

## Quantitative Analysis of Land Mammal Zoogeographical Regions in China and Adjacent Regions

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**Zuo-Fu Xiang, Xing-Cai Liang, Sheng Huo and Shi-Lai Ma (2004)** Quantitative analysis of land mammal zoogeographical regions in China and adjacent regions. *Zoological Studies* 43(1): 142-160. In this paper, our aim was to determine, by means of quantitative analysis, the distribution patterns of the land mammals in China and, adjacent regions using physiographical regions as operative geographical units (OGUs). Based on the pre-sence or absence of 11 orders, 42 families, 197 genera, and 577 species of land mammals in their zoogeographical regions, which were used as OGUs, we studied the biotic boundary between the Oriental Region (OR) and the Palaearctic Region (PR), as well as subregion boundaries. The boundary's statistical significance was tested by G-test as described by McCoy et al. A significantly strong biotic boundary was found to separate the PR from the OR, and there is a weak biotic boundary in the PR, which divides it into 2 subregions. We concluded that the biotic boundary which separates the PR and OR is a strong boundary. We suggest that the Qinghai-Xizang Plateau should be regarded as a subregion of the PR, which can embody its characteristics of high elevations and a frigid climatic, which is called the Qing-Zang subregion of the PR (QZSP).  
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**Key words:** Statistical test, Dendrogram, Cluster analysis, Qinghai-Xizang Plateau.

Zoogeographical regions can usually be distinguished by the distribution of animals in certain physiographical regions. The research on zoogeographical regions can benefit to recognize the history of fauna and the relations among different taxa. In China, there are very intricate topographies, like the Qinghai-Xizang Plateau (QXP), the plains of the lower reaches of the Yangtze River and the Yellow River, etc., variable climates which change from the frigid zone in northernmost to the tropical zone southernmost areas, and very complex geologic histories (i.e., uplift of the QXP). It is these characteristics that make it very difficult to identify the biogeographical patterns of China (Li et al 1981, Committee of Physical Geography of Chinese Academy of Sciences 1985). Integrating the physiography of China and the distribution of special taxa, Zhang (1997) divided Chinese zoogeographical region into 3 subregions, 2 belonging to the Palaearctic Region (PR) and 1 belonging to

the Oriental Region (OR). They are the Northeast Subregion of the PR which is divided into the Northeast Division and the North China Division, the Central Asian Subregion of the PR which is divided into the Mengxin Division and the Qingzang Division, and the Indochinese Subregion of the OR which is divided into the Southwest Division, Central China Division, and South China Division. Recently, many Chinese scholars have undertaken research on the biogeographical patterns of China. For instance, Chen et al. (1996) advocated that the QXP should be regarded as an independent region, which equals the PR and OR, and named it the Qinghai-Xizang Plateau Region (QXPR), in view of the differentiation of the subfamily Schizothroacinae and the genus *Triplophysa* from the Tertiary to the present. Most mammal species have been grouped by many authors, results of which can be found in the literature, e.g., Zheng (1981), Ma et al. (1996), etc. Unfortunately,

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all these studies are based on visual analyses. Nevertheless, as reported by several authors, such as Birks (1987), Real et al. (1992), and Saus-Fuentes and Ventura (2000), the best method for establishing groups of physiographical regions is based on quantitative analyses in order to avoid basic subjective errors and to produce consistent results. Specifically, the main aim of the quantitative analysis of the presence or absence of several taxa in a number of areas is to detect repeatable biogeographical patterns with the data in the form of biotic regions (groups of areas with similar biotas). Some quantitative methods of classification used in defining boundaries between ordered locations can be found in the literature (see McCoy et al. 1986 and references therein). The method outlined by McCoy et al. (1986) is an extension of the probabilistic similarity technique (Crick 1980) used to develop a matrix-analysis method of placing boundaries between the biotas of ordered locations. The advantage of this method is that the G-test can be applied to determine the contingency of groups, which were set up by the unweighted paired-group method using arithmetic averages (UPGMA). This method, complemented by the significance test of the resulting groups according to the approach of Real et al. (1992), constitutes an objective method for measuring the statistical significance of groups obtained from a numerical classification (see Saus-Fuentes and Ventura 2000). However, this method has not been applied to the analysis of land mammal biogeographical patterns of China. Since the foundation of the People's Republic of China (1950s), several important field surveys on land mammals have been carried out in certain regions (i.e., the QXP, Xinjiang region, Transection Mountain region, etc.), all of which have made it become possible for us to apply a quantitative analytical method to the land mammal biogeographical patterns of China and adjacent regions.

The main aim of this paper was to determine the distribution patterns of land mammals in China and adjacent regions by applying quantitative analysis using physiographical regions as operative geographical units (OGUs; Crovello 1981). Specifically, the goals of the study were: (a) to test whether the zoogeographical regions drawn by visual methods are reasonable; and (b) to test whether the QXPR as established by Chen et al. (1996) is rational. In order to achieve these goals, the method of McCoy et al. (1986), complemented by the modifications of Real et al. (1992), the cluster analysis method (UPGMA), the Sokal and

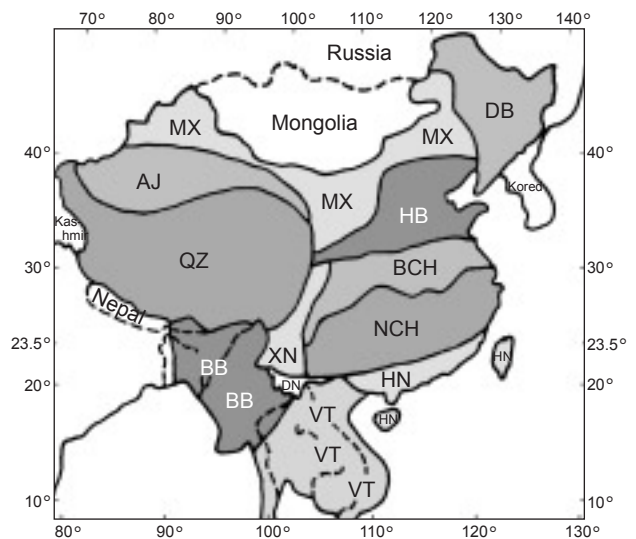
Sneath probabilistic similarity index (Norusis 1997), and Baroni-Urbani and Buser's similarity index (Baroni-Urbani 1976) were used.

## MATERIALS AND METHODS

### Study area

The study area included China, Vietnam, Laos, Thailand, Cambodia, Burma, Bhutan, and part of Bengal and India. For analytical purposes, China was divided into 10 physiographical regions that are defined by the characteristic of geography, climate, and vegetation (adapted from Chen et al. 1996, Zhang et al. 1997 1999), and the other adjacent regions were divided into 2 physiographical regions (Fig. 1).

