Ecological correlates of extinction risk in Chinese terrestrial mammals

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Abstract

Aim: China is among the countries with highest mammal diversity in the world, but a considerable proportion of Chinese terrestrial mammal species is currently at risk of extinction. For effective conservation, it would be fundamental to answer the following questions: (1) Is extinction risk randomly distributed among families in Chinese terrestrial mammals? (2) If not, which families are more threatened than expected by chance? (3) What are the major ecological predictors of extinction vulnerability? (4) Does taxonomic difference exist in ecological correlates of extinction risk? (5) To what extent does anthropogenic disturbance contribute to variations in extinction risk?

Location: China.

Methods: We collected data on biological traits, environmental factors and anthropogenic disturbance for 453 Chinese terrestrial mammals. We used phylogenetically controlled regression models and model selection to identify predictors of extinction risk for the whole species set and for the three large taxonomic groups (Carnivora, Artiodactyla and Lagomorpha) separately.

Results: We found that extinction risk was not randomly distributed among families. Seven families (old world monkeys, gibbons, cats, civets and genets, musk deer, deer and bovids) contained significantly higher proportions of threatened species than expected by chance. Geographic range size was the only factor consistently supported in all the best models for the whole species set and for three large taxonomic groups. Although considered important in the global model for the whole species set, body weight was a poor predictor of extinction risk in taxon-specific analyses. We also detected considerable differences in ecological correlates of extinction risk among Carnivora, Artiodactyla and Lagomorpha. After controlling for phylogeny, anthropogenic disturbance was not significantly correlated with extinction risk.

Main conclusions: For effective conservation, we should pay special attention to those highly threatened families and the species with limited range size. Our results...
also highlight the importance of performing taxon-specific analyses for conservation practice.

**KEYWORDS**

body size, comparative analysis, elevation, extinction risk, geographic range size, human footprint, mammals, Red list

1 | INTRODUCTION

The ongoing worldwide biodiversity loss is a major global crisis nowadays, and the sixth mass extinction is considered to have arrived (Barnosky et al., 2011; Ceballos et al., 2015). By estimation, recent extinction rates are 100–1,000 times their pre-human levels (Pimm et al., 2014). However, extinction risk is generally not randomly distributed (Bennett & Owens, 1997; Purvis et al., 2000; Russell et al., 1998; Schipper et al., 2008), and highly threatened species often share some common traits (Jones et al., 2003; Purvis, Gittleman, et al., 2000). Meanwhile, the spatial variation of the extrinsic drivers of extinction (e.g., habitat loss, human exploitation, land use and climate change) may also contribute to the variation of extinction risk among species. Identifying species traits and extrinsic factors associated with extinction risk is a crucial task for conservation biologists because they can be used to predict vulnerable species and develop efficient conservation strategies.

In recent decades, many ecological and life history traits have been found significantly correlated with extinction risk (Figure 1; Chichorro et al., 2019; Purvis, Gittleman, et al., 2000; Verde Arregoitia, 2016). First, species with small geographic ranges and small populations are predicted to have higher extinction risk, as they are more likely to suffer serious consequences from local catastrophes, demographic stochasticity and inbreeding (Chichorro et al., 2019; Kattan, 1992). Second, species at higher trophic levels are often more vulnerable, due to the cumulative effects of disturbance along the food chain (Crooks & Soule, 1999). Third, species with longer gestation duration or smaller litter size are more likely to be threatened, as it is difficult for them to compensate for population decline (Purvis, Gittleman, et al., 2000; Verde Arregoitia, 2016). Fourth, species with narrow habitat and/or diet breadth are often more vulnerable, as they cannot effectively utilize alternative resources once the habitat or food resources they relied on are severely destructed (Boyles & Storm, 2007; Chichorro et al., 2019). In addition, diurnal species and arboreal species are often more endangered, probably because they are more susceptible to hunting or logging (Purvis, Gittleman, et al., 2000; Tingley et al., 2013). Finally, larger-sized species are often more prone to extinction than smaller-sized species, possibly because they tend to have lower population densities, slower reproductive rates and more likely to be hunted (Cardillo et al., 2005; Chichorro et al., 2019; Purvis, Gittleman, et al., 2000).

Moreover, a variable of extrinsic factors has frequently been hypothesized to influence extinction risk (Figure 1; Böhm et al., 2016; Cardillo et al., 2004; Murray et al., 2014). First, climatic factors (e.g., temperature and precipitation) may largely determine regional resource availability and thus shape population sizes (Owen-Smith et al., 2005). Moreover, higher minimum elevation may imply more restricted range and cause higher susceptibility to extinction (Böhm et al., 2016). Finally, many significant drivers of population decline and diversity loss are highly related to human impacts, such as habitat fragmentation, biological invasion, climate change, logging and overexploitation (Davies et al., 2006). Thus, anthropogenic disturbance such as human population density and human footprint is highly associated with extinction risk (Cardillo et al., 2004; Di Marco et al., 2018; Olalla-Tárraga et al., 2019). Recent studies have highlighted the importance of simultaneously considering the roles of biological, environmental and anthropogenic factors in analysing extinction risk (Cardillo et al., 2004, 2005; Chen, Chen, et al., 2019; Chen, Qu, et al., 2019; Davidson et al., 2009; Gonzalez-Suarez et al., 2013; Murray et al., 2014).

