

Differential Genomic Approach to Explore Phylogenetic Link

Mandakini Singla¹, Sharma VL¹, Sobti RC² and Ananthbandhu Chaudhuri^{3*}

¹Department of Zoology, Panjab University, Chandigarh-160014, India

²BBAU, Lucknow – 226025, India

³Department of Natural Sciences, Stillman College, Tuscaloosa-35401, USA

Abstract

Different approaches are in progress to study phylogenetic relatedness and divergence among organisms. Genomic study is the most effective method for resolving phylogenetic relationships. Multiple genes are preferred over single gene sequence analysis and whole genome sequences are nowadays the best nucleotide sequence-based approach to identify and classify the taxonomically complex group of organisms to deal with several phylogenetic issues. Various bioinformatics tools are providing valuable information to study significant evolutionary relationships such as next generation sequencing, proteomics etc. DNA barcoding technology is also recently used skill to study phylogeny and identify the morphologically ambiguous species by amplifying a small fragment of Cytochrome c Oxidase Subunit I (COI). We recently reported multiple gene phylogenies of Indian termites resulting in incongruent results. However, whole genome analysis will provide a significant outcome to resolve the diverse observations studied in these species.

Keywords: Phylogeny; Whole genome; DNA barcoding; Termites

Editorial

Molecular phylogenies based on single genes often resulted in divergent conclusions and use of multiple gene series was proposed to end these contradictory results. Single gene phylogenies usually produce dissonant results lacking significant support in relation to statistics and produce very small data to resolve phylogenetic relatedness. In contrast, the use of multiple gene analysis and different tree reconstruction methods leads to well-resolved statistically significant differential approach. To reduce differential results, the data containing minimal nonphylogenetic signals should be used to take maximum advantage of the phylogenomics [1].

Whole genome analysis of living organisms using mitochondrial and chloroplast genomes, is best preferred method commonly used to infer phylogeny rather than sequencing single genes. Different attempts to study genome evolution based on binary character encoding, distance methods using software, maximum parsimony, maximum likelihood, method of invariants, Bayesian analysis, statistical approach and mutations related to divergence were observed. Also it has been proposed that genome molecular data should be combined with fossil records to improve the phylogenetic inference of organisms [2].

DNA barcoding technology is another method based on the partial fragments (about 650 bp) mitochondrial cytochrome c oxidase subunit I (COI) gene with the use of a single set of primers for a highly conserved gene that is present in all taxa to make molecular identification and phylogeny analysis of commonly identified species an easy process [3].

Very recently we examined the phylogenetic position of various species of Indian termites belonging to order Isoptera in relation to other termite species of different geographical locations based on 12 SrRNA, COI, COII, ND1 genes [4-7]. The observations by the use of multiple genes contributed differential results and demonstrated the usefulness of the whole genome analysis in further phylogenetic and evolutionary inspection of termites. Also, phylogeny can help in validating the morphological identity which is convenient to recognize unidentified species. This can further be confirmed by using DNA barcoding skill.

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***Corresponding author:** Ananthbandhu Chaudhuri, Assistant Professor, Biology, Stillman College, Tuscaloosa-35401, USA, Tel: (205) 366-8914; E-mail: achaudhuri@stillman.edu

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