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Genetic Diversity and Population Structure of the Tea Lace Bug *Stephanitis chinensis* Drake, 1948 (Hemiptera: Tingidae) in Central China

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ABSTRACT

The tea lace bug, *Stephanitis chinensis* Drake, 1948, a notorious pest, inflicts significant damage on commercial tea cultivation and ornamental gardens across China. In this study, we investigated the genetic diversity, population structure, and demographic history of *S. chinensis* based on the genetic and phylogenetic analysis of mitochondrial cytochrome c oxidase I (*cox1*) sequences. The dataset exhibited 453 polymorphic sites, 315 parsimony informative sites, and 138 singleton variable sites, attesting to the species' genetic complexity. Haplotype diversity varied across populations, with the highest in Ziyang County of Shaanxi Province (SXZY) and lowest in Yongchuan District of Chongqing City (CQYC). Genetic differentiation was primarily within populations, while some pairs showed significant divergence, indicative of geographic barriers and local adaptation. Inconsistent signals from neutrality tests and mismatch distribution analysis suggested historical stability interspersed with growth or bottleneck events. Phylogenetic analysis depicted distinct haplotype clusters, with Mabian County of Sichuan province (SCMB) forming a unique clade. The haplotype network emphasized geographic uniqueness while highlighting shared ancestry between Yongchuan District of Chongqing City (CQYC) and Guwen County of Hunan Province (HNGW). These findings illuminate *S. chinensis*' ecological adaptability, historical dynamics, and potential for adaptive responses to agricultural practices. In addition, the results indicated important implications for pest management, genetic conservation, and the broader understanding of the species' evolutionary trajectory.

Keywords: Genetic diversity, molecular marker, pest management, population genetics, tea lace bug.

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INTRODUCTION

The tea lace bug, *Stephanitis chinensis* Drake, 1948 (Hemiptera: Tingidae), stands as a significant pest with considerable economic and ecological implications for tea plantations in central China. The tea lace bug has a small body size and a large population number (Fig. 1A). It can disperse quickly for a long distance by wind and cause disasters under suitable natural conditions (Yu, Li & Gan, 2016). As a piercing-sucking insect, this pest feeds on the sap of tea plants, causing direct damage by reducing plant vigor and altering leaf quality (Wu & Li, 2014). Its infestations often lead to leaf stippling (Fig. 1B), chlorosis, and even premature leaf drop, resulting in reduced tea yields and compromised product quality (Li, Wang, Chen & Peng, 2017). In response, pest management strategies have predominantly relied on chemical pesticides, raising concerns about their environmental impact, potential for pesticide resistance, and impacts on human health due to the presence of pesticide residues in tea leaves (Luo et al, 2021).

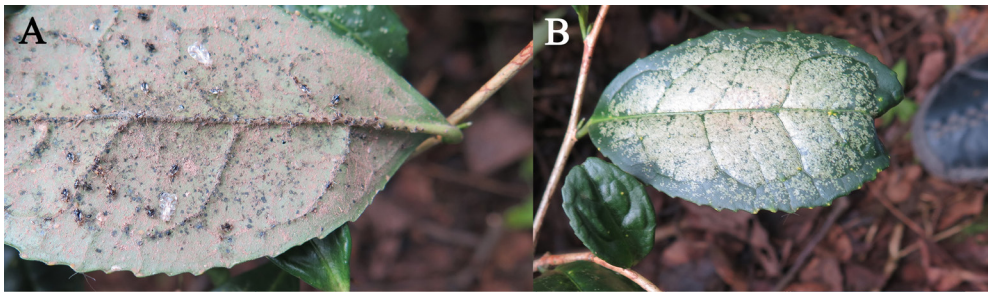

Figure 1. Sample information of *Stephanitis chinensis*. A, Habitus photo. B, Damaged tea leaf.

Beyond its economic significance, the tea lace bug also serves as a model organism for understanding population genetics and evolutionary dynamics. There are numerous molecular genetic studies exploring the species diversity, genetic diversity, and phylogenetic relationships of various lace bug species from around the world (Cassis, 2019; Besedina, Kil, Ismailov & Karpunina, 2020; Hlaka et al., 2021; Lakatos, Tuba, Bender, Kajimura & Tóth, 2021, 2022). However, population genetic studies on *S. chinensis* are scarce, especially for populations from China. The intricate interplay of genetic diversity, population structure, and ecological factors shapes the ability of pests to adapt, disperse, and evolve (Via, 1990). Investigating the genetic makeup of *S. chinensis* populations in central China offers insights into their origins, migration patterns, and potential for local adaptation. Additionally, such studies provide essential knowledge for designing effective management strategies that leverage the pest's genetic vulnerabilities, thereby minimizing the use of chemical pesticides and promoting sustainable pest control.

