F* tests testing whether the inclusion of an allopatric/sympatric term to a power function with an intercept improved model fit (a, b), or whether the inclusion of a tropical/temperate term to a power function with an intercept and an allopatric/sympatric term improved model fit (c, d). The *p*-value for beak shape (d) is from a *F* test comparing a reduced model with an allopatric/sympatric term to a full model with terms allowing both the intercept and slope to differ between tropics and temperate zone. Beak shape evolution is faster in the temperate zone in both allopatry and sympatry compared to the tropics.\

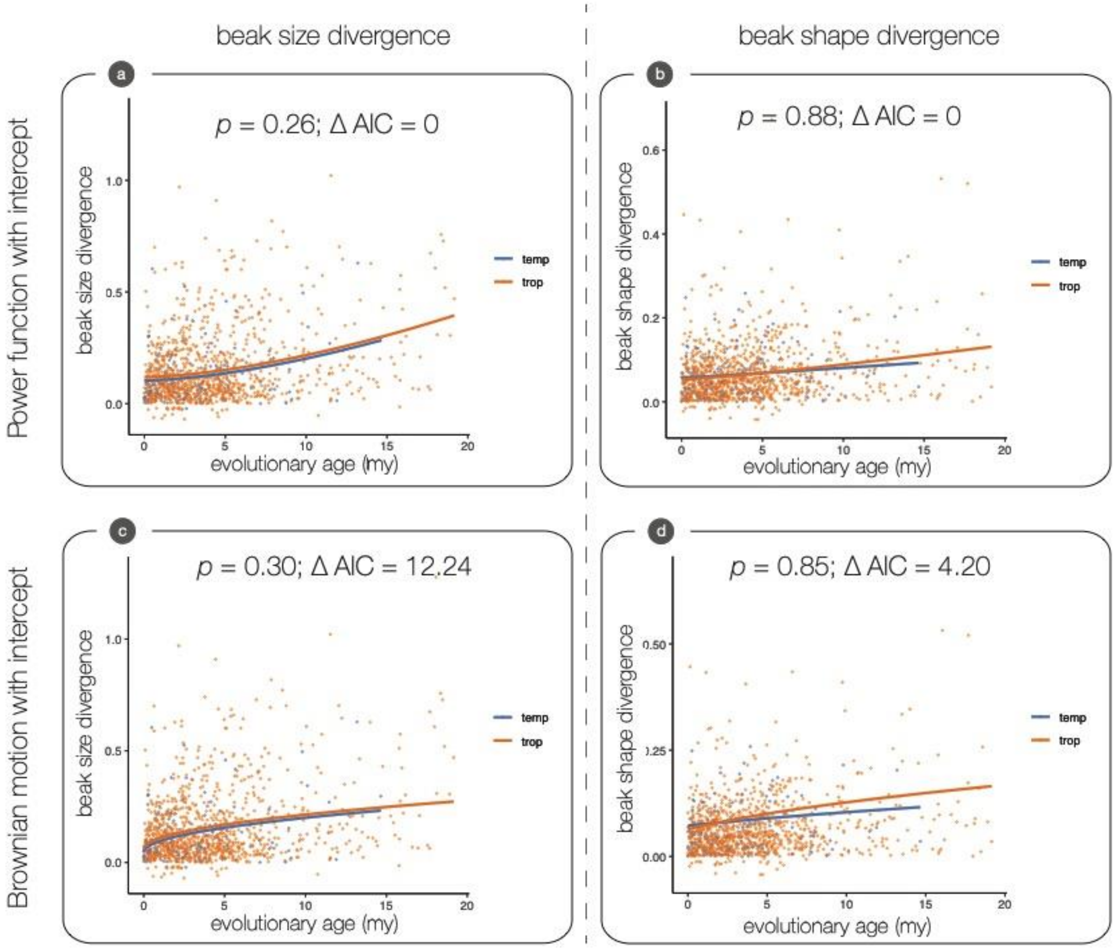

Figure S7. For the resident/non-breeding dataset, rates of beak size evolution are similar between tropics and temperate zone (left panels), but beak shape evolution is faster in the temperate zone (right panels). Model predictions are plotted for the two best models: power functions with an intercept (a, b) and Brownian motion models with an intercept (c, d). *P*-values are from *F* tests testing whether the inclusion of a tropical/temperate term improved model fit. Δ AIC values compare different model fits separately for beak size and beak shape. For results from the resident/breeding dataset see Figure 2.

