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PHYLOGENETIC ANALYSIS OF ECONOMICALLY IMPORTANT AUSTRALIAN CARLIA LIZARDS

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Abstract

Carlia lizards belong to the family Scincidae are generally found in Australia and in New Guinea and also in associated Islands. The present study is based on the phylogenetic analysis of 32 species of Carlia on the basis of their 16S rRNA sequences. All of these species differ in their color, habitat shape and size. These species are widely distributed and are kept in gardens and are non poisonous. These lizards are of major importance as they are assisted in the establishment of the invasive brown tree snake on Guam by providing a food resource. By this phylogenetic analysis we can establish a relation between different species of Carlia, using Bootstrap method. In all four types of tree prepared maximum similarity (100%) was found between C.gracillis, Crhomboidalis, C.jarnoldae, C.rubrigularis.

Keywords: *Carlia, Phylogenetic analysis, Economic importance.*

INTRODUCTION

Phylogenetics and Evolutionary Biology is the field that deals with the study of evolutionary relations among groups of organisms and the computational simulation techniques for the study of biological, behavioral, and social systems. (Brinkman and Leipe, 2001)

The result of a phylogenetic analysis is expressed in the form of phylogenetic tree from which we can deduce to find out the relationship and the conserved pattern. (Brinkman and Leipe, 2001) The branches present in a tree show the hypothesized evolutionary relationship between the organisms and they also shows the evolutionary time of growth of organisms in a phylogram tree. Phylogenetic analysis plays a vital role in identification of species, comparison of more than two species sequences and analysis of gene families, including functional predictions, microbial identification services. (Brinkman and Leipe, 2001) This analysis is done with the help of 16S rRNA sequences. The gene encoding the RNA in the small subunit of the ribosome is often the best choice because, it is present in all cells, it has exactly the same function in all cells, it is conserved enough in sequence and structure of be radially and accurately aligned, horizontal transfer of r RNA gene is absent or rare, there is a large database of aligned sequences available. The 16S rRNA gene codes for one part of ribosomal RNA in a cell. Ribosomal RNA is an integral part of the ribosome which is responsible for making cellular proteins. (Brinkman & Leipe, 2001, Woes and Fox, 1977)

Lizards are reptiles, which mean that they are related to snakes, crocodilians and turtles. Skinks are lizards belonging to family Scincidae. Carlia is a diverse genus of skink found in Australia. Skinks of the present Carlia cluster of species have experienced various degrees of amalgamation and separation during the past two centuries. (Hoskin and Couper, 2012)

The skinks can radially be assign to Carlia gray by the following characteristic features: lower eyelid with a transparent palpebral disc, supranasal scales absent, rostral frontonasal structures as wide as, frontoparietal scales fused, interparietal small and distinct, ear opening with enlarged lobules, dorsal body scales strongly keeled, male with conspicuous breeding colour on flanks.

(Hoskin and Couper, 2012)

These lizards are of major importance as its introduction is thought to have assisted in the establishment of the invasive brown tree snake on Guam by providing a food resource. In addition to the pattern of invasion, we address the mode and timing of translocations and compare the genetic diversity of various introduced populations with populations from native range. (Austin and Rittmeyer, 2011)

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As the phylogenetic analysis of 32 species of the economically important Carlia lizards have never been done earlier as some of them were discovered recently, so the current study was done on Phylogenetic analysis of economically important Carlia lizards by using 16S rRNA sequences. As 41 species of Carlia lizard found in worldwide, by which we found 16S rRNA sequences of 32 species in NCBI. So, for the present study performed with 32 species.

MATERIALS AND METHODS

The literature related to 16S rRNA of Carlia lizards was retrieved with the help of different search engines and 16S rRNA sequences were retrieved from NCBI database. The phylogenetic analysis was done with the help of software MEGA 6. In which the various methods were used for making phylogenetic tree of these species (Fitch and Margoliash, 1967, Harrison and Langdale, 2006). Molecular phylogenetic analysis is the use of macromolecular sequences to reconstruct the evolutionary relationship between organisms.32 species of the Carlia lizards were selected for the present study and these species are, *C.munda, C.storri, C.coensis, C.schmeltzii, C.pectoralis, C.bicarinata, C.rufilatus, C.amax, C.jhonstonei, C.mundivensis, C.scirtetis, C.viax, C.rostralis, C.dogare, C.tetradactyla, C.gracilis, C.rubrigularis, C.jarnoldae, C.rhomboidalis, C.longipes, C.mysi, C.parrhasius, C.luctuosa, C.aenigma, C.eothen, C.decora, C.inconnexa, C.rubigo, C.fusca, C.ailanpalai, C.beccarii, C.pulla*. The phylogenetic analysis was done using the following two methods.