The Aerjin Mountain region (AJ) is an overlapping portion of the QXPR and Mengxin Division. Qing-Zang Plateau region (QZ) is what remains when the AJ is subtracted from the QXPR. The Mengxin region (MX) is what remains when the AJ is subtracted from the Mengxin Division. The Xinan Mountain region (XN) is the Southwest Division minus the portion, which is already included in the QZPR. Along the Yangtze River, the Central China Division is divided into Bei-



**Fig. 1.** Operative geographical Units (OGUs) of China and adjacent regions. (DB, Dongbei region; HB, Huabei region; MX, Mengxin region; AJ, Aerjin Mountain region; QZ, Qing-Zang Plateau region; BCH, Bei-Changjiang region; NCH, Nan-Changjiang region; XN, Xinan Mountain region; HN, Huanan region; DN, Diannan region; BB, Burma-Bengal region; VT, Vietnam-Thailand region).

Changjiang region (BCH) and Nan-Changjiang region (NCH). The South China Division is divided into the Diannan region (DN) and Huanan region (HN). The Dongbei region (DB) and the Huabei region (HB) are equal to the Northeast Division and North China Division, respectively. The adjacent regions of China are divided into the Vietnam-Thailand region (VT) and the Burma-Bengal region (BB).

### Materials and characteristic of animal distribution in OGUs

According to the literature, we obtained a distribution matrix of 577 land mammals in 12 OGUs (see Appendix, presence "1" and absence "0"; information from Corbet 1978 1992, Hong et al. 1986, Wilson et al. 1992, Zhang et al. 1997 1999). Of the land mammals in China, 2 species were not considered for analysis because the common muskrat musquash (*Ondatra zibethica*) is an allochthonous not an acclimated species and David's deer (*Elaphurus davidianus*) is a reintroduced species that is still being raised in some regions of China even after it was extirpated from the field. We also did not consider the distribution shrinkage of some great land mammals (i.e., tiger *Panthera tigris*, panther *Panthera pardus*, etc.), so the results more accurately reflected these natural distribution patterns of the land mammals. The characteristics of the distributions in each of the OGUs are outlined as follows.

**Dongbei region (DB)**, 6 orders, 19 families, 56 genera, 96 species)

Owing to its cold weather, the number of species in this region is sparse. The main species are of Insectivora, especially, *Sorex* in the Soricidae, *Clethrionomys* in the Rodentia, and Mustelidae species of the Carnivora. Representative species are the least shrew (*Sorex mintutus*), wood lemming (*Myopus schisticolor*) and sable (*Martes zibellina*).

**Huabei region (HB)**, 7 orders, 20 families, 55 genera, 83 species)

The number of land mammal species in this region is fewer than that of the DB. Most are southern extension of DB species. Only a few kinds of *Myospalax*, i.e., Rothschild's zokor (*M. rothschildi*) etc., are endemic. But it should be mentioned that some species that are usually distributed in tropical regions, i.e., the masked palm civet (*Paguma larvata*), rhesus monkey (*Macaca mulatta*), etc., appear in this region occasionally.

**Mengxin region (MX)**, 7 orders, 22 families, 76

genera, 139 species)

This region is far removed from the sea, and the weather is arid or semiarid. The majority of species that adapted to this natural condition are of the Rodentia, whose number exceeds 1/2 of the total. Most species of the Cricetinae and Gerbillinae are endemic. Some representative species, i.e., Przewalskii horse (*Equus przewalskii*) and Mongolian wild ass (*E. hemionus*) of the Perissodactyla, and Przewalski's gazelle (*Procapra przewalskii*) of the Artiodactyla, are very remarkable.

**Aerjin Mountain region (AJ)**, 7 orders, 17 families, 48 genera, 73 species)

The natural weather of this region is extreme desert or semidesert, and the faunal diversity is very poor. The primary species are of the Dipodidae and Gerbillinae. The most noticeable species is the wild camel (*Camelus bactrianus*).

**Qing-Zang Plateau region (QZ)**, 8 orders, 21 families, 79 genera, 148 species)

The topography of this region is primary plateau, and the weather is high chilliness. All endemic species are adapted to this extreme environment, i.e., the wild yak (*Bos grunniens*), Tibet gazelle (*Procapra picticaudata*), and mouping pika (*Ochotona* spp.). Most species of the Ochotonidae are distributed in this region. It should be noted that some tropical species such as rhesus monkey (*Macaca mulatta*), Assam macaque (*M. assamensis*), pig-tailed macaque (*M. nemestrina*) and entellus langur (*Semnopithecus entellus*) can be found on the eastern border of the plateau.

**Bei-Chanjiang region (BCH)**, 7 orders, 23 families, 87 genera, 150 species) and **Nan-Changjiang region (NCH)**, 8 orders, 22 families, 80 genera, 149 species)

The number of species in these 2 regions is greater than those of the DB and HB. There is no significant difference between these 2 regions. The most obvious difference concerns species of the Order Pholidota, i.e., common pangolin (*Manis pentadactyla*), found only in the NCH. The number of species of the Order Chiroptera in the NCH is higher than that in the BCH. Some land mammals, such as Chinese river deer (*Hydropotes intermis*) and Reeve's muntjak (*Muntiacus reevesii*), are very common in these regions. In addition, some species that are mainly distributed in the DB, i.e., manchurian hedgehog (*Erinaceus amurensis*), and common hedgehog (*E. europaeus*), are found only in the BCH.

**Xinan Mountain region (XN)**, 8 orders, 28 families, 102 genera, 224 species)

Great mountains and deep gorges in the Transection Mountain produce complex temperature gradients and many kinds of landscape, and these form the basis of the rich diversity of this region. There are many species of Chiroptera, Carnivora, Insectivora, and Rodentia. Some endemic species, such as the giant panda (*Ailuopoda melanolcuca*) and golden monkey (*Rhinopithecus* spp.), are very remarkable species of the world. In addition, there are also many Ochotonidae species, as in the QZ.

*Huanan region* (HN, 9 orders, 26 families, 90 genera, 183 species)

Most species are tropical, with few endemics found in this region. Representative species are Formosan rock monkey (*Macaca cyclopis*), Hainan gibbon (*Hylobates concolor*), and Thamin's deer (*Cervus eldi*).

*Diannan region* (DN, 10 orders, 32 families, 89 genera, 190 species)

This region belongs to the tropical zone, and species of Primates and Chiropteras are significantly enriched. Asia elephant (*Elephas maximus*) is found in this region.

*Burma-Bengal region* (BB, 11 orders, 30 families, 121 genera, 254 species) and *Vietnam-Thailand region* (VT, 11 orders, 32 families, 114 genera, 250 species)

Both regions have many species of Chiropteras, Primates, and Rodentia. The difference at the family level is that the Craseonycteridae and Tragulidae are found in the VT, but not in the BB. Some representative species of these regions, such as the Indian rhinoceros (*Rhinoceros unicornis*), Javan rhinoceros (*R. sondaicus*), Asia two-horned rhinoceros (*Dicerorhinus sumatrensis*), and Asia elephant (*Elephas maximus*), are endemic.

