**Supplementary Material**

**Details on data collection**

For each species we collected information on the type of nest built (the structure that was constructed) and whether this construction was placed inside a cavity or not. If the description mentioned that the species was a cavity nester but did not specify the type of nest inside, then we did not include that species in our analyses. We considered domed nests as those nests that were described as having a roof, as being globular or a ball with a side entrance. When descriptions were not completely clear we looked for photographs online to support our decisions. We did not include species where descriptions were uncertain or ambiguous. Some species were difficult to classify, and additional rationale is included in the ‘additional dataset’ in the Dryad repository. Species were considered open nesters if the nest was an open cup, a platform or a mat or pad of leaves or other materials. Essentially, if the nest did not have a roof, then it was considered an open nest. Some species were initially classified as building ‘deep cups’ if the description specifically mentioned ‘pouch’ or ‘deep purse’, and other species were classified as building ‘both’ types of nests if it was mentioned that they sometimes build cups or domes. Species were classified as cavity nesters if the location of the nest was described as a hollow, cavity, or crevice. All nests were scored by DM and then revised by IM. In our dataset 81.5% of the species where non-migratory, and analyses remain unchanged when including migratory status as a covariable. We obtained information for 3175 species, but there was no data on mid-latitude for 15 species, so sample sizes in models vary depending on whether latitude was included as covariable or not.

Data on time spent building nests was collected from the Handbook of Birds of the World. This data was available for a very small percentage of species (8.7%). We attempted to collect more detailed data such as the number of trips per hour, but this data was not available for most species. Data on time spent nest building was given usually as a range of days (e.g., from 8 to 14 days). In these instances, we took the mid-point of the range given (11 days in the example above). For a few species there was information on average number of days taken to build a nest, and we took this number. We also collected information on who builds the nest (the male, the female, or the couple).

*Nest classifications used and rationale*

We employed three types of nest classifications for PGLS analyses (tip-level analyses). The most specific type of classification included six categories: open (n=1656), domed (n=790), deep cup (n=187), both (n=60), domed in cavity (n=81) and open nest in cavity (n=401). We performed analyses on this category but given that we found no differences between deep cups, both and open nests categories, and some categories had few very species, we merged some of these categories into a simple classification and use this to present main results: open (n=1903), domed (n=790) and cavity (n=482). This last category combines nests of species that place nests in cavities (regardless of whether there is a cup or a dome inside) but we decided to use this classification because the effect of placing a nest inside a cavity could be important, and there were not enough nests in the ‘domed in cavity category’ to split the dataset.
We also created a third category based exclusively on the type of structure constructed, domed (n=871) or open nest (n=2304), this means that we split the cavity category based on what is constructed inside the cavity, a domed or an open nest. This category was specifically designed for the diversification analyses, since we were interested in the evolutionary history of a single trait, which is the construction being built (not where it is placed). This classification was also optimal because it allowed a smaller number of states in the analyses, which facilitates convergence.

Details on elevation analyses

Although our temperature and precipitation PCs already considered altitudinal variation within the range of each species, we thought it would be interesting to test whether different nest types were also related to variation in elevational ranges. To test this, we used previously published information from Quintero and Jetz (2018). This dataset provided mountain system specific elevational ranges per species, for 2832 out of the 3174 species in our dataset (see more details on Quintero and Jetz, 2018). We used the function MCMCglmm in the package MCMCglmm to build a model with elevational range (in m) as response variable, and nest type, body mass (log) and latitude (abs) as predictors. We used mountain system ID as a random factor, to consider that different elevational ranges for each species could be found across mountain systems. We also used species ID and a phylogenetic correlation matrix as random factors, since we had multiple measures within species, and we wanted to control for phylogenetic non-independence.

Details on macroevolutionary analyses

RevBayes analysis

The state-dependent speciation and extinction models implemented in RevBayes are a birth-death process when diversification rates depend on the state of an evolving character. They are based on the original model by Maddison et al. (2007) for a binary character (BiSSE). They provide information on extinction and speciation rates, ancestral states, and transition rates between states. We followed RevBayes (Höhna et al. 2016) code available here (https://revbayes.github.io/tutorials/sse/bisse.html) for SSE (state-dependent speciation and extinction) models. For the MuSSE (Multistate SSE) analysis we specified four states (domed/narrow range, domed/wide range, open/narrow range, open/wide range), with a number of generations of 2500, a tuning interval of 100 and performed two simultaneous runs. We also constrained values in the transition matrix, so that transition rates between diagonal states were set to zero. Results from the two independent runs were combined an analysed using the software Tracer (Rambaut et al. 2018), we used a burnin of 10% and effective sample sizes
were all above 100 and most well above 200. For the HiSSE (Hidden state SSE) analysis we used 4 observed states, two hidden states (A and B) and the same parameters as in the MuSSE analysis. For HiSSE, one chain did not converge, and the effective sample size was below 10 for most parameters, so we only used values from the second run, which had effective sample sizes above 100.

