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Article

Taxonomic Status and Diffusion Trend Prediction under the Effect of Host Plant of the Urban Oligophagous Pest *Histia rhodope*

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Abstract: *Histia rhodope* is an oligophagous pest that only feeds on *Bischofia polycarpa*. Recently, frequent outbreaks of *H. rhodope* have greatly impacted the urban landscape and people's life. The taxonomic status and diffusion trend of *H. rhodope* were studied based on its mitogenome sequence and the MaxEnt model. The mitogenome structure of *H. rhodope* has certain conserved character. The species of lepidopteran moths in each superfamily and family were monophyletic. The genetic distance between *H. rhodope* and *Eterusia aedea* was the closest (0.09). By 2050, the suitable habitat area of *H. rhodope* is expected to increase ($71.63 \times 10^4 \text{ km}^2$). The centroid changes of the distribution of *H. rhodope* shifted from Anhui to Hubei province (distance shifted: 255.71 km). Climate factor like annual mean temperature, mean temperature of driest quarter, precipitation seasonality, and precipitation of coldest quarter affected the distribution of *H. rhodope*, and the suitable habitat of the host plant of biotic factor is the potential invasion area for its further spread. Our results revealed the taxonomic status of *H. rhodope* across lepidopteran moths, emphasized the risk of its spread and the important role of host plant, provided valuable molecular and ecological data for managing and monitoring *H. rhodope*.

Keywords: oligophagous pest; mitogenome; phylogeny; host plant; MaxEnt; suitable habitat

1. Introduction

The urban diurnal moth, *Histia rhodope* Cramer (Lepidoptera: Zygaenidae), is one of the most destructive defoliators, widely distributed in the central and southern provinces of China [1]. *H. rhodope* is an oligophagous pest that mainly feeds on urban landscaping and the street tree (*Bischofia polycarpa*) often causing serious damage. The moth may eat up all the leaves of the host plant, leaving only bare branches and leaf veins, which greatly effects the photosynthesis of the host plants, thus affecting the normal growth and development of *B. polycarpa* [2]. The larvae of *H. rhodope* fall from the tree by spinning silk, which also greatly disturbing the urban landscape and human activities in the city [3,4].

The phylogenetic relationship of the family Zygaenoidea, to which the moth belongs, is in constant change, and its phylogenetic relationship with other moth groups is controversial; therefore, the group is of great interest to lepidopteran researchers and evolutionary biologists [5]. With

advances in DNA sequencing and whole mitochondrial genome sequencing, vast quantities of mitochondrial genome sequences of Lepidoptera species have been obtained [6–8], and the evolutionary relationships across groups have been analyzed [9–12]. The mitochondrial genome is characterized by a simple structure, maternal inheritance, rapid evolutionary rate, and small molecular weight. The mitochondrial genome has been widely used as a molecular marker to study insect population genetics and phylogeny [13,14]. However, data for only two mitochondrial genomes of Zygaenoidea are available and these have not been systematically analyzed in detail [15,16]. Therefore, the phylogenetic status and phylogenetic relationship between *H. rhodope* and other lepidopteran moths must be evaluated urgently.

With excellent wood quality, beautiful tree appearance and wide use and distribution, *B. polycarpa* is the backbone tree for landscaping in many cities in China [2]. However, *H. rhodope* is gradually deteriorating its host plant *B. polycarpa*, *H. rhodope* was found in Zaozhuang (Shandong province), Luoyang (Henan province), and other places [17], and is expected to spread further. Therefore, it is necessary to study its distribution and spread [3]. The prediction of suitable areas for species distribution is an important research field in ecology, and the distribution model is an important tool to study suitable areas for species geographical distribution [18]. As the most commonly used species distribution model, the maximum entropy (MaxEnt) model has the characteristics of simple operation, short running time, high accuracy, and stability of prediction results [19–21]. Because the MaxEnt model has good simulation performance even with sparse species distribution data [22,23], it has been used to predict suitable areas for various pests [24,25]. In summary, based on mitochondrial genome data and the MaxEnt model, this study analyzed the taxonomic status of the *H. rhodope*, their distribution in different suitable areas at present and in 2050, and the main environment factors affecting their geographical distribution. In view of the fact that its host as a street tree mainly through government planning and human planting, we coupling analysis the current distribution of *B. polycarpa* in different suitable areas with the moth *H. rhodope*. These will provide molecular and ecological data for the prevention and control of this urban pest.

2. Materials and Methods

2.1. Sampling and Mitochondrial Genome Sequencing Analysis

H. rhodope was collected from the campus of Yancheng Teachers University, Jiangsu Province (120.20°E; 33.38°N), and stored in the Insect Laboratory of School of Wetlands. The collected live adult insects were put into anhydrous ethanol, and brought back to the laboratory stored in a refrigerator at –20 °C for DNA extraction. DNA extraction kit (Promega Corporation, Madison, WI, USA) was used to extract the total DNA from the chest muscle tissue of *H. rhodope*. NanoDrop 2000 and Quantus Fluorometer (Thermo Fisher Scientific, Wilmington, DE, USA) were used to detect DNA purity (OD260/OD280 ratio) and concentration, respectively. The degree of DNA degradation and the presence of DNA and protein contamination were analyzed by agarose gel electrophoresis. The DNA samples were randomly interrupted by Covaris M220 ultrasonic instrument (Covaris, Woburn, MA, USA) after passing the test, and then the whole library was prepared by terminal repair, sequencing joint addition, purification and other steps. After the library was constructed, Qubit 3.0 and Qseq100 were used for preliminary quantification and detection, and then Q-PCR was used to accurately quantify the effective concentration of the library (concentration > 3nM) to ensure the quality of the library. After qualified library quality detection, different libraries are pooled to flowcell, and cBOT clusters are sequenced using Illumina (HiSeq X, Majorbio Bio-pharm Technology, Shanghai, China) high-quality sequencing platform, and obtained 4 Gb of base data. Using Trimmomatic (<http://www.usadellab.org/cms/?page=trimmomatic>) software to shear of raw data, filter the low quality of sequencing reads, and then use the SPAdes [26] to assemble the cleaned data. The mitoZ program [27] was used to assemble and annotate the individual genes of the mitogenome, and the sequence was then submitted to GenBank (PQ221018).

2.2. Analysis of the Characteristics, Genetic Distances, and Phylogenetic Relationships of the Mitochondrial Genome

MEGA 7.0.26 software (MEGA Software, Paris, France) was used to calculate the nucleotide composition of the mitogenome, the content of C, G, A, and T bases, GC skew and AT skew, and codon usage of amino acid [28,29]. The tRNA genes were predicted secondary structures by tRNAscan-SE v2.0 (<https://lowelab.ucsc.edu/tRNAscan-SE/>) and MITOS WebServer (<http://mitos.bioinf.uni-leipzig.de/>) two online software [30,31]. To measure genetic distances between *H. rhodope* and other lepidopteran moths, we used the mitochondrial genome of *H. rhodope* and the mitogenomes of 64 lepidopteran moths from the NCBI database (Supplementary Table S1). Based on the Kimura 2-parameter model, the genetic distance between species was calculated after sequence alignment using MEGA v7.0.26 [32,33].

To clarify the taxonomic position of *H. rhodope* across the order Lepidoptera in a broader evolutionary condition, we constructed a maximum likelihood tree and a Bayesian inference tree by analyzing 65 mitochondrial genomes from 65 lepidopteran species (Supplementary Table S1), *Papilio slateri* and *Luehdorfia chinensis* were used as outgroups. IQ-TREE software (version 2.2.0) was used for maximum likelihood analysis: the software automatically selected the optimal model as GTR+F+I+R5, and the node support rate of the phylogenetic tree was evaluated by bootstrapping-test confidence (the number of runs was set to 1 000) [34]. The Bayesian phylogenetic tree was constructed using MrBayes 3.2.2 [35], and the operation parameters were set as follows: Operations for running 4 Markov Chain Monte Carlo (MCMC) simultaneously, the operation number was set to 5,000,000 generations, sampling every 1 000 generations, abandoning the results of the first 25% of the data, when the mean standard deviation of the splitting frequency is less than 0.01, the stationarity was reached, and most consistent trees are obtained [36,37].

