Comparison between different individuals of *Bactrocera (Zeugodacus) Scutellata* (Hendel) (Diptera: Tephritidae) reveals differential mutation rates of mitochondrial genes

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**ABSTRACT**

We sequenced and annotated the complete mitochondrial genome (mitogenome) of *Bactrocera scutellata* (Diptera: Tephritidae), which is an economically important pest in many area of East Asia. This mitogenome is 15,850 bp in length with an A + T content of 72.99%, and contains 37 typical animal mitochondrial genes that are arranged in the same order as that of the inferred ancestral insects. All protein-coding genes (PCGs) start with a typical ATN codon, with the exception of *cox1*, which begins with TCG. Ten PCGs stop with termination codon TAA or TAG, whereas *cox1*, *nad1* and *nad5* have single T as the incomplete stop codon. All of the transfer RNA genes present the typical clover leaf secondary structure excepting *trnS1* (AGN) without a DHU-arm. The A + T-rich region (945 bp in length with 84.66% A + T content) is located between *rrnS* and *trnl*, and contains a 20 bp poly-T stretch and 21 bp poly-A stretch. Excepting the control region, the longest intergenic spacer locates between *trnR* and *trnN* which is 56 bp long with an excessive high A + T content (89.29%). Compared with other two mitogenomes of *B. scutellata* revealed that the mutation rates of mitochondrial genes were quite different. For population genetic studies of this species, we recommend using the *cox1* or *nad5* genes.

Fruit flies (Diptera: Tephritidae) are among the most economically important pest species in the world, attacking a wide range of fruits and fleshy vegetables throughout tropical and sub-tropical areas (Vargas et al. 2015). It is estimated that Tephritidae contains more than 4257 species in 471 genera worldwide (Thompson 1998), but to date, very limited mitogenomes have been reported. The striped fruit fly, *Bactrocera* (Zeugodacus) *scutellata* (Hendel) (Diptera: Tephritidae) is a vital quarantine pest that causes damage to Cucurbitaceae plants and has been found in China, Korea, Bhutan, Vietnam, Thailand and Japan (Ryukus) (Kim et al. 2010; Vargas et al. 2015).

The mitogenome of *B. scutellata* (collected from Beibei District, Chongqing, China and the voucher specimen was deposited at the Insect Herbarium of College of Plant Protection, Southwest University under the accession number Di-14-356) was amplified with 2 pairs of primers (available from corresponding author on request) and sequenced in both directions. It (GenBank accession number, KT159731) was 15850 bp in length and with the same number, order and orientation of genes as that of the inferred ancestral insects (Boore 1999). Except the A + T-rich control region, 157 nucleotides ranged from 1 to 56 bp distributed in 15 intergenic spacers. Gene overlaps were 32 bp ranged from 1 to 8 bp distributed in 9 locations with three relatively long overlaps (*trnW-trnC, atp8-atp6* and *nad4L-nad4*) which highly conserved in all sequenced species of Tephritidae except two nucleotide differences occurred in overlap of *trnW-trnC* of *Procecidochares utilis*.

Phylogenetic analysis indicated that *B. scutellata* belonged to the subgenus *Zeugodacus* of *Bactrocera*, and was closest to *B. diaphora* (Figure 1). Since other two mitogenomes of *B. scutellata* had been sequenced (Liu et al. 2017), we analyzed their differences. The results revealed that 121 differential sites (4 in *rrnL*, 1 in *rrnS*, 3 in tRNA genes, 8 in AT-rich region, 2 in intergenic regions and 103 in PCGs) were found and the overall substitution rate was 0.77%. The ratio of nucleotide conversion to transversion reached more than 8 times (108/13). For transversions, except only one occurred between C and G, all other occurred between A and T (8 sites) and
between A and C (4 sites). Although 103 substitutions located in PCGs, only four substitutions caused amino acid change (S74G in \textit{cox1}, N10D in \textit{atp6}, I91M in \textit{nad3} and S514G in \textit{nad5}). Interestingly, none of the substitution site occurred in the second codon position (91 and 12 occurred in first and third codon position respectively).

Overall, mutation rates between mitochondrial genes of \textit{B. scutellata} were significantly different. The mutation rate of PCGs (0.92%) was higher than that of rRNA genes (0.24%) and tRNA genes (0.20%). Among the 13 PCGs, the five highest mutation rates genes were \textit{nad3} (1.412%), \textit{atp6} (1.18%), \textit{cox1} (1.17%), \textit{nad5} (1.11%) and \textit{cox3} (1.01%), while other PCGs were less than 1% (The \textit{atp8} gene even had no mutation). Considering the length of these genes, we suggested that \textit{cox1} and \textit{nad5} were more suitable for population genetic studies of this species.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Figure 1.** Phylogenetic tree was constructed using Bayesian inference and Neighbor-joining method based on the complete mitogenome sequences of the species of Tephritidae. Values at each node indicated percentage Bayesian posterior probabilities and the bootstrap percentages from 1000 replicates. The GenBank accession numbers of species showed in the parentheses. The subgenera of \textit{Bactrocera} represented on the right side of the tree.