Recent advancements in molecular techniques have paved the way for in-depth exploration of species' genetic landscapes. The integration of mitochondrial markers, such as cytochrome c oxidase I (*cox1*) and cytochrome b (*cytb*), empowers researchers to dissect the genetic architecture of populations (Liu et al, 2021). Not only do these

markers provide insights into genetic diversity, but they also facilitate the reconstruction of historical demographic processes and contemporary gene flow dynamics.

This study aims to unravel the genetic diversity and population structure of *S. chinensis* in central China using mitochondrial markers. By delving into the genetic intricacies of this pest population, we seek to uncover hidden patterns of connectivity and differentiation across geographic locations. As the tea industry remains a vital economic pillar in many regions of China, the insights gained from this study shed light on the evolutionary forces shaping the genetic diversity of *S. chinensis* populations and inform strategies for the sustainable management of this pest in the tea-producing regions of central China.

MATERIALS AND METHODS

Sampling and DNA extraction

A total of 60 *S. chinensis* individuals were gathered from six diverse locations spanning five provinces/municipalities across China during the years 2022 and 2023 (Fig. 2; Table 1). Preserving the integrity of each individual, they were immersed in 100% ethanol prior to the subsequent DNA extraction process. The E.Z.N.A. R Tissue DNA Kit (Omega, Norcross, GA, United States) was employed to extract genomic DNA from each specimen, strictly following the manufacturer's recommended protocol. The DNA quality was high, as examined by the electrophoresis. All extracted DNA samples were subsequently stored at -20°C to ensure long-term stability.

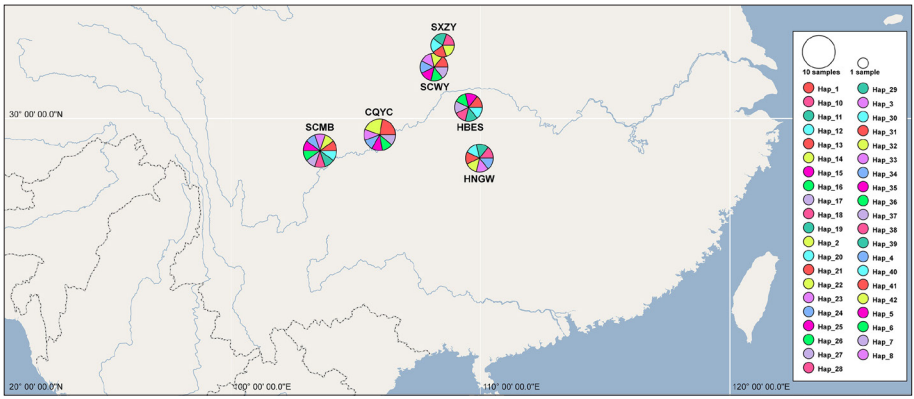

Figure 2. Sampling locations and haplotype frequency of *Stephanitis chinensis*.

Table 1. Sample information in this study.

Code	Sampling location	Latitude	Longitude	Sample size
CQYC	Chongqing City: Yongchuan District, Chashan bamboo sea	29.43613	105.9571	10
HBES	Hubei Province: Enshi City, Longfeng Town	28.62092	109.9564	10
HNGW	Hunan Province: Guwen County	30.38926	109.5162	10
SCMB	Sichuan province: Mabian County, Laodong Town	28.87875	103.5618	10
SCWY	Sichuan Province: Wanyuan City, Gujun Town	31.76862	108.1359	10
SXZY	Shaanxi Province: Ziyang County, Xiangyang Town	32.50617	108.4806	10

PCR reaction and sequencing

Utilizing the universally recognized primers cox1F 5'-ATTCAACCAATCATAAA-GATATTGG-3' and cox1R 5'-TAAACTTCTGGATGTCCAAAAAATCA-3' (Hebert et al, 2004), the mitochondrial *cox1* gene underwent the PCR amplification process. The PCR conditions encompassed an initial denaturation at 95°C for 5 minutes, succeeded by 35 cycles consisting of denaturation at 95°C for 30 seconds, annealing at 55°C for 30 seconds, and extension at 72°C for 45 seconds. A final elongation step at 72°C for 10 minutes concluded the process, followed by preservation at 10°C until manually terminated. Following amplification, PCR products underwent electrophoresis on 1.0% agarose gels and were subsequently purified using the Axygen DNA Gel Extraction Kit (Axygen Biotechnology, Hangzhou, China). The purified PCR fragments were then sequenced utilizing the ABI 3730 automated sequencer (Biozeron Co., Ltd., Shanghai, China).

