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● Taxonomic study on Sphingidae (Lepidoptera) from Dabie Mountains of China



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Abstract: Based on years of surveys and literature review, this study systematically records a total of 55 Sphingidae species belonging to 28 genera and 3 subfamilies in the Dabie Mountains of Hubei, Henan and Anhui Provinces, China, including 4 new record species in Hubei Province, 1 new record species in Henan Province and 1 new record species in Anhui Province. Faunal and cluster analyses indicate that the fauna of Sphingidae insects in the Dabie Mountains exhibit significant characteristics of southern origin. In addition, this study has constructed a comprehensive *COI* DNA barcode database of Sphingidae in the Dabie Mountains and mapped species distribution patterns across different months and altitudes.

Keywords: *COI* gene, hawk moths, Lepidoptera, new records, taxonomy

● 中国大别山区天蛾科（鳞翅目）分类学研究

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摘要: 该研究通过历年调查并结合文献资料, 系统记录了中国鄂豫皖大别山区天蛾科昆虫共计 3 亚科 28 属 55 种, 其中包含湖北省新纪录种 4 种、河南省新纪录种 1 种、安徽省新纪录种 1 种。经区系与聚类分析表明, 大别山区天蛾科昆虫区系具有显著的南方起源特征。此外, 系统构建了大别山区天蛾科昆虫的 *COI* DNA 条形码数据库, 并绘制了不同月份及海拔的物种分布图。

关键词: *COI* 基因, 天蛾, 鳞翅目, 新纪录, 分类学

● Introduction

The Dabie Mountains are located at the junction of Hubei, Henan and Anhui Provinces in China, covering 40 counties and cities. With geographical coordinates ranging from 30°10'N to 32°30'N and 112°40'E to 117°10'E, they stretch approximately 380 kilometers from east to west and about 175 kilometers from north to south, and form a critical watershed between the Yangtze River and the Huaihe River. The region has complex terrain, dominated by mountains with an average altitude of 500-1500 meters, interspersed with hills and rifts. The area has abundant rainfall, a mild and humid climate, and as a critical ecological transition zone from the subtropical to the warm temperate zone, it has both the characteristics of the humid continental monsoon climate in East China and the mountain climate. The unique geographical transition and habitat heterogeneity have nurtured rich biodiversity. In particular, the Lepidoptera fauna in the transition zone between the Palaearctic Realm and the Oriental Realm is a research hotspot. The insect fauna in this region has significant edge effects, while the distribution pattern of Sphingidae species here has not been systematically clarified.

Sphingidae belongs to Bombycoidea, Lepidoptera (van Nieukerken *et al.* 2011). Globally, the family comprises 4 subfamilies, 178 genera and about 1700 species worldwide. In China, more than 280 species belonging to 71 genera and 4 subfamilies are known (Kitching 2025; Jiang & Huang 2023; Deng *et al.* 2024; Jiang & Zhang 2024). Sphingidae insects are medium to large in size with complex life cycles, and most species have multiple generations a year. They have a wide range of hosts. Many species are important agricultural and forestry pests, and others serve as key pollinators. Due to their ecological sensitivity, they are often used as indicator species for ecological environment monitoring (Zhu & Wang 1980, 1997).

Systematic taxonomic researches on Sphingidae insects in the Dabie Mountains have long been lacking, and previous research results are mostly scattered records and regional scientific expedition reports. This study carried out systematic collection and investigation in 35 counties and cities in the Dabie Mountains, systematically determined *COI* gene sequences, constructed a DNA barcode database, established a two-dimensional identification system of morphological and molecular characteristics, and for the first time systematically clarified the species composition and distribution patterns of Sphingidae in the Dabie Mountains of Hubei, Henan and Anhui Provinces. The above series of research results provide basic data for the study on the faunal evolution of Sphingidae in the transition zone and the ecological monitoring and protection work in the Dabie Mountains.

● Material and methods

Specimen Collection and Morphological Identification

The specimens in this study were collected by light trapping in the Dabie Mountains, China (Fig. 1). The map verification number of the map used in this study is GS(2020)4619. All specimens are currently deposited in the Institute of Zoology, Chinese Academy of Sciences, Beijing, China (IZCAS). Images of adult specimens were taken using a Canon EOS 70D camera equipped with an EF 180mm F/3.5L USM lens. Species identification was mainly based on taxonomic literature and relevant academic websites (Jiang & Huang 2023; Kitching 2025). Dissection and mounting of genitalia were conducted following the methods described by Li & Zheng (1996).

Acquisition of DNA Barcodes and Construction of Phylogenetic Tree

DNA was extracted from the leg tissues of dried adult specimens using the TINAamp Genomic DNA Kit (DP304). The 658bp barcode region of the *COI* gene was amplified via PCR using the LepF1 and LepR1 primers (Hajibabaei *et al.* 2006). PCR products were sent to Tianyi Huayu Gene (Wuhan, China; <https://www.tyhygene.com/>) for sequencing with the aforementioned primers. Meanwhile, after obtaining the COI sequences, homologous sequence alignment was performed in the GenBank and BOLD databases, and phylogenetic trees were constructed to assist in verifying the results of morphological identification. Genetic distances between pairwise COI sequences were calculated based on the Kimura 2-Parameter model. A Maximum Likelihood (ML) phylogenetic tree (Fig. 3) was constructed for analysis, with 5000 bootstrap replications (Tamura *et al.* 2021).

