

Supplementary Materials

Applying zeta diversity to understand species turnover patterns of small mammals in the Mountains of Southwest China

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Supplementary Materials and Methods

The MSC (Supplementary Figure S1) is one of the 25 global biodiversity hotspots (Myers et al., 2000), stretching from southeast Qinghai-Tibetan Plateau through western Sichuan Plateau and extending into northwest Yunnan-Kweichow Plateau. The Hengduan Mountains Region occupies most of the MSC, which is composed of a series of rugged mountains and deep river valleys running in a north-south direction, including the Minshan, Qionglai, Daxue, Shaluli, Mangkang-Yunling, Tiantaweng-Nushan, Boshula-Gaoligong Mountains, and the Minjiang, Dadu, Yalong, Jinsha, Lancang and Nujiang rivers (Zhang et al., 1997). These mountains and rivers are one of the main drivers of high biodiversity in the MSC through geographic isolation, which promotes allopatric speciation and endemism (Wen et al., 2016).

The elevational patterns of small mammal diversity have been studied on many different mountains of the MSC. Based on a published presence-absence dataset of small mammals in this region (species trapping data collected from 20 extensive elevational gradients) (Wen et al., 2018), we added the data collected from the Heizhugou (Yue et al., 2020) and Xiaoxiangling gradients (Liu et al., 2022) (Supplementary Figure S1). The three criteria for selecting the 22 gradients were (1) the sampling areas covered the low-elevation evergreen broadleaf forests (dry-hot valley shrublands and tree plantations are also present in some gradients), middle-elevation evergreen and deciduous mixed broadleaf forests and coniferous and deciduous broadleaf mixed forests, and high-elevation dark coniferous forests and meadows (Supplementary Figure S4); (2) the sampling efforts were sufficient (105.2 ± 178.5 trap nights, mean \pm standard error, $n=22$), and the sampling efforts in three elevation zones were comparable (low: 363.8 ± 696.4 trap nights; middle: 343.0 ± 573.9 trap nights; high: 343.6 ± 718.4 trap nights; One-Way ANOVA: $F=0.032$, $P=0.969$); (3) both glires (Rodentia and Lagomorpha) and insectivores (Eulipotyphla) were surveyed based on consistent sampling methods (line transects, quadrats and trap nights).

We employed a number of zeta diversity metrics to measure the compositional change of small mammals among the 22 elevational gradients in the MSC. Zeta diversity (ζ_i) is the average number of species shared by i number of assemblages, where i refers to the zeta order (Hui and Mcgeoch, 2014), for example: ζ_1 is the average number of species per assemblage; ζ_2 is the average number of species shared by any two assemblages; ζ_3 is the average number of species shared by any three assemblages, and so on (Mcgeoch et al., 2019). Therefore, higher orders of zeta ($i > 2$) represent the contribution of increasingly common species to compositional change. Zeta diversity can thus provide information on the relative contributions of rare versus increasingly common species to compositional change (Mcgeoch et al., 2019).

Here, we used three metrics of zeta diversity: zeta decline, retention rate based on the zeta ratio, and zeta decay over space (Hui and Mcgeoch, 2014; Mcgeoch et al., 2019). In brief, zeta decline provides information on the form and rate of how the average number of species shared decreases with an increase in the number of assemblages (orders). Based on the steepness of zeta decline, one may infer whether compositional change is primarily driven by rare or common species (corresponding to

steep and shallow decline, respectively) (Hui and Mcgeoch, 2014; Mcgeoch et al., 2019).

The species retention rates indicate the degree to which common or widespread species are more likely to be retained across different sites than rare species with an increase in zeta order (Mcgeoch et al., 2019). The retention curve is obtained by plotting the zeta ratio (ζ_{i+1}/ζ_i) against the denominator zeta order. The curve of retention rates may show different shapes (e.g., increasing, asymptotic, or modal) under different scenarios that common species remain across sites as the zeta order increases (Mcgeoch et al., 2019). For example, an increasing retention curve indicates that common species are rapidly retained with an increase in zeta order; an asymptotic retention curve shows that some common species are present across all sites; however, a modal retention curve shows that the species composition undergoes a complete turnover when beyond a certain zeta order. Examining species retention rates is also helpful for visualizing turnover at high zeta orders and detecting abrupt shifts in compositional change, as well as comparing differences in retention rates between different taxonomic groups (Mcgeoch et al., 2019).