2.3. Collection and Processing of Distribution Data

The geographical distribution of *H. rhodope* and *B. polycarpa* in China was predicted using data from the following sources: (1) the literature and news reports and field investigations and collection. We conducted a field survey of areas where the adult and larva species of *H. rhodope* are distributed (Figure 1:A), obtaining 102 distribution sites (Supplementary Table S2). We also obtained 243 distribution sites of host plants *B. polycarpa* (Supplementary Table S3), mainly from two parts, including GBIF (Global Biodiversity Information Facility: <https://www.gbif.org/>) database and field investigation. The research data are stored in School of Wetlands, Yancheng Teachers University. Buffer analysis in ArcGIS v10.4.1 was used to screen the distribution data [38]. Buffer radius was set to 10 km. Finally, distribution data for 83 *H. rhodope* and 158 *B. polycarpa* were obtained after deleting 19 and 85 overfitting data, the data distribution condition were shown in the Figure 1: B.

Environmental factors were obtained from the WorldClim database and included 19 environmental factors, of which 11 are temperature related and 5 are rainfall related [39]. The data of environmental factors were based on global meteorological records with spatial resolution of 2.5 arc-minutes. The details of environmental factors are listed in Supplementary Table S4. To improve the simulation accuracy of the model and avoid the transition fitting of the model, 19 environmental factors were extracted to the geographical distribution points of *H. rhodope* by ArcGIS. The data were exported for Pearson's correlation analysis using SPSS 25 software [40]. If the absolute value of the correlation coefficient was >0.90 and significantly correlated, the factors with low contribution rate are eliminated [41].

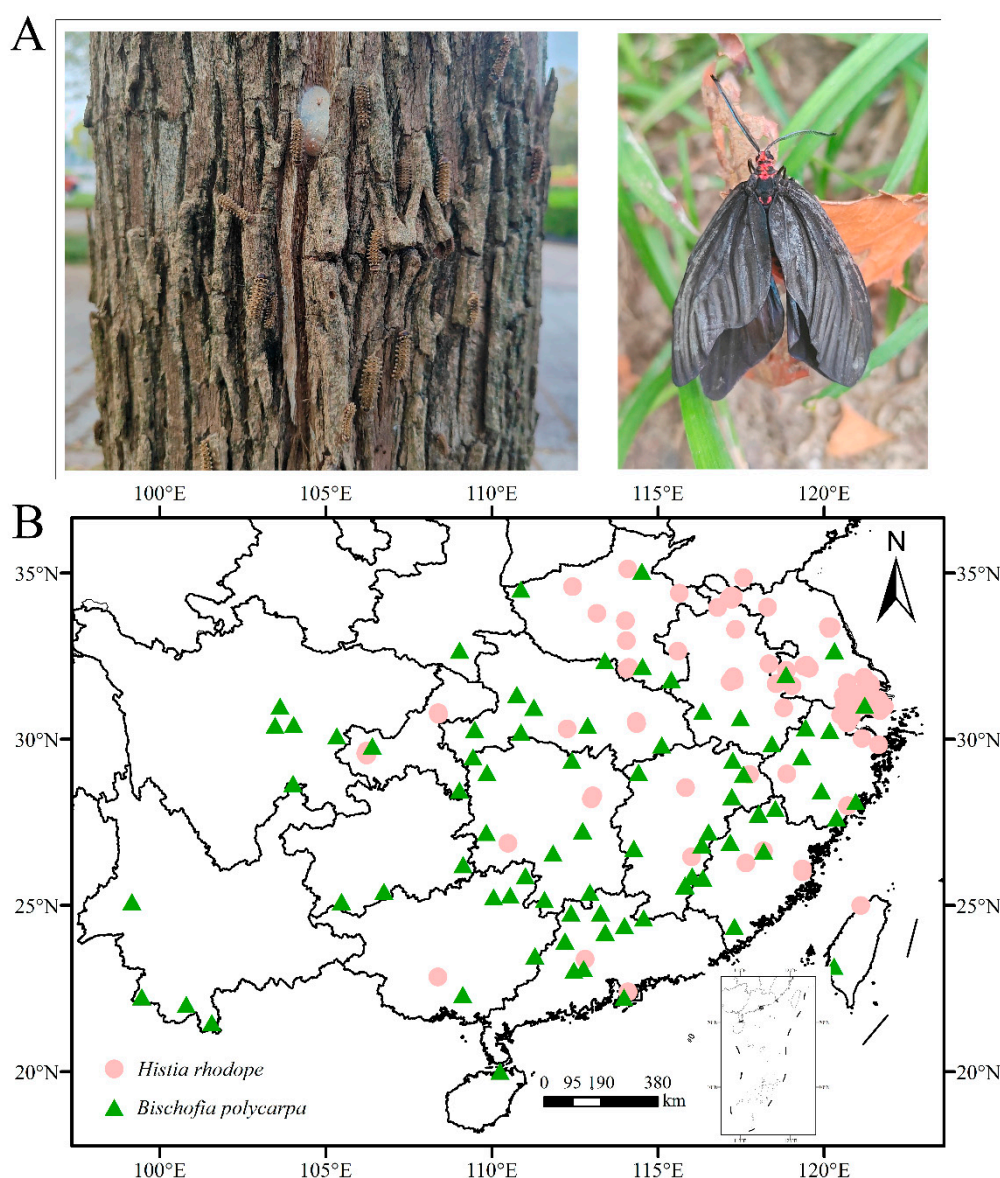


Figure 1. The Larva and adult of *Histia rhodope* (A), and geographical distribution of *H. rhodope* and its host plant *Bischofia polycarpa* (B).

2.4. Optimization and Construction of MaxEnt

The software of MaxEnt v10.4.1 was used to predict the geographical distribution of *H. rhodope* and *B. polycarpa*. The distribution and dominant environmental data obtained for *H. rhodope* by screening were added to MaxEnt software, and the parameters were set [39]. For training data, 75% of the distribution points were randomly selected. For test data, 25% of the distribution points were selected. The validation and prediction models were constructed for the training data and test data, respectively. The Jackknife test was selected to determine the weight of each variable, and the response curve of environmental variables selected was created. The output format was "Logistic," with repeated training run set to "10," maximum number of interactions set to "5000," and repetition mode set to "Subsample" [25]. Area value under receiver operating characteristic curve (ROC curve) was used to evaluate the simulation results of the model. According to a series of different dichotomies, the curve is drawn with false positive rate and true positive rate as the horizontal and vertical coordinates, respectively [42].

2.5. Analysis of Potential Distribution

The output result of the MaxEnt model was the probability of existence of *H. rhodope* and *B. polycarpa* in China, and the data was in ASCII format. First, a format conversion tool (ArcGIS ArcToolbox) was used to convert the data into Raster format, and the results were displayed in ArcGIS [38]. Then, the probability of distribution map of the moth and its host plant in China was obtained by using the “extraction and analysis” function. The “Reclassify” function was used to classify distribution value grades and the corresponding distribution ranges, which were represented by different colors. The classification criteria were as follows: unsuitable areas (probability < 0.05); lowly suitable habitat ($0.05 \leq$ probability of existence < 0.33); and moderately suitable habitat ($0.33 \leq$ probability of existence < 0.66). An area with probability of existence ≥ 0.66 was considered a highly suitable habitat. ArcGIS was used to calculate the ratio of the number of grids in each suitable habitat to the total number of the grids, and the distribution area of *H. rhodope* and *B. polycarpa* was calculated based on their grid proportion to the land area of China [25]. Prediction results were converted into binary files with a threshold of MTSPS using SDM Toolbox in ArcGIS. The SDM Toolbos of “Distribution Changes Between Binary SDMs” and “Centroid Changes (Lines)” were used to determine centroid changes of *H. rhodope* [43].

3. Results

3.1. Mitochondrial Genome Characteristics of *H. rhodope*

The complete length of the mitochondrial genome for *H. rhodope* was 15,201 bp, consisting of 37 regions, including 13 protein genes (PCGs), 22 tRNAs, 2 rRNAs, and 1 non-coding control region (Figure 2). There were 15 gene spacer regions between adjacent mitogenomes (158 bp), with the longest interval between trnH and ND5 (51 bp); 7 overlapping genes (39 bp), with the longest between trnL1 and rrnL (21 bp); and 14 regions with no overlap or interval (Supplementary Table S5). The mitogenome contained 39.81%, 38.64%, 13.41%, and 8.14% of A, T, C, and G, respectively. The content of A + T was 78.45% and that of G + C was 21.55%. The AT-skew value was 0.01% and the GC-skew value was 0.24%, indicating that the percentage of base A and C was higher than that of T and G (Supplementary Table S6).