Genetic analysis

A comprehensive suite of genetic parameters, including gene length, conserved sites, variable sites, parsimony informative sites, singleton sites, and nucleotide contents, were computed employing the MEGA11 software (Tamura, Stecher & Kumar, 2021). Meanwhile, the genetic diversity indices, such as haplotype number (H), number of polymorphic sites (S), haplotype diversity (Hd), and nucleotide diversity (Pi), were estimated utilizing DnaSP ver. 6.12.03 (Librado & Rozas, 2009). To uncover the genetic differentiation and structure, a series of analyses were performed, including molecular variance analysis (AMOVA), pairwise F_{ST} values, and neutrality tests, which were conducted through the Arlequin ver. 3.5 software (Excoffier & Lischer, 2010). Additionally, mismatch distribution analyses were carried out employing both DnaSP and Arlequin.

To gauge gene flow and examine the exchanges between various populations, gene flow analyses were undertaken utilizing Arlequin ver. 3.5 to determine Nm values (M=Nm for haploid data, M=2Nm for diploid data). Correlations between geographic distance and genetic differences were evaluated via an isolation by distance (IBD) analysis, employing the Mantel test implemented through IBD ver. 1.53 (Bohonak, 2002) with a total of 1000 randomizations. To visualize genetic relationships, a Principal Coordinates Analysis (PCoA) was conducted on the genetic distance matrix of the sampled populations.

Phylogenetic analysis

The neighbor-joining (NJ) method in MEGA11 (Tamura et al., 2021) was employed to reconstruct and visualize the phylogenetic relationships between the haplotypes and the sampled individuals. The bootstrap consensus NJ tree, comprising 1000 replicates, was generated to offer insight into the grouping tendencies of associated taxa. The Kimura 2-parameter model was opted for as the substitution model, encompassing both transitions and transversions with uniform rates across sites. In maintaining precision, any ambiguous positions were systematically excluded for each

sequence pair, employing the pairwise deletion option. Furthermore, the TCS method within PopART ver. 1.7 (Leigh & Bryant, 2015) was utilized to infer and visualize the haplotype network and their geographical distribution.

RESULTS

DNA sequencing

A comprehensive dataset of 45 high-quality mitochondrial cytochrome c oxidase I (*cox1*) sequences (GenBank accession numbers OR394910–OR394954) was successfully obtained from a sample pool comprising 60 individuals of *S. chinensis* (other 15 individuals failed due to overlapping peaks in sequencing). Stringent measures were undertaken to ensure data reliability, including the exclusion of double-peak sequences. The finalized dataset consisted of 45 *cox1* sequences, each spanning 658 base pairs (Table 2). The *cox1* gene sequences exhibited an overall average A + T content of 68.2%. Analysis of the *cox1* sequences from *S. chinensis* populations unveiled the presence of 205 invariable (monomorphic) sites, 453 variable (polymorphic) sites, 315 parsimony informative sites, and 138 singleton variable sites. Among the populations examined, distinctive patterns of genetic variation and diversity were observed. Notably, the population from Guwen County of Hunan Province (HNGW) displayed the highest numbers of variable sites (331) and singleton variable sites (200), indicative of its remarkable allelic diversity. Meanwhile, Wanyuan City of Sichuan Province (SCWY) stood out for hosting the greatest number of parsimony informative sites (179). In contrast, Yongchuan District of Chongqing City (CQYC) exhibited comparatively lower genetic variation, with the fewest variable sites (31), parsimony informative sites (26), and singleton variable sites (5). Additionally, the analysis of nucleotide composition shed light on intriguing differences across populations. Ziyang County of Shaanxi Province (SXZY) exhibited the highest A + T content, amounting to 70.9%. Conversely, CQYC featured the lowest A + T content at 66.4%.

Table 2. Content of gene sequences in populations of *Stephanitis chinensis*.