Similar to distance decay of similarity (Nekola and McGill, 2014), zeta decay quantifies the variation in the average number of species shared with increasing distance between sites (or time between samplings) (Mcgeoch et al., 2019). Spatial and temporal compositional similarity for each order of zeta thus provides information on the form of decay for the rare to more common species in the community over distance or time. To assess the effect of geographic distance on the average number of species shared by multiple assemblages, we computed the distance decay of zeta diversity for ζ_2 to ζ_5 .

In addition, we used different sample selection schemes (i.e., ALL and NON) to calculate zeta decline (Mcgeoch et al., 2019) for small mammals. The all combinations (ALL) scheme considers random selection of site combinations and does not take into account the spatial location of sites. As for the non-directional nearest-neighbors (NON) scheme, the spatial location of sites is taken into account (Mcgeoch et al., 2019). By comparing the results of ALL with NON schemes, one can reveal the spatial dependence for compositional change. To avoid the influence of differences in richness between different sites (Mcgeoch et al., 2019), beside using raw zeta values (i.e., the arithmetic mean of the number of shared species), we also used the normalized versions (Sørensen- and Simpson-equivalent) of zeta during the analysis. The Sørensen-equivalent versions of zeta divided the number of shared species by the average number of species over the assemblages; and the Simpson-equivalent versions of zeta, which divided the number of shared species by the minimum number of species over the assemblages, was independent of species richness differences (i.e., nestedness) (Baselga, 2010; Latombe et al., 2018). Computing these two forms of zeta diversity can provide subtle insights into the relative contributions of replacement component (the species at a site are replaced without changing the richness) (Lennon et al., 2001) and nestedness (the composition in one site is a strict subset of the composition that occur in another richer site) (Ulrich et al., 2009) to community compositional change (Baselga, 2010). All the analyses were carried out using the package ‘zetadiv’ ver. 1.2.0

(Mcgeoch et al., 2019) in the R statistical environment.

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Supplementary Table S1 Zeta ratio values (ζ_{i+1}/ζ_i) for orders 1 to 21 using the ALL sample selection scheme and raw zeta values

Order	ALL-Raw data				
	Low	Middle	High	Insectivores	Glires
1	0.432 188	0.417 560	0.340 603	0.378 277	0.507 178
2	0.642 259	0.600 616	0.507 791	0.460 821	0.690 471
3	0.757 072	0.695 824	0.618 703	0.489 386	0.775 630
4	0.831 861	0.761 883	0.697 007	0.500 649	0.827 145
5	0.882 633	0.814 131	0.752 235	0.501 254	0.862 986
6	0.914 559	0.857 768	0.789 561	0.493 152	0.888 154
7	0.932 856	0.894 283	0.812 638	0.477 210	0.905 115
8	0.942 743	0.923 928	0.824 399	0.453 477	0.916 163
9	0.948 083	0.946 976	0.827 272	0.421 634	0.923 367
10	0.951 210	0.964 139	0.823 094	0.381 217	0.928 304
11	0.953 347	0.976 454	0.813 056	0.331 541	0.932 007
12	0.955 048	0.985 024	0.797 699	0.271 429	0.935 082
13	0.956 518	0.990 831	0.776 896	0.198 830	0.937 845
14	0.957 792	0.994 663	0.749 739	0.110 294	0.940 443
15	0.958 838	0.997 113	0.714 240	0.000 000	0.942 944
16	0.959 596	0.998 610	0.666 667	0.000 000	0.945 381
17	0.960 001	0.999 453	0.600 000	0.000 000	0.947 769
18	0.959 978	0.999 863	0.500 000	0.000 000	0.950 107
19	0.959 452	1.000 000	0.333 333	0.000 000	0.952 381
20	0.958 334	1.000 000	0.000 000	0.000 000	0.954 546
21	0.956 521	1.000 000	0.000 000	0.000 000	0.956 521

Supplementary Table S2 Zeta diversity decay across space for ζ_2 to ζ_5 using the ALL sample selection scheme and the Sørensen-equivalent zeta values