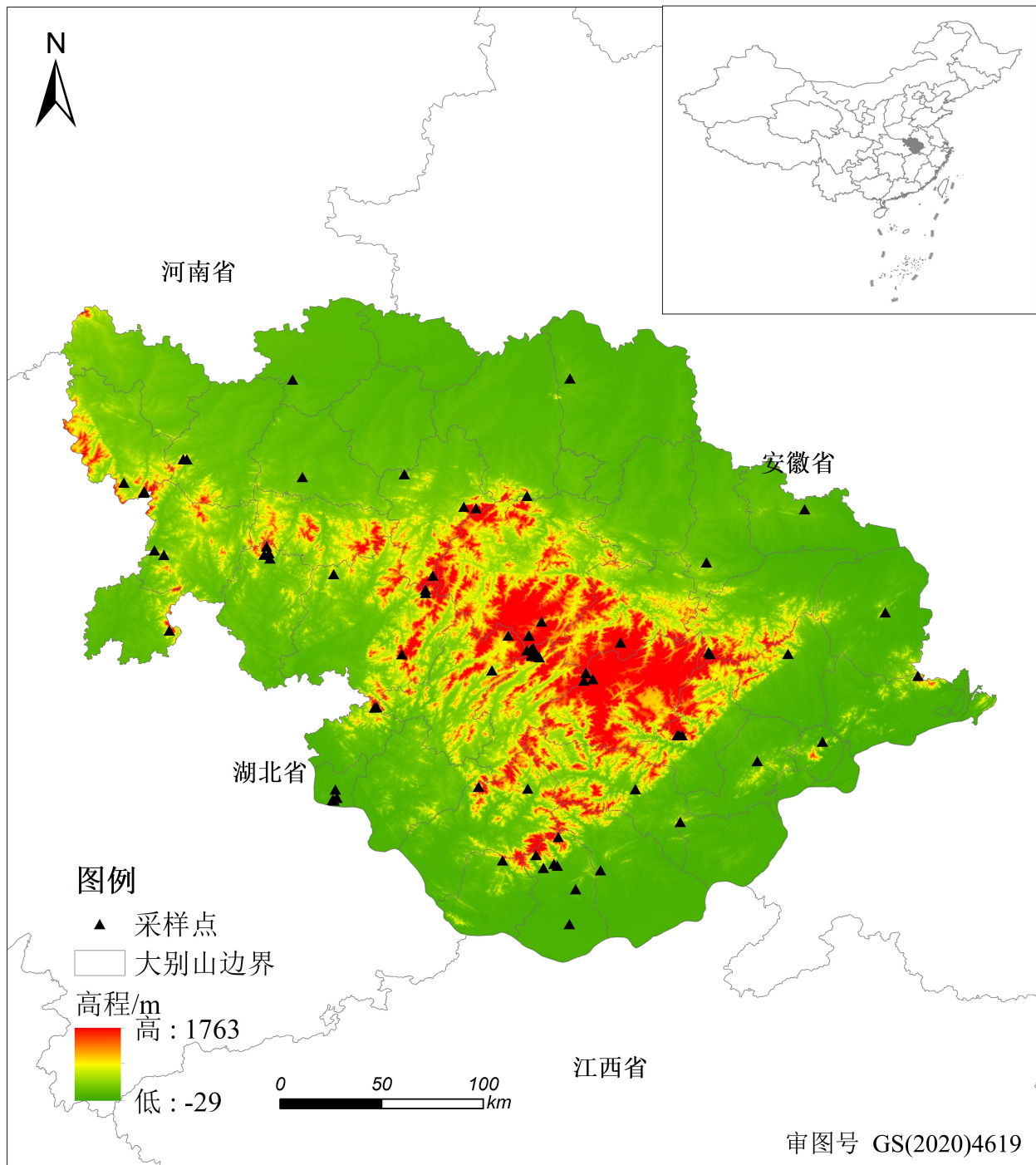


FIGURE 1. Distribution map of specimen collection sites.

Faunistic Analysis and Cluster Analysis

For the analysis of faunistic characteristics, the scheme proposed by Shen (2015) was adopted. This scheme divides China's insect geographical regions into 9 geographical regions, including the Northwestern China region (NWC), Northeastern China region (NEC), Qinghai-Xizang region (QX), Northern China region (NC), Central China region (CC), Changjiang-Huaihe region (CH), Eastern China region (EC), Southwestern China region (SWC), and Southern China region (SC) (Shen *et al.* 2015; Shen *et al.* 2018). Additionally, in the context of this study, HBDM refers to the Dabie Mountains in Hubei, HNDM refers to the Dabie Mountains in Henan, and AHDM refers to the Dabie Mountains in Anhui. Phylogenetic trees, intuitive diagrams illustrating the distribution of species across

different months and altitudes, as well as faunistic analysis diagrams and cluster analysis diagrams, were all plotted using the bioinformatics visualization online platform (<https://www.chiplot.online/>) (Xie *et al.* 2023).

