

# Phylogenetic Analysis of Freshwater Mussel (Bivalvia: Unionoida)

Premalatha Palanivel\*, Saravanan Kaliyaperumal., Karuppunnan Periyasamy and Santhi, M.P.

**Abstract** - Phylogenetics is the study of evolutionary relatedness amongst organisms. The genetic relationships between species can be represented using phylogenetic trees. Studies of the phylogeny of organisms can help explain the similarities and differences among species. There are various techniques used to create phylogenetic trees and most of them rely on aligned genetic sequences to perform this task. Probably the most popular genetic sequence alignment algorithm is ClustalW. The freshwater mussel family Unionidae is one of the largest families in the Bivalvia and includes over 670 species. The present study was carried out for the construction of phylogenetic tree and to evaluate the relationship among the four groups. The mitochondrial COI gene of the different species of *Lamellidens*, *Parreysia corrugata* and *Musculium indicum* was retrieved from GeneBank. Multiple sequence alignment and Phylogenetic tree construction was done by using online software ClustalW. The sequences were converted to FASTA format. From the result of phylogenetic analysis *L. marginalis* and *L. consobrinus* were closely related species and, *L. marginalis* and *Musculium indicum* were distantly related species. From the study it is concluded that all the four species of bivalvia confirmed their relationship among them.

**Key words** - Bivalvia, GeneBank, ClustalW and Phylogenetic tree.

## 1. INTRODUCTION

Freshwater mussels are key components of freshwater ecosystems, and have worldwide ecological and economic significance. The freshwater bivalves are commonly found in freshwater resources like reservoirs, dam, rivers, lake and pond in India. The study of growth and survival of the freshwater mussel is important because it describes mathematical relationship (1). According to modern evolutionary theory, all organisms on earth have descended from a common ancestor, which means that any set of species, extant or extinct, is related. This relationship is called a *phylogeny*, and is represented by *phylogenetic trees*, which graphically represent the evolutionary history related to the species of interest. Phylogenetics infers trees from observations about existing organisms using morphological, physiological, and molecular characteristics (2). Multiple phylogenetic studies have demonstrated that six major lineages (families) of freshwater mussels comprise the Unionoida (3,4,5 and 6) robustly supported phylogenies of the relationships among these groups are still lacking. Thus the present study was carried out to evaluate the phylogenetic relationship among the four groups of freshwater mussels collected from local freshwater bodies.

## 2. METHODOLOGY

The mitochondrial COI gene of the different species such as *Lamellidens marginalis*, *Lamellidens consobrinus*, *Musculium indicum* and *Parreysia corrugata* was retrieved from GeneBank (<http://www.ncbi.nlm.nih.gov/>). Multiple sequence alignment and Phylogenetic tree construction were done by using online software ClustalW (website address). The sequences were converted to FASTA format.

**Figure 1 Images of Different Species of Bivalve**



P.G and Research Department of Zoology,  
Nehru Memorial College (Autonomous) Puthanampatti – 621 007,  
Tiruchirappalli District, Tamil Nadu, South India, India



### 3. RESULT AND DISCUSSION

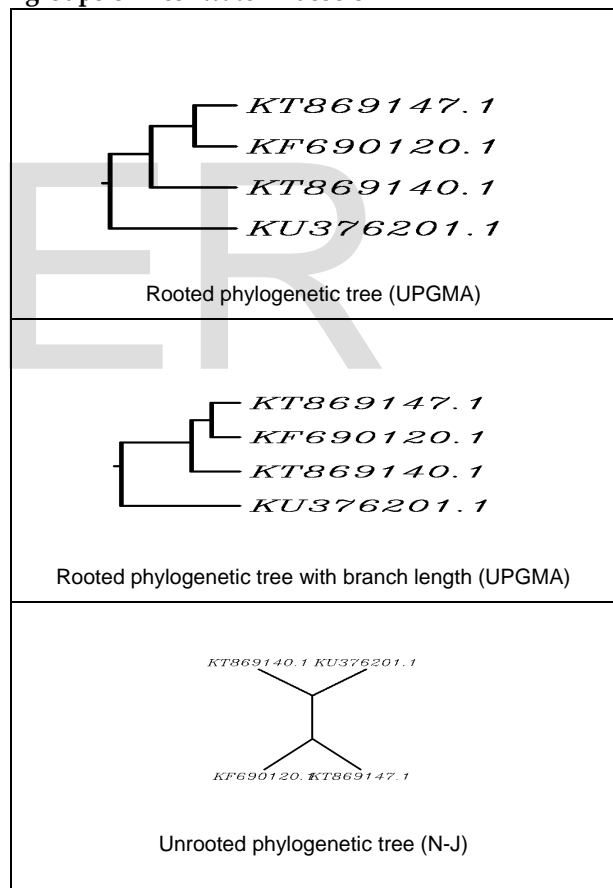
The enzyme cytochrome C oxidase is a well known protein of electron transport chain and is found in both bacteria and mitochondria. The COI and COII genes code for two of seven polypeptide subunits in the cytochrome C oxidase complex. The COI gene consists of approximately 894 bp. COI and/ or COII sequences have been applied to phylogenetic problems at a wide range of hierarchical levels in insects, from closely related species to genera and subfamilies, families, and even orders (7,). It is a good performer in recovering an expected tree (8). So sequencing both the genes represents one of the largest sequence data sets generated for phylogenetic study of any group and also fulfils the putative phylogenetic accuracy.