	Order	Intercept	Slope		Slope significance ^a	Explained deviance
			Coefficient	$Pr(> t)$		
Low	2	4.73E-01	-9.44E-05	3.32E-04	**	0.054 8
	3	3.01E-01	-3.84E-05	8.16E-06	***	0.012 8
	4	2.27E-01	-2.25E-05	3.83E-11	***	0.005 9
	5	1.90E-01	-1.72E-05	<2E-16	***	0.004 4
Middle	2	5.08E-01	-2.07E-04	3.85E-12	***	0.190 2
	3	3.23E-01	-1.14E-04	<2E-16	***	0.090 4
	4	2.21E-01	-6.14E-05	<2E-16	***	0.035 4
	5	1.60E-01	-3.25E-05	<2E-16	***	0.013 0
High	2	4.73E-01	-2.85E-04	<2E-16	***	0.328 6
	3	3.21E-01	-2.21E-04	<2E-16	***	0.303 1
	4	2.56E-01	-1.88E-04	<2E-16	***	0.304 6
	5	2.22E-01	-1.67E-04	<2E-16	***	0.310 3
Insectivores	2	4.80E-01	-2.61E-04	2.61E-09	***	0.143 7
	3	2.75E-01	-1.71E-04	<2E-16	***	0.089 6
	4	1.63E-01	-1.08E-04	<2E-16	***	0.059 1
	5	9.67E-02	-6.63E-05	<2E-16	***	0.038 8
Glires	2	5.74E-01	-1.40E-04	6.78E-07	***	0.102 4
	3	3.87E-01	-5.45E-05	1.31E-08	***	0.020 8
	4	2.86E-01	-1.89E-05	3.89E-06	***	0.002 9
	5	2.25E-01	-1.32E-06	5.20E-01	n.s.	0.000 1

^aSignificance level: ***<0.000 1; **<0.001; *<0.05; n.s.: not available.

Supplementary Table S3: Location coordinates for 22 elevational gradients

Supplementary

Supplementary Table S4: Small mammals presence-absence dataset collected from 22 elevational gradients in the low-elevation zones

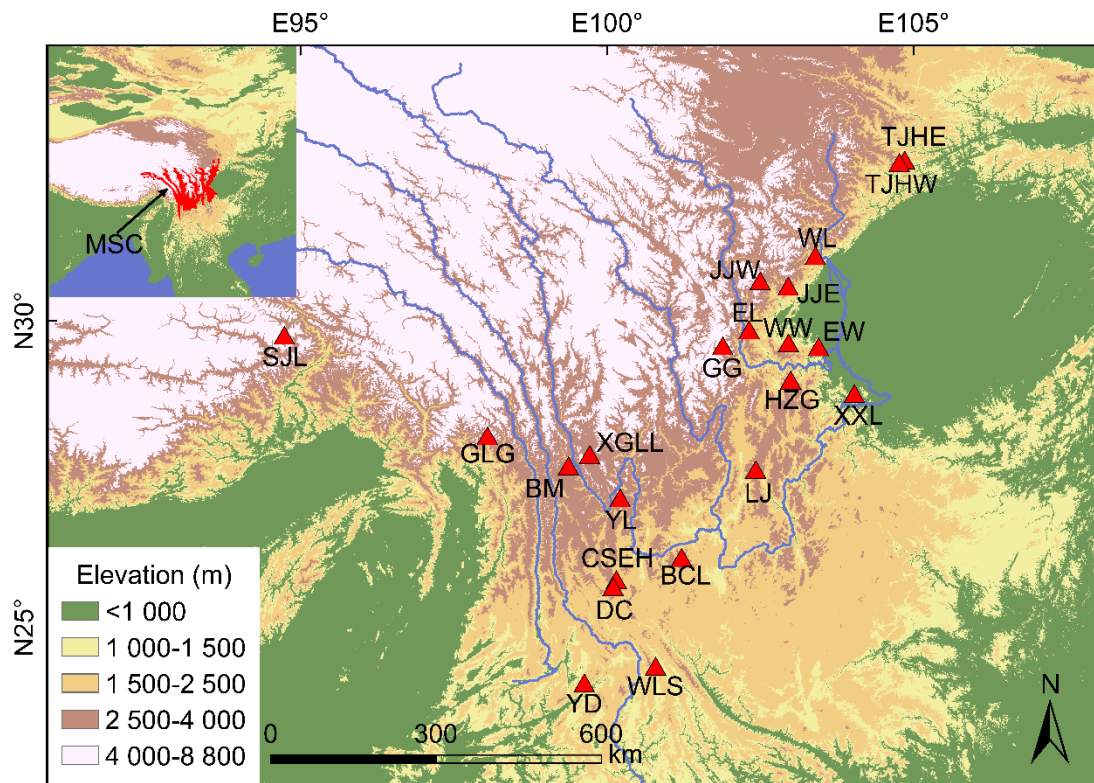
Supplementary Table S5: Small mammals presence-absence dataset collected from 22 elevational gradients in the middle-elevation zones