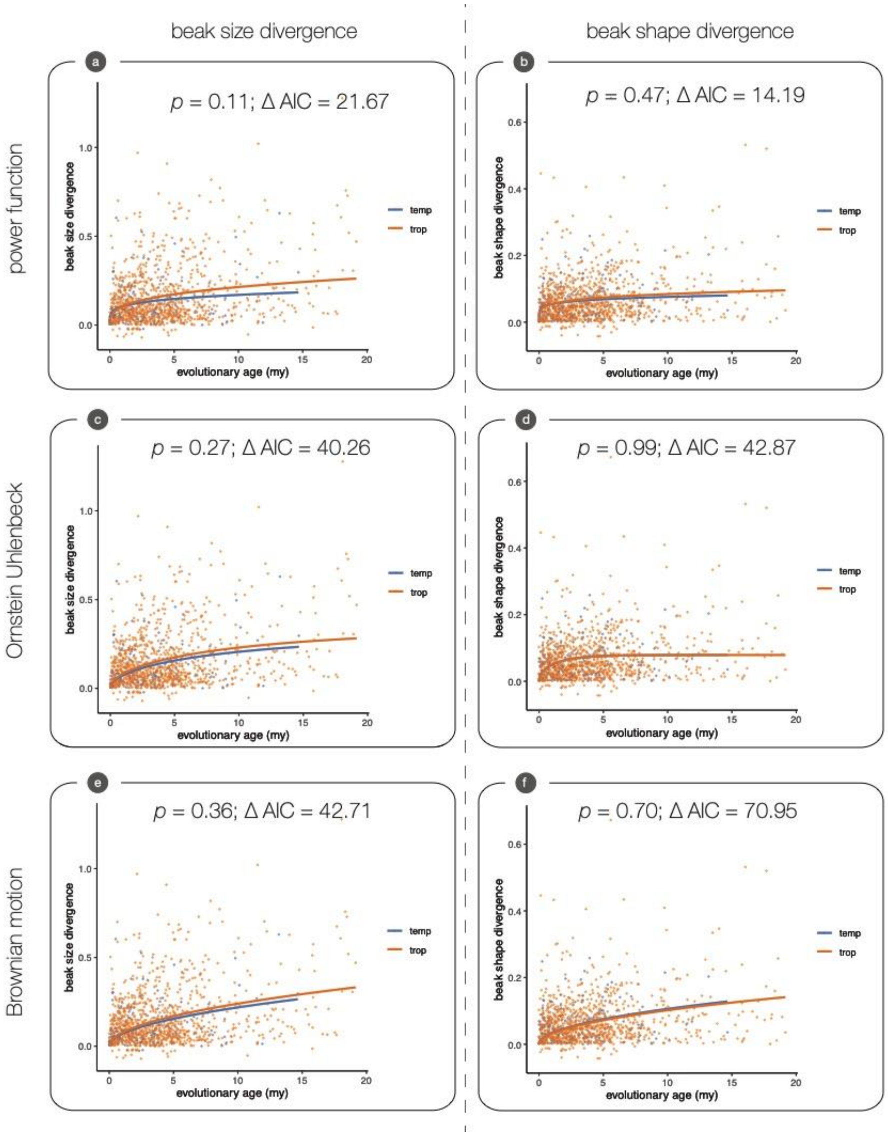

Figure S8. For the resident/non-breeding dataset, rates of beak size and beak shape evolution are similar between tropics and temperate zone (left panels). Model predictions are plotted for power functions forced through the origin (a, b), Ornstein Uhlenbeck models (c, d), and Brownian motion models (e, f). *P*-values are from *F* tests testing whether the inclusion of a tropical/temperate term improved model fit. Δ AIC values compare different model fits for beak size and beak shape relative to the best-fit model, a power function with an intercept.