## OGU classification

Based on the information of the distribution of 577 land mammal species in China and adjacent regions, a presence or absence matrix for species in the 12 OGUs was constructed (see Appendix, presence "1", absence "0"). From the presence or absence matrix, the Sokal and Sneath probabilistic similarity index (SSI; Norusis 1997) matrix was obtained, and applied to classify OGUs. The SSI is defined as follows:  $SSI = (A / (A + B) + B / (A + C) + D / (B + D) + C / (C + D)) / 4$ ; where A is the number of species which are presented in both OGUs; B is the number of species

which are only present in the 1st OGU but not in the 2nd; C is the number of species which are only present in the 2nd OGU but not in the 1st; and D is the number of species which are present in neither of the OGU. The UPGMA, which is also called "between-groups average linkage" in some software packages, was used as a cluster method for classification, which displaying the results as a dendrogram of the 12 physiographical regions (for details see Marquez et al. 1997; in this study, the software package for analysis is SPSS10.0 and STATISTCS).

In order to determine the significance of similarities in the matrix, the probability critical table of the Baroni-Urbani and Busher similarity index (BBI, Baroni-Urbani and Busher 1976) for binary data was used. The BBI is defined as follows:  $BBI = ((A * D)^{0.5} + A) / ((A * D)^{0.5} + A + B + C)$ ; where A, B, C, and D are the same meanings as in the SSI. The similarity values were transformed into 3 categories, represented by "+", "-", and "0" notations, representing significantly higher or lower than expected at random, and with no any significant difference, respectively. The transformed values were regarded as matrices of significant similarities.

Following the method outlined by McCoy et al. (1986) and the approach by Real et al. (1992), for each node of the dendrogram, the presence of strongly or weakly significant segregations between physiographical regions separated by the node was tested. At each node of the dendrogram, a submatrix, which only included the physiographical region involved in the node, was established from the matrix of significant similarities. This submatrix was divided into 3 zones: zone A and B, which corresponds to each group of regions by the node; and zone  $A \times B$ , which corresponds to the intersection between both zones. From the number of "+" and "-" values in each zone, the parameters of  $DW(A \times A)$ ,  $DW(B \times B)$ ,  $DW$ , and  $DS$  were calculated.  $DW$  is a measure of the efficiency of a boundary to separate 2 groups of physiographical regions, whose faunas are similar within but not between each group.  $DW$  can be separated into the parameters,  $DW(A \times A)$  and  $DW(B \times B)$ . These parameters measure the extent to which the similarities higher than expected (+) tend to be in zones A and B, but not in  $A \times B$ , i.e., they measure the internal homogeneity in zones A and B.  $DS$  is another measure of the efficiency of a boundary, giving a measure of whether the similarities lower than expected (-) tend to be located in zones  $A \times B$ , but not in zones A or B. In



a word, these D values (DW and DS) are measures of how well the putative boundary between zones A and B similar locations (weak boundary) or segregates dissimilar locations (strong boundary). The statistical significance of each node of the dendrogram was assessed by a G-test of independence (following the application of Yates' correction) of the distribution of the values of in "+", "-", and "0" in zones A and B and zone A×B of the submatrix. By this test, we obtain parameter GW, for a weak boundary, and GS, for strong segregation (for details see McCoy et al. 1986).

## RESULTS AND DISCUSSION

From the presence or absence matrix of 577 land mammals in the 12 OGUs (see Appendix, presence "1", absence "0"), using the method described above, the Sokal and Sneath probabilistic similarity index matrix was obtained (Table 1), and its corresponding dendrogram was produced (Fig. 2). Using Baroni-Urbani and Busher's similarity index, we obtained the matrix of significant similarities for the 12 OGUs (Table 1). Applying the method outlined by McCoy et al. (1986) and Real et al. (1992), we tested the statistical significance of groups which were determined by

UPGMA, and the results are presented in table 2 (Fig. 2).

The boundary between PR and OR in China is an argumentative focus among many zoologists (e.g., Udvardy 1975, Corbet et al. 1992, Zhang 1997 1999 2002, Hoffman 2001). Applying the site sampling method and analyzing the rules of land mammal faunas at particular sites, Hoffman (2001) believed that a transition zone existed between the PR and OR in China, and the central, southern and northern edges were 30°N, 28°N and 33°N, respectively. The method outlined by McCoy et al. (1986) and Real et al. (1992) revealed 2 operative biogeographical units (OBUs): PR, including DB, HB, MX, AJ, and QZ; and OR, including the remaining BCH, NCH, XN, DN, HN, BB, and VT. Both OBU groups were separated by a weak boundary and a strong boundary (DW, DS > 0; GW and GS were significant; see Table 2; Fig. 2).

Since the configuration and limits of biogeographical regions are strongly related to the type of OGUs considered (see e.g., Real et al. 1996), our results are only one-way of identifying biogeographical units. Thus when using biogeographical units as OGUs, the Q-mode analysis revealed the existence of a biogeographical pattern: in the view of quantitative analysis of the land mammals' zoogeographical patterns, the OR and PR were

**Table 1.** Probabilistic similarity matrix of 12 operative geographical units in China and adjacent region<sup>a,b,c</sup>

	DB	HB	MX	AJ	QZ	BCH	XN	NCH	HN	DN	BB	VT
DB		+	+	+	+	+	0	0	-	-	-	-
HB	0.803		+	+	0	+	0	0	-	-	-	-
MX	0.794	0.724		+	0	-	-	-	-	-	-	-
AJ	0.642	0.616	0.786		+	-	-	-	-	-	-	-
QZ	0.58	0.592	0.563	0.626		+	+	0	0	0	-	-
BCH	0.517	0.575	0.426	0.465	0.688		+	+	-	0	-	-
XN	0.484	0.51	0.403	0.424	0.557	0.673		+	+	0	+	0
NCH	0.485	0.538	0.409	0.429	0.574	0.647	0.769		-	0	0	+
HN	0.617	0.712	0.534	0.496	0.627	0.726	0.623	0.666		0	-	-
DN	0.552	0.596	0.46	0.446	0.582	0.722	0.741	0.794	0.779		0	+
BB	0.39	0.42	0.32	0.365	0.497	0.582	0.711	0.65	0.507	0.6		+
VT	0.402	0.427	0.319	0.355	0.46	0.519	0.73	0.691	0.503	0.627	0.778	

<sup>a</sup>The right upper part of the table is the Baroni-Urbani and Busher probability similarities index, "+", values significantly higher than expected at random,  $p < 0.05$ ; "-", values significantly lower than expected at random,  $p < 0.05$ ; "0", values not different from those expected at random.

<sup>b</sup>The left lower part of the table is the Sokal and Sneath probability similarities index.