Supplementary Table S6: Small mammals presence-absence dataset collected from 22 elevational gradients in the high-elevation zones

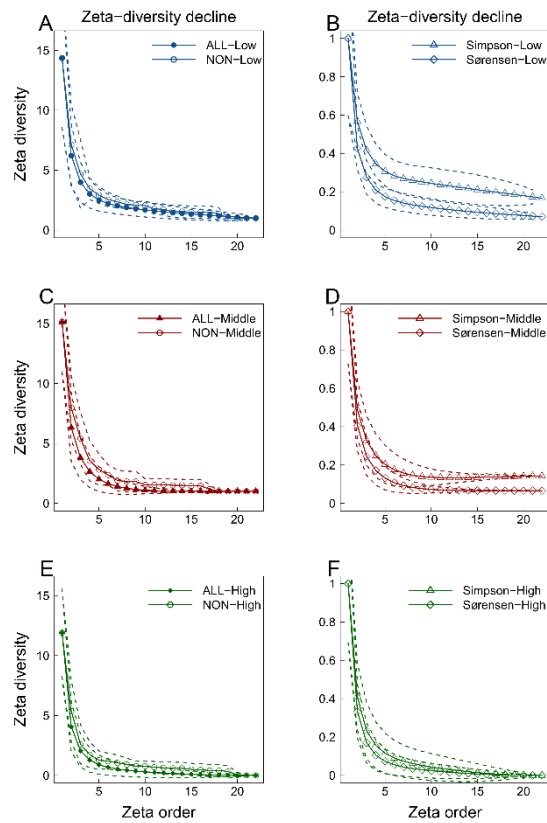
Supplementary Table S7: Presence-absence dataset collected from 22 elevational gradients for the insectivores

Supplementary Table S8: Presence-absence dataset collected from 22 elevational gradients for the glires

Supplementary Table S3–Supplementary Table S8 are listed as separate Excel file due to their large size.

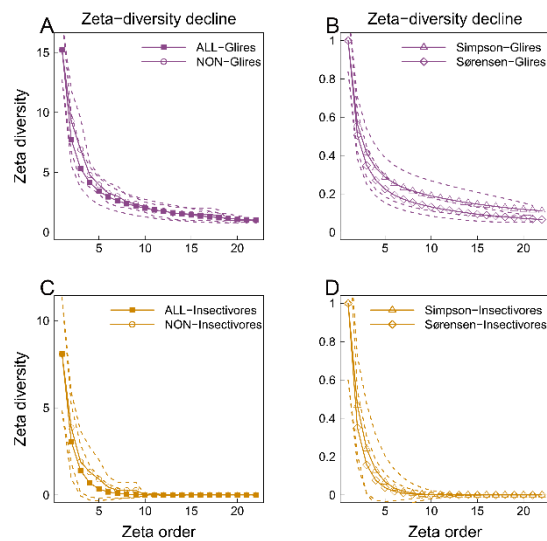


Supplementary Figure S1 Topography of Mountains of Southwest China (MSC)
 Red triangles represent locations of 22 elevational gradients used in this study. See Supplementary Materials for details on 22 elevational gradients.