The arrangement of the PCGs (ND2 – COI – COII – ATP8 – ATP6 – COIII – ND3 – ND5 – ND4 – ND4L – ND6 – CYTB – ND1) for *H. rhodope* is common in Lepidoptera. In terms of codon use, ND1 takes GTG as the start codon, and the remaining PCGs take ATN as the start codon. Except for COII and ND4, which use T and TA as stop codons, respectively, other PCGs use TAA (Supplementary Table S5). Consistently, TAA or TAG are commonly used as stop codons in insect mitogenomes. Leu and Ile (count > 400) were the most used amino acids in PCGs, whereas Arg, Cys, and Gln were the least used (count < 60) (Figure 3). CUA, UUU, and AUU (count > 300) had a relatively high frequency in amino acids, whereas GCG and ACG had the lowest frequency. Consistent results were obtained for *Dendrolimus punctatus* [38], reflecting the AT bias of nucleotide composition. Among the 22 tRNA genes in the mitogenome, 21 can form conventional clover structures, whereas tRNA^{Ser(AGN)} cannot form typical tRNA cloverleaf structures due to the absence of the D-arm (dihydrouridine arms). There were 31 base mismatches in the secondary structure of tRNA, including 22 G–U mismatches, 7 U–U mismatches, and 1 C–A and G–A mismatch each (Supplementary Figure S1). These mismatches conform to the oscillating pairing principle and play an important role in maintaining the stability of tRNA secondary structures.

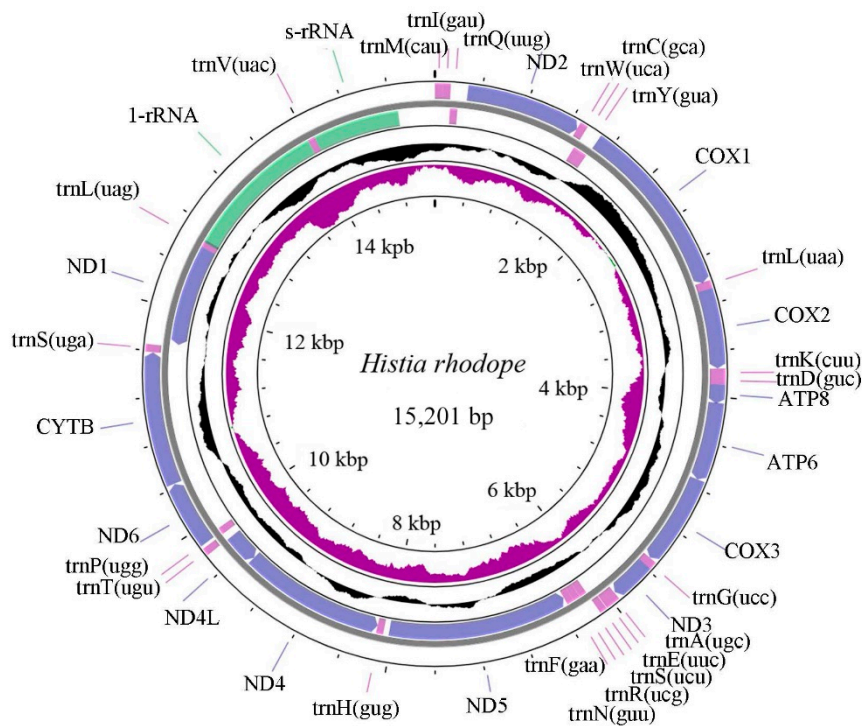


Figure 2. The circle map of the complete mitogenome of *Histia rhodope*. The purple peaks indicated the deviation in GC-skew, and black peaks indicated the deviation of GC% divergence.

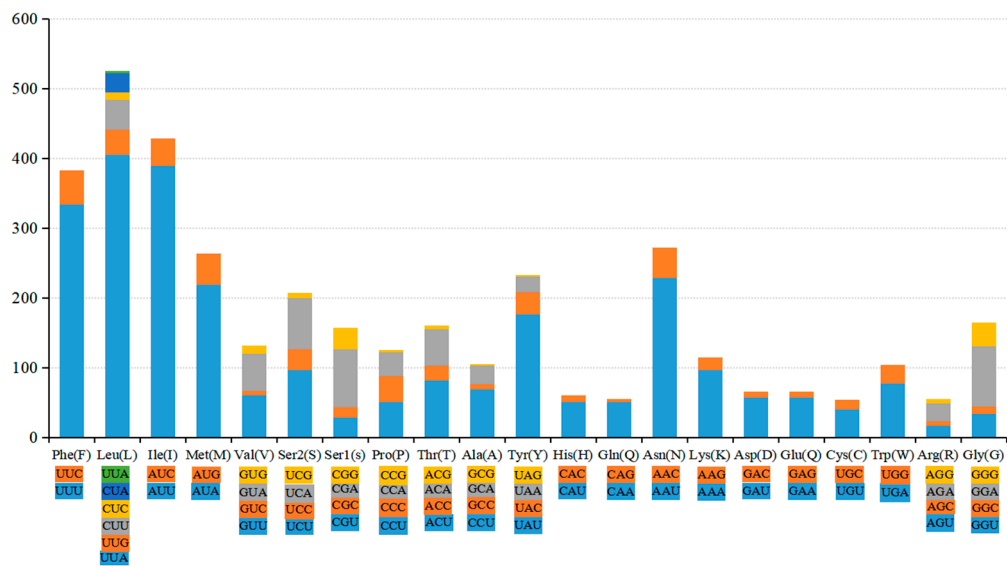


Figure 3. Codon usage of amino acid in *Histia rhodope* mitogenome. Codon families in different color were provided on the horizontal axis, and codon usage were provided on the vertical axis.

3.2. Phylogenetic Relationship and Genetic Distance between *H. rhodope* and Lepidopteran Moths

Using *L. chinensis* and *P. slateri* as outgroups, the Bayesian tree and maximum likelihood model were constructed based on the whole mitochondrial genomes of 65 lepidopteran moths to study the phylogenetic relationship between *H. rhodope* and other moths (Figure 4). *H. rhodope* and *Eterusia aedea* were the most closely related in Zygaenidae, and Zygaenidae were the most closely related to Limacodidae, both of which belong to Zygaenoidea. Zygaenoidea was closely related to Cossioidea and Thyridoidea, with a kinship of Zygaenoidea + (Cossioidea + Thyridoidea). The phylogenetic trees constructed using different methods were similar in structure (Supplementary Figure S2) and supported the monophyly of lepidopteran moths in each family and superfamily. The posterior

probabilities of the phylogenetic trees constructed based on Bayesian construction were >0.91. The phylogenetic relationships of each superfamily were: Gelechioidea + (((((Bombycoidea + Lasiocampoidea) + Geometroidea) + Notuoidea) + Pyraloidea) + (((Hesperioidea + Yponomeutoidea) + Tortricoidea) + (Zygaenoidea + (Cossoidea + Thyridoidea))). Genetic distances between the moths based on complete mitogenome sequences was consistent with their phylogenetic relationships. *E. aedea* had the shortest genetic distance to *H. rhodope* (0.090), and thus the closely related species, whereas *Leucoptera malifoliella* had the greatest distance to *H. rhodope* (0.272) (Supplementary Table S7).