<sup>c</sup>DB, Dongbei region; HB, Huabei region; MX, Mengxin region; AJ, Aerjin mountain region; QZ, Qing-Zang Plateau region; BCH, Bei-Changjiang region; NCH, Nan-Changjiang region; XN, Xinan Mountain region; HN, Huanan region; DN, Diannan region; BB, Burma-Bengal region; VT, Vietnam-Thailand region.

separated by a strong boundary in China, in spite of typical OR species, i.e., masked palm civet (*Paguma larvata*) and rhesus monkey (*Macaca mulatta*), being distributed in the HB, and some typical PR species, i.e., manchurian hedgehog (*Erinaceus amurensis*), common hedgehog (*E. europaeus*), and squirrel (*Sciurus vulgaris*) being found in the BCH. This does not mean that our result is contradictory to the viewpoint mentioned above. In fact, McCoy et al. (1986) pointed out that the implication of this dichotomous dendrogram is to place boundaries between locations where resident species are independently distributed, and this would necessarily result in arbitrary groups. The GW value, which is calculated from a series of a random matrix, may have a bimodal or unimodal distribution pattern, and a range exists in which the GW values are significant. Our results might not conflict with the standpoint of Hoffman (2001). Conversely, applying quantitative analysis, we might conclude that the boundary between the PR and OR adopted by Zhang et al. (1997) was correct.

The Qinghai-Xizang Plateau (QXP) is a special region, with high elevations that average over 4500 m, with many great mountains and a complex geologic history (Li et al. 1979). Chen et al. (1996) discussed this special region from a historically temporal and spatial view, and suggested it should be considered an independent zoogeographical unit, which means that the QXP has an equal position as a zoogeographical region to the PR and OR, which was named the Qinghai-Xizang Plateau Region (QXPR). In our study, we divided the QXPR into the QZ and AJ. Our results reveal that (1) the AJ clusters together with the MX, which equals the DB and HB; (2) between the QZ and AJ, DB, HB, and MX, a weak boundary exists (Fig. 2; Table 2;  $DW > 0$ , GW is significant), which means that the AJ should not be included in the QZPR, and that the QZPR can not be considered

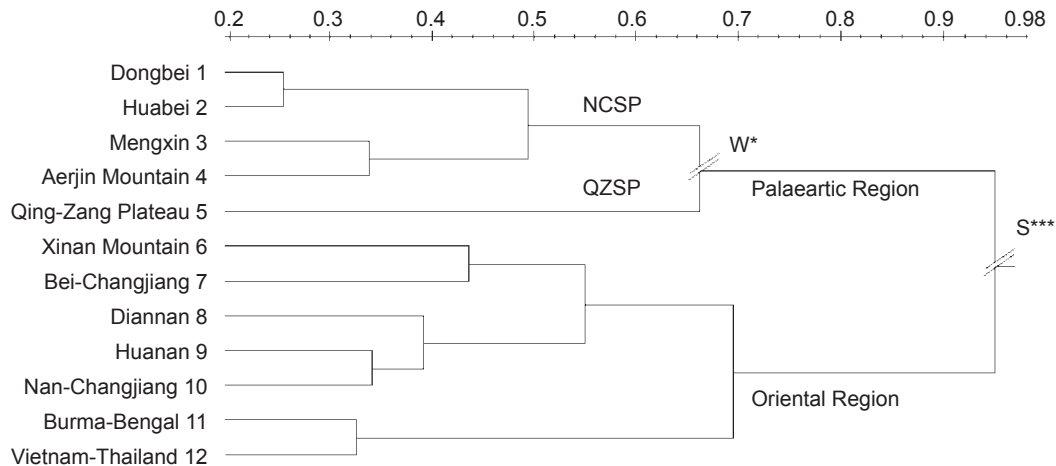
a region independent of the PR and OR. Considering that the QZ is a special region with high elevations and a very cold climate, we suppose that the QZ should be regarded as a subregion of the PR, which is named as Qing-Zang subregion of the PR (QZSP), to embody the land mammal pattern of the high chilliness characteristic fauna as represented by some special species such as the wild yak (*Bos grunniens*), Tibet gazelle (*Procapra picticaudata*), and mouping pika (*Ochotona* spp.). This opinion agrees with the standpoint of Zhang (2002), who supposed that the important geological event (uplifting of the QXP) and different natural environments/natural regions produced a very different fauna in the QXP. Chen et al. (1996) pointed out that the QXP should be regarded as an independent zoogeographic region; however, our results do not agree with this standpoint. It may be the characteristics of different research objects, which are responsible for this discrepancy. Chen et al. (1996) used the subfamily Schizothroacinae and the genus *Triplophysa*, which lack dispersal ability and live in water, as research objects, and geological historical events imposed greater evolutionary pressures on them than on the land mammals that we used in our study. Based on differentiation of the subfamily Schizothroacinae and the genus *Triplophysa*, the QXP can be regarded as an independent zoogeographical region, but based on the differentiation of land mammals, it cannot. In addition, the AJ, MX, DB, and HB should be regarded as another subregion of the PR, which is named the North China subregion of the PR (NCSP). At the same time, according to the results of the cluster analysis (Fig. 2), where DB and HB, and MX and AJ are closely clustered, we suggest taking the DB and HB as a zoogeographical division, which is named the East Division, and the MX and AJ as another division, which is named the West Division.

Corbet et al. (1992) deemed that the XN,

**Table 2.** Significant segregations between the physiographical regions on the dendrogram's fork<sup>a</sup>

	Groups set up by UPGMA			Weak boundary					Strong boundary		
	Group A	Group B	Coefficient	DW (AXA)	DW (BXB)	DW	GW	<i>p</i>	DS	GS	<i>p</i>
Choro-regions	1-5	6-12	0.957	0.515	-0.027	0.299	13.408	***	0.201	17.841	***
	1-4	5	0.667	0.43	0.43	0.467	6.414	*	0	0	n.s
	6-10	11-12	0.669	0.395	0.395	0.4	0.031	n.s	0.062	0.2977	n.s

<sup>a</sup>GW and GS indicate weak segregation and strong segregation between the groups, respectively. \* $p \leq 0.05$ ; \*\*\* $p \leq 0.001$ ; n.s, no significance. DW (AXA) and DW (BXB) quantify the internal homogeneity of each group analyzed. DW and DS quantify the value of each boundary.



**Fig. 2.** Classification dendrogram of the 12 operative geographical units (OGUs) in China and adjacent regions according to the similarity of 577 mammalian fauna. (W, weak segregation; S, strong segregation; \* $p < 0.05$ ; \*\*\* $p < 0.001$ ). NCSP, North China subregion of the PR; QZSP, Qing-Zang subregion of the PR.

BCH, DN, HN, NCH, BB and VT should be regarded as the Indochinese subregion of the OR, while Zhang et al. (1997) also considered the XN, BCH, DN, HN, and NCH to be the Indochinese subregion of the OR. Our quantitative analysis also reveals that there is no weak boundary between the BB and VT, and the XN, BCH, DN, HN, and NCH (Table 2;  $DW > 0$ ,  $GS > 0$ ; GW and GS are not significant). Considering that our results agree with these of Corbet, we suggest to naming it as Indochinese subregion. On account of the cluster analysis results (Fig. 2), we suggest calling the HN, NCH, HN, XN, and DN as the South China Division, and the BB and VT as the Central Peninsula Division.

