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Exploring the Species Richness Pattern and Areas of Endemism of Tenebrionidae (Coleoptera) in Xinjiang, China

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Abstract: Species richness and areas of endemicity (AOE) are the basis of biogeography, which is of great significance for understanding the evolution of species and making conservation plans. The present study aimed to investigate the species richness pattern and AOEs of Tenebrionidae in Xinjiang, China. We collected information on the geographical distribution of 556 species from several sources and obtained 2226 distribution records for the analyses. The AOEs were detected using the parsimony analysis of endemicity (PAE) and endemicity analysis (EA) at 0.5°, 1°, and 1.5° grid sizes, respectively. A total of six AOEs were found, including three mountain ranges (Altai Mountains, Tianshan Mountains, and Kunlun Mountains) and one basin (Junggar Basin), which was largely congruent with the species richness pattern. The results indicated that the complex terrain and stable climate in the mountainous area played an important role in the formation of tenebrionid species diversity and their endemic areas in Xinjiang.

Keywords: Tenebrionidae; species richness; parsimony analysis of endemicity; endemicity analysis; area of endemism; mountainous areas

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1. Introduction

Xinjiang (~166 km^2), a section of Central Asia, is the largest autonomous region located in northwest China, with a complex terrain environment of two basins and three mountains [1,2]. The Tarim Basin and Kunlun Mountains are located in southern and western Xinjiang, Altai Mountain and Junggar Basin are in the north and east areas, and the Tianshan Mountains run through the central areas [3,4]. Xinjiang is surrounded by mountains, which not only leads to complex and varied topography but also to drought and a low-rain climate scenario [5–7]. A large part of the region is arid and semiarid, and one-sixth is covered by desert [3]. Due to the characteristics of its special geographical location, Xinjiang has become a biodiversity hotspot with high species richness and endemic levels, especially breeding many drought-tolerant insect species [8–11]. For example, 84 species of Meloidae Gyllenhal, 1810, accounting for approximately 40% of the total number of species occurring in China, were recorded in Xinjiang [12]. More remarkably, a total of 422 species of Tenebrionidae from Xinjiang were listed [13–16].

Tenebrionidae, a large insect group, is widely distributed in Central Asia [17,18]. It has a high level of species richness in a variety of environments [19,20]. There are approximately 20,000 known species of Tenebrionidae in the world [21,22]. It has been reported that more than 600 species are distributed in the desert and semidesert areas of China, with Xinjiang as the most important geographical component [23]. However, in recent years, a series of events have affected the natural environment in Xinjiang, which may have changed the habitat of some insects, such as the increase in rainfall [24,25], the rise in temperature [5], the prevention and control of desertification [26], and the trend of homogenizing the landscape [20]. As a classic indicator of the desert ecological environment, Tenebrionidae may be affected by the above events to varying degrees in this area [20]. Therefore, it is of significance to study the distribution pattern of Tenebrionidae in the area to identify priority areas for biodiversity conservation [23,27–30]. Some studies have focused on the taxonomy [31,32], adaptive characteristics [17,33], diversity analysis [34], and molecular level [35–37] of tenebrionid beetles, but no formal biogeographical methods have been used to analyse Tenebrionidae in Xinjiang.

The study of the distribution patterns of species richness and endemic areas have always been central issues in biogeography [38–44], which not only represent the highest degree of the historical and ecological imprint of all biological entities [45] but also play an important role in the exploration of biodiversity hotspots [46–51].

Species richness, defined as the number of species in each cell, is the most basic and important indicator for identifying biodiversity hotspots and endemic areas [52,53]. Several studies have been undertaken using species richness as a measure to understand what affects biodiversity [10,48,51,53,54]. However, because species richness is easily affected by external factors (e.g., anthropogenic factors, geographic isolation, environmental change, etc.), simple species richness alone cannot reflect the true level of species spatial distribution [55], and the highest level of species richness does not necessarily mean the highest level of endemism [51]. Therefore, a new index called the areas of endemism (AOEs) has also been used to explore the distribution patterns of organisms [51,53,56].