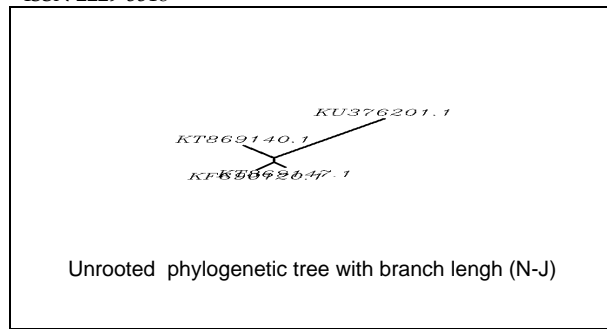
The phylogenetic tree among the four different groups of freshwater mussels showed the closely relationship. The rooted phylogenetic tree was proved the closely relationship among the four groups of freshwater mussels. The unrooted phylogenetic tree also supported to the relationship among the all species. However, *Lamellidens consobrinu* and *Lamellidens marginalis* were closely related species and, *Musculium indicum* and *Lamellidens consobrinus* were distantly related species.

The inference of phylogenies with computational methods has many important applications in medical and biological research, such as drug discovery and conservation biology.

A result published by Korber *et al.* (9) that times the evolution of the HIV-1 virus, demonstrates that ML techniques can be effective in solving biological problems. Phylogenetic trees have already witnessed applications in numerous practical domains, such as in conservation biology (10) (illegal whale hunting), epidemiology (11) (predictive evolution), forensics (12) (dental practice HIV transmission), gene function prediction (13) and drug development (14). Other applications of phylogenies include multiple sequence alignment (15,16) protein structure prediction (17) gene and protein function prediction (18, 19) and drug design (20). A paper by Bader *et al.* 2001 (21) addresses important industrial applications of phylogenetic trees, *e.g.* in the area of commercial drug discovery.

**Figure 2. Phylogenetic tree among the four groups of freshwater mussels**





KT869147.1-*Lamellidens consobrinus*; KF690120.1 - *Lamellidens marginalis*, KT869140.1 - *Parreysia corrugate*; KU376201.1 - *Musculium indicum*.

From the result of phylogenetic analysis *Lamellidens consobrinu* and *Lamellidens marginalis* were closely related species and, *Musculium indicum* and *Lamellidens consobrinus* were distantly related species. However, all the four species were confirmed relationships among them. The close relationship between *Lamellidens consobrinu* and *Lamellidens marginalis* may be due to same habitat. The distance relationship of the two species *Musculium indicum* and *Lamellidens consobrinus* may be depending on the habitat characterization and also morphological and biochemical characterization.

#### 4. CONCLUSION

From the study it is concluded that all the four species of *bivalvia* confirmed their relationship among them. However *Lamellidens consobrinu* and *Lamellidens marginalis* were closely related species and, *Musculium indicum* and *Lamellidens consobrinus* were distantly related species.

#### ACKNOWLEDGEMENT

The authors thanks to the Management, the Principal and Head of the Department of Zoology, Nehru Memorial College (Autonomous), Puthanampatti, Tiruchirappalli District, Tamil Nadu for providing necessary facilities to do the research work. First author acknowledge to the UGC, New Delhi for providing financial support (UGC-RGNF).

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