● Results

Taxonomy

A total of 1,050 specimens of Sphingidae insects were collected during the four-year survey of this study. After identification, they belong to 50 species, 27 genera, and 3 subfamilies. Additionally, 5 species that were recorded in the literature but not collected in this survey were sorted out and verified (Wang & Sun 1999; Huang *et al.* 2023). Thus, the checklist of Sphingidae insects in the Dabie Mountains was compiled, totaling 55 species, 28 genera, and 3 subfamilies. Among them, the subfamily Smerinthinae includes 25 species belonging to 13 genera, the subfamily Macroglossinae includes 23 species belonging to 10 genera, and the subfamily Sphinginae includes 7 species belonging to 5 genera. The checklist is shown in Table 1, the photos of adult specimens are shown in Fig. 2, and the distribution across altitudes and months is shown in Fig. 3.

This study identified 6 new provincial records. Among them, 4 species are new records for Hubei Province: *Macroglossum neotrogiodytus* Kitching & Cadiou, 2000, *Cechenena lineosa* (Walker, 1856), *Cechenena minor* (Butler, 1875), and *Cechetra striata* Rothschild, 1894, one species is a new record for Henan Province: *Meganoton analis analis* (Felder, 1874), and one species is a new record for Anhui Province: *Ambulyx tobii* (Inoue, 1976).

TABLE 1. Checklist of Sphingidae in the Dabie Mountains of Hubei, Henan and Anhui Provinces.

Subfamily	Genus	Species
天蛾亚科	松天蛾属	越中松天蛾 <i>Hyloicus centrovietnama</i> Brechlin, 2015
Sphinginae	大背天蛾属	大背天蛾指名亚种 <i>Meganoton analis analis</i> (Felder, 1874) [†]
	霜天蛾属	丁香天蛾 <i>Psilogramma increta</i> (Walker, 1865)
		霜天蛾 <i>Psilogramma discistriga</i> (Walker, 1856) [#]
	白薯天蛾属	白薯天蛾 <i>Agrius convolvuli</i> (Linnaeus, 1758)
	鬼脸天蛾属	鬼脸天蛾 <i>Acherontia lachesis</i> (Fabricius, 1798)
		芝麻鬼脸天蛾 <i>Acherontia styx</i> Westwood, 1847
目天蛾亚科	目天蛾属	蓝目天蛾 <i>Smerinthus planus</i> Walker, 1856
Smerinthinae	月天蛾属	月天蛾指名亚种 <i>Craspedortha porphyria porphyria</i> (Butler, 1876)
	构月天蛾属	构月天蛾 <i>Parum colligata</i> (Walker, 1856)
	六点天蛾属	椴六点天蛾大陆亚种 <i>Marumba dyras oriens</i> (Butler, 1875)
		红六点天蛾南方亚种 <i>Marumba gaschkewitschii complacens</i> (Walker, 1865)
		黄边六点天蛾华东亚种 <i>Marumba maackii ochreate</i> Mell, 1935
		黑角六点天蛾 <i>Marumba saishivana</i> Okamoto, 1924
		枇杷六点天蛾指名亚种 <i>Marumba spectabilis spectabilis</i> (Butler, 1875) [#]
		栗六点天蛾 <i>Marumba sperchius</i> (Ménétriés, 1857)
	盾天蛾属	盾天蛾指名亚种 <i>Phyllosphingia dissimilis dissimilis</i> (Bremer, 1861)
	枫天蛾属	枫天蛾 <i>Cypoides chinensis</i> (Rothschild & Jordan, 1903)
	绿天蛾属	榆绿天蛾指名亚种 <i>Callambulyx tatarinovii tatarinovii</i> (Bremer & Grey, 1853)
	木蜂天蛾属	木蜂天蛾 <i>Sataspes xylocoparis</i> Butler, 1875
	豆天蛾属	豆天蛾 <i>Clanis bilineata</i> (Walker, 1866)
		灰斑豆天蛾南方亚种 <i>Clanis undulosa gigantea</i> Rothschild, 1894
	蔗天蛾属	甘蔗天蛾 <i>Leucophlebia lineata</i> Westwood, 1847 [#]
	绒天蛾属	白须绒天蛾 <i>Kentrochrysalis sieversi</i> Alphéraky, 1897