Distance based method: This method is use to amount the dissimilarities between two aligned sequences to derive tree. This method measure's the evolutionary distance between each pair of sequences in multiple alignments. This method includes UPGMA and Neighbor joining methods. (Makarenkov *et al.,* 2006)

UPGMA- Unweighted pair group method using arithmetic average. This method assumes that there is a strict molecular clock and all species evolve at the same time. (Nakhleh *et al.,* 2005)

Neighbor joining- This method does not follow the molecular clock theory, so all the species evolve at the different rate. This method is believed to be one of the best methods for the construction of phylogenetic trees. (Nakhleh *et al.,* 2005)

Character based method - This method includes the Maximum parsimony and Maximum likelihood method. (Nakhleh *et al.,* 2005)

Maximum parsimony- The aim of parsimony methods is to find the phylogenetic tree with minimum total length. It includes the minimum number of substitution for all the tree topology. It eliminates the sequence only when there are the more differences. (Makarenkov *et al*., 2006)

Maximum likelihood- It includes specific substitution for all tree topology and a slight difference is eliminate. This method gives more accurate phylogenetic tree. (Makarenkov *et al.,* 2006)

RESULTS

Based on the literature survey we have selected 32 species of Carlia lizard. The following results were obtained from the phylogenetic tree prepared by distance and character based method.

UPGMA TREE- In the phylogenetic tree obtained from UPGMA method 8 clades were obtained. There are no prominent species in clade no. 1, 2, 3 and 8 showing higher similarity. In clade 4 maximum similarities of 100% was found between *C.gracillis, C.rhomboidalis, C.jarnoldae* and *C.rubrigularis*. In clade 5 maximum similarities of 100% was found between *C.longipes, C.mysi and C.parrhasius.* In *clade* 6 maximum similarities of 99% was found between *C.luctosa, C.aenigma* and *C.eothen.* In clade 7 maximum similarities of 99% was found between *C.decora, C.inconnexa* and *C.rubigo.* (Fig.1)