The use of phylogenetic trees (such as those from birdtree.org) that incorporate all species allows us to include tip state information that would be ignored otherwise. However, because non-genetically represented species will vary substantially in their placement across the tree, transition rate estimates could be affected and, as a whole, overestimated (Rabosky 2015). This is particularly problematic if there is an association between being non-genetically represented and having a particular state, for the rates of transition from/to this state would then be biased. In our analyses, 54% of species with domed nests and 81% with open nests had available genetic information. To test whether these potential source of bias could affect our results, we conducted additional analyses in which we only consider species genetically represented in the tree and specify empirical sampling fractions for each state following FitzJohn et al. (2009). The sampling fraction for each state was determined as the number of species with state i that had genetic data over all species with state i. These analyses allow us to test the robustness of our results while accounting for biased sampling in the phylogenetic tree and the state.

For the dataset with only genetic data, we used as sampling parameter a vector Rho that contained the proportion of species sampled per state. We also increased the number of iterations to 6000 due to lack of convergence in chains and low sample size. We combined two chains, but the second chain converged with the other chain only after 4500 iterations, so we used the last 1500 iterations to combine with the other chain (which had 10% burnin). We highlight that this specific implementation (namely, the inclusion of a vector of sampling proportions per state) was customised by Sebastian Höhna for this particular study and is not implemented in the current RevBayes version.

**Castor analysis**

To complement the analysis on RevBayes, and to assess the effect of phylogenetic uncertainty on estimates, we also used the fit_musse function implemented in the R package Castor v1.5.5 (Louca & Doebeli 2018). This function takes as input a phylogenetic tree and a list of tip proxy states (in our case 1 to 4 plus NAs), and fits the parameters of a MuSSE model to the data using maximum-likelihood. Such likelihood is calculated using a variant of a postorder-traversal algorithm, and this function is ideal for large phylogenetic trees and a small number of states (Louca & Pennell 2020), which is why we implemented it on 100 trees, besides the MCC tree. We used a number of trials for fitting the model of 5 (10 for the MCC tree), a number of bootstrap samplings to perform of 5 (10 for the MCC tree), to estimate standard errors, and a maximum model runtime of 5 seconds to evaluate the likelihood of a model. We also specified a transition matrix that would not allow immediate transitions between diagonal states, like we did in the RevBayes analysis.

**BayesTraits analysis**

To explicitly test whether the rates of transition from small to large niches were dependent on the type of nest, we used BayesTraits V3.0.1 (Pagel & Meade 2006) and the RJ MCMC mode implemented in the R package btw developed by Randi Griffin. The traits used were the same in the other diversification analyses: nest type (open/domed) and niche width (wide/narrow), where niche width is correlated to both range size and latitude. We used as input a block of 1000 trees and compared a model of independent trait evolution with a model where two traits evolve in a correlated fashion, and
transition rates in one trait depend on the rates of the second trait. We performed three independent runs of comparisons, using a different number of iterations. Details on iteration number, burnin, stones and stones per iteration are given in table S12. To compare the models, we calculated log bayes factors, using the bayes factor description given in the BayesTraits manual:

\[
\text{Log Bayes Factor} = 2(\log \text{marginal likelihood model 1} – \log \text{marginal likelihood model 2}).
\]

The marginal likelihood for each model corresponds to that of the last iteration. Values above 10 in support of the dependent model suggest very strong evidence of correlated evolution (Pagel & Meade 2006). All analyses gave quantitatively identical results strongly supporting the dependent model of evolution (Table S12). The analysis on the MCC tree gave even stronger results.

Extended discussion

Our analyses revealed interesting patterns that were beyond the scope of the original question, and we discuss these here briefly, in the hope that they can inspire future studies.

Relationship between nest type and body size

One pattern in our dataset (albeit not significant), and which has been reported in other studies, is the fact that species with domed nests tend to have a smaller body size (Martin et al. 2017). This could be explained by the fact that building a domed nest might be even more costly to build for species that are larger. It has been found that the size of the nest is correlated with the size of the builder, and that domed nests are relatively bigger than open nests (Mouton & Martin 2019). Interestingly, it has been shown recently that species that are smaller tend to have higher predation rates (Unzeta et al. 2020), which could suggest selection for domed nests in smaller species, if domed nests offer protection from predation. However, recent studies have also questioned the role of predation in driving nest architecture, since there is no evidence suggesting that domed nests are better at protecting nests from predation (Martin et al. 2017; Mouton & Martin 2019). Future experiments could explore whether there is a factor limiting the prevalence of domed nests in larger species.