Recently, a number of biogeographic and evolutionary studies have implemented and applied AOEs to resolve practical issues [48,49,51–53,56–58]. Although the definition of AOEs has been controversial in the past, it is now generally accepted as the distribution of two or more endemic species [59–62]. AOEs are entities compared in terms of ascertaining earth history based on biological patterns [62,63]. AOEs are important because they represent the operational unit of historical biogeography, which constitutes the first step for biogeographical regionalization [59,64]. In addition, AOEs show unique biota and are considered significant priority areas for biodiversity conservation [65]. Numerous biogeographers and ecologists have shown interest in evaluating the causes for the presence of AOEs [57,58,64,66].

Currently, although a number of alternative protocols and algorithms have been proposed to delimit AOEs [62,67–70], no consensus has emerged on the most appropriate method for detecting endemism. In some cases, more complete results can be obtained by combining two or multiple methods [62,71]. Among several approaches, two of them are most commonly used in exploring AOEs [51,53,56,72,73]. One approach is parsimony analysis of endemicity (PAE), which identifies ecological affinities between species by analysing species composition at local or regional scales [74,75]. The branching diagram is obtained through analysis, and the distance on the branching represents the size of ecological affinity [76]. The other approach is endemicity analysis (EA). Species distribution is analysed in different grid sizes by using the latitude–longitude information of species [72]. The algorithm assigns a score to each species by comparing the composition of species in each grid. The grid score is the sum of the scores of all species in a grid and is used to determine the common area [74].

In the present study, we collected the distribution information for a total of 556 Tenebrionidae species in Xinjiang based on both the literature and the examined material and then analysed the data with an analysis of endemicity using two different methods, aiming to (i) identify the centre of species richness and AOEs; (ii) explore the consistency of species richness and endemic patterns; and (iii) test the hypothesis of whether the centre of species diversity in previous studies is located in mountainous areas [53,56].

2. Materials and Methods

2.1. Species Distribution Data

In the present study, the georeferenced records of 556 species of Tenebrionidae were obtained from published papers [12,18,19,77–86], books [13–15], museum specimens (The Museum of Hebei University), and iNaturalist (https://www.inaturalist.org/ (accessed on 15 June 2022)), and a total of 2322 distribution records were compiled in a geographic database. The distribution records without locations were excluded, and those with a lack of or imprecise coordinates were supplemented and standardized via Google Maps. Ultimately, the distribution information of 433 species with 2226 geographical records with robust coordinates was retained in the following analysis.

2.2. Assessing Sampling Bias and Mapping Species Richness

ArcGIS 10.8 was used to process the latitude and longitude geographic information of the species. In a 1° × 1° cell grid, 115 grid cells with information were obtained, and different colours were used to replace the species richness of different degrees. The incident-based bootstrap estimators were used to construct the species accumulation curve, which was designed to assess species inventory integrity in the study area [51]. EstimateS v9.1 was used to perform 100 randomized matrix analyses, where a matrix was created for the presence (1) or absence (0) of each species in a 1° grid size [87]. In addition, the number of records and the richness of the 1° grid were converted using square roots. Then, a linear regression was fitted to explore the completeness of richness, following previous methods [56].

2.3. Identifying Areas of Endemism

Two methods were used to explore the AOEs of Tenebrionidae: parsimony analysis of endemicity (PAE) and endemicity analysis (EA). In addition, three different grid sizes were used: 0.5° × 0.5°, 1° × 1°, and 1.5° × 1.5°.

For the PAE, matrices were created for the presence (1) or absence (0) of each species in three different grid sizes. Under the New Technical algorithms, TNT v1.5 was used to analyse all matrices, which added all zeros "Root" as the hypothetical outgroup of the tree [88]. The branches with relatively moderate bootstrap values ($\geq$50%) were the candidates for AOEs [53]. Then, AOEs (clades of cells), comprising two or more endemic species restricted to these areas and at least two continuous cells, were mapped using ArcGIS to obtain the final results [52].