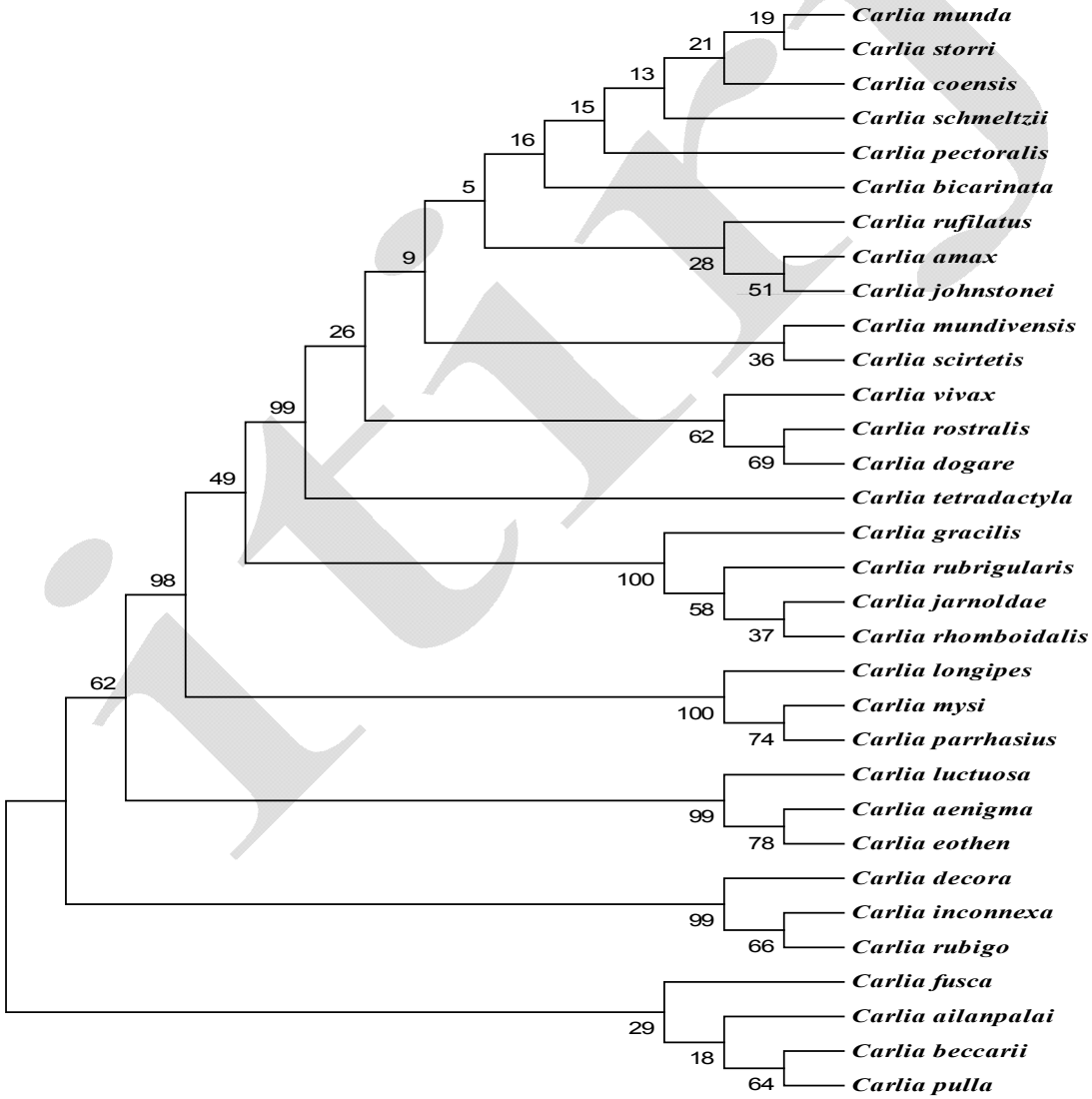
NEIGHBOR JOINING TREE- In the phylogenetic tree obtained from neighbor joining method 7 clades were obtained. There are no prominent species in clade no. 1, 2, 4 and 7 showing higher similarity. In clade 3 maximum similarities of 97% was found between *C.rhomboidalis, C.gracillis, C.jarnoldae* and *C.rubrigularis*. In clade 5 maximum similarities of 99% was found between *C.luctosa, C.aenigma* and *C.eothen.* In clade 6 maximum similarities of 99% was found between *C.decora, C.inconnexa* and *C.rubigo. (*Fig.2)

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MAXIMUM LIKELIHOOD TREE- In the phylogenetic tree obtained from maximum likelihood method 6 clades were obtained. There are no prominent species in clade no. 1, 2 and 6 showing higher similarity. In clade 3 maximum similarities of 97% was in between *C.jarnoldae, C.rubrigularis, C.gracillis* and *C.rhomboidalis.* In clade 4 maximum similarities of 96% was in between *C.luctosa, C.aenigma* and *C.eothen.* In clade 5 maximum similarities of 94% was in between *C.decora, C.inconnexa* and *C.rubigo.* (Fig.3)

MAXIMUM PARCIMONY TREE- In the phylogenetic tree obtained from maximum parsimony method 7 clades was obtained. There are no prominent species in clade no. 1, 2 and 3 showing higher similarity. In clade 4 maximum similarity of 100% was found between *C.gracillis, C.rubrigularis, C.jarnoldae* and *C.rhomboidalis.* In clade 5 maximum similarities of 99% was found between *C.parrhasius, C.longipes* and *C.mysi.* In clade 6 maximum similarities of 100% was found between *C.decora, C.inconnexa* and *C.rubigo.* In clade 7 maximum similarity of 100% was found between, *C.eothen, C.aenigma* and *C.luctosa.* (Fig.4)

Trees prepared by different methods:



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Figure 1. Phylogenetic tree prepared by UPGMA method (Boot strap method)

