LS-7

Assessment Of The Phylogenetic Realtionship Among Coenagrionidae Family (Odonata: Zygoptera) Using Coi Gene Marker

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Abstract

The Suborder Zygoptera of Order Odonata (Insecta) represents the most ancient damselflies with their ancestors known to exist 250 million years ago. They are geographically distributed in all continents except Antartica and ecologically important as bioindicators and biocontrol agents. Coenagrionidae is the most abundant damselfly family among the Zygopterans. In the present study, we assessed the phylogentic relationships of 3 Coenagrionidae members (*Ishnura aurora*, *Ceriagrion coromendelianum* and *Copera marginipes*) using mitochondrial cytochrome oxidase subunit I (COI) gene marker. The partially amplified PCR product of this gene yielded 606 bp, 573 bp and 616 bp long DNAs respectively. The nucleotide BLAST analysis confirmed the taxonotomic identity of all these species. We had taken two species from Coenagrionidae and Calopterigidae families from NCBI GenBank for comparative study. Phylogenetic tree constructed by Neighbour joining method showed that Coenagrionidae members represent monophyletic ancestry due to its consistent divergence from a common ancestor. Among these members, *Ischnura aurora* are having a sister clade relationship with *Copera marginipes* which remained in the same clade and *Ceriagrion coromendelianum* with *Ceriagrion cerinorubellum* in another clade. The average A+T content of all these species are 62.03% while G+C content is 37.97% showing a strong A+T bias. The nucleotide substitution analysis states that *Copera marginipes* is having highest value than other members due to the transition of Cytosine and Thymine. Thus the present study concluded that cytochrome oxidase I is an effective tool for the species identification and phylogenetic relationships of closely related species.

Keywords: *Zygoptera, Coenagrionidae, DNAbarcoding, Cytochrome oxidaseIgene*

Introduction

Dragonflies and damselflies collectively called Odonates are one of the most common insects flying over forests,fields,meadows,ponds and rivers.(Subramanian,K.A,2005).Zygoptera represents the most primitive ancient damselflies with their fossils record dates back to Permian era about 230-280 million years ago.This suborder is the second largest aquatic insect order in the animal kingdom composed of 19 extant families(Dijkstra & Kalkman,2012).They are mostly smallish,slender species with relatively weak flight.They are predacious,hemimetabolous and amphibiotic insects present all kinds of freshwater bodies (Silsby J., and Tiple A.D).Damselflies are good indicators of environmental changes such as sensitive to changes in the habitats,atmospheric temperatures and weather condition. (Corbet PS and Subramanian, K.A).In this work,we presents the phylogenetic hypothesis for the evolutionary relationships of Coenagrionidae members.

Coenagronidae is the most diverse and abundant damselfly family of the suborder zygoptera.About 1100 species are reported from this family making Coenagronidae as the largest damselfly family.This family has 6 subfamilies such as Agriocnemidinae, Arginae, Coenagrioninae, Ischnuriae, Leptobasinae, Psuedogrioninae.Molecular techniques provides powerful tool for the study of insect population ecology and insect systematics. Analysis of mitochondrial DNA (mt DNA) is particularly useful as molecular marker to discriminate between closely related species and to monitor a specific population in the field (Hebert .,2004).A 648 bp region of the cytochrome oxidase I gene in the mtDNA forms the primary DNA barcode sequence for members of animal kingdom.In the present study we have analysed the phylogenetic relationships of three Coenagrionidae members using COI gene marker.

Materials And Methods

Sample Collection And Preservation: Dragonflies were collected by hand sweep netting and random field sampling method was used to cover entire study area. Morphological identification was done from taxonomic experts. Each specimen was then placed in a separate collecting bottle, assigned a code number and stored in 70% ethanol until further use. Morphological identification was done from taxonomic experts. To extract DNA, the middle and hindleg of each specimen was removed leaving the rest of the specimen as vouchers.