NDM/VNDM v3.1 was used for EA analysis under three grid sizes [88]. Due to the incompatibility of the input files, GeX was used to convert the latitude and longitude geographic information of the 433 species into XYD format [51,68,88]. The temporary set was saved with the current score in the 0.99 range. Sets were preserved with two or more endemics species with scores above 3.0. The search was repeated 100 times. Overlapping subsets were maintained when 50% of species were unique [74]. Species with a minimum score of 0.4 were selected in the obtained subsets [89]. Based on strict rules, the consensus area was calculated with a cutoff of 100% similarity in species. Other parameters were applied by using the default value. Finally, consensus areas were overlapped in different grid sizes to obtain the AOEs, and ArcGIS was used to draw the final results [51,53,72,90].

3. Results

3.1. Species Richness Pattern

Inadequate collection is a potential problem in biogeographic research, which may lead to the misidentification of biodiversity hotspots [30,91]. In this study, the 1° grid size species accumulation curves did not show inadequate collection (bootstrap mean approximately 505), with the data integrity for analysis as 86.1% (Figure 1A). The ratio of observed species richness to those predicted by the linear regression models for each grid cell was >69.3% (Figure 1B). This indicates that the data collected were sufficient. The variation in the number of species was well explained by changes in the number of species collected.

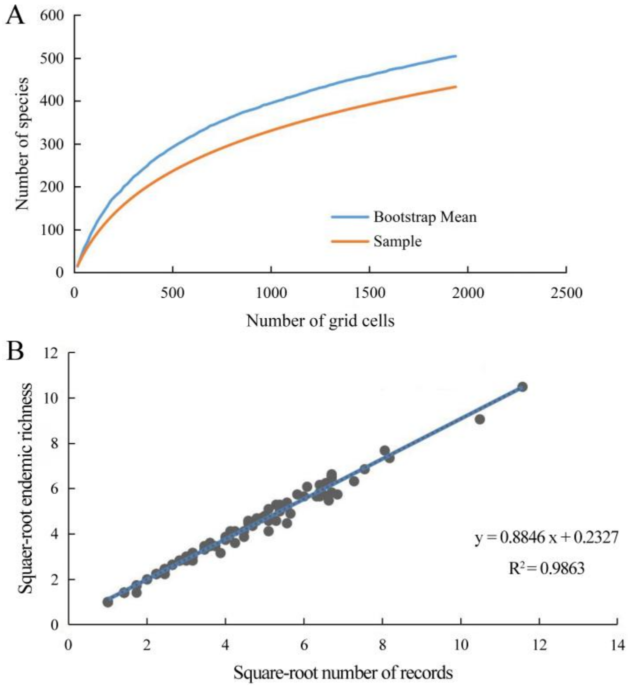

Figure 1. (**A**) Species accumulation curves for Tenebrionidae in Xinjiang, China. (**B**) Linear regression (y = 0.8846x + 0.2327) for the number of records and species richness in a 1° grid. The observed richness in the cells below the regression line was >69.3% of the predicted richness.

Within Xinjiang, most species were found in the Altai Mountains, Tianshan Mountains, and Kunlun Mountains (Figure 2). Among them, 118 species were found in the Altai Mountains, 340 in the Tianshan Mountains, and 80 in the Kunlun Mountains (Table S1).

