The complete mitochondrial genome of *Nilaparvata lugens* (Stål, 1854) captured in Guangxi province, China (Hemiptera: Delphacidae): identification of the origin of *N. lugens* migrated to Korea

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**ABSTRACT**

*Nilaparvata lugens*, called as brown planthoppers (BPH), is one of important pests on rice. To identify the origin of Korean *N. lugens*, we completed mitochondrial genome of *N. lugens* captured in Guangdong province in China. The circular mitogenome of *N. lugens* is 17,606 bp including 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single large non-coding region of 2424 bp. The base composition was AT-biased (89.5%). 90 single nucleotide polymorphisms (SNPs) and 10 insertions and deletions are identified by comparing with Korean *N. lugens*. Phylogenetic trees present that Guangdong BPH may not be an origin of Korean BPH based on distance of two mitochondrial genomes.

*Nilaparvata lugens* (Stål, 1854), called as brown planthoppers (BPH), is one of the important rice pests in rice-cultivated countries, including China and Korea (Sogawa and Cheng 1979). Especially, BPHs have been migrated from China to Korea by westerlies, complete two or three generations, and then affect rice in Korea (Kim et al. 1985; Saxena and Barrion 1979). Especially, BPHs have been migrated from China to Korea by westerlies, complete two or three generations, and then affect rice in Korea (Kim et al. 1985; Saxena and Barrion 1979). BPH, is one of the important rice pests in rice-cultivated countries, including China and Korea (Sogawa and Cheng 1979). Especially, BPHs have been migrated from China to Korea by westerlies, complete two or three generations, and then affect rice in Korea (Kim et al. 1985; Saxena and Barrion 1979). Eight BPH mitochondrial genomes mostly originated from China except one from Korea (Park et al. 2019) were sequenced. Interestingly, five out of eight mitochondrial genomes do not contain putative control region and around 1 kb region between *ND2* and *CO1*, suspecting that they are partial mitochondrial genome. It indicates that more BPH mitochondrial genomes are required to dissect intra-species variation precisely.

Total DNA of *N. lugens* captured at Guangxi provinces in China (25°27′26.35″N, 110°16′58.17″E) was obtained (Samples were deposited at InfoBoss Herbarium (IN); Choi NJ, INH-00016) and extracted using the DNA extraction method manually (Zymo Research, USA). Sequencing was conducted by HiSeqX (Macrogen Inc., Korea) and de novo assembly and confirmation were done by Velvet 1.2.10 (Zerbino and Birney 2008), SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17 (Li 2008), and SAMtools 1.9 (Li et al. 2009). Geneious R11 11.1.5 (Biomatters Ltd, Auckland, New Zealand) was used to annotate mitochondrial genome based on *N. lugens* mitochondrial genome (MK590088; Park et al. 2019) together with ARWEN for tRNAs (Laslett and Canb 2008).

Mitochondrial genome of *N. lugens* (GenBank accession is MK606370) is 17,607 bp, which is between those of *N. lugens* captured in Korea (MK590088; Park et al. 2019) and Guangdong province, China (Park et al. 2019). It contains 13 protein-coding genes (PGCs), 2 rRNAs, and 22 tRNAs. Its nucleotide composition is AT-biased (A + T ratio is 77.1%). The control region, presumably single largest non-coding AT-rich region, is 2,424 bp (AT ratio is 80.7%).

Fouy-seven single nucleotide polymorphisms (SNPs) and 55 insertions and deletions (INDEL) are identified between those of Guangxi and Guangdong BHP mitochondrial genomes, presenting 10 of 13 PGCs have 12 synonymous SNPs (sSNPs) and *ND2* and *CYTB* contain two non-synonymous SNPs (nsSNPs). While, 41 SNPs and 15 INDELs are found between Guangxi and Korea, showing that 19 sSNPs and 2 nsSNPs from *ND2* and *ND5*. In addition, 90 SNPs and 10 INDELs are identified between Guangdong and Korea among which 17 sSNPs and two nsSNPs in *ND5* and *CYTB*. It indicates that mitochondrial genome of Korean BPH (Park et al. 2019) may be originated from Guangxi province, China.

We inferred phylogenetic relationship from 11 Delphacidae complete mitochondrial genomes aligned by MAFFT 7.388 (Katoh and Standley 2013). Neighbor joining, minimum evolution, and maximum likelihood bootstrapped trees were constructed using MEGA X (Kumar et al. 2018). Phylogenetic trees present that intra-species phylogenetic relationship of *N. lugens* is not supported by high bootstrap values and some of clades are incongruent among three trees (Figure 1), indicating that precise analyses of variations from complete mitochondrial genomes together with

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additional samples from China will be required to understand intraspecific relationship of N. lugens.

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