	星天蛾属	大星天蛾 <i>Dolbina inexacta</i> (Walker, 1856)
	鹰翅天蛾属	日本鹰翅天蛾朝鲜亚种 <i>Ambulyx japonica koreana</i> Inoue, 1993
		华南鹰翅天蛾 <i>Ambulyx kuangtungensis</i> (Mell, 1922)
		栎鹰翅天蛾 <i>Ambulyx liturata</i> Butler, 1875
		裂斑鹰翅天蛾 <i>Ambulyx ochracea</i> Butler, 1885
		亚洲鹰翅天蛾指名亚种 <i>Ambulyx sericeipennis sericeipennis</i> Butler, 1875 #
		核桃鹰翅天蛾 <i>Ambulyx schauffelbergeri</i> Bremer & Grey, 1853
		拓比鹰翅天蛾 <i>Ambulyx tobii</i> (Inoue, 1976) †
长喙天蛾亚科	黑边天蛾属	黑边天蛾 <i>Hemaris affinis</i> (Bremer, 1861)
Macroglossinae		锈胸黑边天蛾 <i>Hemaris staudingeri</i> Leech, 1890
	昼天蛾属	葡萄昼天蛾 <i>Sphecodina caudata</i> (Bremer & Grey, 1853)
	锤天蛾属	喜马拉雅天蛾 <i>Neogurelca himachala</i> (Butler, 1876)
		团角锤天蛾 <i>Neogurelca hyas</i> (Walker, 1856) #
	葡萄天蛾属	葡萄天蛾指名亚种 <i>Ampelophaga rubiginosa rubiginosa</i> Bremer & Grey, 1853
	缺角天蛾属	葡萄缺角天蛾东部亚种 <i>Acosmeryx naga metanaga</i> Butler, 1879
		缺角天蛾 <i>Acosmeryx castanea</i> Rothschild & Jordan, 1903
	长喙天蛾属	青背长喙天蛾 <i>Macroglossum bombylans</i> Boisduval, 1875
		长喙天蛾指名亚种 <i>Macroglossum corythus corythus</i> Walker, 1856
		弗瑞兹长喙天蛾 <i>Macroglossum fritzei</i> Rothschild & Jordan, 1903
		小长喙天蛾 <i>Macroglossum neotrogiodytus</i> Kitching & Cadiou, 2000 †
		黑长喙天蛾 <i>Macroglossum pyrrhosticta</i> Butler, 1875
	红天蛾属	红天蛾 <i>Deilephila elpnor</i> (Linnaeus, 1758)
	斜纹天蛾属	西藏斜纹天蛾 <i>Theretra tibetiana</i> Vaglia & Haxaire, 2010
		雀纹天蛾 <i>Theretra japonica</i> (Boisduval, 1869)
		芋单线天蛾指名亚种 <i>Theretra silhetensis siihetensis</i> (Walker, 1856)
		芋双线天蛾指名亚种 <i>Theretra oldenlandiae oldenlandiae</i> (Fabricius, 1775)
	白肩天蛾属	蒙古白肩天蛾 <i>Rhagastis mongoliana</i> (Butler, 1876)
		姬白肩天蛾 <i>Rhagastis dichroae</i> (Mell, 1992)
	背线天蛾属	条背线天蛾 <i>Cechetra lineosa</i> (Walker, 1856) †
		平背线天蛾 <i>Cechetra minor</i> (Butler, 1875) †
		纹背线天蛾 <i>Cechetra striata</i> Rothschild, 1894 †

Note: Species with "##" after their Latin names are those recorded in the literature but for which no specimens were collected in this study (Wang & Sun, 1999; Huang *et al.* 2023), species with "†" after their Latin names are new provincial records discovered in this study.

Molecular Phylogenetic Analysis

A total of 89 *COI* sequences from 48 species of Sphingidae insects in the Dabie Mountains were obtained through bidirectional sequencing. After verification, 2 *COI* sequences of Saturniidae downloaded from the NCBI database, *Loepa sinjaevi* Brechlin, 2004 (GU663523.1) and *Antheraea yamamai* (Guérin-Méneville, 1861) (AB015864.1) were used as outgroups. Genetic distances between pairwise *COI* gene sequences were calculated based on the K2P model, and a maximum likelihood (ML) phylogenetic tree (Fig. 3) was constructed for analysis. At the subfamily level, the overall topology was consistent with the current taxonomic system (Macroglossinae (Smerinthinae, Sphinginae)). However, partial taxonomic groups among the three subfamilies overlapped, with low bootstrap values. This may be attributed to the limited variable sites in the mitochondrial single-gene fragment *COI*, which makes it insufficient for phylogenetic analysis of higher taxa such as subfamilies and tribes.

Species of the same species and genus clustered into a single clade in the phylogenetic tree, which was highly consistent with their morphological characteristics. Genetic distance analysis showed that the minimum intraspecific genetic distance was 0, and the maximum was 4.69%. The maximum intraspecific genetic distance occurred in the clade of *Phyllosphingia dissimilis*. This species has multiple morphologically similar subspecies or species, distributed from Southeast Asia to the Russian Far East. Its taxonomic status and distribution boundaries remain unclear, with a history of confusing taxonomic research, requiring further study with additional specimens from more regions (Kitching 2025; Zolotuhin & Ryabov 2012).