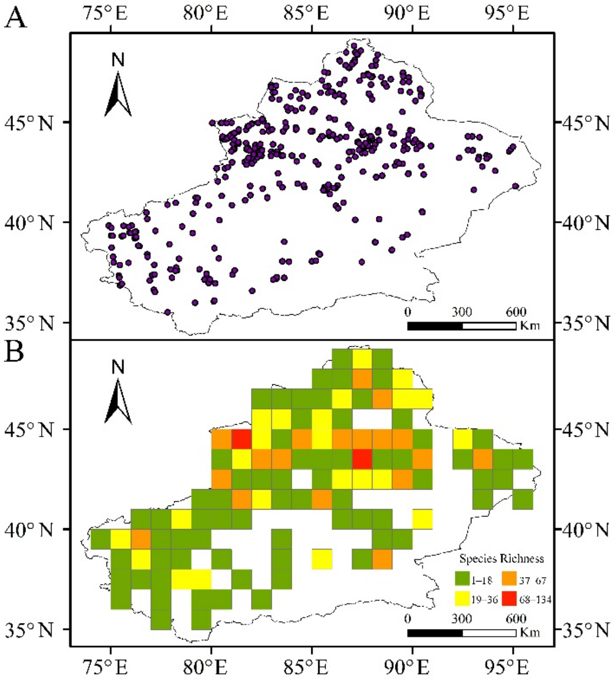

Figure 2. (**A**) The general distribution pattern of Tenebrionidae in Xinjiang, China. (**B**) The species richness pattern identified by a 1° grid size in Xinjiang, China.

3.2. Parsimony Analysis of Endemicity

The four most parsimonious trees for AOE identification were obtained under three different grid cells. The optimal tree at a 1.5° grid size is a candidate for AOE identification (Figure 3). The branches with at least two consecutive cells were considered AOEs. Finally, 10 branches met the criteria and were selected, two of which belonged to Altay Prefecture–Akxoki Prefecture, two to Bortala Mongolian Autonomous Prefecture–Akxoki Prefecture–Changji Hui Autonomous Prefecture–Ili Prefecture, one to Hami Prefecture, two to Kizilsu Kirgiz Autonomous Prefecture–Aksu Prefecture, two to Kashi Prefecture, and one to Hotan prefecture.