Previous comparative analyses suggest that while threatened species may share some traits in common, there is often remarkable variation among taxonomic groups or regions in the correlates of extinction risk (Böhm et al., 2016; Cardillo et al., 2008; Davies et al., 2006; Fritz et al., 2009). This means that different taxonomic groups may respond differently to some extent to the threatening processes (Cardillo et al., 2008), and the relative importance of drivers may also vary across space (Davies et al., 2006). Meanwhile, the explanatory power of global models is often much lower than taxon-specific models (Cardillo et al., 2008; Fisher & Owens, 2004). Therefore, conducting focussed analyses on certain taxonomic groups or countries with highest threat should provide more valuable information for conservation (Fisher & Owens, 2004; Verde Arregoitia, 2016).

Harbouring 673 mammal species, China is among the countries with highest mammal diversity in the world (Jiang et al., 2015). However, a considerable proportion of mammal species in China is suffering serious extinction risk. According to the China Biodiversity Red List released in 2015, 178 mammal species (26.44%) in China were classified as threatened (Critically Endangered, Endangered or Vulnerable), including many flagship species or umbrella species such as the giant panda (*Ailuropoda melanoleuca*), tiger (*Panthera tigris*) and Asian elephant (*Elephas maximus*) (Jiang, Jiang, et al., 2016). Moreover, as human exploitation has been considered as a major threat to Chinese vertebrates (Chen, Qu, et al., 2019; Li & Wilcove, 2005), it...
would be interesting to systematically assess its role in affecting the extinction risk pattern among Chinese mammals. However, to date, very few studies have explicitly examined the ecological drivers that promote extinction risk of Chinese mammals.

In this study, we performed comparative analyses of extinction risk in Chinese terrestrial mammals by considering both species traits and extrinsic factors. We addressed the following questions: (1) Is extinction risk randomly distributed among families in Chinese terrestrial mammals? (2) If not, which families are more threatened than expected by chance? (3) What are the major ecological predictors of extinction vulnerability? (4) Are there taxonomic differences in terms of ecological correlates of extinction risk? (5) To what extent does anthropogenic disturbance contribute to variations in extinction risk among Chinese terrestrial mammals? Answers to these questions are highly important for conservation biologists and policymakers, enabling them to focus on currently and potentially threatened species and to develop effective conservation strategies.

2 | METHODS

2.1 | Data collection

We obtained information on extinction risk of Chinese terrestrial mammals from the recently released China Biodiversity Red List (hereafter CBRL; Jiang, Jiang, et al., 2016). This Red List basically adopted “the IUCN Red List Categories and Criteria” (ver. 3.1) and “Guidelines for Application of IUCN Red List Criteria at Regional and National Levels” (ver. 4.0) to assess the extinction risk of species from China. We used the CBRL rather than the IUCN Red List for three reasons. First, the aim of the present study is to evaluate the local rather than global extinction risk of Chinese mammals. Second, data quality and availability for mammal species at the national scale are often better than those of global scale (Chen, Chen, et al., 2019; Chen, Qu, et al., 2019; Milner-Gulland et al., 2006; Wang et al., 2018). Finally, the findings from country-oriented studies are easier to incorporate into effective conservation strategies.
strategies (Chen, Chen, et al., 2019; Verde Arregoitia, 2016; Wang et al., 2018). Following the protocol used by Purvis, Gittleman, et al. (2000), we defined extinction risk by using ranking numbers: 0 = Least Concern (LC), 1 = Near Threatened (NT), 2 = Vulnerable (VU), 3 = Endangered (EN), 4 = Critically Endangered (CR) and 5 = Extinct (EX) or Extinct in the wild (EW).

Some species were excluded from our analyses for several reasons. First, all the bats (134 species) and marine mammals (44 species) were excluded due to the lack of ecological trait data for most of species. Second, 38 data-deficient (DD) species and Homo sapiens were excluded following the protocol in previous studies (Cardillo et al., 2008; Purvis, Gittleman, et al., 2000; Wang et al., 2018). In addition, we also excluded three regionally extinct (RE) species (Rhinoceros unicornis, R. sondaicus, Dicerorhinus sumatrensis) because of the deficiencies of detailed species data. Finally, a total of 453 species, representing 91.52% of all Chinese terrestrial mammals (Jiang, Li, et al., 2016), were retained to analyse the pattern of extinction risk (Table S1). For the five largest orders in the CBRL, 89.30% of Rodentia (192 species), 89.74% of Soricomorpha (70 species), 98.51% of Artiodactyla (66 species), 91.38% of Carnivora (53 species) and 97.14% of Lagomorpha (34 species) were included in the analyses (Jiang, Li, et al., 2016).