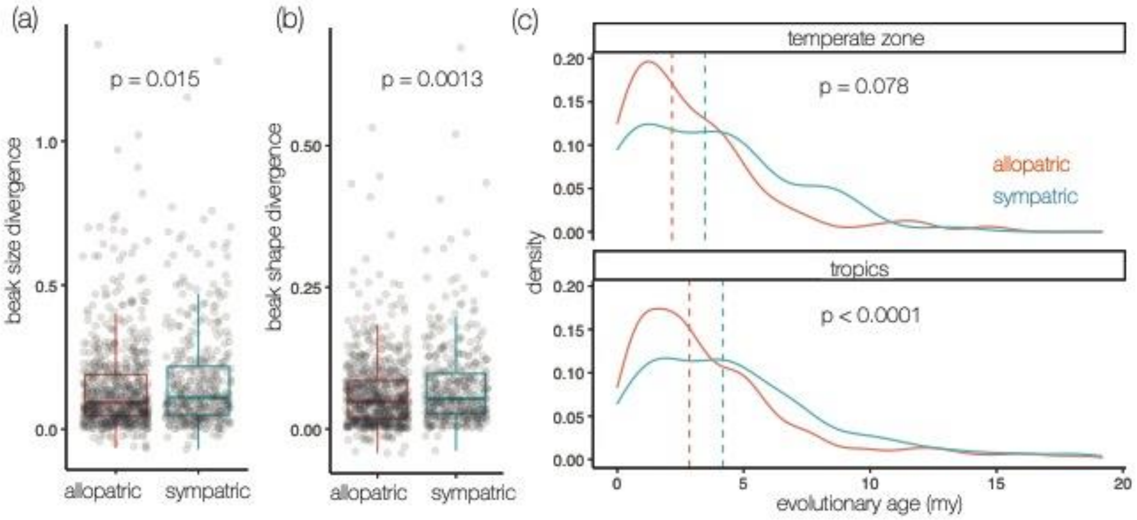

Figure S9. For resident/non-breeding dataset, sympatric sister pairs have greater beak size divergence (a), beak shape divergence (b), and are older (c) than allopatric sister pairs in the non-breeding season analysis. *P*-values are from t-tests of trait divergence or ages between allopatric and sympatric sister pairs; separate t-tests for age for temperate and tropical zones in panel (c). Median values of ages for temperate and tropical sister pairs are plotted as vertical dashed lines. Results are similar for the resident/breeding dataset (see Figure 4).

