



## Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

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To cite this article: Jun-ichi Takahashi, Hisashi Okuyama & Stephen J. Martin (2019) Complete mitochondrial DNA sequence of the small hive beetle *Aethina tumida* (Insecta: Coleoptera) from Hawaii, *Mitochondrial DNA Part B*, 4:1, 1522-1523, DOI: [10.1080/23802359.2019.1601516](https://doi.org/10.1080/23802359.2019.1601516)

To link to this article: <https://doi.org/10.1080/23802359.2019.1601516>



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Published online: 09 May 2019.



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## Complete mitochondrial DNA sequence of the small hive beetle *Aethina tumida* (Insecta: Coleoptera) from Hawaii

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### ABSTRACT

We analyzed the complete mitochondrial genome of the small hive beetle *Aethina tumida*, a major honeybee pest that was accidentally transported to the Hawaii Islands, USA. The mitochondrial genome of *A. tumida* was identified as a 15,198 bp circular molecule containing 13 protein-coding genes, 22 tRNA genes, and two rRNA genes, along with one A + T-rich control region. The average AT content was found to be 76.2%. The heavy strand was predicted to have nine protein-coding and 14 tRNA genes; while the light strand was predicted to contain four protein-coding, eight tRNA, and two rRNA genes. Among the 13 PCGs, the initiation codon ATT was found in five, ATA in three, ATG in four, and TTG in one gene. Six PCGs used TAA as the stop codon, whereas three PCGs used TAG as the stop codon. Incomplete stop codon TA (*COIII*, *ND5*, and *ND4*) and T (*COII*) were identified. We found that the genetic distance between *A. tumida* from Hawaii and the beetles' natural home South Africa, was small, indicating that the Hawaii population may have originated for the South Africa region.

### ARTICLE HISTORY

Received 13 February 2019  
Accepted 23 March 2019

### KEYWORDS

Next generation sequence; small hive beetle; *Aethina tumida*; Hawaii; beekeeping

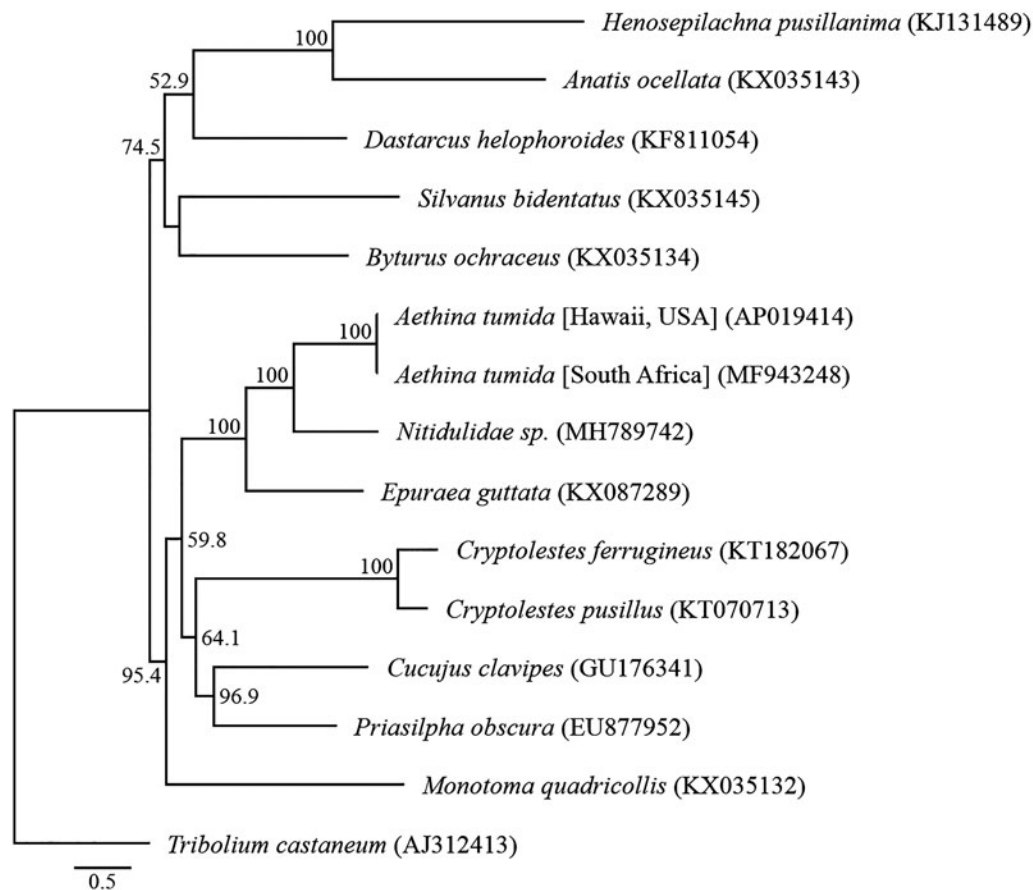
The native distribution of the small hive beetle, *Aethina tumida*, is throughout the sub-Saharan Africa (Neumann and Ellis 2008; Neumann et al. 2013). In the mainland USA, *A. tumida* appeared in 1996 a spread widely throughout the country aided by migratory beekeepers (Hood 2000). Subsequently the beetles have been accidentally introduced into Canada, Mexico, Australia, Italy, and the Philippines (Hood 2004; Ellis 2005; Carreck 2015; Cervancia et al. 2016; Neumann et al. 2016). In 2010, *A. tumida* was discovered in an apiary on Big Island in the Hawaii State of USA (Robson 2012) and quickly spread throughout all the major Hawaiian Islands (Martin 2013).