Population	N	Length (bp)	I	V	Pi	S	A + T (%)	H	Hd ± SD	Pi ± SD	K
CQYC	9	658	627	31	26	5	66.4	7	0.944 ± 0.070	0.02322 ± 0.00354	15.278
HBES	7	658	380	278	100	178	68.3	7	1.000 ± 0.076	0.16732 ± 0.04354	110.095
HNGW	7	658	327	331	131	200	68.2	7	1.000 ± 0.076	0.21523 ± 0.04477	141.619
SCMB	10	658	423	235	38	197	67.2	10	1.000 ± 0.045	0.08734 ± 0.03873	57.467
SCWY	7	658	349	309	179	130	69.8	7	1.000 ± 0.076	0.22311 ± 0.04031	146.810
SXZY	5	658	365	293	107	186	70.9	5	1.000 ± 0.126	0.23632 ± 0.04265	155.500
Whole	45	658	205	453	315	138	68.2	42	0.996 ± 0.006	0.16201 ± 0.01918	106.605

N, number of obtained sequences; I, invariable (monomorphic) sites; V, variable (polymorphic) sites; Pi, parsimony informative sites; S, singleton variable sites; A + T, average A + T content; H, number of haplotypes; Hd, haplotype (gene) diversity; Pi, nucleotide diversity; SD, standard Deviation; K, average number of nucleotide differences.

Haplotype diversity and distribution

Within the 45 *S. chinensis* samples, a remarkable diversity of 43 haplotypes was identified. Haplotype counts varied across populations, ranging from 5 in SXZY to 10

in Mabian County of Sichuan province (SCMB) (Fig. 2). In totality, 42 haplotypes were recorded when considering all populations as a whole. While each population harbored a minimum of five haplotypes, most haplotypes exhibited population specificity. An exception was Hap_1, which was shared by three individuals from CQYC and HNGW. Haplotypic diversity (Hd) was highest in SXZY (Hd = 1.000 ± 0.126), along with the highest nucleotide diversity (Pi = 0.23632 ± 0.04265). Conversely, CQYC displayed the lowest haplotype diversity (Hd = 0.944 ± 0.070) and nucleotide diversity (Pi = 0.02322 ± 0.00354). Correspondingly, the average number of nucleotide differences was greatest in SXZY (k = 155.500) and lowest in CQYC (k = 15.278). On the whole, the collective population exhibited high levels of haplotype diversity (Hd = 0.996 ± 0.006), nucleotide diversity (Pi = 0.16201 ± 0.01918), and average nucleotide differences (k = 106.605).

Genetic variation and differentiation

Assessment of molecular variance (AMOVA) demonstrated that genetic differentiation was predominantly observed within populations (85.93% of molecular variance), overshadowing differentiation among populations (14.07%) (Table 3). Pairwise F_{ST} values revealed a diverse spectrum, ranging from -0.06899 between populations Enshi City of Hubei Province (HBES) and HNGW to 0.519 between populations CQYC and SXZY (Fig. 3A). Among the 15 population comparisons, eight displayed significant ($p < 0.05$) genetic differentiation, five of which were highly significant ($p < 0.01$). Notably elevated genetic differentiation ($F_{ST} > 0.25$, $p < 0.05$) was evident between specific pairs of populations, such as CQYC and SCWY, as well as SCMB and SXZY (Fig. 3B, Table 4). Considerable gene flow was observed among populations, as most Nm values exceeded 1. The highest Nm value was observed between HBES and HNGW, HNGW and SCWY, and SCWY and SXZY. In contrast, the isolation by distance (IBD) analysis showed no significant correlation ($r = 0.3885$, $p \leq 0.1230$) between geographic distance and genetic distance among *S. chinensis* populations (Fig. 4).

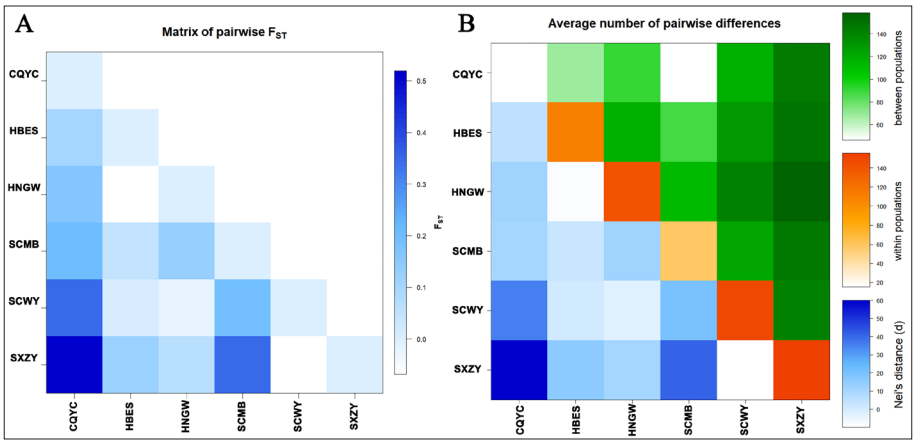

Figure 3. Pairwise comparison of six populations of *Stephanitis chinensis*. A, Matrix of pairwise FST. B, Average number of pairwise differences.