Information on eight life history and ecological traits was collected for each species (Table S1). We selected these traits because they are commonly suggested to affect extinction vulnerability and are available for most species involved in this study. These traits were body weight, litter size, habitat use, active period, trophic level, habitat breadth, diet breadth and geographic range size. We used mean adult body weight as a measure of body size (Cardillo et al., 2008). Litter size was defined as median number of offspring per litter (Thornton et al., 2011). Habitat use was classified as fresh water (1), subterranean (2), terrestrial (3) and arboreal (4) (Davidson et al., 2009). Active period was defined as nocturnal (1), crepuscular (2), diurnal (3) and cathemeral (4) (Chen, Qu, et al., 2019). Trophic level was classified as omnivore (1), herbivore (2) and carnivore (3) (Thornton et al., 2011). To obtain information on habitat breadth, we adopted the IUCN habitat classification scheme to classify the major habitats as forest, savanna, shrubland, grassland, inland wetlands, rocky areas, caves, desert, marine neritic, marine oceanic, marine coastal, marine intertidal, artificial terrestrial/aquatic and exotic vegetation. We then calculated habitat breadth as the number of habitats that a species has reportedly occurred in (Wang et al., 2015). Similarly, we classified seven major food types for mammals as vertebrate, invertebrate, egg, nectar, leaf/stem/flower, fruit and seed. Diet breadth was represented by the number of food types that a given species has reportedly utilized (Meyer et al., 2008; Thornton et al., 2011). To obtain recent geographic range size, we digitized the latest distribution map for each species from the book China’s Mammal Diversity and Geographic Distribution (Jiang et al., 2015) and calculated the range size within China (in km²) by using ArcGIS 10.1 (ESRI Inc., 2016). Compared with the frequently used IUCN range maps, the distribution maps provided in this book were more accurate and fine-grained (Jiang et al., 2015). In the above species traits, habitat use was categorical, while activity period and trophic level were ordinal, with larger numbers indicating higher extinction risk.

All the above trait data were collected from the most recent sources, including IUCN (2019) and many research papers, most of which were published in Chinese. Huisheng Gong and Zhigao Zeng provided some unpublished data on insectivores, Rodentia and large herbivores. Global databases such as PanTHERIA (Jones et al., 2009) and Amniote (Myhrvold et al., 2015) were used as supplementary references.

Within the geographic range of each species, we also collected data on six environmental and geographical variables: mean annual temperature (MAT), mean annual precipitation (MAP), centroid latitude (LA), average elevation (MeanE), minimum elevation (MinE) and maximum elevation (MaxE) (Table S1). Data sets of climatic factors (representing mean values of multi-year recordings obtained from local weather stations) and the digital elevation model with a 1 × 1 km resolution were provided by the Data Center for Resources and Environmental Sciences, Chinese Academy of Sciences (RESDC, http://www.resdc.cn). We then used ArcGIS 10.1 (ESRI Inc., 2016) to calculate MAT, MAP, as well as the average, minimum and maximum elevations within the geographic range for each species.

We used two variables to represent the level of anthropogenic disturbance: human footprint index (HFP) in 2015 within geographic range and human exploitation (whether the species was reportedly exploited by human or not) (Table S1). Following the protocols proposed by Venter et al. (2016), we used relevant data sets on land use/land cover, artificial light at night, roadways and railways (provided by RESDC, all scaled to a 1 × 1 km resolution) to calculate the HFP of China in 2015. To estimate HFP, each type of human pressure was scored between 1 and 10 according to its estimated impact on the environment and the scores in each 1-km² grid cell were then summed up to generate a total score (Venter et al., 2016). To quantify human exploitation, we collected the relative information on human exploitation from IUCN (2019) and a variety of Chinese publications such as Medicinal Fauna of China and Identification atlas of common illegal trade wild animals and products (Li et al., 2013; Yang & Hu, 2016). As a supplement, we also conducted an extensive survey on a Chinese search engine (www.baidu.com) for reliable Chinese reports on hunting, trade and smuggling of mammals. For each species, human exploitation was roughly set to 1 (reportedly utilized) or 0 (unutilized). We used an equal area projection (1 × 1 km resolution) for all the above environmental and anthropogenic variables to avoid the influences of the scale dependence of range maps (Hurlbert & Jetz, 2007).

2.2 | Statistical analyses

2.2.1 | The pattern of extinction risk in Chinese terrestrial mammals

We used the simulation method proposed by Bennett and Owens (1997) to evaluate whether variation in extinction risk among Chinese mammal families can be attributed to random processes. According to the CBRL, 150 out of the 453 species were classified as threatened.
(Critically Endangered, Endangered or Vulnerable) (Jiang, Jiang, et al., 2016). We thus randomly picked 150 species from the 453 species and recorded which families these species were from using the classification of Jiang et al. (2015). We calculated the proportion of species that were randomly selected in each family. This simulation was repeated 10,000 times so that no significant variation in proportions was found. We then drew a histogram of the mean number of families in each proportion class across the 10,000 simulations. The histogram was divided into ten bins, each with a magnitude of 0.1. This histogram thus provided the predicted distribution based on random processes. It is expected that such a predicted distribution should not significantly differ from the observed pattern, if extinction risk was randomly distributed among families (Bennett & Owens, 1997). We then conducted a chi-square test to test the null hypothesis that the observed and predicted distributions did not differ (Sokal & Rohlf, 1995). Before conducting the chi-square test, we combined several threatened groups into one group (0.5–0.9) as these threatened groups consist of very small predicted frequencies.

To identify which families contained an unexpected large number of threatened species, we followed the protocol of Bennett and Owens (1997). For each family, we developed a predicted distribution based on the null hypothesis that the species in each family are threatened randomly. Under this hypothesis, the probability for a family of N species to contain K threatened species should follow a binomial distribution, with the overall probability of a species as threatened being 0.3311 (150/453) for the CBRL. As we tested this issue independently for each of the 33 families, we used the Dunn–Sidak method to adjust the critical values. For 33 independent tests, the adjusted critical values corresponding to significance levels of 5% and 1% are \( p < 1.55 \times 10^{-3} \) and \( p < 3.05 \times 10^{-4} \), respectively.