Except for *Phyllosphingia dissimilis*, the intraspecific genetic distances of all other species were less than 3%. Interspecific genetic distances ranged from 1.52% to 18.80%, with an average of 11.21%. The maximum interspecific genetic distance was observed between *Clanis undulosa gigantea* and *Theretra oldenlandiae oldenlandiae*, the minimum interspecific genetic distance, with a high bootstrap value, was between *Ambulyx schauffelbergeri* and *Ambulyx japonica koreana*. However, these two species did not cluster into the same smallest clade and do not belong to the same species group (Jiang *et al.* 2025). There was an overlap between intraspecific and interspecific genetic distances, with no clear DNA barcode gap (Jin *et al.* 2017). Therefore, identification cannot rely solely on the *COI* DNA barcode, and accurate results require a combination of genital morphological characteristics and phylogenetic trees.

Faunistic Analysis and Clustering Analysis

The results of the faunistic analysis (Fig. 4) showed that all Sphingidae species in the Dabie Mountains are widespread species, with their faunistic proportions exhibiting a significant gradient: Changjiang-Huaihe region (100.00%), South China region (98.18%), East China region (98.18%), Southwest China region (98.18%), Central China region (96.36%), North China region (72.73%), Qinghai-Tibet region (65.45%), Northeast China region (50.91%), and Northwest China region (16.36%).

The results of the cluster analysis of Sphingidae faunas in the Dabie Mountains are shown in Fig 4: ((Changjiang-Huaihe region (100.00%) + South China region (98.18%) + East China region (98.18%)) + (Southwest China region (98.18%) + Central China region (96.36%))) + (North China region (72.73%) + Qinghai-Tibet region (65.45%)) + (Northeast China region (50.91%) + Northwest China region (16.36%)).

The full coverage in the Changjiang-Huaihe region indicates a high adaptability of Sphingidae species to the local environment. The high overlap (>95%) and clustering among the faunas of the South China, East China, Southwest China, and Central China regions may result from climatic similarity and convergent vegetation types. The low proportions in the Qinghai-Tibet region (65.45%), Northeast China region (50.91%), and Northwest China region (16.36%) reveal the ecological filtering effect of arid and alpine environments on Sphingidae dispersal. Meanwhile, the high connectivity (98.15% each) between the South China and Southwest China faunas may reflect insect migration along the South China-Southwest dispersal corridor in the East Asian monsoon region.

This pattern not only reflects historical biogeographical processes such as the Quaternary glacial refugium effect but also provides model parameters for predicting species migration paths under climate change. Therefore, the faunistic characteristics of Sphingidae in the Dabie Mountains are the combined result of its geographical location, climatic transition, and topographic heterogeneity. Future studies should integrate genomics and ecological niche models to quantify the contributions of various driving factors.