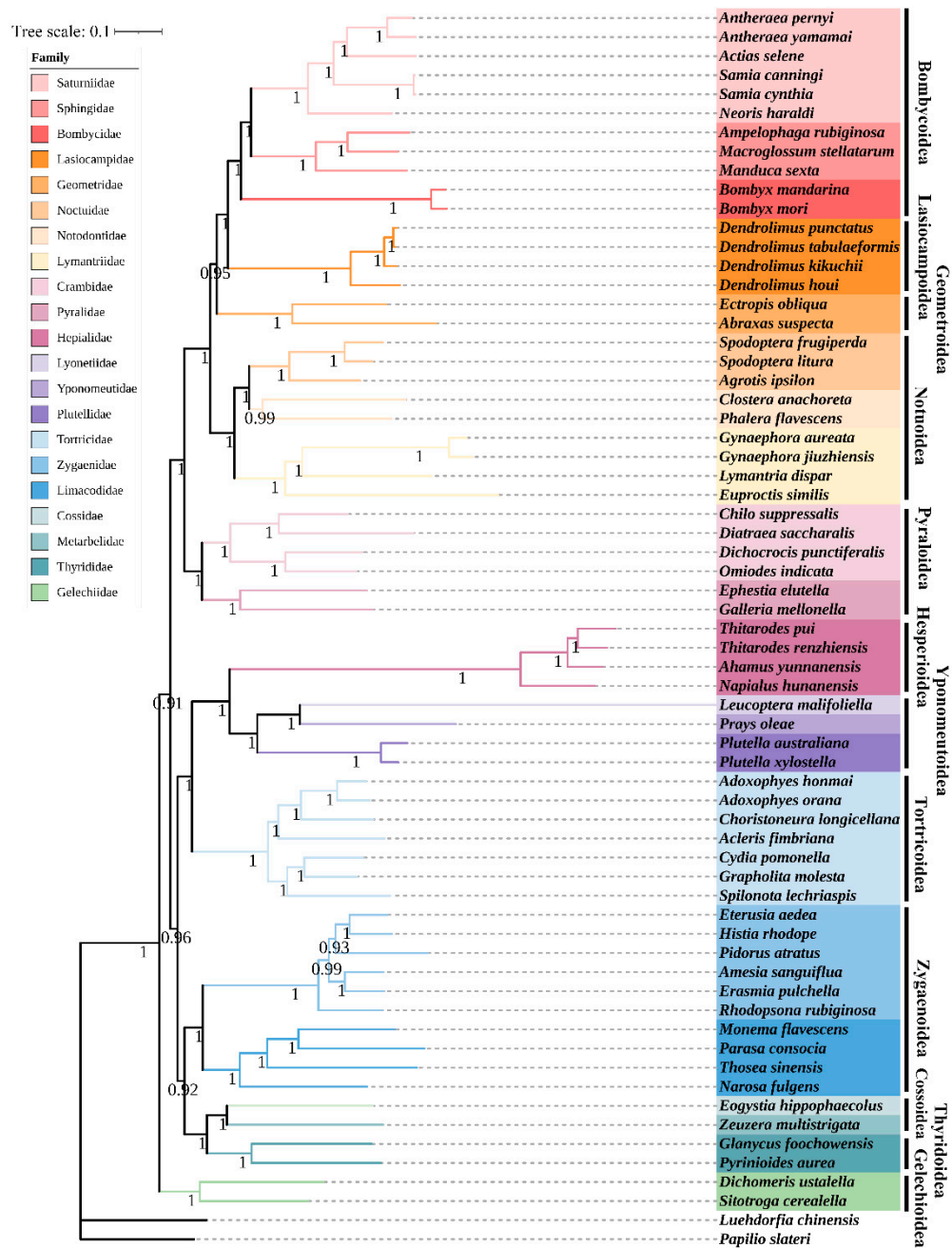


Figure 4. Phylogenetic tree constructed by the mitogenomes from lepidopteran moths using BI (Bayesian inference). Numbers at the nodes were Bayesian posterior probabilities for the BI tree, and different colored clades indicate different families.

3.3. Screening of Key Environmental Factors and Suitable Area Predictions

The contribution rates of 19 environmental factors simulated based on the MaxEnt model were selected and combined with the results obtained by Spearman correlation analysis (Supplementary

Table S8). Finally, six major environmental factors were selected as follows: annual mean temperature (bio1), mean temperature of driest quarter (bio9), mean temperature of coldest quarter (bio11), precipitation seasonality (bio15), precipitation of warmest quarter (bio18), and precipitation of coldest quarter (bio19). The accumulate contribution percent of the six major environmental factors was 88.5% (Supplementary Table S4).

The Jackknife simulation calculated the scores for “without variable,” “with only variable,” and “with all variables,” reflecting the contribution of environmental factors to distribution gain. For “without variable,” the scores of annual mean temperature (bio1), mean temperature of driest quarter (bio9), precipitation seasonality (bio15), and precipitation of coldest quarter (bio19) were higher than the scores of mean temperature of coldest quarter (bio11) and precipitation of warmest quarter (bio18), with little difference under test gain, regularized training gain, and AUC. These findings indicated that the four environmental factors contributed the most to the distribution of *H. rhodope* and were the dominant environmental factors affecting the geographical distribution of *H. rhodope* (Figure 5).

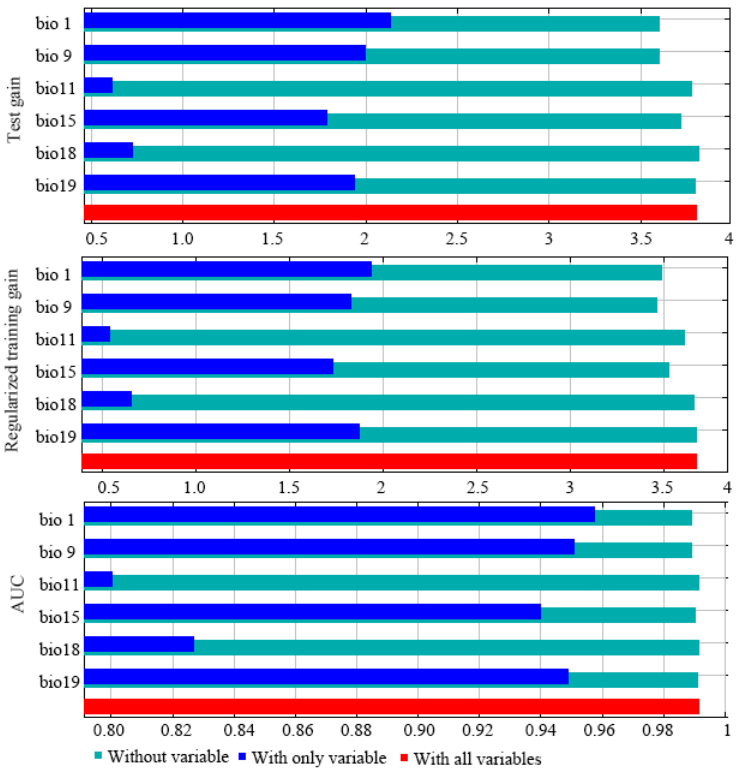


Figure 5. Jackknife test gain of environmental factors for predicting potential geographical distribution of *Histia rhodope*.

3.4. Forecasting Suitable Distribution of *H. rhodope* in Current Year and 2050

The reliability of the MaxEnt model prediction results was tested by ROC curve analysis based on six major environmental factors and 83 fitted distribution data. After 10 repetitions, the AUC values predicted for current and 2050 population distribution of *H. rhodope* were 0.995 and 0.994, respectively, (i.e., >0.9) (Supplementary Figure S3). The predicted results reached an excellent level, indicating that MaxEnt model built in the study was reliable in predicting the suitable distribution areas of *H. rhodope*.

Based on the dominant environmental factors and their geographical distribution data, MaxEnt model was constructed, which was divided into four grades: unsuitable habitat, lowly suitable habitat, moderately suitable habitat, and highly suitable habitat. Finally, the current and 2050 suitable habitat distribution map of *H. rhodope* was obtained. The results showed that *H. rhodope* was mainly distributed in the southern provinces of China (Figure 6). The total area of distribution was $147.09 \times 10^4 \text{ km}^2$. The areas of highly suitable habitat, moderately suitable habitat, and lowly suitable habitat

were 27.46×10^4 , 44.60×10^4 , and 75.03×10^4 km², respectively (Figure 7). However, the distribution area of *H. rhodope* had a significant trend of diffusion. In 2050, the total area was 219.74×10^4 km². The areas of highly suitable habitat, moderately suitable habitat, and lowly suitable habitats were 87.44×10^4 , 61.02×10^4 , and 71.28×10^4 km², respectively.