However, binomial tests are less effective for relatively small families, which may contain disproportionately high phylogenetic diversity (Bennett & Owens, 1997; Chen, Chen, et al., 2019). To overcome this problem, we calculated the phylogenetic originality (OG) proposed by Pavoine et al. (2005) for each of the 33 families. This metric represents the terminal branch of the evolutionary history within a family, indicating how unique that evolutionary history is in the whole phylogeny (Vamosi & Wilson, 2008). In this sense, families with a higher mean OG per threatened species deserve additional conservation attention. We then conducted a t test to compare the mean OG per species between small (defined as those families with 6 or fewer species per family, \( n = 17 \)) and large families (families with at least 7 species per family, \( n = 16 \)). We also used the Mann–Whitney U test to determine whether small families possessed a higher proportion of threatened species than large families.

### 2.2.2 Ecological correlates of extinction risk in Chinese terrestrial mammals

We built phylogenetic generalized least squares (PGLS) models to evaluate the relative roles of species traits and extrinsic factors in determining extinction risk, while controlling for the non-independence between species (Orme et al., 2012). A set of relevant PGLS models were fitted using the “pgls” function of the “caper” package in R (Orme et al., 2012). As a branch length transformation indicating the strength of the phylogenetic signal, Pagel's λ (Pagel, 1999) was optimized for each model by the maximum likelihood method, while the other two branch length transformations (κ and e) were set as constant (1) (Orme et al., 2012). All continuous variables were log-transformed to meet the assumption of normality.

As geographic range size is often used as a criterion of vulnerability assessment (IUCN Criteria B and D2) (Baillie et al., 2004), there is a danger of circular inference in exploring the causal relationship between geographic range size and extinction risk (Cooper et al., 2008; Verde Arregoitia, 2016). To overcome this problem, we simply excluded 118 species assessed as threatened on the basis of small range size from analyses (Table S1) following previous studies (Cooper et al., 2008; Jones et al., 2003; Wang et al., 2018). Therefore, our PGLS modelling was based on the remaining 335 Chinese mammal species. We built the phylogenetic tree for these species (Figure 2) using the updated global phylogenetic tree of mammals provided by Upham et al. (2019).

We first conducted univariate PGLS models to evaluate the significance of each of the sixteen explanatory factors (Chen, Qu, et al., 2019; Jones et al., 2003; Purvis, Gittleman, et al., 2000). We then used correlations between variables to assess the potential effect of multicollinearity on the results of multiple regressions (Neter et al., 1996). Some highly correlated (Pearson R > .6) variables were excluded from analyses to avoid multicollinearity (Table S2). We further tested the significance of the possible combinations of important predictors (the marginally significant variables with \( p < .1 \) found in the previous step) in promoting extinction vulnerability (Table S3; Chen, Zeng et al., 2019; Price & Gittleman, 2007). The Akaike information criterion corrected for small sample size (AICc) was used for model selection, with models differing by less than 2 AIC units considered equivalent. In this scenario, we also reported results from model averaging by using the conditional averaged models (Barton, 2014; Burnham & Anderson, 2002).

To avoid the skewed distribution often associated with ordinal-scaled data (Davidson et al., 2009), we also used a standard phylogenetic binomial regression implemented in the R package “phyr” to repeat the above modelling procedures with the dependent variable dichotomized into 0 (non-threatened) and 1 (threatened) (Dinnage et al., 2018; Li et al., 2019). As the results were generally similar (Tables S4–S5), we only reported the results for the non-dichotomized response variable.

In order to explore whether there were differences in ecological correlates of extinction risk among taxonomic groups, after excluding the species assessed as threatened on the basis of small range size, we repeated the PGLS analysis procedures described above separately for each of the three orders: Carnivora (33 species), Artiodactyla (15 species) and Lagomorpha (33 species) (Table S3). Rodentia (179 species) and Soricomorpha (59 species) were excluded from analyses because all endangered species in these two orders were evaluated based on small range size (Jiang, Jiang, et al., 2016).
RESULTS

3.1 The pattern of extinction risk in Chinese terrestrial mammals

Among the 453 terrestrial mammal species considered in our study, a total of 150 (33.11%) species were classified as threatened by the CBRL (Critically Endangered, Endangered or Vulnerable) (Table S1). Within these threatened species, 3 species were extinct in the wild, 54 were critically endangered, 45 were endangered, and 48 were vulnerable. Moreover, 100 (22.07%) species were near-threatened and 203 (44.81%) species were currently not threatened (Least Concern) (Table S1).

The predicted and observed frequency distribution patterns of extinction risk among families were significantly different ($\chi^2 = 35.35, df = 5, p < .001$; Figure 3). Seven families were found...
to contain significantly more threatened species than expected by chance (Table 1): cats (Felidae), gibbons (Hylobatidae), musk deer (Moschidae), old world monkeys (Cercopithecidae), civets and genets (Viverridae), deer (Cervidae) and bovids (Bovidae). Although all the species in six small families were threatened (100%), including bears (Ursidae), slow lorises (Lorisidae), pangolins (Manidae), elephants (Elephantidae), red pandas (Ailuridae) and wild camels (Camelidae), these high proportions were not statistically significant (Table 1).