Males building nests take longer to build

Our analysis on nest building time revealed that, overall, species that build domed nests take longer to construct their nest compared to species that build open nests. Two interesting patterns also emerged from this analysis: nests constructed by males tend to take less time to be built, and when males build there are no differences in the time taken to build open and domed nests. We think the reason for both patterns is related to the role of nest building in sexual selection. In many weaver species males build and display nests to females, which subsequently lay their eggs in these nests (Quader 2005). In several species, males that build a larger number of nests, have higher reproductive success (Savalli 1994; Friedl & Klump 2000). This could select for nests that are built in a short time. Our sample size for this category (males building nests) was relatively low, but future studies could explore whether sexual selection favours nests that can be built more rapidly. In general, we know extremely little about the energetic costs of building nests.

Species with specific nest types could have even higher ecological success

The analysis on specific nest categories offered interesting patterns, that we did not discuss in the main text because they were not strong enough due to the small sample size in some of the categories. For instance, in some models, we found that species that build both types of nests (open and domed) had slightly wider temperature niches than species with open nests. This is an interesting pattern, and could suggest that having certain flexibility in the type of nest that a species builds could be related to their ecological success. Unfortunately, species that build both nest types are quite rare (1.8%), but
studying this particular type of species could offer insights into the drivers and consequences of building different nest types.

In addition, our analysis showed that species that build domed nests inside cavities have smaller ranges and narrower niches compared to species that build open nests inside cavities. This mirrors our main findings for species that do not use cavities, and supports the idea that building a domed structure can be related with different measures of ecological success.
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Table S1. Loadings of environmental PCs.

Table S2 to S5. PGLS results using different response variables and alternative nest type classifications.

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Table S9. Ancestral reconstruction and speciation and extinction rates.

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Table S11. PGLS of niche width when controlling for the link between niche width and latitude.

Table S12. BayesTraits results.

Table S13. Analysis of link between nest type and urban environments, when considering range size.
**Table S1.** Loadings and proportion of variance explained by Principal Component Analysis on 7 temperature (top) and 7 precipitation (bottom) variables (14 Worldclim and CHELSEA variables), for whole (top) and breeding (bottom) range.

|                              | PC1        | PC2        |
|------------------------------|------------|------------|
| Annual Mean Temperature      | 0.39781638 | -0.1035411 |
| Max Temperature of Warmest Month | 0.37505071 | 0.42206511 |
| Min Temperature of Coldest Month | 0.37927389 | -0.4247252 |
| Mean Temperature of Wettest Quarter | 0.35001639 | 0.50696388 |
| Mean Temperature of Driest Quarter | 0.37858277 | -0.3315879 |
| Mean Temperature of Warmest Quarter | 0.37772064 | 0.35649025 |
| Mean Temperature of Coldest Quarter | 0.38564379 | -0.3697304 |
| **Proportion of variance**   | **88.17**  | **7.81**   |
| Annual Precipitation         | -0.4688086 | -0.0037371 |
| Precipitation of Wettest Month | -0.3841517 | 0.41625139 |
| Precipitation of Driest Month | -0.3265992 | -0.5267115 |
| Precipitation of Wettest Quarter | -0.4009754 | 0.39720579 |
| Precipitation of Driest Quarter | -0.3384351 | -0.5134339 |
| Precipitation of Warmest Quarter | -0.3556069 | 0.28877697 |
| Precipitation of Coldest Quarter | -0.3524245 | -0.2108404 |
| **Proportion of variance**   | **60.99**  | **26.23**  |
| Annual Mean Temperature      | -0.4028813 | -0.0200359 |
| Max Temperature of Warmest Month | -0.3763478 | -0.4297463 |
| Min Temperature of Coldest Month | -0.3814137 | 0.4361592 |
| Mean Temperature of Wettest Quarter | -0.3474579 | -0.3535348 |
| Mean Temperature of Driest Quarter | -0.366922 | 0.37914777 |
| Mean Temperature of Warmest Quarter | -0.3802803 | -0.4423161 |
| Mean Temperature of Coldest Quarter | -0.3880732 | 0.40037289 |
| **Proportion of variance**   | **84.68**  | **7.98**   |
| Annual Precipitation         | -0.463081 | 0.01557181 |
| Precipitation of Wettest Month | -0.3918944 | -0.3992453 |
| Precipitation of Driest Month | -0.34207 | 0.50482491 |
| Precipitation of Wettest Quarter | -0.3980048 | -0.3962535 |
| Precipitation of Driest Quarter | -0.3453694 | 0.50052908 |
| Precipitation of Warmest Quarter | -0.3656054 | -0.3332687 |
| Precipitation of Coldest Quarter | -0.3218816 | 0.25864709 |
| **Proportion of variance**   | **63.13**  | **24.9**   |

