Journal of Asia-Pacific Entomology 21 (2018) 233–238

Contents lists available at ScienceDirect

Journal of Asia-Pacific Entomology

journal homepage: www.elsevier.com/locate/jape

Short Communication

Comparing the genetic diversity and structure of indigenous Korean and Chinese populations of *Laodelphax striatellus* Fallén using mitochondrial haplotypes

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ARTICLE INFO

Keywords:
Laodelphax striatellus
Population genetics
Genetic structure
Haplotype
Population tree

ABSTRACT

The small brown planthopper, *Laodelphax striatellus* Fallén, is a major migratory pest from China to Korea and transmits viral diseases of rice plants. In this study, we compared the genetic structures of overwintered indigenous Korean and Chinese populations. The eight Korean populations consisted of 33 haplotypes, and 16 of these were newly identified. The genetic diversity of the Korean population revealed high haplotype diversity (Hd) and low nucleotide diversity (π) of 0.86 ± 0.017 and 0.0024 ± 0.0001 on average, respectively. These values for the Chinese population were Hd = 0.92 ± 0.016 and $\pi = 0.0026 \pm 0.0002$. Overall, genetic distances by pairwise F_{ST} were generally low, ranging from −0.022 to 0.089. Moreover, the Korean population revealed its ongoing population expansion by showing negative values in the neutrality test (Tajima's $D = -1.4$, Fu's $Fs = -15.8$) and a unimodal pattern in the mismatch distribution analysis. The genetic structures and population relationships were determined using 8 indigenous Korean and 30 Chinese populations by Bayesian approaches and population tree construction, respectively. The genetic structure was inferred as five (K = 5), and all indigenous Korean populations as well as 10 Chinese populations from the Shanghai city, Anhui, Henan, Jiangsu, Liaoning, Shandong, and Zhejiang provinces were grouped into 'G3'. These results provide partial support for unidirectional gene flow by migratory Chinese populations into Korea. Further analysis conducted using specimens from China and Korea collected in similar periods is necessary to clarify the migration population's origin and its effect on the genetic structure of the indigenous populations.

Introduction

The small brown planthopper (*Laodelphax striatellus* Fallen, SBPH) is an important migratory pest that transmits plant viruses in eastern Asia (Falk and Tsai, 1998). In Korea, it is a major vector of rice stripe virus (RSV) (Chung and Lee, 1971) and rice black-streaked dwarf virus (RBSDV) (Chung, 1974), both of which affect rice yield. SBPHs occasionally migrate with low-pressure-gradient wind currents from China to western coastal areas of Korea between mid-May and early June (Kim et al., 2011). Therefore, the Korean SBPH population could be divided largely among indigenous and migratory populations. Moreover, the migratory population would affect the genetic diversity and structure of the indigenous population after settlement.

Population genetics analysis can be a powerful tool for understanding the effects of migratory insects on genetic structure (Kim and Sappington, 2013). It provides valuable information pertaining to population relatedness in specific regions, genetic diversity, and genetic structure. Proper sampling using the same molecular markers is an essential step for properly comparing the population structures between Korea and China. In China, the genetic structures of 26 populations had already been analyzed using mitochondrial and nuclear molecular markers (Sun et al., 2015). The SBPH revealed a lack of significant differences in its genetic structures due to extensive gene flow. Moreover, mitochondrial DNA markers revealed a non-random distribution and correlated well with geographic distance along climatic gradients.

Here, as a preliminary study, we compare the genetic diversity and structure between Korean and Chinese populations, including 30 nationwide Chinese populations, using haplotype variations from mitochondrial cytochrome *c* oxidase subunit I (COI) and tRNA-Leu gene obtaining mitochondrial cytochrome *c* oxidase subunit II (tRNA-Leu