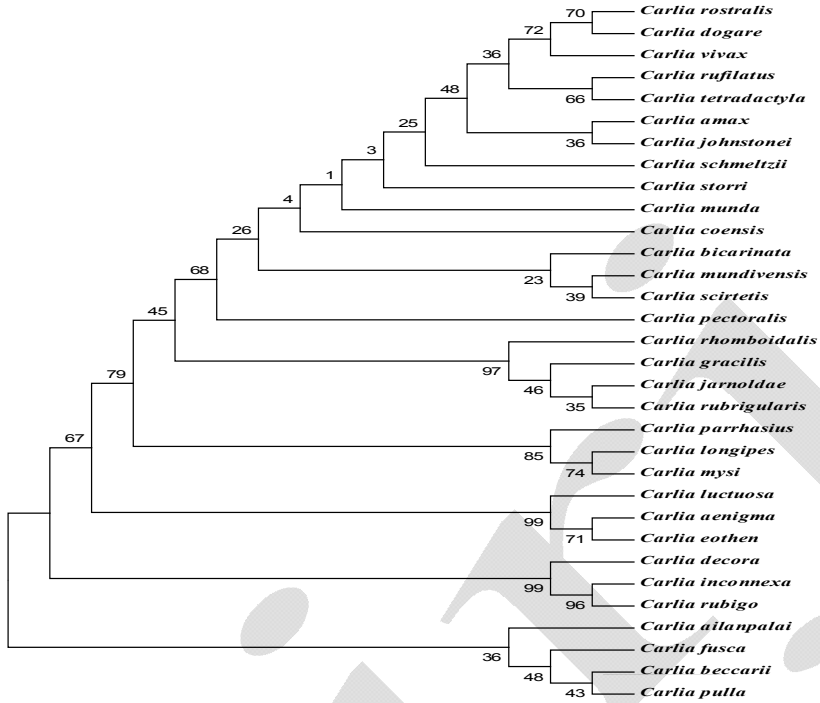


Figure 2. Phylogenetic tree prepared by Neighbor joining method (Boot strap method)

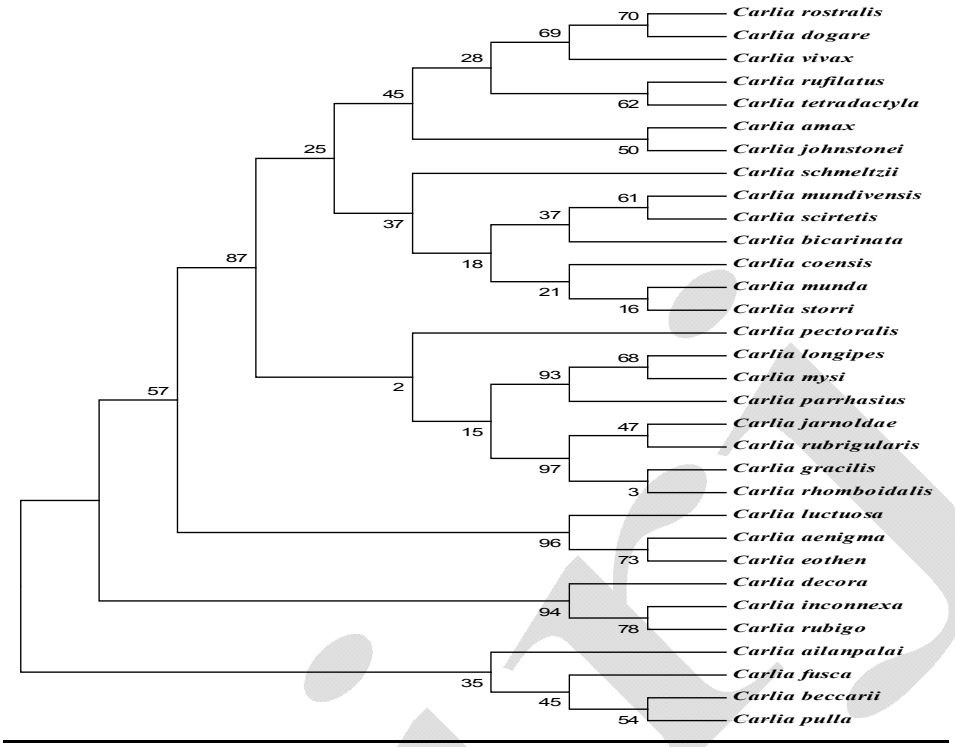


Figure 3. Phylogenetic tree prepared by Maximum likelihood method (Boot strap method)