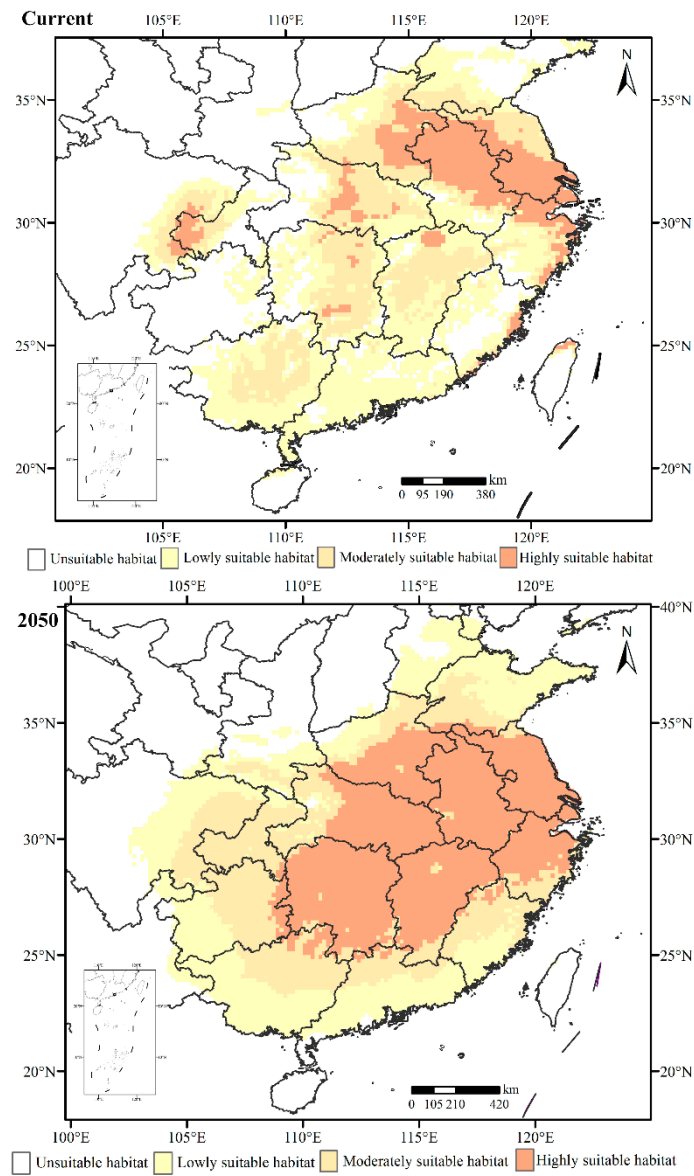


Figure 6. Potential distribution of *Histia rhodope* in different habitat areas of China under current year and 2050 climatic conditions (inspection number: GS(2024) 0650).

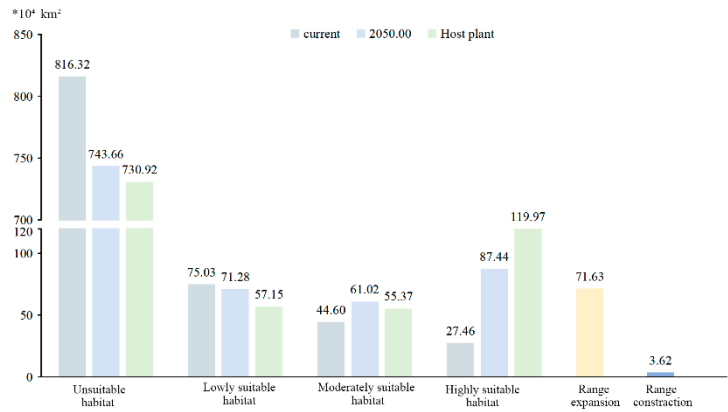


Figure 7. Histogram of predicted suitable habitat area changes based on the MaxEnt model.

3.5. Centroid migration and current host plant *B. polycarpa* distribution of *H. rhodope*

In 2050, the area of range expansion of *H. rhodope* was $71.63 \times 10^4 \text{ km}^2$, and the area of range contraction was $3.62 \times 10^4 \text{ km}^2$. The centroids of the distribution regions of the species were 117.29°E , 31.57°N and 115.00°E , 30.37°N in the current year and 2050, respectively. The centroid locations shifted from Anhui Province to Hubei province, and the centroid transfer distance was 255.71 km (Figure 8:A). The current distribution prediction results of *B. polycarpa*, the host plant of *H. rhodope*, showed that the AUC value was 0.990 (Supplementary Figure S4), and the distribution habitat area of *B. polycarpa* was mainly distributed in southern China (Figure 8:B), and the distribution area of high, moderate and low suitable habitat were 119.97×10^4 , 55.37×10^4 , and $57.15 \times 10^4 \text{ km}^2$, respectively. The host distribution area can basically cover the current and 2050 suitable areas of *H. rhodope*.

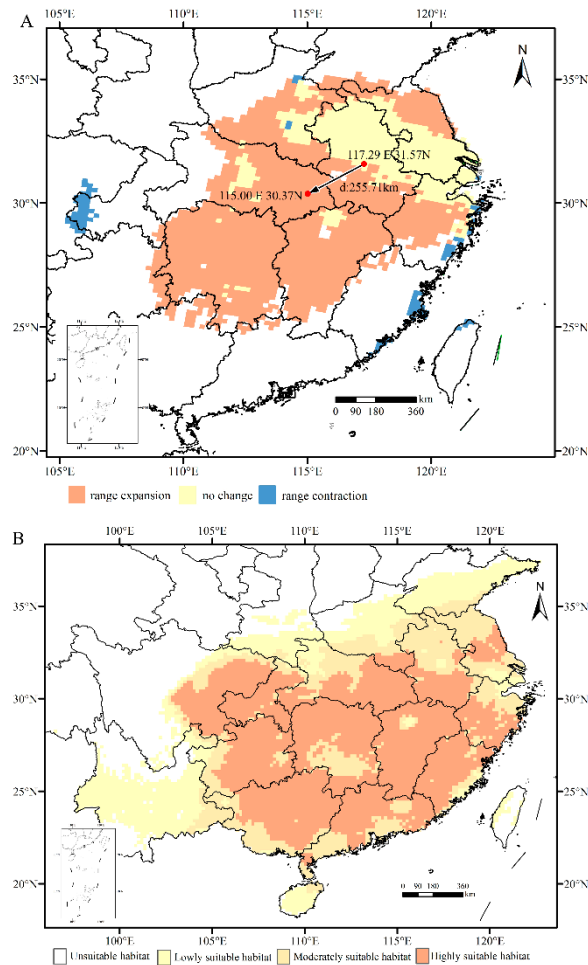


Figure 8. Centroid migration of *Histia rhodope* habitat suitability areas (A) and its host plant distribution (B). (inspection number: GS(2024) 0650).

4. Discussion

In this study, we got the whole mitochondrial genome of *H. rhodope*, revealing the conservation of the mitogenome structure. The arrangement of protein genes in the mitogenome of *H. rhodope* indicated the same pattern as reported for other lepidopteran insects, among which the arrangement of trnM-trnI-trnQ is typical of Lepidoptera [10]. The base content of mitochondrial genome was $A > T > C > G$, the content of $A + T$ was 78.45 %, and the content of $A + T$ was much higher than the content of $G + C$, consistent with other Lepidoptera species, such as *Leucinodes orbonalis* [44], *Neptis thisbe*, and *Athyma zeroa* [45]. Except for *ND1* in the PCG of *H. rhodope*, which has GTG as its start codon, all other genes had ATN as their start codon. In insects, the start codon exhibits diversity, including quadruplet codons (ATTA, ATAA, and TTAG) and sextuplet codons (TATTAG and TTTTAG) [46–48]. Most genes used TAA as stop codon. *COII* and *ND4* used T and TA, respectively. These incomplete stop codons can be converted into TAA through post-transcriptional processing [8]. With the exception of tRNA^{Ser} (AGN), which lacks the D-arm, the other 21 tRNAs are classical cloverleaf structures. These are also found in other insect groups [6,13,14]. The mismatch in their structure is dominated by G–U, which possibly occurs because mitochondrial genomes lack recombination. The mismatch can be corrected by RNA editing, which did not hinder tRNA transport [8,10]. The conservation of the mitochondrial genome of *H. rhodope* indicates that it is suitable to solve the phylogenetic relationship of higher order species, such as family and order.