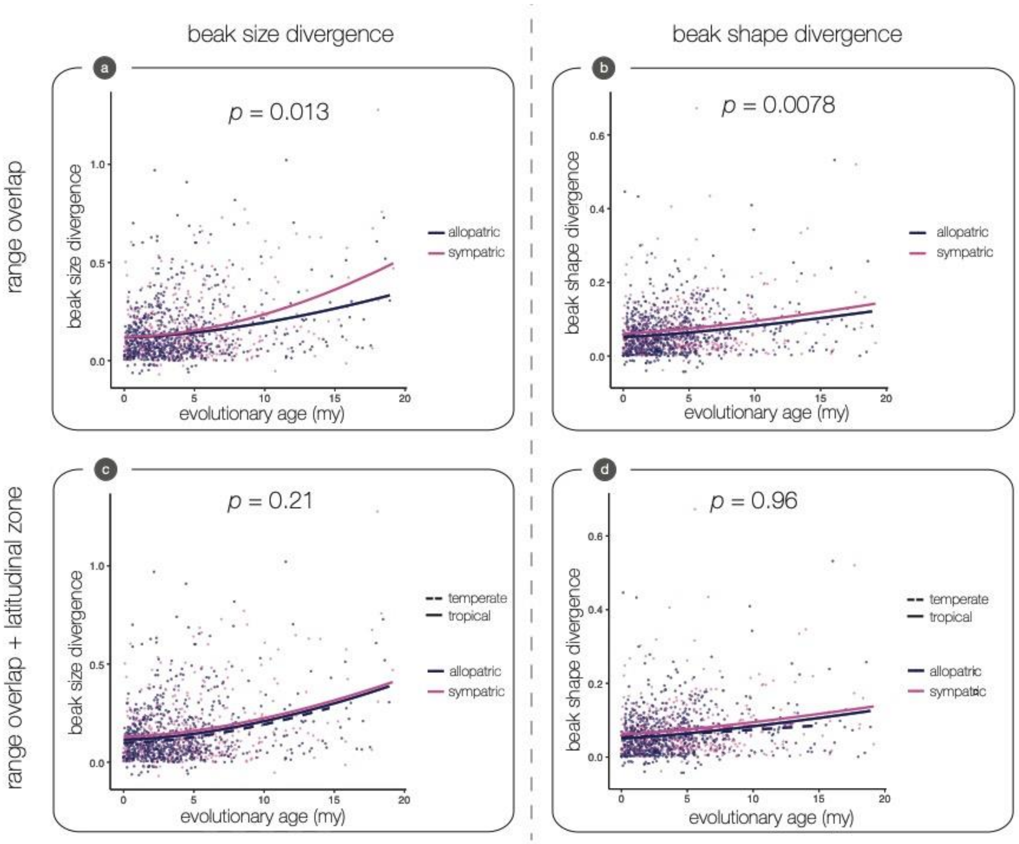

Figure S10. For the resident/non-breeding dataset, rates of beak size and beak shape evolution are faster in sympatric (n = 422) than allopatric (n = 727) sister pairs. *P*-values are from *F* tests testing whether the inclusion of an allopatric/sympatric term to a power function with an intercept improved model fit (a, b), or whether the inclusion of a tropical/temperate term to a power function with an intercept and an allopatric/sympatric term improved model fit (c, d). The *p*-value for beak shape (d) is from a *F* test comparing a reduced model with an allopatric/sympatric term to a full model with terms allowing both the intercept and slope to differ between tropics and temperate zone. Beak shape evolution is faster in the temperate zone in both allopatry and sympatry compared to the tropics. Results for beak shape evolution are similar for the resident/breeding dataset, with the exception that beak size evolution is not faster in sympatric sister-pairs in the resident/breeding dataset (see Figure 4)

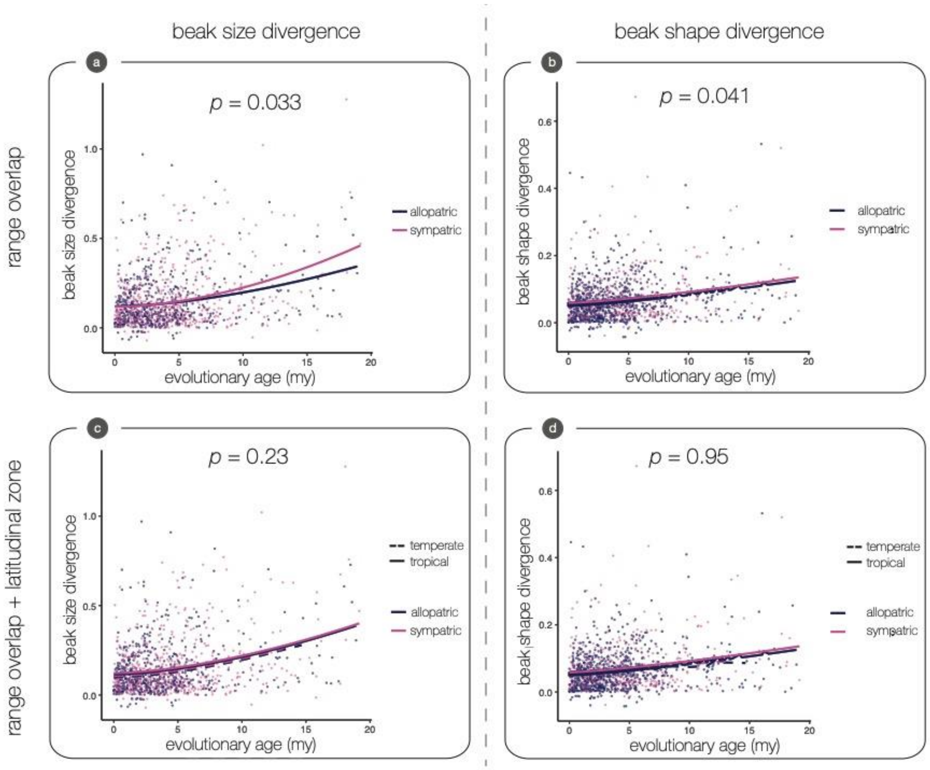

Figure S11. For the resident/non-breeding dataset, rates of beak size and beak shape evolution are faster in sympatric (n = 497) than allopatric (n = 652) sister pairs when defining sister pairs as sympatric when they have any range overlap at all (> 0 % range overlap). *P*-values are from *F* tests testing whether the inclusion of an allopatric/sympatric term to a power function with an intercept improved model fit (a, b), or whether the inclusion of a tropical/temperate term to a power function with an intercept and an allopatric/sympatric term improved model fit (c, d). The *p*-value for beak shape (d) is from a *F* test comparing a reduced model with an allopatric/sympatric term to a full model with terms allowing both the intercept and slope to differ between tropics and temperate zone. Beak size and shape evolution are faster in sympatry in both the tropics and the temperate zone.