Among the above 13 families, except Camelidae, Viverridae and Bovidae, all families also contained high proportions of threatened species global as assessed by IUCN (>50%, Figure 4). Elephantidae, Manidae, Camelidae, Lorisidae, Castoridae, Tragulidae and Equidae were the seven families with mean originality (OG) per threatened species larger than 1% (Table S6). Generally, small families (mean OG = 0.025) possessed significantly higher OG per species than large families (mean OG = 0.002) (t = 2.62, df = 31, p < .05; Table S6). Compared with larger families, small families also contained a marginally higher proportion of threatened species (Mann-Whitney test, p < .1). However, four families were significantly less threatened than expected by chance (Table 1): hamsters (Cricetidae), rats (Muridae), squirrels (Sciuridae) and shrews (Soricidae).

### 3.2 Ecological correlates of extinction risk in all species

Univariate PGLS models suggested that the extinction risk of Chinese terrestrial mammals increased significantly with small range size, large body weight, decreased nocturnality, narrow habitat or diet breadths, high minimum elevation and low maximum elevation (Table 2). Human exploitation and human footprint index (HFP) were not significantly correlated with extinction vulnerability after controlling for phylogeny (Table 2).

According to model selection based on AIC<sub>c</sub>, the best multivariate model suggested that Chinese terrestrial mammals were more vulnerable to extinction if they had smaller range size and larger body weight, and were less nocturnal (Table 3). Range size and body weight were included in all the eight best models (with ΔAIC<sub>c</sub> < 2), while the effects of diet breadth, maximum elevation and habitat breadth were inconsistent among models (Table 3). Model averaging suggested similar results, with geographic range size and body weight being identified as the two most important predictors of extinction risk (Table 4).

### 3.3 Ecological correlates of extinction risk in major taxonomic groups

For Carnivora, univariate PGLS analyses showed that high extinction risk was significantly related to small range size, narrow diet breadth, low maximum elevation and human footprint index (HFP) (Table 2). However, the best multivariate model based on AIC<sub>c</sub> suggested that only small range size and narrow diet breadth were important predictors of extinction risk (Table 3). Model averaging also indicated that geographic range size and diet breadth were the two most consistent predictors among models (Table 4).

For Artiodactyla, small range size, activity period, mean and maximum elevation were significantly correlated with extinction risk in the univariate PGLS analyses (Table 2). However, multivariate PGLS analyses and model averaging could not be conducted due to the small sample size of Artiodactyla (n = 15) (Table 2). For Lagomorpha, small range size and minimum elevation were the only two important predictors of extinction risk identified by univariate PGLS analyses (Table 2), which preventing the use of model averaging.

### 4 DISCUSSION

In this study, we conducted the most extensive study to date to explore the patterns and ecological drivers of extinction risk in Chinese terrestrial mammals. Although Liu and Li (2005) also conducted a similar research, only two intrinsic traits (body size and litter size) were used in their study. Our study thus has obvious advantages and can obtained comprehensive results as it was based on sixteen biological traits and environmental factors. We found that the extinction risk in Chinese terrestrial mammals was not randomly distributed among families. Certain families were unusually threatened and thus deserve special attention. However, ecological correlates of extinction risk varied greatly among taxonomic groups and geographic range size was the only common predictor that received consistent support.

### 4.1 The pattern of extinction risk in Chinese terrestrial mammals

We found that the extinction risk in Chinese terrestrial mammals was not randomly distributed among families. Seven families were found to contain unexpectedly high number of threatened species, including monkeys, gibbons, cats, civets and genets, deer.
and musk deer. As the binomial test is relatively less powerful when a family is small (Bennett & Owens, 1997; Sokal & Rohlf, 1995), six small families (bears, slow lorises, pangolins, red pandas, wild camels and elephants) containing unusually high proportions (100%) of threatened species were not assessed as significantly threatened. Actually, our results suggest that small families tend to suffer higher extinction risk. As in birds and amphibians (Bennett & Owens, 1997; Chen, Chen, et al., 2019), these small families often represent a large portion of diversity in terms of ecology and life history. Therefore, these small endangered families also need prior conservation attention because species extinction from these families may imply a disproportionally large loss of biodiversity.

It should be noted that all the above 13 families containing unusually high proportions (>70%) of threatened species assessed by the CBRL are large-sized mammals (Table S1). Their threat pattern is thus typically associated with their large body size (Cardillo et al., 2005). These families also tend to fall above the 5 kg cut-off mentioned in several studies (Cardillo, 2003), for which threatening processes are similar across taxonomic groups.