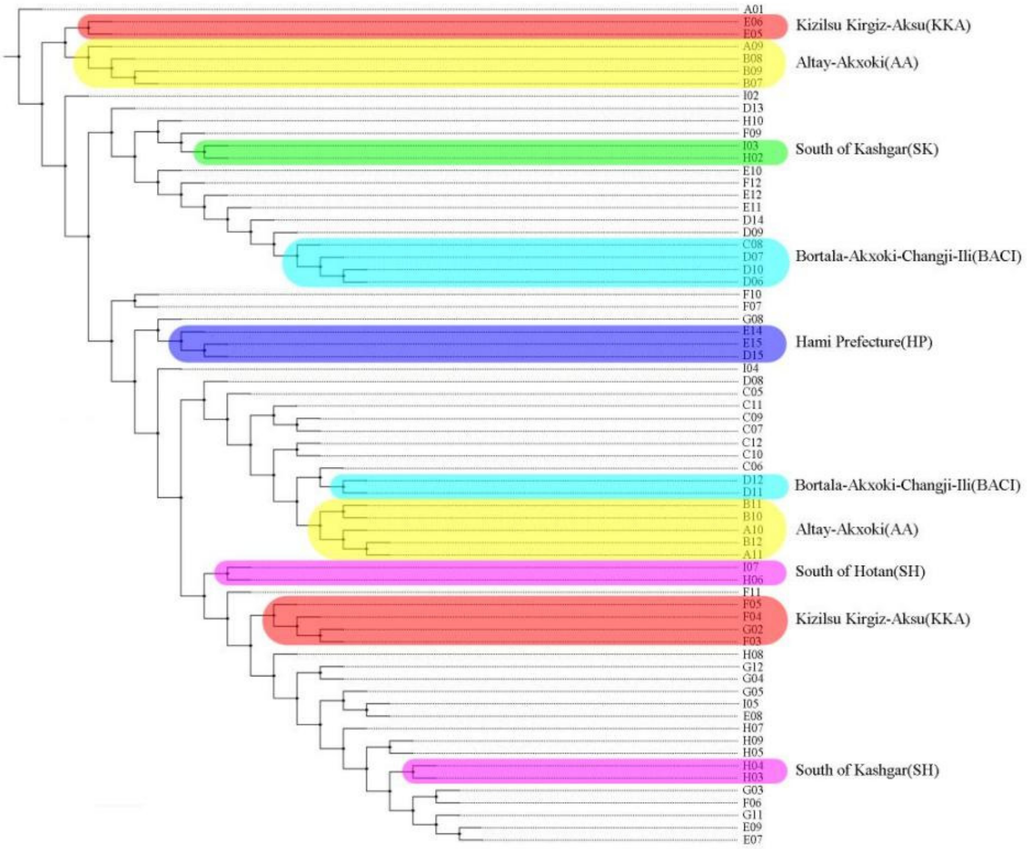

Figure 3. The optimal tree obtained by PAE using TNT v1.5 under a 1.5° grid size. Different coloured shadows represent different AOEs.

Under the criteria of identification, six AOEs were obtained (Table S2 and Figure 4): (i) Altay–Akxoki (AA), which shared 135 species; (ii) Bortala–Akxoki–Changji–Ili (BACI), which shared 264 species; (iii) Hami Prefecture (HP), which shared 21 species; (iv) Kizilsu Kirgiz–Aksu (KKA), which shared 73 species; (v) South of Kashgar (SK), which shared 41 species; and (vi) South of Hotan (SH), which shared 7 species.

3.3. Endemicity Analysis

In the EA analysis, three sizes were analysed by NDM/VNDM v3.1 under 0.5°, 1°, and 1.5° grid cells, and 3, 12, and 25 consensus areas were obtained, respectively. The consensus areas under the 0.5° grid size were only related to the Tianshan Mountains (TM) (Figure S1), and those under a 1° × 1° cell grid (Figures S2 and S3) were similar to those under the 1.5° grid (Figures S4–S7); both were related to the Altai Mountains (AM), Tianshan Mountains (TM), Kunlun Mountains (KM), and Junggar Basin (JB) (Figure 5). By overlapping the consensus areas with different grid sizes, a total of four AOEs were finally detected.

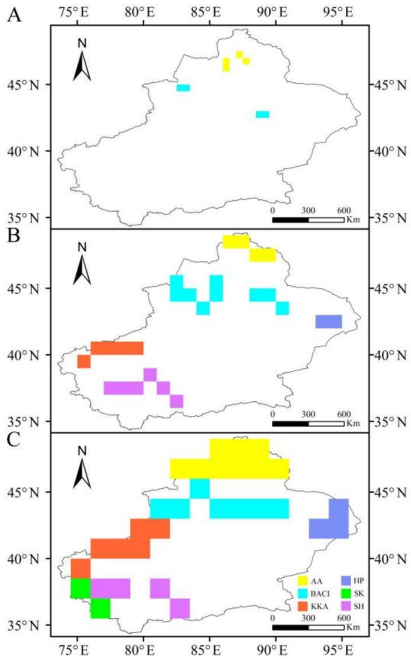

Figure 4. AOEs obtained for Tenebrionidae by PAE using three different cells in Xinjiang, China: (**A**) 0.5° grid size, (**B**) 1° grid size, and (**C**) 1.5° grid size.

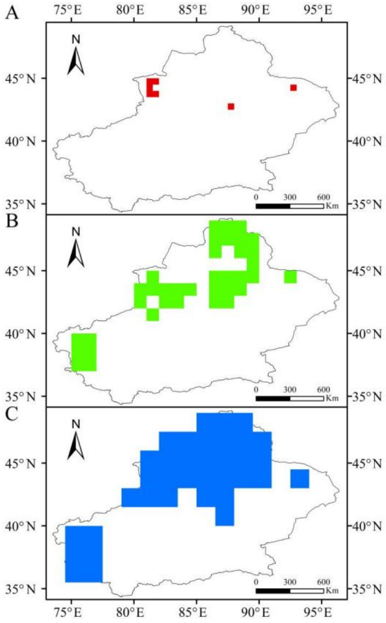

Figure 5. AOEs obtained for Tenebrionidae by EA analysis using three different cells in Xinjiang, China: (**A**) 0.5° grid size (red shadows); (**B**) 1° grid size (green shadows); and (**C**) 1.5° grid size (blue shadows).