*These PC axes were inverted in posterior analyses (*-1) so that higher values represent more variation.*
Table S2. Results of PGLS analyses using different datasets. Top: Using all species (both continental and insular (n= 3160). Middle: Using all species but using breeding range variables instead of whole range (n=3054). Bottom: Using only continental species and breeding range (n=2488).

| Predictor         | Range size | Temperature | Precipitation |
|-------------------|------------|-------------|---------------|
|                   | Estimate   | t-value     | P-value       | Estimate   | t-value     | P-value       | Estimate   | t-value     | P-value       |
| Open vs Domed     | -0.573     | -3.268      | 0.001         | -0.471     | -2.871      | 0.004         | -0.028     | -0.195      | 0.846         |
| Open vs Cavity    | 0.135      | 0.818       | 0.413         | 0.397      | 2.644       | 0.008         | 0.001      | 0.011       | 0.991         |
| log(body mass)    | -0.397     | -4.340      | < 0.001       | -0.321     | -3.597      | < 0.001       | -0.076     | -0.987      | 0.324         |
| Latitude(abs)     | 0.057      | 16.178      | < 0.001       | -          | -           | -             | -          | -           | -             |
| Open vs Domed     | -0.538     | -3.036      | 0.002         | -0.349     | -2.089      | 0.037         | 0.185      | 1.243       | 0.214         |
| Open vs Cavity    | 0.139      | 0.839       | 0.402         | 0.581      | 3.748       | < 0.001       | 0.04       | 0.295       | 0.768         |
| log(body mass)    | -0.375     | -4.101      | < 0.001       | -0.276     | -3.127      | 0.002         | 0.029      | 0.363       | 0.717         |
| Latitude(abs)     | 0.046      | 12.848      | < 0.001       | -          | -           | -             | -          | -           | -             |
| Open vs Domed     | -0.573     | -4.395      | < 0.001       | -0.245     | -1.376      | 0.169         | 0.281      | 1.791       | 0.073         |
| Open vs Cavity    | 0.319      | 2.547       | 0.011         | 0.708      | 4.319       | < 0.001       | 0.108      | 0.746       | 0.456         |
| log(body mass)    | -0.208     | -3.106      | 0.002         | -0.194     | -1.96       | 0.05          | 0.031      | 0.353       | 0.724         |
| Latitude(abs)     | 0.034      | 12.293      | < 0.001       | -          | -           | -             | -          | -           | -             |
Table S3. Results of PGLS models using alternative nest type classifications, for whole range
Top: Only when differentiating between open and domed nests. Bottom: When
differentiating between five different nest types (open, domed, deep cup, domed inside
cavity, open inside cavity and either domed or open).

| Predictor          | Range size (n=3160) | Temperature (n=3174) |
|--------------------|---------------------|----------------------|
|                    | Estimate            | t-value   | P-value | Estimate | t-value   | P-value |
|                    | mcc                 |           |         | mcc      |           |         |
| Domed vs Open      | 0.542               | 3.164     | 0.002   | 0.589    | 3.629     | < 0.001 |
| log(body mass)     | -0.390              | -4.267    | < 0.001 | -0.312   | -3.492    | < 0.001 |
| latitude           | 0.058               | 16.356    | < 0.001 | -        | -         | -       |
| Open vs Domed      | -0.529              | -2.821    | 0.005   | -0.525   | -2.94     | 0.003   |
| Open vs Deep cup   | 0.076               | 0.238     | 0.812   | 0.019    | 0.066     | 0.947   |
| Open vs Cav Domed  | -0.030              | -0.127    | 0.899   | -0.231   | -1.088    | 0.277   |
| Open vs Cav Open   | 0.193               | 1.079     | 0.281   | 0.499    | 3.08      | 0.002   |
| Open vs Both       | 0.469               | 1.448     | 0.148   | 0.256    | 0.891     | 0.373   |
| log(body mass)     | -0.392              | -4.286    | < 0.001 | -0.318   | -3.563    | < 0.001 |
| latitude           | 0.057               | 16.104    | < 0.001 | -        | -         | -       |
**Table S4.** Results of PGLS models using alternative nest type classifications, for breeding range

Top: Only when differentiating between open and domed nests. Bottom: When differentiating between six different nest types (open, domed, deep cup, domed inside cavity, open inside cavity and either domed or open).