### TABLE 1

| Family      | Common name     | No. species in the family | No. species threatened | Proportion threatened | Binomial probability |
|-------------|-----------------|--------------------------|------------------------|-----------------------|----------------------|
| Felidae     | Cat             | 12                       | 12                     | 1.00                  | 1.74 × 10^−2        |
| Hylobatidae | Gibbon          | 6                        | 6                      | 1.00                  | 1.32 × 10^−1        |
| Moschidae   | Musk deer       | 6                        | 6                      | 1.00                  | 1.32 × 10^−1        |
| Ursidae     | Bear            | 4                        | 4                      | 1.00                  | 0.012                |
| Lorisidae   | Loris           | 2                        | 2                      | 1.00                  | 0.11                 |
| Manidae     | Pangolin        | 2                        | 2                      | 1.00                  | 0.11                 |
| Aluridae    | Red panda       | 1                        | 1                      | 1.00                  | 0.33                 |
| Camelidae   | Camel           | 1                        | 1                      | 1.00                  | 0.33                 |
| Elephantida | Elephant        | 1                        | 1                      | 1.00                  | 0.33                 |
| Cercopithecidae | Old world monkey | 17                    | 16                     | 0.93                  | 2.37 × 10^−2        |
| Viverida    | Civet and genet | 11                      | 9                      | 0.82                  | 1.18 × 10^−1        |
| Cervidae    | Deer            | 27                       | 24                     | 0.82                  | 2.64 × 10^−2        |
| Bovidae     | Bovid           | 30                       | 24                     | 0.80                  | 1.60 × 10^−2        |
| Cricetidae  | Hamster         | 63                       | 1                      | 0.016                 | 1.53 × 10^−1        |
| Muridae     | Rat             | 53                       | 3                      | 0.057                 | 5.06 × 10^−2        |
| Sciuridae   | Squirrel        | 43                       | 4                      | 0.093                 | 5.19 × 10^−1        |
| Soricidae   | Shrew           | 53                       | 5                      | 0.094                 | 1.29 × 10^−1        |

Note: Binomial probability was calculated based on \( p = 0.3311 \) (150 threatened species out of a total of 453 terrestrial mammal species).

*Adjusted significantly at the 5% level allowing for multiple comparisons.; **Adjusted significantly at the 1% level allowing for multiple comparisons.

**FIGURE 4**  Families containing high proportions of threatened species according to the China Biodiversity Red List (2015) (red colour) and IUCN (2019) (blue colour). The numbers above the bars are number of species in a family.
4.2 | Ecological correlates of extinction risk in Chinese terrestrial mammals

We found that after excluding those species assessed as threatened based on restricted range size, geographic range size is still the most important factor in determining extinction vulnerability in Chinese terrestrial mammals. Range size is the only explanatory factor consistently supported in both the global model and the three taxon-specific models, suggesting its universal importance in promoting extinction risk. The relationship between range size and extinction has previously been observed in amphibians (Chen, Chen, et al., 2019; Chichorro et al., 2019). Small range size may contribute to extinction vulnerability through many ways, such as increasing risk of inbreeding, demographic stochasticity and local catastrophes (Cooper et al., 2008; Jones et al., 2003). In addition, small range size is often indicative of past decline, and therefore increased species vulnerability to extinction (Turvey et al., 2015, 2017).

As body size is often closely associated with many important factors that put species at risk (Cardillo et al., 2005; Purvis, Gittleman, et al., 2000), it is reasonable to predict a strongly positive relationship between body size and extinction risk. However, sometimes larger body size may also be beneficial, as larger species may have better dispersal ability (Jenkins et al., 2007), larger ranges and higher survival rates (McCarthy et al., 2008). The association between body size and extinction risk may thus be complex (Chen, Zeng, et al., 2019; Meyer et al., 2008). Our study presents mixed results on the role of body size in extinction risk of Chinese terrestrial mammals. After controlling for range size, body weight is the most significant factor in all mammal species. However, this is not the case in taxon-specific models. None of the three orders support the association between extinction vulnerability and body weight. This implies that body weight may not be a reliable predictor when focusing on narrow taxonomic groups, and its significant role detected in the global model may be a cumulative result across taxa.

We found that environmental factors also played a role in regulating the extinction risk of Chinese terrestrial mammals. For Lagomorpha, minimum elevation was positively associated with higher extinction risk in the univariate PGLS analyses. Moreover, maximum elevation was negatively correlated with extinction risk in Artiodactyla. Minimum elevation was found to be negatively correlated with maximum elevation (Table S2). The positive relationship between minimum elevation and extinction risk in Chinese mammals is probably because higher minimum elevation results in smaller altitudinal range, reflecting a narrower climatic niche which may put species at risk (Chen, Chen, et al., 2019; Chichorro et al., 2019).

As many crucial processes related to extinction (such as habitat loss, logging and biological invasion) are caused by human pressure, it would be reasonable to infer that HFP is an important

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**TABLE 2** Results of univariate PGLS models predicting extinction risk in Chinese terrestrial mammals using the criteria of China Biodiversity Red List (2015)

| Variable                        | All species (335 spp.) | Carnivora (33 spp.) | Artiodactyla (15 spp.) | Lagomorpha (33 spp.) |
|---------------------------------|------------------------|---------------------|------------------------|-----------------------|
|                                 | Slope | t (p) | Slope | t (p) | Slope | t (p) | Slope | t (p) |
| Range size                      | -0.17 | -9.25*** | -0.38 | -4.18*** | -0.52 | -3.66*** | -0.31 | -6.33*** |
| Body weight                     | 0.10  | 2.56*  | 0.01  | 0.02  | 0.23  | 0.52  | -0.11 | -0.70  |
| Activity period                 | 0.13  | 2.26*  | -0.13 | -0.65  | 1.02  | 2.13*  | 0.21  | 0.97   |
| Microhabitat                    | 0.13  | 1.07   | -0.14 | -0.48  | /     | /     | /     | /     |
| Trophic level                   | 0.10  | 1.04   | 0.29  | 1.31   | 1.93  | 1.05   | /     | /     |
| Litter size                     | -0.02 | -0.56  | -0.10 | -0.87  | -0.26 | -0.68  | 0.10  | 0.65   |
| Habitat breadth                 | -0.09 | -1.93+ | 0.03  | 0.30   | -0.65 | -1.75  | -0.21 | -0.87  |
| Diet breadth                    | -0.10 | -1.92+ | -0.40 | -3.35** | -0.48 | -1.28  | -0.43 | -1.00  |
| Mean elevation                  | 0.01  | 0.13   | 0.45  | 1.09   | -1.24 | -2.18* | 0.13  | 0.75   |
| Maximum elevation               | -0.44 | -4.47***| -1.49 | -2.49* | -2.52 | -4.34***| -0.26 | -0.79  |
| Minimum elevation               | 0.01  | 3.34*** | 0.01  | 1.84+  | 0.01  | 0.31   | 0.01  | 3.36** |
| Mean latitude                   | -0.32 | -1.47  | -0.73 | -0.90  | -1.16 | 0.47   | -0.35 | -0.41  |
| Mean annual precipitation       | -0.03 | -0.33  | -0.17 | -0.65  | -0.19 | -0.34  | -0.20 | -0.93  |
| Mean annual temperature         | 0.01  | 1.27   | 0.01  | 0.21   | 0.07  | 1.26   | -0.01 | -0.04  |
| Human footprint index           | 0.06  | 0.31   | -4.64 | -2.72* | 0.37  | 0.13   | 0.37  | 0.73   |
| Human exploitation index        | 0.03  | 0.23   | -0.98 | -1.97+ | /     | /     | 0.27  | 0.59   |