(i) Altai Mountains (AM): The AM included consensus areas 6, 8, 9, 10, 36, and 40. The consensus regions scored 3.250000, 3.916667, 4.071429, 3.357143, 6.966667, and 3.000000 (Table S3 and Figures S2, S3, S6 and S7). One hundred and eleven species were found in both areas, including *Scythis altaicus*, *S. affinis*, *S. arenarius arenarius*, *S. vitorovianus*, *S. intermedia intemedia*, *Anatolica dashidorzsi subalpina*, *A. subpolita*, etc.

(ii) Tianshan Mountains (TM): These AOEs included consensus areas 1, 2, 3, 4, 5, 7, 11, 13, 14, 15, 16, 18, 20, 22, 24, 25, 26, 27, 28, 29, 30, 32, 33, 34, 37, 38, and 39 (Table S3 and Figures S1–S6). The consensus area scores were 3.70000, 3.250000, 3.000000, 3.666667, 4.375000, 3.928571, 3.000000, 3.458974, 3.000000, 3.333333, 5.000000, 9.869374, 7.947520, 10.089686, 3.000000, 6.558036, 5.207238, 7.365209, 3.333333, 6.672132, 3.230769, 6.400000, 7.418164, 10.898350, 5.583333, 4.641865, and 3.000000. Three hundred seventy-five species were counted in both regions, for example, *Colposphena brevlcollis*, *Scythis banghaasi*, *S. bulganicus*, *S. tatarica pseudoscythis*, *S. vitorovianus*, *S. angusticollis angusticollis*, *S. intermedia intemedia*, *Anatolica gobioltaica altaica*, and *A. hoboksarana*.

(iii) Kunlun Mountains (KM): The consensus areas 12, 31, and 35 were covered by KM, scoring 3.541667, 3.871429, and 5.250000, respectively (Table S3 and Figures S3, S5 and S6). Eighty-eight species were supported in these AOEs, including *Anatolica sternalis*, *Ascelosodis concinnus*, *Microdera* (*Microdera*) *parvicollis*, *M.* (*Microdera*) *laticollis laticollis*, *M.* (*Dordanea*) *elegans*, *M.* (*Dordanea*) *mongolica*, *Colposcelis* (*Scelocolpis*) *damone*, and *C.* (*Scelocolpis*) *forsteri*.

(iv) Junggar Basin (JB): This region contained consensus areas 17, 19, 20, 21, 23, 27, and 33 (Table S3 and Figures S4–S6). The scores were 4.783780, 5.188492, 7.947520, 3.500000, 6.387500, 7.365209, and 7.418164. A total of two hundred and twenty-one species were supported in these consensus areas, e.g., *Scythis altaicus*, *S. banghaasi*, *S. sculptilis*, *S. affinis*, *S. arenarius arenarius*, *S. vitorovianus*, *Anatolica dashidorzsi subalpina*, and *A. subpolita*.

4. Discussion

4.1. Congruent Patterns between Species Richness and Endemism Areas

In general, the species richness centres and endemism areas in this study were mainly found in the Altai, Tianshan, and Kunlun Mountains and Junggar Basin, which indicated that the species richness pattern of Tenebrionidae was basically consistent with the AOEs. This condition is found not only in insects [48,51,53,58,73] but also in other groups, such as plants [91], mammals [72], and birds [92]. This supports the hypothesis that AOEs have historically served as speciation centres [51,53], because AOEs characterized by stable climates and diverse habitats could maintain the long-term existence of organisms [51,53,72,93]. It is worth noting that there is an AOE in the basin area. In the centre of the basin, the vegetation coverage is lower than that around the basin, resulting in a more arid environment [94]. However, the Tenebrionidae there have evolved and adapted to the arid and semiarid environment in morphology, biology, and behaviour, which contributed to the high species richness in the middle of the basin [17,23,28,95].