## CONCLUSIONS

In conclusion, using the physiographical regions in China and adjacent region as OGUs, we applied a classification to them, and tested the significance of the resulting groups. Although the results obtained constitute the first quantitative approach to the zoogeography of the land mammals of China and adjacent regions, and just tests whether the zoogeographical regions that already recognized are reasonable, we suggest that the QZ should be regarded as a subregion of the PR and conclude that the boundary between the PR and OR is strong. At the same time, we suggest that one should use an objective method, such as

quantitative analysis, rather than a subjective method, such as visual analysis, when analyzing the zoogeography of a region in the future.

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**Appendix:** Presence (1) or absence (0) of 577 mammalian species in each OGU<sup>a</sup>.

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Hylomys suillus</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Neohylomys hainanensis</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Neotetracus sinensis</i>	0	0	0	0	0	0	1	0	0	0	1	1
<i>Erinaceus europaeus</i>	1	1	0	0	0	1	0	0	1	0	0	0
<i>Erinaceus amurensis</i>	1	1	0	0	0	1	0	0	0	0	0	0
<i>Hemiechinus dauuricus</i>	1	1	1	1	0	0	0	0	0	0	0	0
<i>Hemiechinus hughii</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Hemiechinus auritus</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Sorex mintutus</i>	1	0	1	1	0	0	0	0	0	0	0	0
<i>Sorex caecutiens</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Sorex araneus</i>	1	1	1	0	0	1	1	0	1	0	0	0
<i>Sorex unguiculatus</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Sorex daphaenodon</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Sorex mirabilis</i>	1	0	0	0	0	0	0	0	0	0	0	0
<i>Sorex cylindricauda</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Sorex bedfordiae</i>	0	0	0	0	0	1	1	1	0	0	1	0
<i>Sorex buchariensis</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Blarinella quadratacauda</i>	0	0	0	0	0	1	1	1	1	0	1	0
<i>Soriculus macrurus</i>	0	0	0	0	0	1	1	1	1	0	1	1
<i>Soriculus lamula</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Soriculus parca</i>	0	0	0	0	0	0	1	0	1	0	1	1
<i>Soriculus nigrescens</i>	0	0	0	0	1	0	0	0	0	0	1	0
<i>Soriculus caudatus</i>	0	0	0	0	0	1	1	0	1	0	1	0
<i>Soriculus leucops</i>	0	0	0	0	0	0	1	1	0	0	1	1
<i>Soriculus hysibius</i>	0	0	0	0	1	1	1	0	0	0	0	0
<i>Soriculus parva (simithii)</i>	0	0	0	0	0	0	1	1	1	0	0	0
<i>Soriculus salenskii</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Soriculus sodalis (fumidus)</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Neomys fodiens</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Suncus murinus</i>	0	0	0	0	0	0	1	0	0	1	1	1
<i>Suncus etruscus</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Suncus stoliczkanus</i>	0	0	0	0	0	0	0	1	0	0	0	0
<i>Crocidura horsfieldi</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Crocidura suaveolens</i>	1	1	0	1	1	0	1	0	0	0	0	0
<i>Crocidura russula</i>	0	0	0	0	0	1	1	1	1	1	0	0
<i>Crocidura leucodon</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Crocidura attenuata</i>	0	0	0	0	0	1	1	1	1	1	1	1
<i>Crocidura dracula</i>	0	0	0	0	1	0	1	1	1	1	1	1
<i>Crocidura lasiura</i>	0	0	0	0	0	0	0	0	1	0	0	0
<i>Crocidura fuliginosa</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Anourosorex squamipes</i>	0	0	0	0	0	1	1	1	1	0	1	1
<i>Chimarrogale himalayica</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Chimarrogale styani</i>	0	0	0	0	0	0	1	0	0	0	1	0
<i>Nectogale elegans</i>	0	0	0	0	1	0	1	0	0	0	1	0
<i>Uropsilus soricipes</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Uropsilus gracilis</i>	0	0	0	0	0	1	1	0	1	0	1	0
<i>Uropsilus andersoni</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Scaptonyx fuscicauda</i>	0	0	0	0	0	1	1	0	1	0	1	0
<i>Scapanulus oweni</i>	0	1	0	0	0	1	1	0	0	0	0	0
<i>Talpa longirostris</i>	0	0	0	0	0	1	1	1	1	0	0	1
<i>Talpa grandis</i>	0	0	0	0	0	1	1	0	0	0	1	0
<i>Talpa micrura</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Parascaptor leucura</i>	0	0	0	0	0	0	1	1	0	0	1	0

## Appendix: (Cont.)

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Scaptochirus moschalus</i>	1	1	1	0	0	1	0	0	0	0	0	0
<i>Mogera robusta</i>	1	0	0	0	0	0	0	0	0	0	0	0
<i>Mogera wogura</i>	0	0	0	0	0	1	0	0	0	1	0	0
<i>Mogera insularis</i>	0	0	0	0	0	0	0	0	1	1	0	0
<i>Tupiaia belangeri</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Denrogale murina</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Rousettus leschenaulti</i>	0	0	0	0	0	0	1	1	0	1	1	1
<i>Pteropus dasymallus</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Pteropus giganteus</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Pteropus lylei</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Pteropus intermedius</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Pteropus vampyrus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Sphaerias blanfordi</i>	0	0	0	0	1	0	0	0	0	0	1	1
<i>Cynopterus horsfieldii</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Cynopterus sphinx</i>	0	0	0	0	1	0	0	0	0	1	1	1
<i>Cynopterus brachyotis</i>	0	0	0	0	0	0	0	0	0	1	1	1
<i>Eonycteris spelaca</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Macroglossus minimus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Macroglossus sobrinus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Megaerops ecaudatus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Megaerops niphanae</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Taphozous melanopogon</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Taphozous longimanus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Taphozous theobaldi</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Taphozous nudiventris</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Taphozous saccolaimus</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Megaderma lyra</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Megaderma spasma</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Rhinolophus ferrumequinum</i>	1	1	0	0	0	0	1	1	1	0	0	0
<i>Rhinolophus affinis</i>	0	0	0	0	0	1	1	1	1	1	1	1
<i>Rhinolophus rouxii</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Rhinolophus thomasi</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Rhinolophus cornutus</i>	0	0	0	0	1	1	0	0	1	1	0	0
<i>Rhinolophus blythi</i>	0	0	0	0	1	0	1	1	0	1	1	1
<i>Rhinolophus lepidus</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Rhinolophus monoceros</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Rhinolophus luctus</i>	0	0	0	0	0	0	1	1	0	1	1	1
<i>Rhinolophus pearsoni</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Rhinolophus macrotis</i>	0	0	0	0	0	0	0	1	1	1	0	1
<i>Rhinolophus rex</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Rhinolophus trifoliatus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Rhinolophus paradoxolophus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Rhinolophus marshalli</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Rhinolophus ceolophyllus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Rhinolophus shameli</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Rhinolophus yunanensis</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Rhinolophus acuminatus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Rhinolophus subbadius</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Rhinolophus megaphyllus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Rhinolophus borneensis</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Rhinolophus malayanus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Hipposideros larvatus</i>	0	0	0	0	0	0	0	0	0	1	1	1
<i>Hipposideros pomona</i>	0	0	0	0	0	0	0	1	1	1	1	1