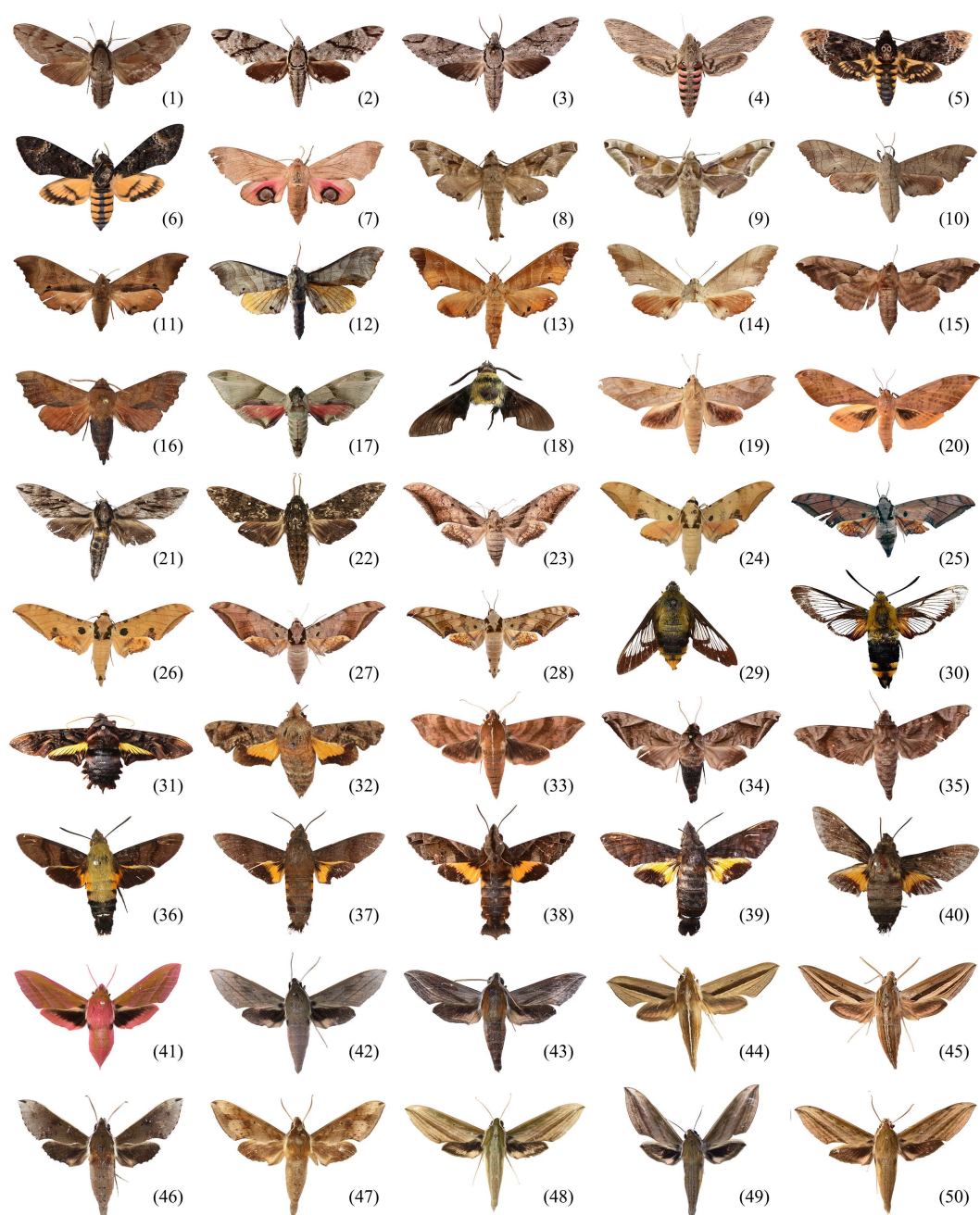


FIGURE 2. Adult specimens of Sphingidae from the Dabie Mountains: (1) *Hyloicus centrovietnama* (2) *Meganoton analis analis* (3) *Psilogramma increta* (4) *Agrius convolvuli* (5) *Acherontia lachesis* (6) *Acherontia styx* (7) *Smerinthus planus* (8) *Craspedortha porphyria porphyria* (9) *Parum colligata* (10) *Marumba dyras oriens* (11) *Marumba gaschkewitschii complacens* (12) *Marumba maackii ochreata* (13) *Marumba saishivana* (14) *Marumba sperchius* (15) *Phyllosphingia dissimilis dissimilis* (16) *Cypoides chinensis* (17) *Callambulyx tatarinovii tatarinovii* (18) *Sataspes xylocoparis* (19) *Clanis bilineata* (20) *Clanis undulosa gigantea* (21) *Kentrochrysalis sieversi* (22) *Dolbina inexacta* (23) *Ambulyx japonica koreana* (24) *Ambulyx kuangtungensis* (25) *Ambulyx liturata* (26) *Ambulyx ochracea* (27) *Ambulyx schauffelbergeri* (28) *Ambulyx tobii* (29) *Hemaris affinis* (30) *Hemaris staudingeri* (31) *Sphecodina caudata* (32) *Neogurelca himachala* (33) *Ampelophaga rubiginosa rubiginosa* (34) *Acosmeryx naga metanaga* (35) *Acosmeryx castanea* (36) *Macroglossum bombylans* (37) *Macroglossum corythus corythus* (38) *Macroglossum fritzei* (39) *Macroglossum neotrogiodytus* (40) *Macroglossum pyrrhosticta* (41) *Deilephila elpnor* (42) *Theretra tibetiana* (43) *Theretra japonica* (44) *Theretra silhetensis siihetensis* (45) *Theretra oldenlandiae oldenlandiae* (46) *Rhagastis mongoliana* (47) *Rhagastis dichroae* (48) *Cechetra lineosa* (49) *Cechetra minor* (50) *Cechetra striata*.