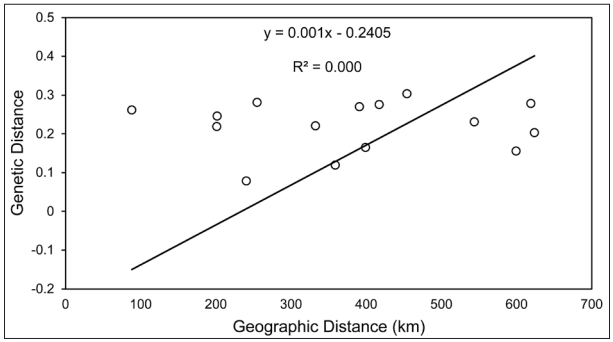

Figure 4. Plots of the isolation by distance analysis (IBD) of the six populations of *Stephanitis chinensis*.

Table 3. Analysis of molecular variance (AMOVA) for the different populations of *Stephanitis chinensis*.

Source of variation	degree of freedom	Sum of squares	Variance components	Percentage of variation	Fixation index
Among populations	5	519.029	7.66749 Va	14.07	FST = 0.14070, p = 0.00391
Within populations	39	1826.283	46.82776 Vb	85.93	
Total	44	2345.311	54.49525		

The first two coordinates of the PCoA explained 99.07% of the total variation among the six populations (Fig. 5). The first and second axes accounted for 89.96% and 9.11% of the variation, respectively. All populations on the PCoA graph are segregated from each other. HBES and HNGW from Hunan Province were closer to each other than to the other populations. SCMB and SCWY from Sichuan Province were distantly located.

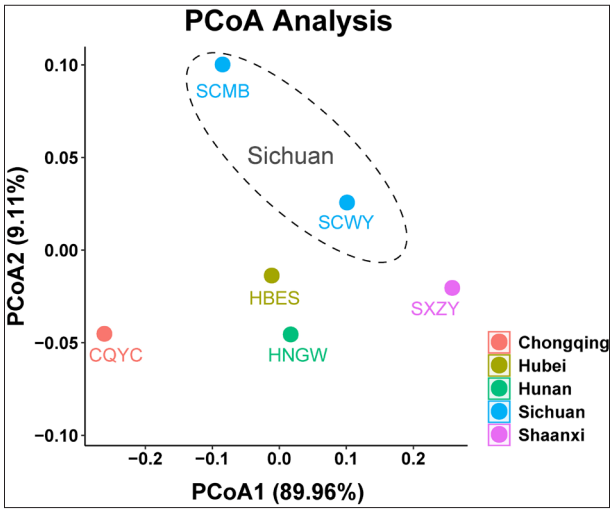

Figure 5. Two-dimensional plot of the principal coordinates analysis of the six populations of *Stephanitis chinensis*.

Table 4. Matrix of pairwise F_{ST} (below diagonal) and Nm values (above diagonal) among the populations of *Stephanitis chinensis*.

	CQYC	HBES	HNGW	SCMB	SCWY	SXZY
CQYC		2.238885	1.24096	0.973685	0.47391	0.231695
HBES	0.10045*		inf	4.880555	40.52039	1.85794
HNGW	0.16768**	-0.06899		1.681065	inf	3.570285
SCMB	0.2043**	0.04873	0.12946*		1.07287	0.47301
SCWY	0.34535**	0.00613	-0.01691	0.18898		inf
SXZY	0.519**	0.1186	0.06544	0.34578*	-0.06842**	

* Significant: p < 0.05. ** Highly significant: p < 0.01.

Demographic history and expansion patterns

Tajima's *D* and Fu's *Fs* neutrality tests were conducted to probe into the demographic history of central Chinese *S. chinensis* populations (Table 5). Tajima's *D* values were positive for CQYC, HNGW, SCWY, and SXZY, but none of these values reached statistical significance. Similarly, Fu's *Fs* values were positive for most populations, except for SCMB, and all these values were not statistically significant. When considering the entire dataset, Tajima's *D* was positively inclined but insignificant, whereas Fu's *Fs* demonstrated negative insignificance.

Table 5. Neutrality test and the corresponding p-values for the populations of *Stephanitis chinensis*.

