

Phylogenetic position of Indian termites (Isoptera: Termitidae) with their respective genera inferred from DNA sequence analysis of the mitochondrial cytochrome oxidase gene subunit I compared to subunit II

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Abstract The present work was aimed to investigate the phylogenetic analysis of different species of Indian termites belonging to the family termitidae based on mitochondrial genes *COI* and *COII*. The sequences so obtained from public database revealed grouping of termites according to their ecological distribution. The sequences of the species under investigation were characterized on the basis of frequencies of nucleotide bases and in most of the species, a significantly high percentage of A+T base composition was observed. Phylogenetic tree revealed positioning of species according to the analysis of their cytochrome oxidase subunits.

Keywords Termitidae · Mitochondrial genes · Sequence analysis · Nucleotide bases · Phylogenetic tree

Introduction

Isopterans are the most elegant engineers of nature and are known for their superarchitectural ability, cryptobiotic nature of life, and enormous economic importance. They constitute a marvelous group of social insects with highly evolved organization, cast system, and division of labor. With almost 3,000 species, out of which 300 are from Indian region, Order Isoptera continues to evolve and become more

and more specialized for a variety of climates. Termites are the most destructive insect pests of wood in the world. In United States, it was estimated that termites cause more than US \$2 billion damage each year, more than that caused by fire and wind storm combined. In Australia, it was estimated that more than \$ 200 million worth of damage was caused by termites each year. Termites in fact are found almost anywhere in the world especially the tropical and sub-tropical regions. In India, it had been reported that an entire township was gradually destroyed by termites eventually resembled a bombed-out ghost town [1, 2]. Besides being an economically important pest, termites are also ecologically important to forest ecosystems. They are closely linked with biogeochemical (nutrient) cycling. The termite gut is host to protozoan and bacterial symbionts that are able to digest wood cellulose and thus release the energy otherwise unavailable to the insects [3].

Because of their vast economic importance, it has become vital to thoroughly study them to unravel their origin and taxonomic position. Proper identification of species is imperative for generating good termite taxonomy and to construct their accurate phylogenies [4]. The importance of constructing accurate termite phylogenies is to tailor effective management strategies, including recognizing special susceptibility (or resistance) based on genetic bottlenecks or single invasion events and delineating the boundaries of particular species groups in complex ecosystems [5]. Though a good deal of work has been carried out on the taxonomy of Indian termites based on their morphological aspects, [6, 7] identifying workers and separating soldiers of different species is very difficult and inspite of using precise measurements, overlap may occur. Molecular studies have now demonstrated a great potential for DNA sequence analysis in the interpretation of phylogeny and gene flow in various termite species [8].

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