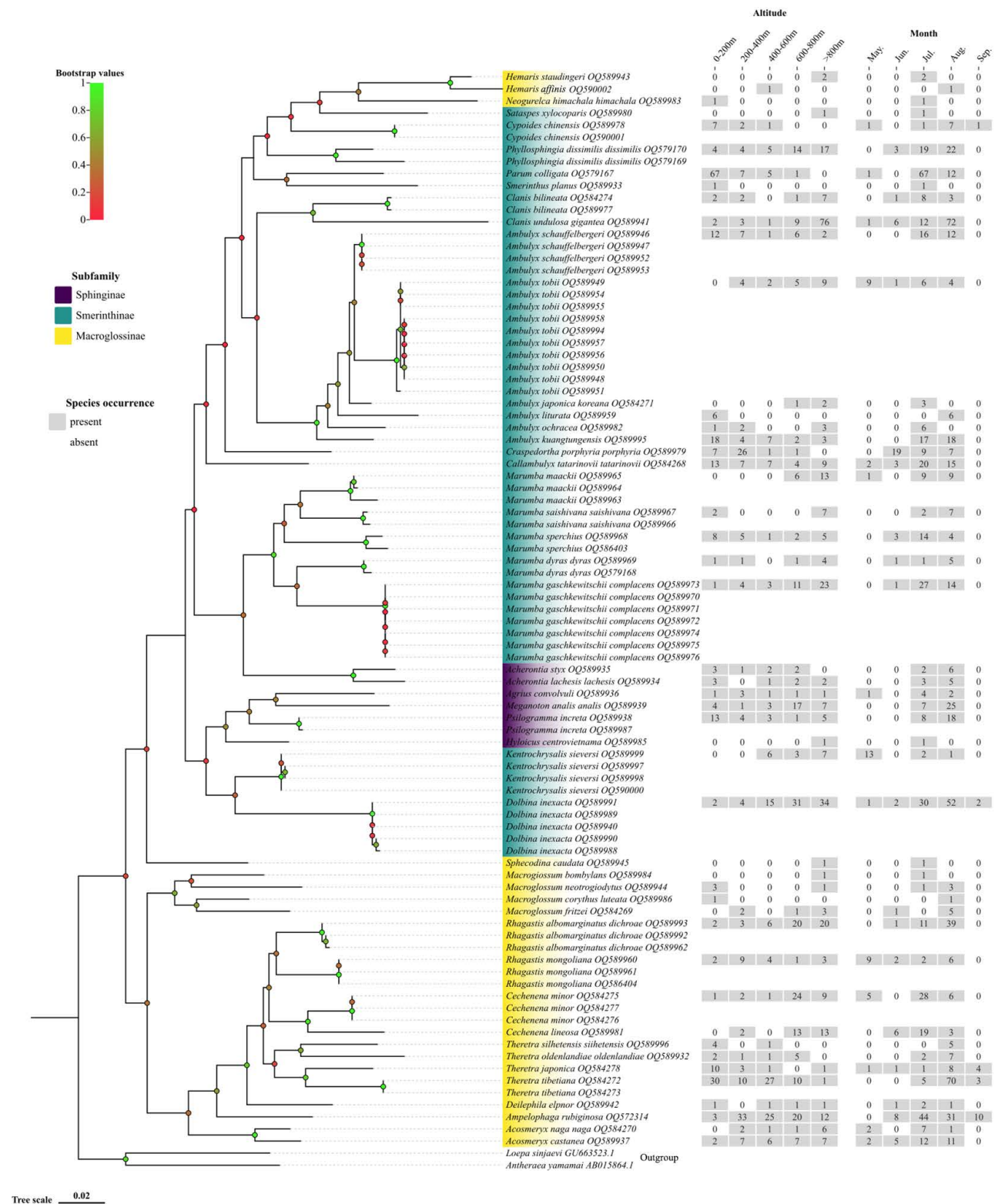


FIGURE 3. ML tree topology constructed by 89 *COI* sequences of Sphingidae species in the Dabie Mountains based on K2P model, combining species occurrence maps in different months and altitudes.

● Discussion

By combining morphological and molecular biological methods, this study conducts, for the first time, a comprehensive and systematic taxonomic investigation on the Sphingidae in the Dabie Mountains spanning Hubei, Henan, and Anhui provinces, clarifying the species composition and distribution pattern. Among them, the dominant position of the subfamily Smerinthinae indicates that the region may have a relatively complex agricultural ecosystem. For example, some species of the genera *Clanis* and *Phyllosphingia* often harm economic crops such as beans and cotton, and some of these species have a high population density in the region, which may have an important impact on local agricultural production and ecological balance. Future research should further explore the ecological functions of these species and their specific effects on agricultural and forestry production. Some species of the subfamily Macroglossinae are important pollinators, playing a key role in maintaining the balance of the ecosystem. In addition, due to their strong flying ability and migratory characteristics, some Sphingidae species can serve as important indicator species for monitoring climate change and ecosystem health, and relevant research in this region should be strengthened in the future.

During the research, it was found that the *COI* DNA barcode can be used as an important auxiliary technology for the identification of hawk moth species, which is similar to other groups such as Notodontidae and Geometridae, as well as previous studies (Jin *et al.* 2017; Yang *et al.* 2020; Sun *et al.* 2021; Wang *et al.* 2021; Jiang *et al.* 2025). However, there is overlap among species of Sphingidae and a lack of division thresholds—for example, between *Ambulyx schauffelbergeri* and *Ambulyx japonica koreana*. Additionally, some species exhibit significant intraspecific individual differences, or closely related species have minimal differences in appearance; a case in point is the intraspecific variation within *Phyllosphingia dissimilis*. Therefore, when constructing a DNA barcode library, it is necessary to conduct comprehensive identification by combining morphological characteristics and phylogenetic trees to obtain accurate results, so as to ensure the reliability of subsequent identification (Jin *et al.* 2017). It is not fully applicable to the division of high-level taxa at the subfamily and tribe levels, which is consistent with previous studies. In-depth analysis still requires mitochondrial genomes or multi-gene combined tree construction (Yang *et al.* 2020).