Population	Tajima's D test	D significance (*p*)	Fu's Fs test	Fs significance (*p*)
CQYC	1.70472	0.98500	1.16602	0.66000
HBES	-0.17482	0.40900	1.58112	0.49700
HNGW	0.28377	0.62500	1.84977	0.53000
SCMB	-1.53936	0.05200	-0.09763	0.27400
SCWY	0.96469	0.88300	1.88784	0.52800
SXZY	1.70472	0.77500	2.72160	0.56100
Whole	0.10711	0.61400	-3.00443	0.12000

The observed mismatch distribution curves from DnaSP exhibited a distinctive multimodal pattern (Fig. 6A, B). The simulated mismatch distribution under the population growth-decline model correlated more closely with the observed data than the constant population size model. The goodness-of-fit test by Arlequin yielded a sum of squared deviation (SSD) of 0.00823628 under the sudden expansion model (Table 6), which was not statistically significant ($p = 0.79$). Similarly, the Harpending's raggedness index (HRI) was 0.00271809 and also not statistically significant ($p = 0.8$). Conversely, under the spatial expansion model, the goodness-of-fit test for the entire dataset of *S. chinensis* resulted in an SSD of 0.00637913, which was not statistically significant ($p = 0.96$). Likewise, the HRI was 0.00271809 and not significant ($p = 0.99000000$).

Table 6. Mismatch distribution and the corresponding p-values for *Stephanitis chinensis*.

Model	Sum of squared deviation	SSD p-value	Harpending's raggedness index	Raggedness p-value
Sudden expansion	0.00823628	0.79000000	0.00271809	0.80000000
Spatial expansion	0.00637913	0.96000000	0.00271809	0.99000000

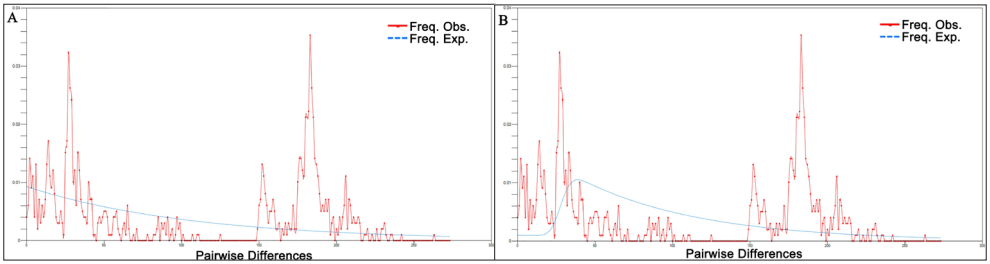

Figure 6. Mismatch distributions of *Stephanitis chinensis*. A, Under constant population size model. B, Under population growth-decline model

Phylogenetic relationships and population structure

NJ trees generated from *cox1* sequences illustrated the relationships among haplotypes (Fig. 7A) and individual specimens (Fig. 7B) of *S. chinensis*. While a specific cluster emerged for haplotypes from SCMB, no other substantial clusters were identified (Fig. 7A). Individual sequence-based NJ tree revealed a discernible cluster of eight individuals from SCMB of Sichuan Province (Fig. 7B). However, the overall pattern displayed dispersion, making the distinction of geographic populations challenging (Fig. 7B).

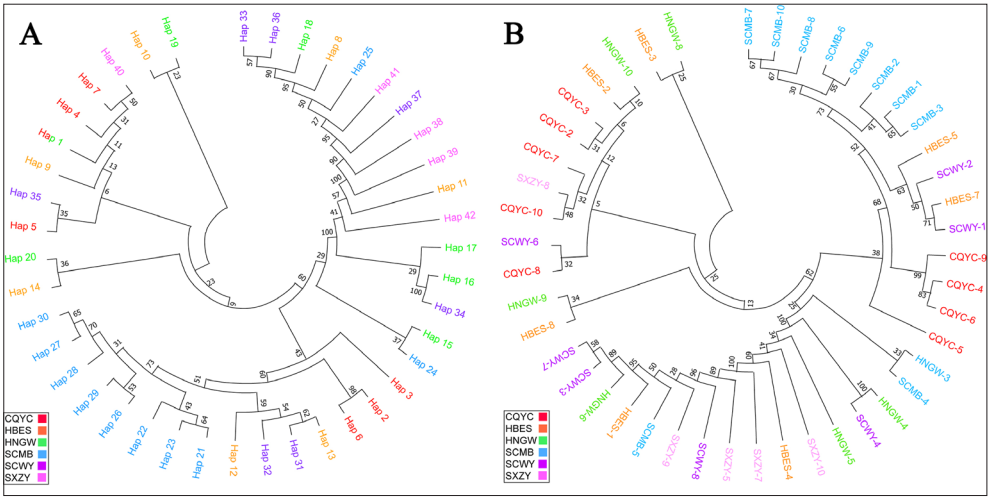

Figure 7. Phylogeographic analysis of *Stephanitis chinensis*. A, Neighbor-joining tree of haplotypes. B, Neighbor-joining tree of individuals. Bootstrap values are shown on the nodes

