

Supplemental Information

Echolocators are smaller than their non-echolocating relatives: agility counts in dark, three-dimensional habitats

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Taxon	Sub-Taxa	Echolocators (N)	Non-echolocators (N)	Estimate	SE	Z/t	P-value
All	All	1327	4878	0.454	0.065	6.984	<0.001
Class	Mammalia	1309	4429	0.509	0.061	8.388	<0.001
Order	Caprimulgiformes	18	449	0.189	0.112	1.685	0.093
	Chiroptera	1216	174	1.017	0.028	35.846	<0.001
	Rodentia	4	2258	0.752	0.287	2.625	0.009
	Afrosoricida	4	51	-0.664	0.248	-2.673	0.008
	Cetacea	76	14	1.866	0.203	9.177	<0.001
	Eulipotyphla	9	465	-0.031	0.085	-0.366	0.714
Family	Apodidae	17	76	0.424	0.083	5.115	<0.001
	Pteropodidae	8	174	0.22	0.184	1.192	0.233
	Platacanthomyidae	4	1	-	-	-	-
	Tenrecidae	4	27	-0.93	0.221	-4.202	<0.001
	Soricidae	5	398	-0.046	0.12	-0.381	0.703
	Talpidae	4	41	0.597	0.154	3.865	<0.001

Table S1. Statistical results from PGLS and GLMM models for the body mass of echolocating vs. non-echolocating taxa. Fixed factors in bold indicate (marginal) significant differences ($P < 0.1$).

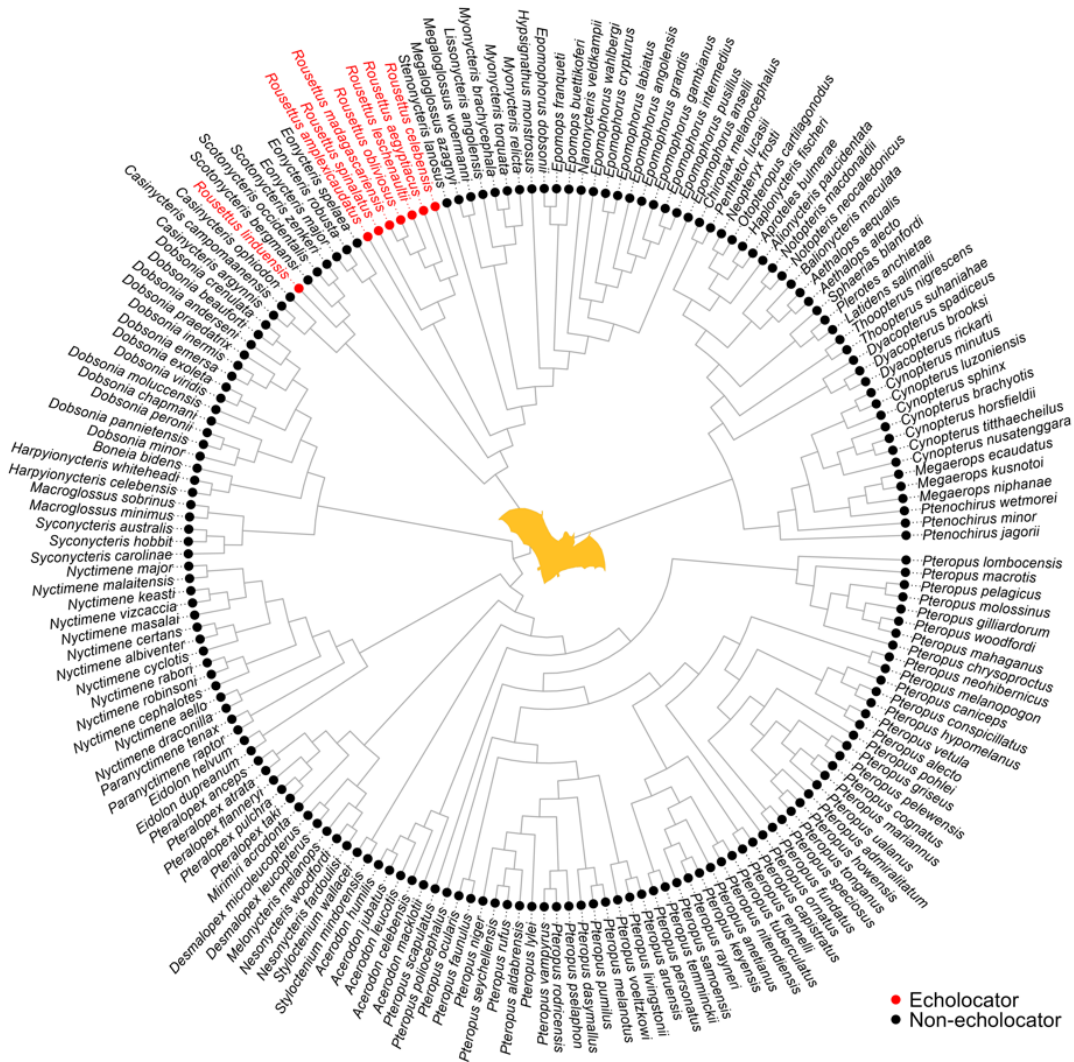


Figure S1. Phylogenetic tree of echolocating and non-echolocating species in the Pteropodidae (i.e., fruit bats).

