

First complete mitochondrial genome sequence of phytophagous ladybird beetle *Henosepilachna pusillanima* (Mulsant) from India

Ladybird beetles within the insect family Coccinellidae are considered to be the predatory beneficial insect and have been playing important role in biological control of insect pests. However, the sub-family Epilachninae within family Coccinellidae has phytophagous ladybird beetle and are considered to be the most economically important beetles in the World because of the crops damage caused by them to the plant families Cucurbitaceae and Solanaceae. The genus *Epilachna* Dejean was considered to be the one genus only, but due to the existence of unique morphological features in some species within this genus, the new genus *Henosepilachna* Li being erected. The species of the genus *Henosepilachna* are phytophagous ladybird beetles and among this *Henosepilachna pusillanima* (Mulsant) is one of the important pest species of cucurbitaceous crops in India. In the literature *H. pusillanima* has been also known as *Epilachna dodecastigma* (Wiedemann) or in some cases by other names but now *H. pusillanima* has been accepted as synonym of *E. dodecastigma*. The family Coccinellidae has both phytophagous and non-phytophagous ladybird beetles and despite of their importance in agriculture, the evolutionary relationships between these two groups is poorly understood. In this study we have sequenced the complete mitochondrial genome of first phytophagous species of ladybird beetle from the sub-family Epliachninae. The size of complete mitochondrial genome of the *H. pusillanima* was determined to be 16216-bp long and circular in nature (Fig. 1) and which has a total of 13 protein coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes and one control region (A+T-rich region). The size of control region was estimated to be 1690-bp. The gene arrangement and orientations of assembled mitogenome were identical to the reported coleopteran insect species including predatory ladybird beetle *Coccinella septempunctata* L. All tRNA genes have the classic 'clover-leaf' secondary structures, and the large and small rRNA genes were each 1,040bp and 765bp long respectively. The complete assembled and annotated genome has been submitted to the NCBI vide Genbank Accession Number: KJ131489. This would be the first completely sequenced coleopteran genome from the beetle subfamily Epilachninae and also the first insect mitogenome from India. Together with the published complete mitogenome of seven spotted ladybird beetle (predatory/beneficial ladybird beetle), *C. septempunctata* (NCBI Accession No: JQ 321839), our research would certainly help to establish the evolutionary relationships between predatory and phytophagous ladybird beetles.

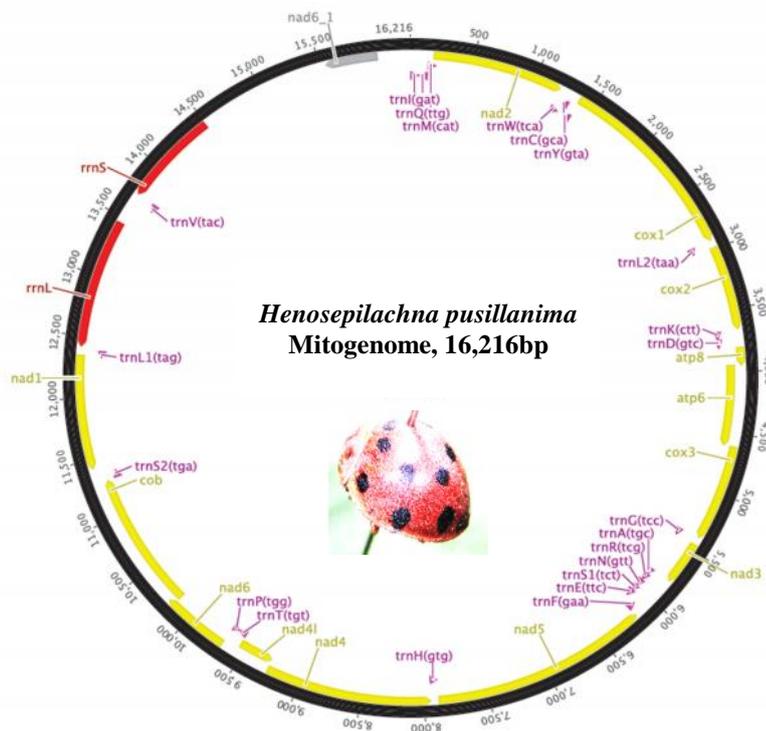


Fig 1. Circos plot of *H. pusillanima* mitogenome (16,216bp). The abbreviation *COI*, *COII* and *COIII* refer to cytochrome oxidase subunits, *CytB* refer to cytochrome b, and *NDI-6* refers to NADH dehydrogenase components. Yellow and grey colour represents protein coding genes (PCGs) and red colour represents large and small subunits ribosomal RNA.