The TCS haplotype network could help to unravel the genetic relationships among the sequenced *S. chinensis* populations (Fig. 8). The network analysis revealed that the majority of haplotypes were unique to their specific geographic groups, which unveiled a distinctive genetic fingerprint for the majority of haplotypes by establishing a compelling link between their genetic makeup and specific geographic origins. A notable exception was haplotype 1, which is shared by populations CQYC and HNGW. Additionally, the aggregation of nine distinct haplotypes originating from the

SCMB population in Sichuan Province implies a pronounced genetic affinity among these haplotypes rooted in a localized context. In contrast, the broader distribution of remaining haplotypes is characterized by a scattered arrangement within the network, defying discernible spatial patterns of clustering.

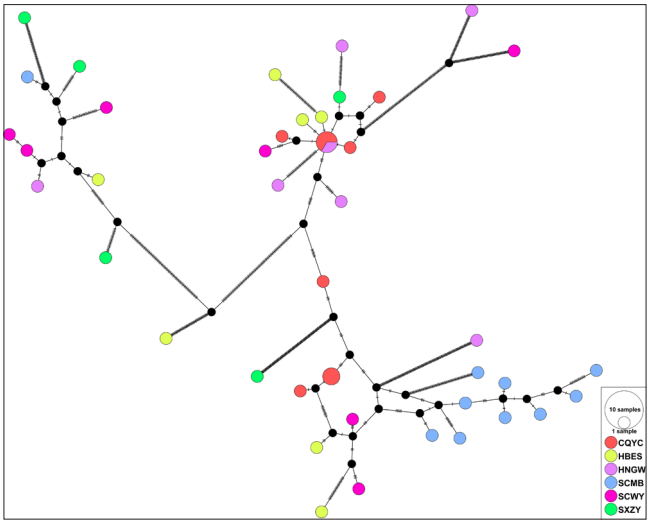

Figure 8. The TCS network of the haplotypes of *Stephanitis chinensis*. Branch lengths are proportional to the number of differences. Bars indicate the number of point mutations between two haplotypes, and small black circles indicate undetected haplotypes.

DISCUSSION

Genetic diversity

The elucidation of genetic diversity and variation within populations of *S. chinensis* in central China provides valuable insights into the evolutionary dynamics of this pest species. The abundance of polymorphic sites, parsimony informative sites, and singleton variable sites underscores the genetic complexity within these populations. These polymorphic sites represent allelic variation that has accumulated over time due to factors such as mutation and selection, potentially influencing the species' adaptability to changing environments (Takahata, 1990). The pronounced number of parsimony informative sites implies that these genetic variants have accumulated and been maintained over time, potentially due to selection acting on specific sites (Carbone, Jakobek, Ramirez–Prado & Horn, 2007). In contrast, the singleton variable sites might represent recent mutations or rare alleles that contribute to unique genotypic profiles (Linck & Battey, 2019). The differences in genetic variation among populations, exemplified by the high allelic diversity in HNGW and the pronounced number of parsimony informative sites in SCWY, highlight the distinct genetic signatures present in different geographic locations.

The observed diversity of 43 haplotypes among the *S. chinensis* samples further illuminates the intricate genetic architecture of this pest. The variation in haplotype counts across populations underscores the localized genetic distinctiveness, where specific geographic regions harbor unique genetic variants. This scenario could arise due to factors such as limited gene flow, genetic drift, and selection acting differentially across habitats (Takahata, 1990; Carbone, Jakobek, Ramirez-Prado & Horn, 2007). The high genetic diversity is also found in other lace bugs, such as the macadamia lace bug, *Ulonemia decoris* Drake, 1942 (Cassis, 2019) and the sycamore lace bug, *Corythucha ciliata* (Say, 1832) (Besedina et al, 2020; Lakatos et al, 2021). Interestingly, the shared haplotype (Hap_1) between CQYC and HNGW provides a glimpse into potential historical gene flow or shared ancestry between the two populations from Chongqing City and Hunan Province. Conversely, the aggregation of SCMB haplotypes within a single clade could signify either a potential common genetic lineage rooted in local adaptations or selective pressures peculiar to this specific region in Sichuan Province.