The results of the faunistic analysis show that the hawk moths in the Dabie Mountains are dominated by the subfamily Smerinthinae, and all are widespread species, which is relatively similar to the research results in adjacent regions, possibly due to similar habitats (Huang *et al.* 2023). The Changjiang-Huaihe region, East China region, South China region, and Central China region are connected with a large common latitudinal area, and their climate and vegetation types are relatively similar. Both the South China region and East China region are close to the Southwest China region, where species originated, and there is no barrier of the Himalayas, with relatively flat terrain. Being adjacent to the East China Sea and the South China Sea and affected by the north-south monsoon climate, they are convenient for species migration and diffusion. Moreover, hawk moths have strong migration ability. It may be due to the above factors that the hawk moth community in the Dabie Mountains is more similar to those in the South China region, East China region, and Southwest China region. Considering factors such as terrain, climate, and latitude in a comprehensive manner, this study puts forward a hypothesis: the origin and diffusion path of species in the Dabie Mountains may proceed gradually along the route of Southwest China Region - South China Region, East China Region - Dabie Mountains (Changjiang-Huaihe Region). To verify this hypothesis, it will be necessary in the future to further obtain more extensive specimens and comprehensive data, integrate analytical methods of landscape genomics and ecological niche models, quantify the contribution of each driving factor to this diffusion process, and ultimately provide theoretical support for cross-faunal biodiversity conservation.

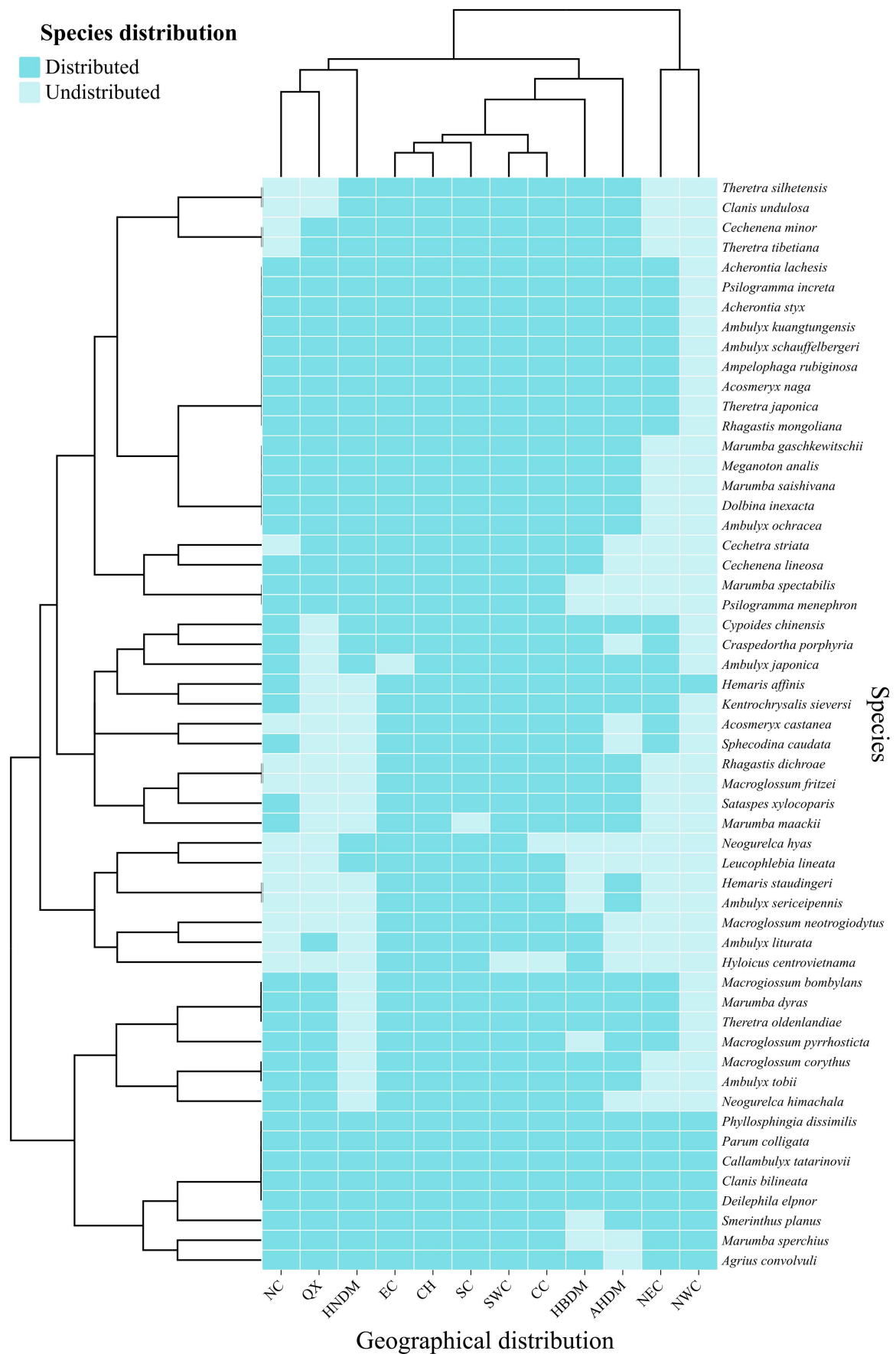


FIGURE 4. The clustering results of the geographical fauna of Sphingidae species and their distribution patterns in Hubei, Henan and Anhui provinces in the Dabie Mountains.

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● Additional information

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