The small hive beetle larvae consume the honeybee brood, pollen and honey, which can result in the death of the colony in weak colonies, becoming a major pest in areas where it was introduced (Elzen et al. 1999; Neumann and Elzen 2004). Mitochondrial DNA sequence data can provide useful information to estimate the invasion route of alien species (Evans et al. 2000). Therefore, we report here on the complete mitochondrial genome of the beetle's found in Hawaii.

We collected several *A. tumida* adults from an *Apis mellifera* hive from an apiary in Big Island, Hawaii, in May 2012 (19°29'18.5"N 155°52'42.1"W). The adult beetles were transferred immediately to 99% ethanol for mitochondrial DNA analysis. These specimens were stored the National Museum of Nature and Science, Japan. Genomic DNA isolated from one beetle was sequenced using Illumina's MiSeq platform

(Illumina). The complete mitochondrial genome of the *A. tumida* was used as a reference sequence (Duquesne et al. 2017). The resultant reads were assembled and annotated using the MITOS web server (Bernt et al. 2013) and Geneious R9 (Kearse et al. 2012). The 13 protein-coding gene (PCG) sequences were aligned using MEGA 6 (Tamura et al. 2013). The phylogenetic analysis was performed under the maximum likelihood (ML) criterion using TREEFINDER (Jobb 2011).

We succeeded in sequencing the entire mitochondrial genome of *A. tumida* from Hawaii (DDBJ accession number AP019414). The genome consisted of a closed loop 15,198 bp long, which included 13 PCGs, 22 tRNA genes, two rRNA genes, and one AT-rich control region, which represents a typical Coleopteran mitochondrial genome. The genes *ATP8* and *ATP6* shared four nucleotides, *ATP6* and *COIII* shared one nucleotide, *ND4* and *ND4L* shared seven nucleotides, whereas the genes *ND6* and *Cytb* shared one nucleotide. All the tRNA genes possessed a cloverleaf secondary structure except for *tRNA-Phe*, *tRNA-Asn*, *tRNA-Pro*, *tRNA-Thr*, *tRNA-Trp*, and *tRNA-Ser* (*AGN*). The number of mutation sites between *A. tumida* from Hawaii and South Africa, was identified as one site in *ND2*, two in *ND5*, and one in non-coding regions. A phylogenetic analysis was constructed using 13 PCGs across 14 beetle taxa (Figure 1). The mutation sites that differed between *A. tumida* from Hawaii and South Africa were a few, indicating that they are genetically common enough to be considered of South Africa origin.



**Figure 1.** Phylogenetic relationships (maximum likelihood) of the Coleopteran based on the nucleotide sequences of the 13 protein-coding genes of the mitochondrial genome. The numbers at the nodes indicate the bootstrap support inferred from 1000 bootstrap replicates. Alphanumeric terms indicate the DNA Database of Japan accession numbers.

## Acknowledgments

We are grateful to Mr. Gentaro Shishimi of University of Hawaii for kindly providing laboratory for helping our research.

## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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