4.2. AOEs of Tenebrionidae

Here, Tenebrionidae beetles were selected as the subjects to detect AOEs in Xinjiang for the first time, and a total of four AOEs were detected by two different methods, including three mountain regions (AM, TM, and KM) and one basin (JB).

4.2.1. AOEs in Montane Areas

Mountains often harbour high biodiversity due to their complex topography and stable climate. The formation of mountains is geological uplift, which is usually caused by the collision of continental plates [96,97]. The complex terrain and diverse environments in montane areas hinder the exchange of species, but they also provide the basis for the emergence of new species [98,99]. In addition, the complex terrain increases the number of ecological niches, which also promotes the formation of new species [99–101].

(i) AA belongs to the Altai Mountains. There was no significant difference in the AOEs between the PAE and EA under a 1.5° grid size, while the PAE had a larger consensus region than the EA under a 0.5° grid size. Under a 1° × 1° cell grid, the EA detected larger AOEs, which were mainly located in the southern Altai Mountains. The Altai Mountains have a northwest to southeast trend and cross China diagonally. The Altai Mountains first appeared during the Caledonian movement, and the Himalayan movement caused the Altai Mountains to rise along the NW-trending fault block displacement, which provided shelters for several species and contributed to the high biodiversity of the areas [102,103].

(ii) BACI, HP, and KKA belong to the Tianshan Mountains. The EA detected more consensus areas in the region. Compared to PAE, the AOEs detected by EA were more widely distributed, mainly located in the southeastern and southwestern Tianshan Mountains. Significant differences could be observed in the 1.5° grid size. This may be caused by the different height gradients of the crustal changes in the late Cenozoic [104]. Tianshan

Mountain is located in the hinterland of Eurasia running from east to west and accounts for approximately one-third of the entire area of Xinjiang. The annual precipitation gradually decreases from west to the east on the same slope, which enhanced the adaptation of Tenebrionidae to the special climate and provided a certain guarantee for their survival, reproduction, and evolution [105,106].

(iii) The Kunlun Mountains include SK and SH. Within the 1° and 1.5° cells, the consensus area was mostly distributed in the western part of the northern slope of the Kunlun Mountains. Although the consensus areas of the EA and PAE were similar, the AOEs identified by the PAE were more widely distributed in this area, which is mainly located in the middle of the northern slope of the Kunlun Mountains. The neotectonic movement of the Kunlun Mountains is extremely strong, showing high values in the west and low values in the east [107]. The northern slope belongs to the Tarim Desert and Qaidam Desert in the warm temperate zone with low precipitation. With the increase in altitude, its terrain transitions from warm temperate desert into alpine desert, and the precipitation in this area also increases [25,99]. The higher topography of the west provides greater opportunities for the geographical isolation of species, which may be one reason why endemic areas are widespread in the west [108–110].

In addition, the high level of AOEs is closely related to the geological events experienced by the region [56]. The collision of the Indian plate with the Asian plate caused the Kunlun Mountains and the Qinghai-Tibet Plateau uplift, which is known as 'the roof of the world' [51,99,111,112]. Because the Qinghai–Tibet Plateau has affected the northwards movement of westerlies and the blocking of water vapour; hence, warm and wet air cannot reach Xinjiang across the Qinghai–Tibet Plateau, which leads to the arid climate in Xinjiang [4,5,24,99,106,113]. Tenebrionidae has adapted to arid environments, which contributes to the high species richness in this region [17,23].

4.2.2. AOE in the Basin

Basins with high surroundings (mountains or plateaus) and low central areas (plains or hills) can be divided into two types according to the influence of special geology and surface external force changes [114,115]. The Junggar Basin was formed as a result of plate movement [100,103,116,117]. Although the vegetation coverage of the basin is low, the surrounding mountains or plateaus have higher plant coverage than the central region [94], which provides certain environmental conditions for the existence of organisms.

