Comparative analysis of the complete mitochondrial genome of the small brown planthopper *Laodelphax striatellus* Fallén from Zhejiang and Beijing populations in China

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The small brown planthopper (SBPH), *Laodelphax striatellus* Fallén (Hemiptera: Delphacidae) is an important pest of rice, corn and wheat, in terms of direct sap-sucking and vector of many virus diseases, in north-eastern Asia. The acquiring mitochondrial genome information of the insect will help to understand its geographical differentiation and evolutionary relationship with other hemipterans.

In this study, the complete nucleotide sequence of the mitochondrial genome of the planthopper was determined to be 15,943 bp with a total A+T content of 77.4% from Zhejiang population. It has typical gene content and codon usage for an animal mitogenome, while its size and nucleotide composition are well in the range of other hemipteran species. However, compared with the hypothesized ancestral arthropod mitochondrial genome arrangement, there are two regions where gene rearrangements occur in SBPH. *tRNACys* transposes with *tRNATrp*, and a shuffling occurs among *tRNAThr* , *tRNAPro* and *nad6*.

All 13 protein-coding genes were observed to have a putative ATG methionine or ATT isoleucine codons as start signals. Canonical TAA and TAG termination codons were found in nine protein-coding genes, and the remaining four have incomplete termination codons. The *atp8* gene has the smallest size among known hexapods and the *nad6* gene has the largest size among known hemipterans.

Twenty two kinds of tRNAs were found. The anticodons of all tRNAs are identical to those observed in *Drosophila yakuba*, and can be folded in the form of a typical clover-leaf structure except for *tRNASer(AGN)*, *tRNASer(UCN)* and *tRNAHis*. *tRNASer(AGN)* and *tRNASer(UCN)* lose the DHU arm, while *tRNAHis* lose the TΨC arm.

The A+T-rich region of the SBPH mitogenome can be divided into four parts. In the second part a single stem-and-loop structure which harbors the conserved elements is identified and a 23 bp poly-T stretch is found to be located downstream of this structure on the majority strand. In the third part there are eleven 21 bp repeat units.

We also compared the *L. striatellus* mitogenomes of Beijing (Song and Liang, 2009) and Zhejiang (current study) populations, and summarized the characteristics in the aspects of nucleotide substitutions, synonymous and nonsynonymous substitutions and the variations of protein-coding genes. Compared to the protein-coding genes in the mitochondrial genome on Beijing population, Zhejiang population is absent in amino acid residues SKLISLS from 24 to 30 in *nad2*, YALSDWN from 211 to 217 in *cox2*, CLNKNSFWDFGDSNKDLKK from 2 to 20 in *nad5*, LESNLFK from 439 to 445 in *nad4*, KLIKFKFFFKKKKKEKKKK from 152-170 in *nad6*, LAPFNLVKLMKN from 306 to 317 in *nad1*. In other side, Zhejiang population has residues KFIQAMMMTNTMLSMWMKHPISMGTLLM from 2 to 29 in *nad6*, which was absent in Beijing population. Beijing and Zhejiang population has residues GSKTLFV and VRKHYLM from 26-32 in *nad4l*, respectively. Those amino acid residues presented in Beijing population but absent in Zhejiang population had the possibility of zero, very low or average as homologous to other species, while reverse situation had high homologous possibility with other species. The regions of Mt sequence of Zhejiang population different to Beijing population were confirmed by SBPH samples collected from Shangdong of China, Kyushu of Japan, etc. These results suggest that SBPH populations in eastern China and Korea and

Japan are quiet uniform and probably resulted from frequent migration from south-eastern China to north-eastern China and Korea and Japan.

References

Song N and AP Liang. 2009. Complete Mitochondrial Genome of the Small Brown Planthopper, *Laodelphax striatellus* (Delphacidae: Hemiptera), with a Novel Gene Order. Zoological Science 26: 851-860.