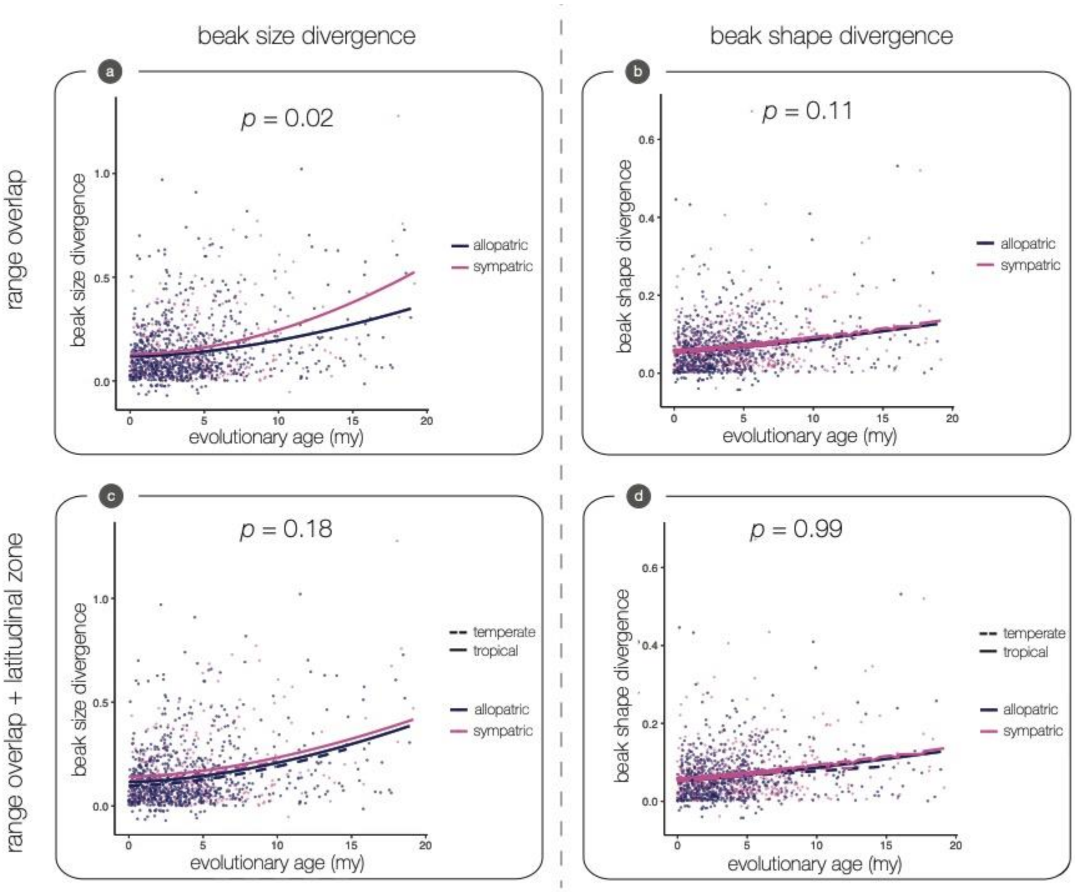

Figure S12. For the resident/non-breeding dataset, rates of beak size evolution are faster in sympatric (n = 275) than allopatric (n = 874) sister pairs (left panels), but beak shape evolution is similar between sympatric and allopatric sister pairs (right panels), when defining sister pairs as sympatric when they have 50% or greater range overlap. *P*-values are from *F* tests testing whether the inclusion of an allopatric/sympatric term to a power function with an intercept improved model fit (a, b), or whether the inclusion of a tropical/temperate term to a power function with an intercept and an allopatric/sympatric term improved model fit (c, d). The *p*-value for beak shape (d) is from a *F* test comparing a reduced model with an allopatric/sympatric term to a full model with terms allowing both the intercept and slope to differ between tropics and temperate zone. Beak size evolution is faster in sympatry in both the tropics and the temperate zone.