(iv) The Junggar Basin (JB) is the second largest inland basin in China located in the northern part of Xinjiang. The basin is located between the Altai Mountains and the Tianshan Mountains, with the north being slightly higher than the south [94,103]. In addition, special geographical conditions prevent water vapour from moving northwards, which causes climatic changes and produces many arid and semiarid regions [1]. The Gurbantunggut Desert lies in the middle of the basin. The flourishing of the Tenebrionidae in this region is facilitated by adapting to the environment in arid and semiarid regions. In terms of morphology, beetles have adapted to merged anterior wings, degeneration of posterior wings, variable legs, formation of a subelytral cavity, and a well-developed tarsus [17]. Meanwhile, in biology and behaviour, they have suspended animation and self-defence through the release of smelly fluids, gregariousness, and diurnal activity [17,23].

4.3. Limitations of Dataset and Methods

Although the taxonomy of the Tenebrionidae from Xinjiang, China, is well studied and documented with rich geographical data, under-collecting remains a potential problem in biogeographical research. Due to the harsh environment and technological limitations, we were unable to make a systematic survey for the species distribution of each cell. However, the data integrity for analysis showed an adequate collection. This suggests that the geographic data we collected were sufficient, and the variation in numbers of species was explained well by the variation in the numbers of collections [51].

In general, although slight differences were shown in the two approaches, both of them detected similar AOEs. The results of the EA had one more AOE than those of the PAE method, which might be explained by the different algorithms of the two methods [51]. There is no widely accepted answer as to which method can identify AOEs more accurately [62,118], and more accurate AOEs cannot be obtained by using a fixed method [53,56,93,119]. Thus, we adopted the PAE and EA results to provide more comprehensive AOE information.

Moreover, the grid sizes are also an important factor affecting the results of AOEs [72,93]. The smaller grid sizes will produce narrow and accurate consensus areas, but too small may also lead to the fragmentation of consensus areas [51], such as 0.5° in the present study. However, a grid size that is too large may also cause inaccurate consensus areas, such as a 1.5° grid size. Therefore, in the present study, we overlapped the consensus areas by different methods and three grid sizes to obtain more comprehensive endemism areas, following previous studies [51,56].

5. Conclusions

The geographical patterns of species richness and endemic areas of Tenebrionidae in Xinjiang, China, were analysed using the PAE and EA. We found that the species richness pattern was consistent with the AOEs of Tenebrionidae. In addition, the AOEs of Tenebrionidae in Xinjiang were mostly located in mountainous areas and basins, such as the Altai Mountains, Tianshan Mountains, Kunlun Mountains, and Junggar Basin. This is mainly due to the complex terrain and stable climate of the mountainous area, which promote long-term persistence, speciation, and species accumulation. Our findings indicate that greater conservation efforts should be expended in montane areas. Future studies should explore the relation between the AOEs and evolution histories at the molecular level.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/d14070558/s1, Table S1: A list of Tenebrionidae distributed in Altai Mountains, Tianshan Mountains and Kunlun Mountains; Table S2: Summary information of areas of endemism (AOEs) of Tenebrionidae using Parsimony analysis of endemicity (PAE) based on 1.5° cell grid; Table S3: Summary information on the consensus areas of Tenebrionidae using endemicity analysis (EA), with their respective score, number of cells for each consensus area, the maximum scores and grid size of each consensus areas; Figure S1: Consensus areas 1–3 detected by endemicity analysis (EA) using 0.5° grid size; Figure S2: Consensus areas 4–9 detected by endemicity analysis (EA) using 1° grid size; Figure S3: Consensus areas 10–15 detected by endemicity analysis (EA) using 1° grid size; Figure S4: Consensus areas 16–23 detected by endemicity analysis (EA) using 1.5° grid size; Figure S5: Consensus areas 24–31 detected by endemicity analysis (EA) using 1.5° grid size; Figure S6: Consensus areas 32–39 detected by endemicity analysis (EA) using 1.5° grid size; Figure S7: Consensus areas 40 detected by endemicity analysis (EA) using 1.5° grid size.

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Conflicts of Interest: The authors declare no conflict of interest.

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