

The First Complete Mitochondrial Genome of Melon Thrips, *Thrips palmi* (Thripinae: Thysanoptera): Vector for Tospoviruses

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Abstract : The melon thrips, *Thrips palmi* is a serious pest of a wide range of agriculture crops and also act as vectors for plant viruses (genus Tospovirus, family Bunyaviridae). More molecular data on this species is required to understand the cryptic speciation and evolutionary affiliations. Mitochondrial genomes have been widely used in phylogenetic and evolutionary studies in insect. So far, mitogenomes of five thrips species (*Anaphothrips obscurus*, *Frankliniella intonsa*, *Frankliniella occidentalis*, *Scirtothrips dorsalis* and *Thrips imaginis*) is available in the GenBank database. In this study, we sequenced the first complete mitogenome *T. palmi* and compared it with available thrips mitogenomes. We assembled the mitogenome from the whole genome sequencing data generated using Illumina HiSeq2500. Annotation was performed using MITOS web-server to estimate the location of protein coding genes (PCGs), transfer RNA (tRNAs), ribosomal RNAs (rRNAs) and their secondary structures. The boundaries of PCGs and rRNAs was confirmed manually in NCBI. Phylogenetic analyses were performed using the 13 PCGs data using maximum likelihood (ML) in PAUP, and Bayesian inference (BI) in MrBayes 3.2. The complete mitogenome of *T. palmi* was 15,333 base pairs (bp), which was greater than the genomes of *A. obscurus* (14,890bp), *F. intonsa* (15,215 bp), *F. occidentalis* (14,889 bp) and *S. dorsalis* South Asia strain (SA1) (14,283 bp), but smaller than the genomes of *T. imaginis* (15,407 bp) and *S. dorsalis* East Asia strain (EA1) (15,343bp). Like in other thrips species, the mitochondrial genome of *T. palmi* was represented by 37 genes, including 13 PCGs, large and small ribosomal RNA (*rrnL* and *rrnS*) genes, 22 transfer RNA (tRNAs) genes (with one extra gene for *trn-Serine*) and two A+T-rich control regions (CR1 and CR2). Thirty one genes were observed on heavy (H) strand and six genes on the light (L) strand. The six tRNA genes (*trnG*, *trnK*, *trnY*, *trnW*, *trnF*, and *trnH*) were found to be conserved in all thrips species mitogenomes in their locations relative to a protein-coding or rRNA gene upstream or downstream. The gene arrangements of *T. palmi* is very close to *T. imaginis* except the rearrangements in tRNAs genes: *trnR* (arginine), and *trnE* (glutamic acid) were found to be located between *cox3* and CR2 in *T. imaginis* which were translocated between *atp6* and CR1 in *T. palmi*; *trnL1* (Leucine) and *trnS1* (Serine) were located between *atp6* and CR1 in *T. imaginis* which were translocated between *cox3* and CR2 in *T. palmi*. The location of CR1 upstream of *nad5* gene was suggested to be ancestral condition of the thrips species in subfamily Thripinae, was also observed in *T. palmi*. Both the Maximum likelihood (ML) and Bayesian Inference (BI) phylogenetic trees generated resulted in similar topologies. The *T. palmi* was clustered with *T. imaginis*. We concluded that more molecular data on the diverse thrips species from different hierarchical level is needed, to understand the phylogenetic and evolutionary relationships among them.

Keywords : thrips, comparative mitogenomics, gene rearrangements, phylogenetic analysis

Conference Title : ICE 2018 : International Conference on Entomology

Conference Location : Paris, France

Conference Dates : October 29-30, 2018