## Appendix: (Cont.)

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Rhinopithecus roxellanae</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Rhinopithecus bieti</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Rhinopithecus avunculus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Rhinopithecus brelichi</i>	0	0	0	0	0	0	0	0	1	0	0	0
<i>Pygathrix nemaeus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Pygathrix pileatus</i>	0	0	0	0	0	0	1	0	0	0	1	0
<i>Semnopithecus entellus</i>	0	0	0	0	1	0	0	0	0	0	1	0
<i>Semnopithecus phayrei</i>	0	0	0	0	0	0	1	1	0	0	1	1
<i>Semnopithecus francoisi</i>	0	0	0	0	0	0	0	0	1	1	0	1
<i>Semnopithecus cristatus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Semnopithecus geei</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Hylobates pileatus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Hylobates lar</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Hylobates hoolock</i>	0	0	0	0	0	0	0	1	0	0	1	0
<i>Hylobates concolor</i>	0	0	0	0	0	0	0	1	0	1	0	1
<i>Hylobates leucogenys</i>	0	0	0	0	0	0	0	1	0	0	0	1
<i>Hylobates gabriellae</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Canis lupus</i>	1	1	1	1	1	1	1	1	1	1	0	0
<i>Canis aureus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Vulpes vulpes</i>	1	1	1	1	1	1	1	1	1	1	0	0
<i>Vulpes corsac</i>	1	0	0	0	1	0	1	0	0	0	0	0
<i>Vulpes ferrilata</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Nyctereutes procyonoides</i>	1	1	0	0	0	1	0	1	1	1	0	1
<i>Cuon alpinus</i>	1	0	1	1	1	1	1	1	1	1	1	1
<i>Ursus ursinus</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Ursus thibetanus</i>	1	0	0	0	1	1	1	1	1	1	1	1
<i>Ursus arctos</i>	1	0	1	1	0	0	0	0	0	0	0	0
<i>Ursus pruinus</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Ursus malayanus</i>	0	0	0	0	0	0	0	1	0	0	0	0
<i>Ailurus fulgens</i>	0	0	0	0	1	1	1	1	0	0	1	0
<i>Ailuopoda melanoleuca</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Martes foina</i>	0	1	1	1	1	0	1	0	0	0	0	0
<i>Martes zibellina</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Martes flavila</i>	1	1	0	0	1	1	1	1	1	1	1	1
<i>Gulo gulo</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Mustela altaica</i>	1	1	1	1	1	1	1	0	0	0	0	0
<i>Mustela erminea</i>	1	1	1	1	0	0	0	0	0	0	0	0
<i>Mustela nivalis</i>	1	0	1	1	1	0	1	0	0	0	0	0
<i>Mustela kathiah</i>	0	0	0	0	0	1	1	1	1	1	1	1
<i>Mustela amurensis</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Mustela sibirica</i>	1	1	1	0	1	1	1	1	1	1	1	1
<i>Mustela strigidorsa</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Mustela eversmanni</i>	1	1	1	1	1	1	1	0	0	0	0	0
<i>Vormela peregusna</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Melogale moschata</i>	0	0	0	0	0	1	1	1	1	1	1	0
<i>Melogale personata</i>	0	0	0	0	0	0	0	0	0	1	1	1
<i>Meles meles</i>	1	1	1	1	1	1	1	1	1	1	0	0
<i>Arctonyx collaris</i>	0	1	1	0	1	1	1	1	1	1	1	1
<i>Lutra summatrana</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Lutra lutra</i>	1	0	1	0	1	1	1	1	1	1	1	1
<i>Lutra perspicillata</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Aonyx cinerea</i>	0	0	0	0	1	0	1	1	1	1	1	1
<i>Viverra zibetha</i>	0	0	0	0	1	1	1	0	1	1	1	1



## Appendix: (Cont.)

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Viverra megaspila</i>	0	0	0	0	0	0	0	1	1	1	1	1
<i>Vivericula indica</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Prionodon pardicolor</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Paradoxurus hermaphroditus</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Paguma larvata</i>	0	1	0	0	1	1	1	1	1	1	1	1
<i>Arctictis binturong</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Cynogale lowei</i>	0	0	0	0	0	0	0	1	0	0	0	1
<i>Arctogalidia trivirgata</i>	0	0	0	0	0	0	1	1	0	0	1	1
<i>Chrotogale owstoni</i>	0	0	0	0	0	0	0	1	0	1	0	1
<i>Herpestes javanicus</i>	0	0	0	0	0	0	0	1	1	1	1	1
<i>Herpestes urva</i>	0	0	0	0	0	1	1	1	1	1	1	1
<i>Felis libyca</i>	0	0	0	1	1	0	0	0	0	0	0	0
<i>Felis bieti</i>	0	0	1	1	1	0	1	0	0	0	0	0
<i>Felis chaus</i>	0	0	0	0	0	0	1	1	0	1	1	1
<i>Felis manul</i>	1	0	1	1	1	0	1	1	0	0	0	0
<i>Felis marmorata</i>	0	0	0	0	0	0	1	0	0	0	1	1
<i>Felis lynx</i>	1	0	1	1	1	0	1	0	0	0	0	0
<i>Felis temmincki</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Felis bengalensis</i>	1	1	0	0	0	1	1	1	1	1	1	1
<i>Felis viverrina</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Pardofelis nebulosa</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Panthera pardus</i>	1	1	1	0	1	1	1	1	1	1	1	1
<i>Panthera tigris</i>	1	1	1	1	1	1	1	1	1	1	1	1
<i>Panthera uncia</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Elephas maximus</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Rhinoceros unicornis</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Rhinoceros sondaicus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Dicerorhinus sumatrensis</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Equus przewalskii</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Equus hemionus</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Sus scrofa</i>	1	1	1	1	1	1	1	1	1	1	1	1
<i>Sus salvanus</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Camelus bactrianus</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Tragulus javanicus</i>	0	0	0	0	0	0	0	1	0	0	0	1
<i>Tragulus napu</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Moschus moschiferus</i>	1	1	1	0	0	0	0	0	0	0	0	0
<i>Moschus berezovskii</i>	0	0	0	0	1	1	1	1	1	1	0	1
<i>Moschus sifanicus</i>	0	0	0	0	1	0	1	0	1	0	0	0
<i>Moschus chrysogaster</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Moschus fuscus</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Hydropotes inermis</i>	0	0	0	0	0	1	0	0	1	1	0	0
<i>Muntiacus rooseveltorum</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Muntiacus gongshanensis</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Muntiacus muntjack</i>	0	0	0	0	1	0	1	1	1	1	1	1
<i>Muntiacus reevesii</i>	0	0	0	0	0	1	1	1	1	1	0	0
<i>Muntiacus crinifrons</i>	0	0	0	0	0	0	0	0	1	0	0	0
<i>Muntiacus feae</i>	0	0	0	0	0	0	1	0	0	0	1	1
<i>Elaphodus cephalophus</i>	0	0	0	0	1	1	1	1	1	1	1	0
<i>Axis porcinus</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Cervus duvaucelii</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Cervus unicolor</i>	0	0	0	0	1	0	1	1	1	1	1	1
<i>Cervus eldii</i>	0	0	0	0	0	0	0	0	0	1	0	1
<i>Cervus nippon</i>	1	1	0	0	0	1	1	1	1	1	0	1