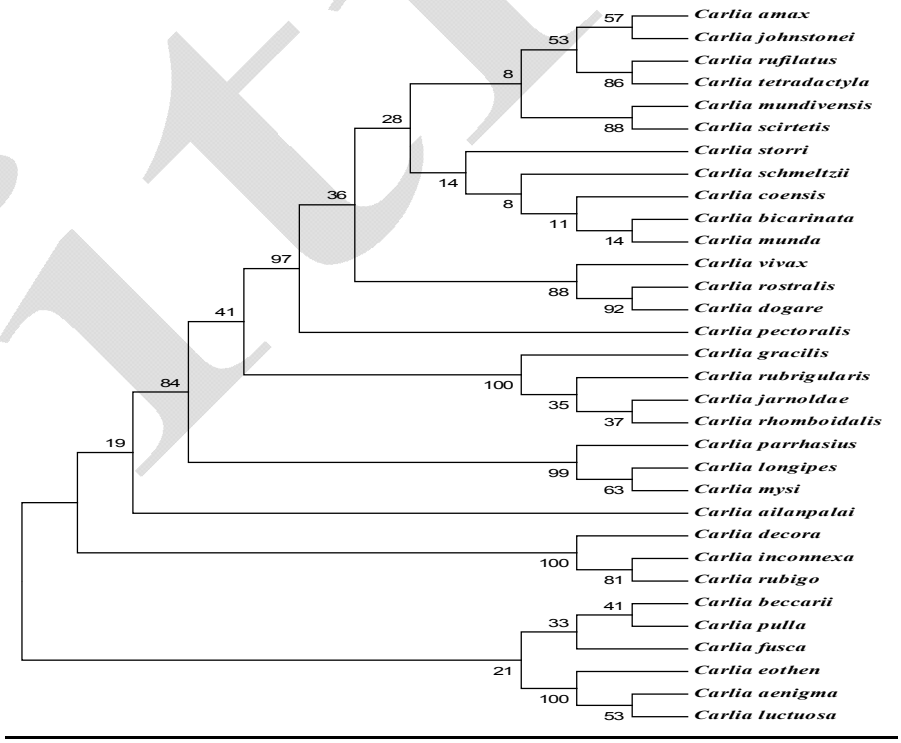


Figure 4. Phylogenetic tree prepared by Maximum parcimony method (Bootstrap method)

Table 1. Comparative Analysis of the Tree Topology Obtained from the UPGMA, Neighbor Joining, Maximum parsimony, Maximum Likelihood Methods

Groups	UPGMA	Neighbour joining	Maximum Parsimony	Maximum Likelihood
Polyphyletic group	8	7	7	6
monophyletic group	0	0	0	0
Root nodes	0	0	0	0
Dichotomy	9	9	10	11
Polytomy	0	0	0	0
Out groups	0	0	0	0
Nodes	30	30	30	30
Branches	62	62	62	62
Terminal nodes	32	32	32	32
Sister group	9	9	10	11

DISCUSSION

In the above results it was observed that *C.parrhasius, C.longipes, C.mysi* show maximum similarity of 100% in UPGMA and of 99% in Maximum parsimony trees. This may be due to all the three species of Carlia also have similarities in their characters like Head and nuchal scales smooth, populations likely are sexually dimorphic in adult coloration and or morphometry, and hence the above results were obtained (Stuart-Fox, 2002). *C.eothen, C.aenigma, C.luctosa* show maximum similarity of 99% in UPGMA, of 100% in Maximum parsimony, of 95% in Maximum likelihood and of 99% in Neighbor joining trees, these species of Carlia show similarities in their characters like Head and nuchal scales smooth, Trunk scales smooth to weakly tricarinate dorsally and laterally, hence the above results were observed (Stuart-Fox, 2002). *C.inconnexa, C.rubigo, C.decora,* show maximum similarity of 99% in UPGMA, of 100% in Maximum parsimony, of 95% in Maximum likelihood and of 99% in neighbor joining tree, these species of Carlia show similarities in their characters like body robust with keeled dorsal scales. Head barely distinct from neck, the similar results we observed in our study (Stuart-Fox, 2002). *C.gracillis, C.rubrigularis*, *C.jarnoldae, C.rhomboidalis* show maximum similarity of 100% in UPGMA, of 97% in Neighbor joining, of 97% in Maximum likelihood and of 100% in Maximum parsimony, these species of Carlia show similarities in their characters like northern and southern *C. rubrigularis* and between these and *C. rhomboidalis*, there is negligible morphological divergence among these lineages other than for throat colour, which is red in *C.rubrigularis* and red and blue in *C. rhomboidalis* (Nakhleh, 2004).

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