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MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of *Exorista japonica* (Townsend, 1909) (Diptera:Tachinidae)

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ABSTRACT

Exorista japonica (Townsend, 1909), a dipteran tachinid fly, is an endoparasitoid of lepidopteran larvae as a potential biological agent. We have determined a 17,663 bp mitogenome of *E. japonica* which includes 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNAs, and a single large non-coding region of 2,773 bp. The base composition was AT-biased (81.4%). Phylogenetic trees present monophyly of Tachinidae and Exoristinae, where two *Exorista* species are clustered in single clade, Exoristini. The *E. japonica* mitogenome will be a good resource for understanding phylogenetic relationship among species of Tachinidae presenting morphological and ecological complexities.

Exorista japonica (Townsend, 1909), a dipteran endoparasitoid, belongs to Exoristini and Exoristinae in Tachinidae where there are more than 8,500 species and 1,520 genera (O'Hara 2012). Tachinidae presents diverse host ranges (Hemiptera, Lepidoptera, Coleoptera, and Hymenoptera) and ovipositional strategies (Stireman et al. 2006; O'Hara 2013). *Exorista japonica* is distributed in Inida, Nepal, Vietnam, China, Taiwan, Japan, and Korea (Crosskey 1976; Park et al. 2016). Its female adult directly attaches milky eggs to the larval integument of 18 lepidopteran families (mainly Lymantriidae, Lasiocampidae, Noctuidae, and Arctiidae), e.g. *Mythimna separata*, *Spodoptera litura*, *Lymantria dispar*, and *Mamestra brassicae*. Hatched *E. japonica* larva penetrates host body resulting in death of host finally (Nakamura 1994; Dindo and Nakamura 2018).

Recently, molecular phylogenetic analyses combining quantitative morphologies or ecological traits have been conducted in Tachinidae at tribal or subfamily level utilizing several loci (Stireman 2002; Tachi and Shima 2010; Cerretti et al. 2014; Stireman et al. 2018). Several unresolved relationships within Dexiinae, Tachininae, and Exoristinae (Stireman et al. 2018) require more molecular marker sequences; however, only six Tachinidae mitogenomes are available till now (Shao et al. 2012).

To compensate this short-coming, we completed mitogenomes of *E. japonica* collected in Gimje-si, South Korea in 2018 (35°46′11″N, 126°49′20″E; Voucher was deposited in InfoBoss Cyber Herbarium (IN; Seo BY, INH-00020; South Korea)). Genomic DNA was extracted using CTAB-based DNA extraction method (iNtRON biotechnology, Inc., Korea). HiSeqX was used for sequencing (Macrogen Inc., Korea).

Filtering, *de novo* assembly, and gap filing processes were done by Velvet 1.2.10 (Zerbino and Birney 2008), Trimmomatic 0.33 (Bolger et al. 2014), SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17 (Li 2013), and SAMtools 1.9 (Li et al. 2009). Geneious R11 11.1.5 (Biomatters Ltd, Auckland, New Zealand) and ARWEN (Laslett and Canbäck 2008) were used to annotate *E. japonica* mitogenome based on both *Nemorilla maculosa* (NC_039823) and *E. sorbillans* mitogenomes (NC_014704; Shao et al. 2012).
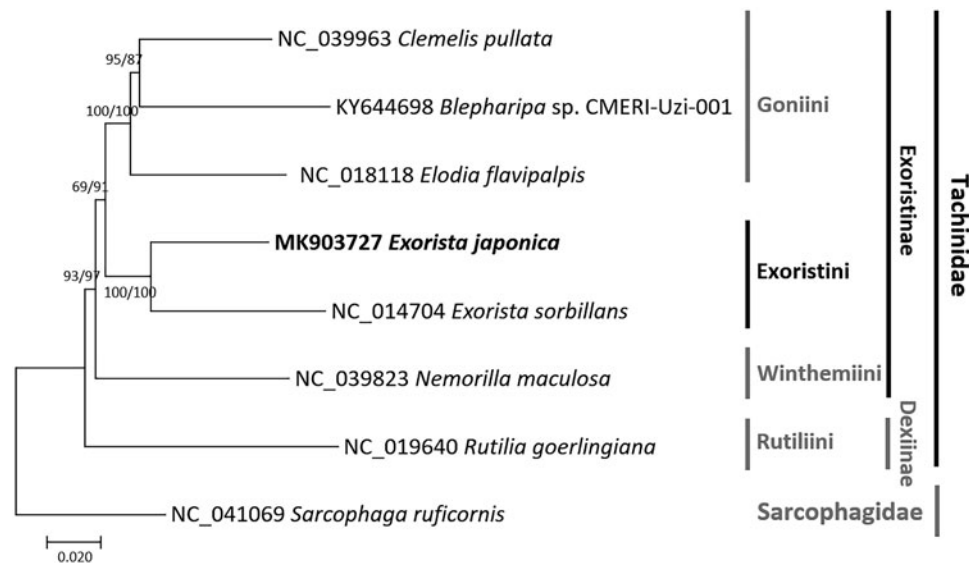
Exorista japonica mitogenome (GenBank accession is MK903727) is 17,663 bp long and GC ratio is 18.6%. It contains 13 protein-coding genes, 2 rRNAs, and 22 tRNAs (63bp to 72 bp in size). Gene order is same to those of other Tachinids. Interestingly, its control region (2,773 bp), single long non-coding AT-rich region (AT ratio is 84.3%), is the longest among seven mitogenomes of Tachinidae while *E. sorbillans* is the shortest (105 bp). This extreme difference within same genus suggests several evolutionary events in AT-rich region inside this genus.

We inferred the phylogenetic relationship of seven Tachinids including *E. japonica* and one outgroup species, *Sarcophaga ruficornis* (Sarcophagidae). Multiple sequence alignment was conducted by MAFFT 7.388 (Katoh and Standley 2013) using these complete mitogenomes. Bootstrapped neighbor-joining and maximum likelihood trees were constructed using MEGA X (Kumar et al. 2018). *E. japonica* closely clustered with *E. sorbillans* with high bootstrap value (Figure 1). Additional mitochondrial genomes of *Exorista* are strongly required for understanding inter-species distribution of extreme difference in AT-rich region. In addition, these mitochondrial genomes are expected to give an

Figure 1. Neighbor-joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1000) phylogenetic tree of seven Tachinidae species and one Oestroidea species: *Exorista japonica* (MK903727 in this study), *E. sorbillans* (NC_014704), *Elodia flavipalpis* (NC_018118), *Clemelis pullata* (NC_039963), *Blepharipa* sp. CMERI-Uzi-001 (KY644698), *Nemorilla maculosa* (NC_039823), *Rutilia goerlingiana* (NC_019640), and *Sarcophaga ruficornis* (NC_041069). Phylogenetic tree was drawn based on neighbor-joining phylogenetic tree. Grey bars in right side indicate tribes, subfamilies, and families, respectively. The numbers above branches indicate bootstrap support values of maximum likelihood and neighbor-joining phylogenetic trees, respectively.

insight into phylogenetic relationship and evolutionary history of *Exorista* species in morphologically and ecologically complex Tachinidae.

Disclosure statement

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