| Predictor          | Range size (n=3054) |                     | Temperature (n=3068) |                     |
|--------------------|---------------------|---------------------|----------------------|---------------------|
|                    | Estimate  | mcc   | t-value | P-value | Estimate  | mcc   | t-value | P-value |
| Domed vs Open      | 0.511     | 2.958 | 0.003   |         | 0.421     | 2.564 | 0.01    |         |
| log(body mass)     | -0.369    | -4.032| < 0.001 |         | -0.266    | -3.002| 0.003   |         |
| latitude           | 0.047     | 13.025| < 0.001 |         | -         | -     | -       |         |
| Open vs Domed      | -0.494    | -2.611| 0.009   |         | -0.3      | -1.673| 0.095   |         |
| Open vs Deep cup   | 0.080     | 0.248 | 0.804   |         | 0.463     | 1.547 | 0.122   |         |
| Open vs Cav Dome   | -0.080    | -0.342| 0.732   |         | -0.159    | -0.73 | 0.465   |         |
| Open vs Cav Open   | 0.200     | 1.111 | 0.267   |         | 0.666     | 3.974 | < 0.001 |         |
| Open vs Both       | 0.539     | 1.625 | 0.104   |         | 0.68      | 2.219 | 0.027   |         |
| log(body mass)     | -0.371    | -4.051| < 0.001 |         | -0.27     | -3.066| 0.002   |         |
| latitude           | 0.046     | 12.780| < 0.001 |         | -         | -     | -       |         |
Table S5. Results of PGLS models using SD of Bioclim 8 (Variation in temperature during wettest quarter), instead of PC\textsubscript{TEMP}. Patterns remain unchanged, possibly because Bioclim8 is very correlated with PC\textsubscript{TEMP}. Model for continental species presented.

| Comparison            | Estimate | t-value | p-value |
|-----------------------|----------|---------|---------|
| Open vs. Domed        | -3.413   | -1.976  | 0.048   |
| Open vs. Cavity domed | 2.135    | 0.755   | 0.45    |
| Open vs. Deep cup     | -4.013   | -1.641  | 0.1     |
| Open vs. Cavity open  | 5.999    | 3.732   | 0.0001  |
| Open vs. both         | 3.759    | 1.297   | 0.194   |
| log(body mass)        | -1.186   | -1.345  | 0.178   |
| Domed vs. Open        | -3.041   | 1.603   | 0.057   |
| Domed vs. Cavity      | 5.103    | 3.440   | < 0.001 |
| log(body mass)        | -1.194   | -1.353  | 0.176   |
| Domed vs. Open        | 4.225    | 2.681   | 0.007   |
| log(body mass)        | -1.097   | -1.236  | 0.216   |
Table S6a. Model comparison to test the importance of nest type in predicting range size (complete dataset: 3175 spp.). Evidence ratio: 199.

| Model | Intercept | Latitude | Body mass | Nest type | df | AICc | Delta | Weight |
|-------|-----------|----------|-----------|-----------|----|------|-------|--------|
| 8     | 26.42     | 0.057    | -0.396    | +         | 5  | 14469| 0     | 0.995  |
| 4     | 26.11     | 0.058    | -0.375    |           | 3  | 14479| 10.61 | 0.005  |

Table S6b. Model comparison to test the importance of nest type in predicting breeding range size (complete dataset: 3054 spp.). Evidence ratio: 82.33.

| Model | Intercept | Latitude | Body mass | Nest type | df | AICc | Delta | Weight |
|-------|-----------|----------|-----------|-----------|----|------|-------|--------|
| 8     | 26.53     | 0.046    | -0.375    | +         | 5  | 13950| 0     | 0.988  |
| 4     | 26.23     | 0.047    | -0.353    |           | 3  | 13959| 8.90  | 0.012  |

Table S6c. Model comparison to test the importance of nest type in predicting range size (continental dataset: 2583 spp.). Evidence ratio: 993.

| Model | Intercept | Latitude | Body mass | Nest type | df | AICc | Delta | Weight |
|-------|-----------|----------|-----------|-----------|----|------|-------|--------|
| 8     | 25.97     | 0.046    | -0.242    | +         | 5  | 10158| 0     | 0.993  |
| 4     | 26.25     | 0.048    | -0.214    |           | 3  | 10195| 36.74 | 0.001  |

Table S6d. Model comparison to test the importance of nest type in predicting breeding range size (continental dataset: 2583 spp.). Evidence ratio: 978.

| Model | Intercept | Latitude | Body mass | Nest type | df | AICc | Delta | Weight |
|-------|-----------|----------|-----------|-----------|----|------|-------|--------|
| 8     | 26.19     | 0.033    | -0.207    | +         | 5  | 9789 | 0     | 0.978  |
| 4     | 26.43     | 0.035    | -0.178    |           | 3  | 9821 | 32.28 | 0.001  |
Table S7. Results of MCMCglmm exploring the link between nest type and elevational range (N= 8563 observations, 2832 species).