In this study, phylogenetic trees were constructed for 65 moths species from 21 families and 12 superfamilies. The phylogenetic trees strongly supported the monophyly of species of each family and superfamily in Lepidoptera. Only two families, Zygaenidae and Limacodidae, were only involved in the superfamily Zygaenoidea. However, the morphological analysis of five families showed that limacodid clades included in Aididae, Dalceridae, Megalopygidae, and Limacodidae, but not Zygaenidae [49], and other molecular studies were gradually clarifying the study [50,51], as the mitochondrial genomes of other families, such as Megalopygidae, Dalceridae, and Cyclotornidae, have yet to be sequenced, which will further elucidate the phylogenetic relationships across families in Zygaenoidea. The phylogenetic relationship between Cossoidea, Thyridoidea, and Zygaenoidea follows Zygaenoidea +(Cossoidea +Thyridoidea); however, Lu et al. [52] hypothesized that Zygaenoidea and Cossoidea are sister groups and that the result was unstable, which might be related to the lack of mitogenome data on Thyridoidea. In general, the phylogenetic relationships of each family established in this study were consistent with the findings of Timmermans et al. [53] and Liu et al. [54]. The definition and internal phylogeny of Zygaenoidea remain in flux, and the phylogenetic relationships across lepidopteran moth species must be further resolved. The mitochondrial genome data of Lepidoptera and other lower genera are limited, and representative species of each family cannot be widely selected for analysis, resulting in unbalanced data sets. However, each tree building method has its application scope and conditions, which affect the topology of the final phylogenetic tree. Therefore, to obtain a more comprehensive and reliable phylogenetic relationship, a large number of molecular data representative of species are needed [8].

Nineteen environmental factors are commonly used by the MaxEnt model to predict the geographical distribution of *H. rhodope*, of which many environmental factors have problems of multiple linear repetition and autocorrelation [55]. This redundant information may affect the precision and conclusion of the prediction results. Therefore, during modeling, this study first performed correlation analysis on the environmental factors based on the geographical distribution sites of *H. rhodope* and eliminated redundant information. Using the method of Guo et al. [56] as reference, combined with the results of importance of environmental factors and contribution rate to *H. rhodope* distribution as criteria for evaluating environmental factors, environmental factors with a small contribution to *H. rhodope* distribution were eliminated. Finally, four predominant environmental factors were identified as follows: annual mean temperature, mean temperature of driest, precipitation seasonality, and precipitation of coldest quarter. In most of its distribution areas

of China, *H. rhodope* occurs four generations a year, and the old larvae form cocoons in bark cracks, ground leaves or wall corners to overwinter. Yang et al. [3] studied its overwintering overcooling point and found that the cold tolerance of *H. rhodope* has seasonal changes, and the changes of biochemical substances in the larvae are related to the changes of temperature and humidity in winter. Therefore, the changes of these environmental factors may have a significant impact on the outbreak degree of *H. rhodope* in the next year, and the extent of the impact needs to be further studied.

In addition to the influence of external environmental factors, especially as an oligophagous insect, the availability of host plants may play a greater role in the geographical distribution of *B. polycarpa*. As an important street tree species in China, the planting distribution of *B. polycarpa* is mainly affected by the government's landscape species selection and artificial planting. Therefore, we only studied the distribution of its current suitable areas, and its distribution area basically covered the current and 2050 suitable areas of *H. rhodope*. The distribution area of the current suitable area, especially the highly suitable habitat, is significantly lower than the distribution area in 2050, which is mainly related to the limited species distribution data we used. In some areas, there may be less harm and less reported, resulting in a gap between these data and the actual distribution data. However, the distribution data of host plants are easier to obtain, so using the distribution data of *B. polycarpa* to analyze the potential prediction range of *H. rhodope*, especially for this oligophagous pest, can better analyze its spread trend. The area of total suitable habitat and highly suitable habitat of *B. polycarpa* under current condition are larger than that of *H. rhodope* under 2050 climate condition, respectively. Besides, the forecast results for the year 2050 show that the area of highly suitable habitat for *H. rhodope* will increase by $59.98 \times 10^4 \text{ km}^2$ compared to the current area of highly suitable habitat. The areas of Hubei, Hunan, and Jiangxi provinces will increase significantly, indicating that the moth will cause further harm. The centroid locations for the distribution regions of *H. rhodope* in the current year and 2050 were 117.29°E, 31.57°N and 115.00°E, 30.37°N, respectively. The centroid locations shifted from Anhui Province to Hubei province, and the centroid transfer distance was 255.71 km. In this year, the cities of Wuhan and Xiangyang in Hubei province have frequently reported that *H. rhodope* has caused trouble to pedestrians, and has gradually aroused great attention of landscaping and greening industry personnel. With global warming, the environmental temperature is gradually approaching the optimal level for pest development. The severity of pest damage is expected to increase, reducing the thermal constraints of population dynamics [57]. In addition, the distribution of this moth is influenced by its own flight ability, human factors, geographical barrier, and species interaction [11,58–60], the way in which these factors are added to model predictions needs to be further studied. In summary, the forecast results for 2050 confirmed its further spread trend, and we also believed that the current distribution range of its host plants is also the potential invasive distribution of this urban pest, because *B. polycarpa* is not only the most important food source of the moth, but also the main habitat of its older larvae during the overwintering stage [61]. Ultimately, these results will facilitate a more accurate assessment of the risk of the spread and outbreak of this pest, thereby improving our early prevention and response capabilities.

5. Conclusions

In conclusion, this study conducted sequencing and feature analysis of the mitogenome of *H. rhodope*, clarified the conservative features of gene arrangement, codon usage, and tRNA structure characteristics; By analyzing the genetic distance and phylogenetic relationship between *H. rhodope* and other lepidopteran moths, the taxonomic status of the species was preliminarily determined; The maximum entropy model was used to predict the distribution of the suitable habitat of *H. rhodope* and its host *B. polycarpa*, and mastered the diffusion trend and the dominant environmental factors (Annual mean temperature, mean temperature of driest quarter, precipitation seasonality, and precipitation of coldest quarter) affecting the distribution of *H. rhodope*. The distribution of the suitable area of the host plant *B. polycarpa* is the main biological factor affecting the distribution of the suitable area of the oligophagous insect *H. rhodope*, and also the potential invasion area for the further spread of this urban pest. This study enriched insect mitogenome data, clarified the risk of further

spread, and emphasized the importance of host plants in predicting the distribution of pests, providing reference and data support for the control and monitoring of this oligophagous urban pest.

Supplementary Materials: The following supporting information can be downloaded at the website of this paper posted on Preprints.org, Figure S1: Secondary structures for tRNA genes from the mtDNA of *Histia rhodope*; Figure S2: Phylogenetic tree inferred from the mitogenomes of lepidopteran moths using maximum likelihood method; Figure S3: ROC curve and AUC value of *Histia rhodope* generated using the MaxEnt model during the climate conditions of the current year (left) and 2050 (right). Figure S4: ROC curve and AUC value of *Bischofia polycarpa* generated using the MaxEnt model during the climate conditions of the current year. Table S1: List of sample information of the mitogenomes of 65 published moth species of Lepidoptera; Table S2: Original distribution data of *Histia rhodope*; Table S3: Table S3 Original distribution data of *Bischofia polycarpa*; Table S4: Information on the 19 environmental factors; Table S5: Organization of the mitochondrial genome of *Histia rhodope*; Table S6: Base composition of the mitochondrial genomes of *Histia rhodope*; Table S7: Genetic distance between lepidopteran moths; Table S8: Correlation of environmental factors based on the geographic distribution of *Histia rhodope*.