Note: Significant correlations were marked in bold: +p < .1, *p < .05, **p < .01, ***p < .001. Variables underlined were excluded in the following analyses to avoid the multicollinearity (see Table S2 for details). Variables with zero variance were marked with slashes (/).
predictor of extinction risk (Venter et al., 2016). In our study, however, HFP was not significantly related to extinction risk of Chinese terrestrial mammals. An explanation for this result is that a considerable time lag may exist between human pressure and significant population decline, so that current extinction risk is more associated with past rather than relatively recent level of human activities (Turvey et al., 2015, 2017). According to the extinction filter effects (Balmford, 1996), some vulnerable species may have already disappeared from those densely populated areas. Nowadays, many highly threatened species can only be found in Chinese natural reserves, where changes in human pressure are relatively low. In summary, our results suggest that the relationship between human pressure and extinction vulnerability may be more complex than previously thought.

It is suggested that human exploitation is a major threat to Chinese vertebrates (Chen, Qu, et al., 2019; Li & Wilcove, 2005). However, human exploitation on Chinese terrestrial mammals was not an important predictor of extinction risk after controlling for phylogeny. An explanation for this result is that human exploitation is concentrated in certain clades (Chen, Qu, et al., 2019; Li et al., 2013), so that it is not a general correlate of extinction risk. Another possible reason is that our estimate of human overexploitation is quite coarse. At present, we can only quantify human exploitation qualitatively (whether the species are utilized or unutilized), not quantitatively (magnitude of exploitation).

### Table 3: The performance of PGLS models predicting the extinction risk of Chinese terrestrial mammals using the criteria of China Biodiversity Red List (2015)

| Model Details | k | AICc | ΔAICc | wi |
|---------------|---|------|-------|----|
| All species   |   |      |       |    |
| RS + BW + AP  | 4 | 728.679 | 0 | 0.1209 |
| RS + BW + DB  | 4 | 729.101 | 0.422 | 0.0979 |
| RS + BW       | 3 | 729.148 | 0.469 | 0.0956 |
| RS + BW + AP + DB | 5 | 729.199 | 0.520 | 0.0932 |
| RS + BW + AP + MaxE | 5 | 729.895 | 1.216 | 0.0658 |
| RS + BW + MaxE | 4 | 730.295 | 1.616 | 0.0539 |
| RS + BW + DB + MaxE | 5 | 730.503 | 1.824 | 0.0486 |
| RS + BW + AP + DB + MaxE | 6 | 730.626 | 1.948 | 0.0457 |
| Carnivore     |   |      |       |    |
| RS + DB       | 3 | 85.007 | 0 | 0.2186 |
| RS + HFP      | 3 | 85.484 | 1.478 | 0.1044 |
| RS           | 2 | 85.561 | 1.554 | 0.1005 |
| RS + DB + HEI | 4 | 85.683 | 1.677 | 0.0945 |
| RS + DB + HFP | 4 | 86.008 | 2.002 | 0.0804 |
| RS + DB + MaxE | 4 | 86.512 | 2.505 | 0.0625 |
| RS + HEI      | 3 | 87.04 | 3.033 | 0.048 |
| RS + HFP + HEI | 4 | 87.146 | 3.139 | 0.0455 |
| RS + DB + HFP + HEI | 5 | 87.811 | 3.805 | 0.0326 |
| RS + MaxE     | 3 | 87.868 | 3.862 | 0.0317 |

Note: The table shows model rank, AICc, ΔAICc from the top model and model weight (wi). Only those with ΔAICc < 4 were listed.

Abbreviations: AP, Active period; BW, Body weight; DB, Diet breadth; HB, Habitat breadth; HEI, Human exploitation index; HFP, human footprint index; LS, Litter size; MaxE, Maximum elevation; MeanE, Mean elevation; MH, Microhabitat; MinE, Minimum elevation; MT, Mean temperature; RS, Range size.
We found considerable differences in ecological correlates of extinction risk among taxonomic groups. For Carnivora, high extinction risk was correlated with small range size and narrow diet breadth. For Lagomorpha, small range size and minimum elevation were two important predictors of extinction risk. For Artiodactyla, small range size, activity period, mean and maximum elevation were correlated with extinction risk. The main reason for their differences in correlates of extinction risk may be due to the huge differences in ecological and life history traits, and responses to environmental factors and human disturbance among taxonomic groups (Cardillo et al., 2008; Jiang, Jiang, et al., 2016; Jiang et al., 2015). The results also suggest that these taxonomic groups should be conserved with different management measures by considering their taxon-specific correlates of extinction risk.