## Appendix: (Cont.)

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Cervus albirostris</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Cervus elaphus</i>	1	1	1	1	1	0	1	1	0	0	0	0
<i>Capreolus capreolus</i>	1	1	1	1	1	1	0	0	0	0	0	0
<i>Alces alces</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Rangifer tarandus</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Bos gaurus</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Bos grunniens (mutus)</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Bos banleng (javanicus)</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Bos sauveli</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Bubalus arnee</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Procapra picticaudata</i>	0	0	0	0	1	1	1	0	0	0	0	0
<i>Procapra przewalskii</i>	0	0	1	0	1	0	0	0	0	0	0	0
<i>Procapra gutturosa</i>	1	1	1	0	0	0	0	0	0	0	0	0
<i>Gazella subgutturosa</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Pantholops hodgsoni</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Saiga tatarica</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Budorcas taxicolor</i>	0	0	0	0	1	1	1	0	0	0	1	0
<i>Naemorhedus cranbrooki</i>	0	0	0	0	1	0	0	0	0	0	1	0
<i>Naemorhedus goral</i>	1	1	1	0	1	1	1	1	1	1	1	1
<i>Naemorhedus sumatraensis</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Naemorhedus swinhoei</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Hemitragus jemlahicus</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Capra ibex</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Pseudois nayaur</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Pseudois schaeferi</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Ovis ammon</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Manis pentadactyla</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Manis crassicaudata</i>	0	0	0	0	0	0	1	0	0	1	1	0
<i>Manis javanica</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Trogopterus xanthipes</i>	0	1	0	0	1	1	1	0	1	1	0	0
<i>Trogopterus pearsonii</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Petaurista petaurista</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Petaurista yunnanensis</i>	0	0	0	0	0	0	0	1	0	0	1	0
<i>Petaurista hainana</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Petaurista alborufus</i>	0	0	0	0	0	1	1	1	1	1	0	0
<i>Petaurista pectoralis</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Petaurista xanthotis</i>	0	0	0	0	1	1	1	0	0	0	0	0
<i>Petaurista magnificus</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Petaurista philippensis</i>	0	0	0	0	0	0	0	1	1	1	1	1
<i>Petaurista marica</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Petaurista elegans</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Petaurista sybilla</i>	0	0	0	0	0	0	0	1	0	0	1	0
<i>Aeretes melanopterus</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Pteromys volans</i>	1	1	1	0	0	1	1	0	1	0	0	0
<i>Petinomys setosus</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Petinomys electilis</i>	0	0	0	0	0	0	0	0	0	1	0	1
<i>Hylopetes alboniger</i>	0	0	0	0	0	1	1	1	1	0	1	1
<i>Eupetaurus cinereus</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Sciurus vulgaris</i>	1	1	1	1	0	0	0	0	0	0	0	0
<i>Callosciurus erythraeus</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Callosciurus phayrei</i>	0	0	0	0	0	0	0	1	0	0	1	0
<i>Callosciurus pygerythrus</i>	0	0	0	0	1	0	0	1	0	0	1	0
<i>Callosciurus caniceps</i>	0	0	0	0	0	0	0	0	0	1	1	1

## Appendix: (Cont.)

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Callosciurus quinquestriatus</i>	0	0	0	0	0	0	0	1	0	0	1	0
<i>Callosciurus finlaysonii</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Callosciurus inornatus</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Tamiops maclellandii</i>	0	0	0	0	1	1	1	1	0	1	1	1
<i>Tamiops swinhoei</i>	0	0	1	0	1	1	1	1	1	1	1	1
<i>Tamiops rodolphii</i>	0	0	0	0	0	0	0	0	0	0	0	1
<i>Dremomys lokriah</i>	0	0	0	0	1	0	1	0	0	0	1	0
<i>Dremomys pernyi</i>	0	0	0	0	0	1	1	1	1	1	1	0
<i>Dremomys rufogenis</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Dremomys pyrrhomerus</i>	0	0	0	0	0	0	0	1	1	1	0	0
<i>Dremomys gularis</i>	0	0	0	0	0	0	0	1	0	0	0	1
<i>Ratufa bicolor</i>	0	0	0	0	0	0	1	1	0	1	1	1
<i>Menetes berdmorei</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Sciurotamias davidianus</i>	0	1	0	0	0	0	1	0	0	1	0	0
<i>Sciurotamias forresti</i>	0	0	0	0	0	0	1	1	0	0	0	0
<i>Eutamias sibiricus</i>	1	1	1	0	0	1	1	0	0	0	0	0
<i>Citellus dauricus</i>	1	1	1	0	0	0	0	0	0	0	0	0
<i>Citellus reliclus</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Citellus major</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Citellus erthrogenys</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Citellus undulatus</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Marmota baibacina</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Marmota bobak</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Marmota himalayana</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Marmota caudata</i>	0	0	0	1	0	0	0	0	0	0	0	0
<i>Castor fiber</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Sicista concolor</i>	1	0	1	1	1	0	0	0	0	0	0	0
<i>Sicista subtilis</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Eozapus setchuanus</i>	0	1	0	0	1	1	1	0	0	0	0	0
<i>Cardiocranium paradoxus</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Salpingotus kozlovi</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Salpingotus crassicauda</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Euchoreutes naso</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Allactaga sibirica</i>	1	1	1	1	1	0	0	0	0	0	0	0
<i>Allactaga elater</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Allactaga bullata</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Alactagulus pumilio</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Dipus sagitta</i>	1	0	1	1	1	0	0	0	0	0	0	0
<i>Stylodipus telum</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Atherurus macrourus</i>	0	0	0	0	0	0	0	1	0	1	1	1
<i>Hystrix hodgsoni</i>	0	0	0	0	0	1	1	1	1	1	1	1
<i>Hystrix yunnanensis</i>	0	0	0	0	0	0	0	1	0	0	0	0
<i>Dryomys nitedula</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Chaetocauda sichuanensis</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Cricetulus migratorius</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Cricetulus barabensi</i>	1	1	1	0	0	1	0	0	0	0	0	0
<i>Cricetulus longicaudatus</i>	0	1	1	1	1	1	0	0	0	0	0	0
<i>Cricetulus kamensis</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Cricetulus eversmanni</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Cricetulus triton</i>	1	1	1	0	0	1	0	0	1	0	0	0
<i>Cricetulus canus</i>	0	0	0	0	0	1	1	0	0	0	0	0
<i>Phodopus sungorus</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Phodopus roborovskii</i>	1	1	1	1	1	0	0	0	0	0	0	0