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References

- Huang, B.K. A study on the bionomic characteristics and control of the *Bischofia* burnet *Histia rhodope* Cramer. *J. Fujian Agric. Coll.* **1980**, *1*, 61-79.
- Yang, H.B.; Dong, J.F.; Sun, Y.L.; Hu, Z.J.; Lv, Q.H.; Li, D.X. Antennal transcriptome analysis and expression profiles of putative chemosensory soluble proteins in *Histia rhodope* Cramer (Lepidoptera: Zygaenidae). *Comp. Biochem. Phys. D.* **2020**, *33*, 100654.
- Yang, H.B.; Hu, Z.J.; Dong, J.F.; Zhu, P.H.; Li, D.X. Changes in the cold hardiness of overwintering larvae of *Histia rhodope* (Lepidoptera: Zygaenidae). *Acta. Entomol. Sin.* **2019**, *62*, 979-986.
- Yang, H.; Dong, J.; Sun, Y.L.; Hu, Z.; Lu, Q.H.; Li, D. Identification and expression profiles of candidate chemosensory receptors in *Histia rhodope* (Lepidoptera: Zygaenidae). *PeerJ* **2020**, *8*, e10035.
- Mitter, C.; Davis, D.R.; Cummings, M.P. Phylogeny and Evolution of Lepidoptera. *Annu. Rev. Entomol.* **2017**, *62*, 265-283.
- Pang, S.Y.; Zhang, Q.W.; Liang, L.L.; Qin, Y.T.; Li, S.; Bian, X. Comparative Mitogenomics and Phylogenetic Implications for Nine Species of the Subfamily Meconematinae (Orthoptera: Tettigoniidae). *Insects* **2024**, *15*, 413.
- Shah, B.; Hassan, M.A.; Xie, B.Q.; Wu, K.Q.; Naveed, H.; Yan, M.; Dietrich, C.; Duan, Y.N. Mitogenomic Analysis and Phylogenetic Implications for the Deltocephaline *Tribe chiasmini* (Hemiptera: Cicadellidae: Deltocephalinae). *Insects* **2024**, *15*, 253.
- Du, H.C.; Fang, J.X.; Shi, X.; Zhang, S.F.; Liu, F.; Yu, C.M.; Zhang, Z.; Kong, X.B. Comparative analysis of eight mitogenomes of bark beetles and their phylogenetic implications. *Insects* **2021**, *12*, 949.
- Li, X.Y.; Yan, L.P.; Pape, T.; Gao, Y.Y.; Zhang, D. Evolutionary insight into bot flies (Insecta: Diptera: Oestridae) from comparative analysis of the mitochondrial genomes. *Int. J. Biol. Macromol.* **2020**, *149*, 371-380.
- Du, H.C.; Wang, Y.; Fang, J.X.; Zhang, Z.Y.; Zhang, S.F.; Liu, F.; Zhang, Z.; Kong, X.B. Sequencing and analysis of the complete mitochondrial genome of *Dendrolimus punctatus* (Lepidoptera: Lasiocampidae). *Sci. Silvae Sin.* **2019**, *12*, 16-172.
- Du, H.C.; Liu, M.; Zhang, S.F.; Liu, F.; Zhang, Z.; Kong, X.B. Lineage divergence of *Dendrolimus punctatus* in Southern China based on mitochondrial genome. *Front. Genet.* **2020**, *11*, 65.
- Du, Z.Y.; Hasegawa, H.; Cooley, J.R.; Simon, C.; Yoshimura, J.; Cai, W.Z.; Li, H. Mitochondrial genomics reveals shared phylogeographic patterns and demographic history among three periodical cicada species groups. *Mol. Biol. Evol.* **2019**, *36*, 1187-1200.
- Su, C.Y.; Zhu, D.H.; Abe, Y.; Ide, T.; Liu, Z.W. The complete mitochondrial genome and gene rearrangements in a gall wasp species, *Dryocosmus liui* (Hymenoptera: Cynipoidea: Cynipidae). *PeerJ* **2023**, *11*, e15865.

14. Li, F.P.; Zhang, Y.; Zhong, T.; Heng, X.; Ao, T.C.; Gu, Z.F.; Wang, A.M.; Liu, C.S.; Yang, Y. The Complete Mitochondrial Genomes of Two Rock Scallops (Bivalvia: Spondylidae) Indicate Extensive Gene Rearrangements and Adaptive Evolution Compared with Pectinidae. *Int. J. Mol. Sci.* **2023**, *24*, 13844.
15. Tang, M.; Tan, M.; Meng, G.; Yang, S.; Su, X.; Liu, S.; Song, W.; Li, Y.; Wu, Q.; Zhang, A.; et al. Multiplex sequencing of pooled mitochondrial genomes- a crucial step toward biodiversity analysis using mito-metagenomics. *Nucleic Acids Res.* **2014**, *42*, e166.
16. Qin, Z.P.; Song, G.J.; Liu, P.; Li, G.P.; Liang, X.; Wang, H.T. Test on chemical control of *Histia rhodope*. *Shandong For. Sci. Technol.* **2018**, *5*, 78-80.
17. Peng, S.Y.; Jia, W.R.; Huang, Z.J.; Wang, Y.C.; Li, Y.; Huang, Z.R.; Zhang, Y.F.; Zhang, X.; Ding, J.H.; Geng, X.X.; Li, J. Complete mitochondrial genome of *Histia rhodope* Cramer (Lepidoptera: Zygaenidae). *Mitochondrial DNA B.* **2017**, *2*, 636-637.
18. Booth, T.H.; Nix, H.A.; Busby, J.R.; Hutchinson, M.F. Bioclim: the first species distribution modeling package, its early applications and relevance to most current MaxEnt studies. *Divers. Distrib.* **2014**, *20*, 1-9.
19. Li, Y.; Johnson AJ, Gao L, Wu CX, Hulcr J. Two new invasive *Ips* bark beetles (Coleoptera: Curculionidae) in mainland China and their potential distribution in Asia. *Pest Manag. Sci.* **2021**, *77*, 4000-4008.
20. Wang, Y.J.; Zhao, R.; Zhou, X.Y.; Zhang, X.L.; Zhao, G.H.; Zhang, F.G. *Agastache rugosa* Prediction of potential distribution areas and priority protected areas of based on Maxent model and Marxan model. *Front. Plant Sci.* **2023**, *14*, 1200796.
21. Elith, J.; Graham, C.H.; Anderson, R.P.; Dudík, M.; Ferrier, S.; Guisan, A.; Hijmans, R.J.; Huettmann, F.; Leathwick, J.R.; Lehmann, A.; et al. Novel methods improve prediction of species' distributions from occurrence data. *Ecography* **2006**, *29*, 129-151.
22. Phillips, S.J.; Miroslav, D. Modeling of species distributions with Maxent: new extensions a comprehensive evaluation. *Ecography* **2008**, *31*, 161-175.
23. Waldo, C.; Stuart-Smith, R.D.; Albouy, C.; Cheung, W.L.; Edgar, G.J.; Mouillot, D.; Tjiputra, J.; Pellissier, L. A quantitative review of abundance-based species distribution models. *Ecography* **2022**, *1*, 2022.
24. Lin, S.L.; Yao, D.D.; Jiang, H.X.; Qin, J.; Feng, Z. Predicting current and future potential distributions of the greater bandicoot rat (*Bandicota indica*) under climate change conditions. *Pest Manag. Sci.* **2024**, *80*, 734-743.
25. Zhang, G.L.; Liu, S.; Xu, C.Q.; Wei, H.S.; Guo, K.; Xu, R.; Qiao, H.L.; Lu, P.F. Prediction of Potential Distribution of *Carposina coreana* in China under the Current and Future Climate Change. *Insect* **2024**, *15*, 411.
26. Dmitry, A.; Anton, K.; McLean, J.S.; Pevzner, P.A. HYBRIDSPADES: An algorithm for hybrid assembly of short and long reads. *Bioinformatics* **2016**, *7*, 1009-1015.
27. Meng, G.; Li, Y.; Yang, C.; Liu, S. MitoZ: A toolkit for animal mitochondrial genome assembly, annotation and visualization. *Nucleic Acids Res.* **2019**, *47*, e63.
28. Kumar, S.; Tamura, K. MEGA5: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol. Biol. Evol.* **2016**, *33*, 1870-1874.
29. Perna, N.T.; Kocher, T.D. Patterns of nucleotide composition at fourfold degenerate sites of animal mitochondrial genomes. *J. Mol. Evol.* **1995**, *41*, 353-358.
30. Lowe, T.M.; Chan, P.P. tRNAscan-SE On-line: Integrating search and context for analysis of transfer RNA genes. *Nucleic Acids Res.* **2016**, *44*, 54-57.
31. Bernt, M.; Donath, A.; Jühling, F.; Externbrink, F.; Florentz, C.; Fritzsch, G.; Pütz, J.; Middendorf, M.; Stadler, P.F. MITOS: Improved de novo metazoan mitochondrial genome annotation. *Mol. Phylogenet. Evol.* **2013**, *69*, 313-319.
32. Tamura, K.; Stecher, G.; Peterson, D.; Filipski, A.; Kumar, S. MEGA6: Molecular evolutionary genetics analysis version 6.0. *Mol. Biol. Evol.* **2013**, *30*, 2725-2729.
33. Kumar, S.; Stecher, G.; Tamura, K. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Mol. Biol. Evol.* **2016**, *33*, 1870-1874.
34. Minh, B.Q.; Schmidt, H.A.; Chernomor, O.; Schrempf, D.; Woodhams, M.D.; Von Haeseler, A.; IQ-TREE, R.L. 2: New models and efficient methods for phylogenetic inference in the genomic era. *Mol. Biol. Evol.* **2020**, *37*, 1530-1534.
35. Ronquist, F.; Huelsenbeck, J.P. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **2003**, *19*, 1572-1574.
36. Clary, D.O.; Wolstenholme, D.R. The ribosomal RNA genes of *Drosophila* mitochondrial DNA. *Nucleic Acids Res.* **1985**, *13*, 4029-4045.
37. Huelsenbeck, J.P.; Ronquist, F.; Nielsen, R.; Bollback, J.P. Bayesian inference of phylogeny and its impact on evolutionary biology. *Science* **2001**, *294*, 2310-2314.
38. Ji, W.; Gao, G.; Wei, J.F. Potential global distribution of *Daktulosphaira vitifoliae* under climate change based on MaxEnt. *Insects* **2021**, *12*, 347.
39. Hijmans, R.J.; Cameron, S.E.; Parra, J.L.; Jones, P.G.; Jarvis, A. Very high resolution interpolated climate surfaces for global land areas. *Int. J. Climatol.* **2005**, *25*, 1965-1978.