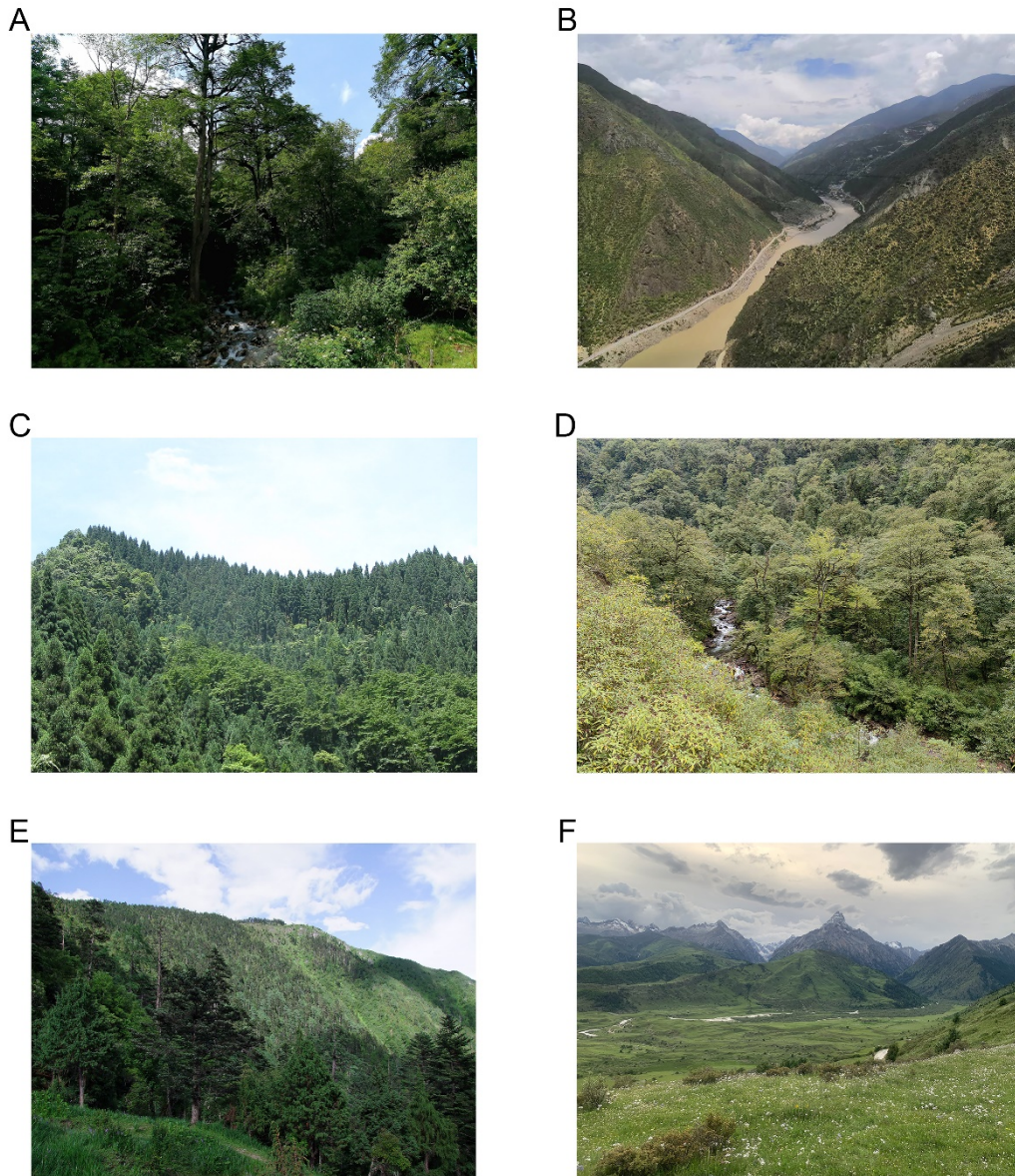
Supplementary Figure S2 Zeta diversity decline curves obtained using different sample selection schemes and normalized zeta values for small mammal communities at low- (A, B), mid- (C, D), and high-elevation zones (E, F)

A, C, E: Different sample selection schemes (all combinations: ALL; non-directional nearest-neighbors: NON). B, D, F: Different normalized zeta values (Simpson- and Sørensen-equivalent). ALL combination sample selection scheme was used for normalized zeta values (B, D, F). Dashed lines indicate 95% confidence intervals.



Supplementary Figure S3 Zeta diversity decline curves obtained using different sample selection schemes and normalized zeta values for glire (A, B) and insectivore communities (C, D) for all elevation zones

A, C: Different sample selection schemes (ALL and NON). B, D: Different normalized zeta values (Simpson- and Sørensen-equivalent). ALL combination sample selection scheme was used for normalized zeta values (B, D). Dashed lines indicate 95% confidence intervals.



Supplementary Figure S4 Typical habitat types in MSC

A: Evergreen broadleaf forests. B: Dry-hot valley shrublands. C: Coniferous and deciduous broadleaf mixed forests. D: Evergreen and deciduous mixed broadleaf forests. E: Dark coniferous forests. F: Meadows.