|                      | Estimate | 95% lower CI | 95% higher CI | pMCMC |
|----------------------|----------|--------------|---------------|-------|
| Domed vs. Open       | 40.458   | -56.907      | 136.149       | 0.415 |
| Domed vs. Cavity     | 177.087  | 63.058       | 292.117       | 0.002 |
| log(body mass)       | 37.397   | -11.379      | 84.795        | 0.137 |
| abs(Latitude)        | 8.726    | 6.492        | 11.239        | < 0.001 |
Table S8. Results of MCMCglmm exploring the link between nest type and the likelihood of living in urban environments (n=2888). Top: Model using the MCC tree. Bottom: Model when using 1300 different trees, one at each iteration. Species with domed nests are less likely to occupy urban environments.

| Comparison         | Estimate | Lower 95% | Upper 95% | pMCMC  |
|--------------------|----------|-----------|-----------|--------|
| Open vs Domed      | -1.858   | -2.825    | -0.828    | 0.001  |
| Open vs Cavity     | -0.210   | -0.928    | 0.476     | 0.569  |
| log(body size)     | 0.227    | -0.230    | 0.679     | 0.326  |
| Open vs Domed      | -1.720   | -2.668    | -0.754    | 0.001  |
| Open vs Cavity     | 0.034    | -0.662    | 0.772     | 0.938  |
| log(body mass)     | -0.045   | -0.482    | 0.419     | 0.848  |
Table S9. Results of ancestral reconstruction (two first rows) and diversification analyses from three different methods (MuSSE in RevBayes and castor, and HiSSE in RevBayes). Each row shows the results for the four states in the analyses, and in black are highlighted the highest two values per rows. For diversification analyses we present the HPD intervals from the analyses on the MCC tree. The last rows show the HPD intervals from the castor analyses on 100 different trees. Results on the MCC are a good representation of results across trees.

| State               | Domed/Small | Open/Small | Domed/Large | Open/Large |
|---------------------|-------------|------------|-------------|------------|
| Probability MuSSE   | 0.469       | 0.066      | **0.464**   | 0.001      |
| Probability HiSSE   | 0.566       | 0.035      | **0.398**   | 0.001      |
| Speciation rates MuSSE | 0.181 (0.161 to 0.209) | 0.19 (0.180 to 0.2) | 0.094 (0.077 to 0.113) | 0.108 (0.1 to 0.119) |
| Extinction rates MuSSE | 0.016 (0.000001 to 0.006) | 0.0007 (0.00001 to 0.028) | **0.005 (0.000001 to 0.072)** | 0.0008 (0.00001 to 0.024) |
| Speciation rates castor | 0.22 (0.20 to 0.23) | 0.23 (0.23 to 0.24) | 0.06 (0.046 to 0.07) | 0.06 (0.052 to 0.063) |
| Extinction rates Castor | 0.024 (0.015 to 0.028) | 0 (0 to 0.007) | **0.0001 (0 to 0.0006)** | 0 (0 to 0.006) |
| Speciation rates HiSSE (states A) | 0.126 (0.116 to 0.147) | 0.121 (0.113 to 0.129) | 0.069 (0.05 to 0.083) | 0.073 (0.066 to 0.080) |
| Extinction rates HiSSE (states A) | 0.0008 (0 to 0.005) | 0.0003 (0 to 0.001) | **0.0006 (0 to 0.003)** | 0.0001 (0 to 0.0006) |
| Speciation castor (HPD 100 trees) | 0.15 to 0.25 | **0.20 to 0.27** | 0.037 to 0.122 | 0.050 to 0.07 |
| Extinction Castor (HPD 100 trees) | 0 to 0.048 | 0 to 0.002 | **0 to 0.07** | 0 to 0.002 |
| Speciation (only genetic) | 0.167 | 0.194 | **0.3066** | 0.1498 |
| Extinction (only genetic) | **0.00428** | 0.00183 | 0.151 | 0.00082 |
Table S10a. Association between nest type, body mass and latitude with range size (log). Dataset using only tropical species, with middle latitudes between -5 and 5 degrees (PGLS).