Genetic differentiation within and among populations of *S. chinensis* offers insights into the interplay between evolutionary forces and geographic isolation. The predominance of genetic divergence within populations indicates the existence of unique genetic compositions in different regions. The spectrum of pairwise F_{ST} values, ranging from negative to positive, highlights the varying degrees of genetic differentiation between populations. Notably, the significant genetic differentiation observed in specific population pairs emphasizes the influence of factors such as limited gene flow, geographic barriers, and local adaptation (Dionne, Caron, Dodson & Bernatchez, 2008; Tigano & Friesen, 2016). Nevertheless, the gene flow analysis suggests that migration and genetic exchange of *S. chinensis* populations are ongoing, contributing to the maintenance of genetic diversity across populations. The migration of *S. chinensis* appears frequent since their host tea plant is an important economic crop being traded globally (Kumar, Kakkar, McKenzie, Seal & Osborne, 2013). The non-significant correlation in the isolation by distance (IBD) analysis implies that factors beyond geographic proximity, such as historical colonization or specific habitat preferences, also play a role in shaping the observed genetic patterns. The IBD analysis further suggests the complexity of the population structure of *S. chinensis*.

Demographic History

The evaluation of demographic history through neutrality tests and mismatch distribution analysis offers contrasting insights into the historical dynamics of *S. chinensis* populations. The non-significant Tajima's *D* and Fu's *Fs* values suggest a history of relatively stable population sizes without undergoing pronounced demographic shifts (Tajima, 1989; Fu, 1997), potentially maintained by factors such as stable environments and consistent reproductive dynamics. The non-significant SSD and HRI values in both the sudden expansion and spatial expansion models indicate that the genetic diversity patterns observed in the *S. chinensis* populations may not be well explained by these specific demographic scenarios. However, the multimodal pattern of the observed mismatch distribution curves indicates that the species'

demographic history is more complex. The closer fit of the mismatch distribution to the population growth-decline model than the constant population size model suggests that past population expansion and contraction events might have contributed to the observed genetic diversity. This apparent conflict underscores the complexity of the species' demographic history, which likely involves a combination of stable periods and episodes of population growth or bottleneck events.

Phylogenetic analysis provides a window into the genetic relationships among haplotypes and individual specimens of *S. chinensis*. The observed patterns, including the presence of specific clusters and the shared haplotype, offer glimpses into the species' evolutionary past and potential gene flow dynamics. The TCS haplotype network serves as a visual representation of these relationships, underscoring the uniqueness of most haplotypes to specific geographic regions. The shared haplotype between CQYC and HNGW might point to historical migration or common ancestry between the two populations. Therefore, special attention should be paid to limit the transfer of *S. chinensis* between Chongqing City and Hunan Province, such as strengthening the monitoring of pests on tea products from the two areas. The clustering of most SCMB haplotypes within a single clade may indicate a localized genetic affinity of lace bugs in Sichuan Province, potentially reflecting localized ecological adaptations or historical founder effects within this region. However, the dispersed arrangement of other haplotypes suggests ongoing genetic exchange and complex historical interactions.

Ecological and evolutionary implications

The findings of this study have significant implications for understanding the ecological and evolutionary dynamics of *S. chinensis* in central China. The high genetic diversity observed within populations indicates the species' ability to adapt to diverse environments and suggests that it can respond to selective pressures, including those imposed by pesticides or host plants. Therefore, it is not safe to rely on chemical agents for control of *S. chinensis*, but also need more backup strategies to prevent the development of pesticide resistance.

The presence of localized genetic clusters suggests potential adaptation to specific ecological niches and may influence the pest's interactions with its host plants, predators, and parasites. The observed gene flow between populations highlights the potential for rapid genetic exchange, potentially influencing the spread of traits related to pesticide resistance or host plant utilization. It is necessary to strengthen the supervision of tea products between different regions.

The interplay between the demographic history inferred from neutrality tests and mismatch distribution analysis underscores the complexity of the species' historical trajectory. The apparent contradiction suggests that the species has experienced phases of equilibrium punctuated by events that have influenced population dynamics and genetic diversity. These fluctuations could be linked to changes in host plant availability, climate conditions, or human interventions such as using pesticides.

Understanding these historical patterns is crucial for predicting the pest's response to changing environments and for designing effective management strategies. In this case, *S. chinensis* has a strong ability to maintain a stable population and cope with various interference.

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