## Appendix: (Cont.)

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Cricetus cricetus</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Myospalax fontanieri</i>	1	1	1	0	1	1	0	0	0	0	0	0
<i>Myospalax psilurus</i>	1	1	1	0	0	1	0	0	0	0	0	0
<i>Myospalax smithi</i>	0	0	0	0	0	1	0	0	0	0	0	0
<i>Myospalax rothschildi</i>	0	0	0	0	0	1	0	0	0	0	0	0
<i>Myospalax aspalax</i>	1	1	1	0	0	0	0	0	0	0	0	0
<i>Typhlomys cinereus</i>	0	0	0	0	0	1	0	1	1	1	0	1
<i>Rhizomys pruinosus</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Rhizomys sumatrensis</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Rhizomys sinensis</i>	0	0	0	0	0	1	1	1	1	1	1	1
<i>Cannomys badius</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Myopus schisticolor</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Clethrionomys rutilus</i>	1	1	1	1	0	0	0	0	0	0	0	0
<i>Clethrionomys frater</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Clethrionomys rufocanus</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Eothenomys shanseius</i>	1	1	1	0	0	1	0	0	0	0	0	0
<i>Eothenomys melanogaster</i>	0	0	0	0	1	1	1	1	1	1	1	1
<i>Eothenomys miletus</i>	0	0	0	0	0	0	1	1	1	1	1	0
<i>Eothenomys eleusis</i>	0	0	0	0	0	0	1	1	1	0	1	1
<i>Eothenomys olitor</i>	0	0	0	0	0	0	1	0	1	0	1	0
<i>Eothenomys proditor</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Eothenomys chinensis</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Eothenomys wardi</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Eothenomys cachinus</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Eothenomys inez</i>	0	1	0	0	0	1	0	0	0	0	0	0
<i>Eothenomys eva</i>	0	1	0	0	0	1	1	0	0	0	0	0
<i>Alticola argentata</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Alticola strelzowi</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Alticola stracheyi</i>	0	0	0	1	1	0	0	0	0	0	0	0
<i>Alticola stoliczkanus</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Lagurus lagurus</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Lagurus luteus</i>	0	0	1	1	1	0	0	0	0	0	0	0
<i>Arvicola terrestris</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Pitymys leucurus</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Pitymys irene</i>	0	0	0	0	1	1	1	0	0	0	1	0
<i>Pitymys sikimensis</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Pitymys judaschi</i>	0	0	0	1	1	0	0	0	0	0	0	0
<i>Microtus socialis</i>	0	0	1	1	0	0	0	0	0	0	0	0
<i>Microtus arvalis</i>	1	0	1	1	0	0	0	0	0	0	0	0
<i>Microtus fortis</i>	1	1	1	0	0	1	0	0	1	0	0	0
<i>Microtus clarkei</i>	0	0	0	0	0	0	0	1	0	0	1	1
<i>Microtus kikuchii</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Microtus musseri</i>	0	0	0	0	0	0	0	1	0	0	0	0
<i>Microtus ilaeus</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Microtus agrestis</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Microtus oeconomus</i>	0	1	1	1	1	0	1	0	0	0	0	0
<i>Microtus millicens</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Microtus brandti</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Microtus mandarinus</i>	0	1	1	0	0	1	0	0	0	0	0	0
<i>Microtus fuscus</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Microtus gregalis</i>	1	1	1	1	0	1	0	0	0	0	0	0
<i>Microtus maximowiczii</i>	1	1	1	0	0	0	0	0	0	0	0	0
<i>Proedromys bedfordi</i>	0	0	0	0	0	1	1	0	0	0	0	0





## Appendix: (Cont.)

Species	Operative geographical unit (OGU)											
	DB	HB	MX	AJ	QZ	BCH	XN	DN	NCH	HN	BB	VT
<i>Maxomy musschenbroekii</i>	0	0	0	0	0	0	0	0	1	0	0	1
<i>Mus musculus</i>	1	1	1	1	1	1	1	1	1	1	1	1
<i>Mus famulus</i>	0	0	0	0	0	0	1	1	0	0	1	1
<i>Mus caroli</i>	0	0	0	0	0	0	0	1	0	1	0	1
<i>Mus cervicolor</i>	0	0	0	0	0	0	1	0	0	0	1	1
<i>Mus pahari</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Mus booduga</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Mus shortridgei</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Millardia kathleenae</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Bandicota savilei</i>	0	0	0	0	0	0	0	0	0	0	1	1
<i>Bandicota bengalensis</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Bandicota indica</i>	0	0	0	0	0	0	1	1	1	1	1	1
<i>Nesokia indica</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Lepus capensis</i>	1	1	1	1	0	1	0	0	1	0	0	0
<i>Lepus peguensis</i>	0	0	0	0	0	0	0	0	0	1	1	1
<i>Lepus hainanus</i>	0	0	0	0	0	0	0	0	0	1	0	0
<i>Lepus timidus</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Lepus oiostolus</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Lepus sinensis</i>	0	0	0	0	0	0	1	1	1	1	0	0
<i>Lepus mandschuricus</i>	1	0	1	0	0	0	0	0	0	0	0	0
<i>Lepus yarkandensis</i>	0	0	0	1	0	0	0	0	0	0	0	0
<i>Lepus comus</i>	0	0	0	0	0	0	1	1	1	0	0	0
<i>Lepus melainus</i>	1	0	0	0	0	0	0	0	0	0	0	0
<i>Caprolagus hispidus</i>	0	0	0	0	0	0	0	0	0	0	1	0
<i>Ochotona thibetana</i>	0	0	0	0	1	1	1	1	0	0	0	0
<i>Ochotona nubric</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Ochotona huangensis</i>	0	1	0	0	0	1	1	0	0	0	0	0
<i>Ochotona cansus</i>	1	0	0	0	1	0	1	0	0	0	0	0
<i>Ochotona thomasi</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Ochotona himalayana</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Ochotona roylei</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Ochotona macrotis</i>	0	0	0	1	1	0	1	0	0	0	0	0
<i>Ochotona rutila</i>	0	0	0	1	0	0	1	0	0	0	0	0
<i>Ochotona daurica</i>	0	1	1	0	0	0	1	0	0	0	0	0
<i>Ochotona forresli</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Ochotona iliensis</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Ochotona curzoniae</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Ochotona koslowi</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Ochotona gaoligongensis</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Ochotona alpina</i>	1	1	1	0	0	0	0	0	0	0	0	0
<i>Ochotona pallasii</i>	0	0	1	0	0	0	0	0	0	0	0	0
<i>Ochotona shaanxiensis</i>	0	1	0	0	0	0	0	0	0	0	0	0
<i>Ochotona kamensis</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Ochotona erythrotis</i>	0	0	0	0	1	0	0	0	0	0	0	0
<i>Ochotona gloveri</i>	0	0	0	0	1	0	1	0	0	0	0	0
<i>Ochotona ladacensis</i>	0	0	0	0	0	0	1	0	0	0	0	0
<i>Ochotona muliensis</i>	0	0	0	0	0	0	1	0	0	0	0	0

<sup>a</sup>Abbreviations are described in Materials and Methods, and the legend of figure 1.