| Species between -5 and 5 degrees | Whole range (599 spp.) | Breeding range (582 spp.) |
|----------------------------------|------------------------|---------------------------|
|                                  | estimate | t-value | p-value | estimate | t-value | p-value |
| Domed vs. Open                   | 0.805    | 2.156   | 0.031   | 0.823    | 2.166   | 0.031   |
| Domed vs. Cavity                 | 1.782    | 3.575   | 0.001   | 1.739    | 3.314   | 0.001   |
| log(body mass)                   | -0.489   | -2.582  | 0.01    | -0.47    | -2.464  | 0.014   |
| abs(Latitude)                    | -0.04    | -0.064  | 0.948   | -0.03    | -0.414  | 0.678   |
| Continental                      |          |         |         | 496 spp. |         | 482 spp. |
| Domed vs. Open                   | 0.547    | 2.247   | 0.027   | 0.491    | 2.031   | 0.04    |
| Domed vs. Cavity                 | 1.333    | 3.858   | 0.001   | 1.164    | 3.299   | 0.001   |
| log(body mass)                   | -0.395   | -3.018  | 0.003   | -0.366   | -2.846  | 0.004   |
| abs(Latitude)                    | -0.035   | -0.588  | 0.556   | -0.059   | 0.985   | 0.324   |

Table S10b. Association between nest type, body mass and latitude with range size (log) for continental species. Dataset using only species with specific body mass (PGLS).

| Small size (< 15 g, 870 spp.) | Medium (15 to 30 g, 802 spp.) | Large ( > 30 g, 902 spp.) |
|-------------------------------|--------------------------------|---------------------------|
| estimate | t-value | p-value | estimate | t-value | p-value | estimate | t-value | p-value |
| Domed vs. Open | 0.581 | 3.411 | 0.0006 | 0.813 | 3.784 | 0.0001 | 0.731 | 2.606 | 0.009 |
| Domed vs. Cavity | 0.563 | 2.663 | 0.0078 | 1.103 | 4.279 | < 0.001 | 1.413 | 4.497 | < 0.001 |
| log(body mass) | -0.607 | -2.481 | 0.013 | -0.204 | -0.604 | 0.546 | 0.051 | 0.353 | 0.724 |
| abs(Latitude) | 0.034 | 7.597 | < 0.001 | 0.049 | 10.572 | < 0.001 | 0.044 | 9.764 | < 0.001 |
Table S11. Results of model where range predicts $PC_{\text{TEMP}}$ for continental species. The effect of nest type is reduced, suggesting that the effect of nest type on niche width possibly occurs through range size or latitude, given larger ranges and niches occur in temperate species. The pattern is similar for the complete dataset (continental plus island species).

| With Latitude          | estimate | t-value | p-value |
|------------------------|----------|---------|---------|
| Open vs. Domed         | -0.164   | 1.237   | 0.215   |
| Cavity vs. Domed       | 0.222    | 1.777   | 0.075   |
| log(Weight)            | -0.168   | -2.348  | 0.018   |
| abs(Latitude)          | 0.103    | 38.174  | < 0.001 |

| With range             | estimate | t-value | p-value |
|------------------------|----------|---------|---------|
| Open vs. Domed         | -0.054   | -0.346  | 0.729   |
| Open vs. Cavity        | 0.271    | 1.893   | 0.058   |
| log(Weight)            | -0.086   | -0.949  | 0.342   |
| log(range)             | 0.500    | 24.992  | < 0.001 |
Table S12. Results from BayesTraits RJ MCMC analyses on models of dependent and independent evolution of traits. Dependent models were strongly favoured over independent models of evolution. Bayes Factors above 10 indicate very strong evidence of correlated evolution. Marginal likelihood values presented correspond to the last iteration of each run.

|            | Lh Dependent | Lh independent | Bayes Factor | Iterations | Stones | Stones per it | Burnin |
|------------|--------------|----------------|--------------|------------|--------|---------------|--------|
| Run 1      | -2794.584    | -2818.661      | 43.795       | 1 million  | 100    | 1000          | 10000  |
| Run 2      | -2797.549    | -2817.064      | 43.008       | 5 million  | 100    | 1000          | 50000  |
| Run 3      | -2798.921    | -2816.945      | 43.031       | 30 million | 1000   | 10000         | 300000 |
| MCC tree   | -2830.814    | -2885.891      | 107.30       | 1 million  | 100    | 1000          | 10000  |
Table S13. Association between nest type and probability of living in an urban environment when including range size in the model. Domed-nesting species are still less likely to be present in urban environments, even when there is a strong effect of range size.