Other ecological traits that had been suggested to significantly affect extinction vulnerability of mammals were not included in the present study. For example, sleep-or-hide behaviour, home range size, gestation length, weaning age and population fluctuation are found to promote extinction vulnerability of mammals (Henle et al., 2004; Liow et al., 2009; Verde Arregoitia, 2016; Vucetich et al., 2000). It is possible that these traits (alone or in combination) would explain some of the remaining variation in extinction vulnerability in Chinese terrestrial mammals. However, the reliable values of these traits are currently not available for a large proportion of mammal species in our study and therefore cannot be incorporated in analyses at this stage.

There are a few important implications from this study that need fleshing out. First, the binomial test has relatively less statistical power when a family is small (Sokal & Rohlf, 1995) in spite of the fact small families may contain unusually high proportions of threatened species (Bennett & Owens, 1997; Wang et al., 2018). Future studies should try to propose more sensitive statistical methods to overcome this potential limitation. Second, although body weight was important in the global model for the whole species set, it was a poor predictor of extinction risk in the taxon-specific analyses. This taxonomic effect of body weight on extinction risk should be considered in future studies. Finally, we found that after controlling for phylogeny, human exploitation and HFP were not related to extinction risk. However, this does not mean that the negative effects of human pressure should be ignored. As documented above, the lack of significance may suggest that several clades have suffered disproportionately high level of exploitation (Chen, Qu, et al., 2019; Li et al., 2013) and that a time lag exists between human exploitation and becoming threatened or extinct (Balmford, 1996). Therefore, the effects of past human disturbance and current exploitation on mammals require more research.

### 4.3 Conservation implications

The results of our study have several general conservation implications for Chinese terrestrial mammals. First, we highlight the non-random distribution of extinction risk among families of Chinese terrestrial mammals. We found seven families (monkeys, gibbons, cats, civets and genets, musk deer, deer, bovids) that possessed significantly larger proportions of threatened species and thus deserve some priorities in conservation effort. As documented above, the lack of significance may suggest that several clades have suffered disproportionately high level of exploitation (Chen, Qu, et al., 2019; Li et al., 2013) and that a time lag exists between human exploitation and becoming threatened or extinct (Balmford, 1996). Therefore, the effects of past human disturbance and current exploitation on mammals require more research.

### TABLE 4 Model-averaged parameter estimates (β), unconditional standard errors (SE) and relative variable importance (w_i) for each variable in the 95% confidence set for predicting the extinction risk of Chinese terrestrial mammals using the criteria of China Biodiversity Red List (2015)

|                      | Lower CI       | Upper CI       | SE          | Z value | p               |
|----------------------|----------------|----------------|-------------|---------|-----------------|
| All species          |                |                |             |         |                 |
| (Intercept)          | 3.033          | 1.622          | 4.444       | 0.72    | 4.214 <.001     |
| Range size           | -0.168         | -0.207         | -0.128      | 0.02    | 8.385 <.001     |
| Body weight          | 0.90           | 0.084          | 0.017       | 0.151   | 0.034 2.465 <.05|
| Activity period      | 0.54           | 0.079          | -0.024      | 0.181   | 0.052 1.5 .133  |
| Diet breadth         | 0.45           | -0.058         | -0.145      | 0.03    | 0.045 1.298 .194|
| Maximum elevation    | 0.32           | -0.088         | -0.288      | 0.111   | 0.102 0.868 .386|
| Habitat breadth      | 0.25           | -0.007         | -0.087      | 0.073   | 0.041 0.168 .867|
| Carnivore            |                |                |             |         |                 |
| (Intercept)          | 7.093          | 0.86           | 13.325      | 3.18    | 2.231 .026      |
| Range size           | 0.97           | -0.321         | -0.544      | -0.099  | 0.114 2.83 <.01 |
| Diet breadth         | 0.59           | -0.252         | -0.482      | -0.022  | 0.117 2.143 <.05|
| Human footprint      | 0.35           | -2.028         | -5.418      | 1.361   | 1.729 1.173 .241|
| Human exploitation   | 0.30           | -0.43          | -1.316      | 0.455   | 0.452 0.952 .341|
| Maximum elevation    | 0.23           | -0.04          | -1.774      | 1.694   | 0.885 0.045 .964|

Note: Important variables (p < .05) were marked in bold.
consistently supported factor in determining the extinction risk of Chinese terrestrial mammals. Generally, paying special attention to small-ranged species should be important for effective conservation of Chinese terrestrial mammals. Finally, considerable differences in ecological correlates of extinction risk exist among taxonomic groups, suggesting that mechanisms observed for one taxon may not apply to other taxa. Therefore, we should use taxon-specific models to direct the conservation practice for each taxonomic group.

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DATA AVAILABILITY STATEMENT
The data used for analyses can be found in the online Supporting Information (Table S1).

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Biosketches

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Supporting Information

Additional supporting information may be found online in the Supporting Information section.

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