Supplemental Experimental Procedures

Collating echolocating and non-echolocating species lists

To compare body size between echolocating and non-echolocating species, we utilized the comprehensive global list of 1,329 echolocating species (belonging six orders, Figure 1A) provided by Wu *et al.*^{S1}, including Chiroptera (N = 1,218), Cetacea (N = 76), Afrosoricida (N = 9), Eulipotyphla (N = 4), Rodentia (N = 4), and Caprimulgiformes (N = 18). The taxonomy of non-echolocating taxa referenced from Wu *et al.*^{S1} was verified against the “*Handbook of the Mammals of the World*”^{S2} (henceforth “HMW”) for mammals and against the BirdLife Taxonomic Checklist v8.1 for birds. Given that mammals accounted for the substantial majority (98.65%) of echolocating taxa, we included all non-echolocating closely related mammals (by class, order and family) in our comparative group to ensure appropriate sample representation. Echolocating birds constituted only a small percentage (1.35%) of echolocating taxa, exclusively occurring in the Caprimulgiformes; therefore, we restricted our comparative non-echolocating group to species within this order. Because the taxonomy of species in our list differed from phylogenetic information in the VertLife database^{S3} (vertlife.org), we matched our list of non-echolocating taxa with the VertLife phylogenetic database (N = 4,647). For unmatched species (N = 226), we cross-referenced against taxonomic updates from HMW^{S2}, and online databases (GBIF www.gbif.org; IUCN Red List, www.iucnredlist.org; Catalogue of Life, www.catalogueoflife.org). Ultimately, we identified phylogenetic relationships for 6,207 species, including 1,329 echolocating and 4,878 non-echolocating species.

Body mass

Body mass data were sourced from the TetrapodTraits 1.0 database^{S4}, which integrates global published trait data for Tetrapod species based on the VertLife phylogenetic database. This database employs phylogeny-informed imputation to address missing data, thereby improving data completeness and usability for ecological and evolutionary studies, thus allowing for better representation and analysis of global biodiversity patterns. For species with missing body mass data (N = 44) or outliers (N = 40), we supplemented our database

using additional searches for body mass references in Google Scholar, HMW, and the National Museum of Natural History (naturalhistory.si.edu). Only the body mass of *Eumops chimaera* and *Carollia monohernandezii* could not be obtained. Ultimately, this body mass dataset comprised 6,205 species, with all values log₁₀-transformed prior to analysis.

Phylogeny

To account for phylogenetic relatedness between species, we constructed a supertree using available phylogenies (Loeffler-Henry et al.^{S5} and Healy et al.^{S6,S7}). Firstly, we generated 10,000 random trees for mammals and birds, based on the pseudo-posterior distributions of the trimmed tree from VertLife^{S3, S8}. We then calculated the ultrametric maximum clade credibility (MCC) tree from these trees using the “maxCladeCred” and “chronos” functions in the “phangorn” and “ape” R packages for both mammals and birds^{S9, S10}. To create a phylogenetic distribution encompassing both mammals and birds, we merged them into a combined tree using the “tree.bind” function in the “mulTree” package^{S11}. The age of the amniote node was set to 315 million years, corresponding to the common ancestor of all amniotes (i.e., *Archerpeton anthracos*^{S5}). Ultimately, after matching species with complete body mass data, our dataset included 1,327 species for echolocators, and for 4,873 species for non-echolocators, and this was the sample size for our main analyses (DATA S1).

Statistical analysis

To thoroughly examine differences in body size between echolocators and related non-echolocators, and considering that echolocators are distributed across different phylogenetic branches within the total tree (i.e., Mammalia, Caprimulgiformes, and Eulipotyphla; Figure 1A), we employed Phylogenetic Generalized Least Squares (PGLS) regressions separately for the mean body mass of each species using the “phylolm” function in the “phylolm” package^{S12}. In parallel, because echolocators are distributed on the same phylogenetic branches within their respective orders, we conducted analyses sequentially for these orders and all families using Generalized Linear Mixed Models (GLMM) with the “glmmTMB” function in the “glmmTMB” package^{S13}. Since there was only one non-echolocating species (*Platacanthomys Lasiurus*) in the Platacanthomyidae, the sample

77 size was too small to be included in the final model analysis. All statistical analyses were
78 conducted using R version 4.3.0^{S14}.

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83

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86 N.W., J.W., J.L., H.X.; Formal analysis, J.G., N.W., Y.Z.; Visualization, J.G., N.W.; Writing –
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