|                        | Estimate | Lower 95% | Upper 95% | pMCMC |
|------------------------|----------|-----------|-----------|-------|
| Open vs. Domed         | -1.370   | -2.316    | -0.406    | 0.004 |
| Open vs. Cavity        | -0.474   | -1.213    | 0.281     | 0.220 |
| Log(range size)        | 0.647    | 0.513     | 0.802     | < 0.001 |
| Log(body mass)         | 0.311    | -0.097    | 0.745     | 0.137 |
Figure S1. Association between different response variables used in the models. The variables with the prefix ‘Var’ refer to the first principal component of the analyses described in the main text, and represent variation in a climatic variable across the range of a species. BR refers to the breeding range.
Figure S2. Association between predictor variables. There are significant correlations between nest type and latitude (Domed vs. Open, $B=2.850$, $t$-value=3.055, $p=0.002$; Domed vs. Cavity, $B=5.569$, $t$-value=5.534, $p$-value < 0.001) but not between body mass and nest type (Domed vs. Open, $B=-0.004$, $t$-value=-0.132, $p=0.894$; Domed vs. Cavity, $B=0.050$, $t$-value=1.572, $p=0.115$), with tropical species being more likely to build domed nests. Despite this, there is enough variation in each variable and variance inflation factors (VIF) in the model are low (domed: 2.183, open: 2.016, body mass: 1.12, latitude:1.074).
Figure S3. Results of alternative nest type classifications for range size and temperature niche. For further analyses ‘pouch’ and ‘both’ categories were grouped along with the ‘open’ category, and domed and open cavity nesters were merged as well. Note that within cavity nesters the broad scale patterns are similar: domes in cavities tend to have smaller ranges than open nests in cavities.
Figure S4. Species with open and cavity nests are more likely to be urban than species with domed nests.
Figure S5. Speciation and extinction rates for three different analyses, HiSSE, MuSSE in RevBayes and Castor.
Figure S6. Transition matrix for MuSSE analysis performed using the Castor R package.
Figure S7. Transition matrix for HiSSE analysis, using the software RevBayes.
Figure S8. Transition matrix for MuSSE analysis, using the software RevBayes and vector of sampling proportions per state and information only on genetic data.
References

1. FitzJohn, R.G., Maddison, W.P. & Otto, S.P. (2009). Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Systematic biology*, 58, 595-611.

2. Friedl, T.W. & Klump, G.M. (2000). Nest and mate choice in the red bishop (Euplectes orix): female settlement rules. *Behavioral Ecology*, 11, 378-386.

3. Höhna, S., Landis, M.J., Heath, T.A., Boussau, B., Lartillot, N., Moore, B.R. *et al.* (2016). RevBayes: Bayesian phylogenetic inference using graphical models and an interactive model-specification language. *Systematic biology*, 65, 726-736.

4. Louca, S. & Doebeli, M. (2018). Efficient comparative phylogenetics on large trees. *Bioinformatics*, 34, 1053-1055.

5. Louca, S. & Pennell, M.W. (2020). A General and Efficient Algorithm for the Likelihood of Diversification and Discrete-Trait Evolutionary Models. *Systematic biology*, 69, 545-556.

6. Maddison, W.P., Midford, P.E. & Otto, S.P. (2007). Estimating a binary character's effect on speciation and extinction. *Systematic biology*, 56, 701-710.

7. Martin, T.E., Boyce, A.J., Fierro-Calderón, K., Mitchell, A.E., Armstad, C.E., Mouton, J.C. *et al.* (2017). Enclosed nests may provide greater thermal than nest predation benefits compared with open nests across latitudes. *Functional Ecology*, 31, 1231-1240.

8. Mouton, J.C. & Martin, T.E. (2019). Nest structure affects auditory and visual detectability, but not predation risk, in a tropical songbird community. *Functional Ecology*, 33, 1973-1981.

9. Pagel, M. & Meade, A. (2006). Bayesian analysis of correlated evolution of discrete characters by reversible-jump Markov chain Monte Carlo. *The American Naturalist*, 167, 808-825.

10. Quader, S. (2005). Elaborate nests in a weaverbird: A role for female choice? *Ethology*, 111, 1073-1088.

11. Quintero, I. & Jetz, W. (2018). Global elevational diversity and diversification of birds. *Nature*, 555, 246-250.

12. Rabosky, D.L. (2015). No substitute for real data: a cautionary note on the use of phylogenies from birth–death polytomy resolvers for downstream comparative analyses. *Evolution*, 69, 3207-3216.

13. Rambaut, A., Drummond, A., Xie, D., Baele, G. & Suchard, M. (2018). Posterior summarisation in Bayesian phylogenetics using Tracer 1.7. *Systematic Biology* syy032.
14. Savalli, U.M. (1994). Mate choice in the yellow-shouldered widowbird: correlates of male attractiveness. *Behavioral Ecology and Sociobiology*, 35, 227-234.

15. Unzeta, M., Martin, T.E. & Sol, D. (2020). Daily nest predation rates decrease with body size in passerine birds. *The American Naturalist*, 196, 743-754.