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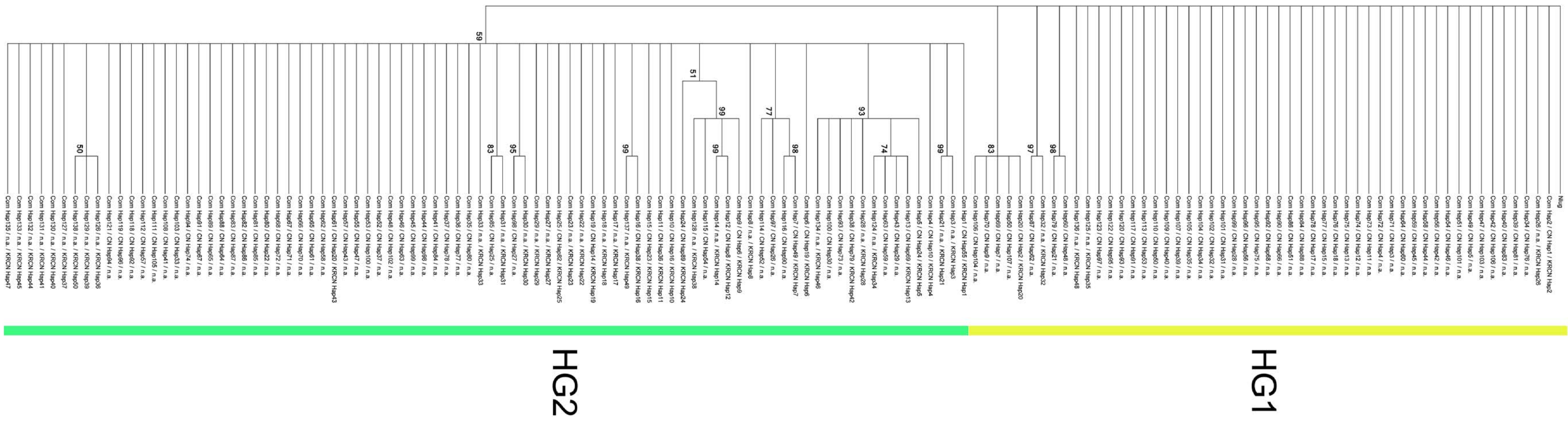
https://doi.org/10.1016/j.aspen.2017.12.004
Received 29 August 2017; Received in revised form 7 December 2017; Accepted 12 December 2017

Table 1
Sample collection site.

Country	Province	Locality	Population	Collection dates	Number of specimen	Specimen composition	Coordinate	Host plants
Korea	CB	Chungju	KR_15_CB_CJu	08-Apr-15	23	15♀ + 4♂ + 4(4th)	N36.9875892, E127.7687763	Stub of rice
Korea	CN	Taean	KR_15_CN_TAn	15-Mar-15	24	18(4th) + 6(3rd)	N36.4481695, E126.3838149	Stub of rice
Korea	GGi	Gimpo	KR_15_GGi_GPo	28-Apr-15	23	3♂ + 11(4th) + 9(3rd)	N37.6972475, E126.6152749	Stub of rice
Korea	GSN	Sacheon	KR_15_GSN_SCn	21-Apr-15	21	21♀ + 0♂	N34.9930854, E128.0552451	Stub of rice
Korea	JB	Buan	KR_15_JB_BuA	16-Apr-15	23	23♀ + 0♂	N35.7788525, E126.6448133	Stub of rice
Korea	JN	Haenam	KR_15_JN_HNm	17-Apr-15	23	15♀ + 8♂	N34.648338, E126.6016974	Stub of rice
Korea	JN	Shinan	KR_15_JN_SAn	16-Apr-15	24	6♀ + 18(4th)	N34.9015934, E126.319738	Stub of rice
Korea	JN	Younggwang	KR_15_JN_YG	23-Mar-15	24	24♀ + 0♂	N35.308271, E126.5376537	Stub of rice
China	JS	Taizhou	CN_16_JS_TZ1	17-May_16	24	2(3rd) + 16 (4th) + 6 (5th)	N32.6406, E120.0725	Wheat
China	JS	Taizhou	CN_16_JS_TZ2	17-May_16	19	2(1st) + 3 (2nd) + 1 (3rd) + 8 (4th) + 5 (5th)	N32.6796, E120.0748	Wheat
China	SHG	Shenjiabang	CN_16_SHG_SJB	18-May_16	24	24 (5th)	N30.8974, E121.362	Wheat
China	ZJ	Jiaxing	CN_16_ZJ_JX	19-May_16	24	8 (4th) + 16 (5th)	N30.7151, E120.5234	Wheat



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