40. Muscarella, R.; Galante, P.J.; Soley-Guardia, M.; Boria, R.A.; Kass, J.M.; Uriarte, M.; ENMeval, R.A. An R package for conducting spatially independent evaluations and estimating optimal model complexity for MAXENT ecological niche models. *Methods Ecol. Evol.* **2014**, 12261, 1198-1205.
41. Li, J.; Deng, C.; Duan, G.; Wang, Z.; Zhang, Y.; Fan, G. Potentially suitable habitats of *Daodi goji berry* in China under climate change. *Front. Plant Sci.* **2024**, 14, 1279019.
42. Peterson, A.; Soberón, J.; Pearson, R.; Anderson, R.; Martínezmeyer, E.; Nakamura, M.; Araújo, M. *Ecological Niches and Geographic Distributions*; Princeton University Press: Princeton, NJ, USA, **2011**.
43. Song, Z.K.; Fan, G.H.; Deng, C.R.; Duan, G.Z.; Li, J.L. Predicting the Distribution of *Neoceratitis asiatica* (Diptera: Tephritidae), a Primary Pest of Goji Berry in China, under Climate Change. *Insects* **2024**, 15, 558.
44. Despabiladeras, J.B.; Bautista, M.A.M. Complete Mitochondrial Genome of the Eggplant Fruit and Shoot Borer, *Leucinodes orbonalis* Guenée (Lepidoptera: Crambidae), and Comparison with Other Pyraloid Moths. *Insects* **2024**, 15, 4, 220.
45. Liu, N.; Fang, L.J.; Zhang, Y.L. The Complete Mitochondrial Genomes of Four Species in the Subfamily Limenitidinae (Lepidoptera, Nymphalidae) and a Phylogenetic Analysis. *Insects* **2022**, 13, 16.
46. Kim, I.; Lee, E.M.; Seol, K.Y.; Yun, E.Y.; Lee, Y.B.; Hwang, J.S.; Jin, B.R. The mitochondrial genome of the Korean hairstreak, *Coreana raphaelis* (Lepidoptera: Lycaenidae). *Insect Mol. Biol.* **2006**, 15, 217-225.
47. Wilson, K.; Cahill, V.; Ballment, E.; Benzie, J. The complete sequence of the mitochondrial genome of the crustacean *Penaeus monodom*: Are malacostracan crustaceans more closely related to insects than to branchiopods?. *Mol. Biol. Evol.* **2000**, 17, 863-874.
48. Spanos, G.; Koutroumbas, G.; Kotsyfakis, M.; Louis, C. The mitochondrial genome of the mediterranean fruit fly, *Ceratitis capitata*. *Insect Mol. Biol.* **2000**, 9, 139-144.
49. Epstein, M.E. Revision and phylogeny of the Limacodid-group families, with evolutionary studies on slug caterpillars (Lepidoptera: Zygaenoidea). *Smithson. Contrib. Zool.* **1996**, 582, 1-102.
50. Mutanen, M.; Wahlberg, N.; Kaila, L. Comprehensive gene and taxon coverage elucidates radiation patterns in moths and butterflies. *Proc. R. Soc. B* **2010**, 277, 2839-2848.
51. Regier, J.C.; Mitter, C.; Zwick, A.; Bazinet, A.L.; Cummings, M.P.; et al. A large-scale, higher-level, molecular phylogenetic study of the insect order Lepidoptera (moths and butterflies). *PLOS ONE* **2013**, 8, e58568.
52. Lu, B.; Yonghen, Z.; Xing, G.; Yuefang, G.; Youben, Y. The complete mitochondrial genome of *Etersia aedeia* (Lepidoptera, Zygaenidae) and comparison with other zygaenid moth. *Genomic* **2019**, 11, 1043-1052.
53. Timmermans, M.J.T.N.; Lees, D.C.; Simonsen, T.J. Towards a mitogenomic phylogeny of Lepidoptera using next generation sequence technology. *Mol. Phylogenet. Evol.* **2014**, 79, 169-178.
54. Liu, Q.N.; Xin, Z.Z.; Bian, D.D.; Chai, X.Y.; Zhou, C.L.; Tang, B.P. The first complete mitochondrial genome for the subfamily Limacodidae and implications for the higher phylogeny of Lepidoptera. *Sci. Rep-uk*. **2016**, 6, 35878.
55. Wang, S.Y.; Lu, Y.Y.; Han, M.Y.; Li, L.L.; He, P.; Shi, A.; Bai, M. Using MaxEnt model to predict the potential distribution of three potentially invasive scarab beetles in China. *Insects* **2023**, 14, 239.
56. Guo, Y.; Li, X.; Zhao, Z.; Nawaz, Z. Predicting the impacts of climate change, soils and vegetation types on the geographic distribution of *Polyporus umbellatus* in China. *Sci. Total Environ.* **2019**, 648, 1-11.
57. Skendžić, S.; Zovko, M.; Živković, I.P.; Lešić, V.; Lemić, D. The impact of climate change on agricultural insect pests. *Insects* **2021**, 12, 440.
58. Du, H.C.; Fang, J.X.; Shi, X.; Yu, C.M.; Deng, M.; Zhang, S.F.; Liu, F.; Zhang, Z.; Han, F.Z.; Kong, X.B.; Insights into the Divergence of Chinese *Ips* Bark Beetles during Evolutionary Adaptation. *Biology* **2022**, 11, 384.
59. Aidoo, O.F.; Souza, P.G.C.; Silva, R.S.; Santana, P.A.; Picano, M.C.; Kyerematen, R.; Sètamou, M.; Ekesi, S.; Borgemeister, C. Climate-induced range shifts of invasive species (*Diaphorina citri* Kuwayama). *Pest. Manag. Sci.* **2022**, 78, 2534-2549.
60. Berzitis, E.A.; Minigan, J.N.; Hallett, R.H.; Newman, J.A. Climate and host plant availability impact the future distribution of the bean leaf beetle (*Ceratomya trifurcata*). *Glob. Change Biol.* **2014**, 20, 2778-2792.
61. Dang, Y.Q.; Zhang, Y.L.; Wang, X.Y.; Xin, B.; Quinn, N.F.; Duan, J.J. Retrospective analysis of factors affecting the distribution of an invasive wood-boring insect using native range data: the importance of host plants. *J. Pest Sci.* **2021**, 94, 981-990.

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