Studies on Coleopteran Diversity and Phylogenetic Analysis in Agroecosystem of Koduvayur, Palakkad District, Kerala

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Abstract- Order Coleoptera is the largest and most diverse order of class insects. Beetles constitute the major part of our biodiversity. Coleopteran diversity study was done in Koduvayur gramapanchayat (ward 11) of Palakkad District for a period of 5 months (October 2021 to February 2022) and phylogenetic analysis was performed based on the identified species in the study. During the study period 48 species belong 40 genera of 15 families were identified. Most of the Beetles are observed as terrestrial but some of them are aquatic in habit. The sizes of the observed beetles were ranged between about 3 mm to 6 cm. The highest species diversity obtained in this study belongs to the family scarabaeidae (38%) with 18 species of 14 genera. The second largest species in the study was family Chrysomelidae (21%). The evolutionary relationship between beetles has been analyzed using Clustal X. Based on the phylogenetic analysis, the family Dytiscidae showed lowest root distance (0.086110), hence only few changes had occurred in the genetic makeup with respect extant taxa and it can be the close relative of the common ancestor. Family Hydrophilidae represents recent taxon which shows the highest root distance (0.842630). Highest diversity shown (0.12550)family Scarabaeidae melonidae(0.12570) belongs to same clade with almost same root distance. Scarabaeidae lies intermediate between Dytiscidae and Hydrophilidae with moderate evolution which indicate highly adapted species in this locality.

Index Terms- Ancestor, Beetles, Coleoptera, Phylogenetic analysis

I. INTRODUCTION

Beetles (Coleoptera) are species-rich and evolutionarily successful group of animals that dominate terrestrial and aquatic habitats all over the world. The diversity and evolution of Coleoptera is a growing topic in scientific research. New methods in the study of morphology or the application of

phylogenomics to reconstruct the evolutionary relationships of beetle continually challenge our understanding of beetle diversity and evolution. The order Coleoptera (Beetles) is the most diverse group of organisms on Earth, constituting about 25% of all described animal species (Zhang et al., 2018). As is the case with most vertebrates, greater habitat complexity is generally correlated with greater beetle species richness (Lassau et al., 2005). In India Western Ghats is the one of the hottest Hotspot in the world. The biodiversity study conducted in the Western Ghats revealed rich diversity and abundance in the region (Aland et al., 2012). In Kerala also there are many biodiversity studies in Coleoptera conducted. Many of them are special reference to particular families. At present the biodiversity studies of Beetles in Palakkad is not especially in gramapanchayat. A study of the most diverse group of insects, that is, beetles, not only will help to assess the diversity of this area but also will help to carry out further studies to conserve the biodiversity of this area. The aim of present study is to understand the Beetles (coleptera) diversity in Koduvayur gramapanchayat (ward 11) of Palakkad District and phylogenetic analysis.

II. MATERIALS AND METHODS

Study area: The biodiversity study of beetles was conducted in selected area in Koduvyur Gramapanchayat (Ward XI) of Chittur Taluk, Palakkad District, Kerala. The study was conducted from october 2021 to February 2022 over a period of 5 months. Koduvayur is about 16 km away from the Palakkad town.

Field method: Beetles were collected and identified mainly during 7.30 am to 11.30 am and in the

evening from 16.00 pm to 20.00pm. Beetles were collected using various methods based on the nature of beetles. Areal net, sweep net, beating sheet are the simple devices used for collection. Some of the beetles are not much harmful hence hand picking also adopted. The nocturnal insects are light attracted and they are collected manually as well as using nets. All specimens were initially separated from other material and identified to the family level using the taxonomic keys (Lindroth, 1992;Bousquet, 1990). The specimens were also identified to the lowest taxonomic level possible using Hangay & Zborowski (2010) and Slipinksi & Lawrence (2013).

Data analysis: The important focus of the study is to estimate beetle diversity in the study area. Shannon diversity index were the most important and it was used to calculate the beetle diversity index. The graphical representation (pie-diagram) of families with number of species was done using MS Excel.

Shannon diversity index:

$$H = -\sum_{i=1}^{S} p_i \ln p_i$$

Where, pi = the observed relative abundance of a particular species in Shannon-Wiener index. Higher the value of H, higher the diversity of species in a particular community. Lower the value of H, lower the diversity. A value of H = 0 indicates a community that only has one species.

Phylogenetic analysis: The phylogenetic analysis of identified beetles was analyzed up to family level by Clustal X using retrieved Cytochrome oxidase I (CO I) gene sequence of identified beetles from NCBI. Based on the sequence alignment the phylogenetic tree was visualized using PHYLODRAW.

III. RESULT AND DISCUSSION

DIVERSITY ANALYSIS

A total of 48 species belonging to 40 genera under 15 families (Table.1) were recorded during the present study from Koduvayur gramapanchayat (ward-11). Out of the 15 families recorded during the study period the maximum diversity was recorded from the world's largest family Scarabaeidae (18 species belonging to 13 genera). Second largest species diversity was recorded from in the family Chrysomelidae, about 10 species belong to 8 genera. Six species belong to 5 genera

and 3 species belong to 3 different genera was reported from the family Coccinellidae and Cerambycidae respectively. The family Cantharidae, Carabidae, Dytiscidae, Elateridae, Eucnemidae, Histeridae, Hydrophilidae, Lampyridae, Melonidae, Anobiidae and Tenebrionidae has reported one species each.

Table.1.Beetle diversity in Koduvayur Gramapanchayath

SL NO 1	FAMILY CANTHARIDAE	NAME RHAGONYCHA	NUMBER
	CANTHARIDAE	RHAGONYCHA	1
2		FULVA	38
1	CARABAEIDAE	PHERESOPHUS JESSOENSIS	28
3	CERAMBYCIDAE	BATOCERA RUFOMACULATA	15
		MONOCHAMUS URUSSOVI	17
		MACROTOMA SERRIPES	10
4	CHRYSOMELIDAE	AULACOPHORA FEMORALIS	98
		AULACOPHORA NIGRIPENNIS	87
		AUALCOPHORA FOVEICOLLIS	92
		ASPIDIMORPHA MILIARIS	50
		CASSIDA CIRCUMDATA	63
		CHARIOTELLA SEXPUNCTATA	67
		CHIRIDOPSIS BIPUNCTATA	53
		LILIOCERIS LILII	43
		CHRYSOCHUS COBALTINUS	45
		CALIGRAPHA CALIFORNICA	67
5	COCCINELLIDAE	COCCINELLA SEPTEMPUNCTATA	71
		HARMONIA AXYRIDIS	88
		COCCINELLA TRANSVERALIS	100
		HENOSEPILACHNA ARGUS	94
		CURINUS COERULEUS	66
		BRUMOIDES SUTURALIS	58
6	DYTISCIDAE	GRAPHODERUS LIBERUS	12
7	ELATERIDAE	LANEGANUS SULCICOLLIS	21
8	EUCENMIDAE	EURYOSTUS REICHEI	12
9	HISTERIDAE	OMALODES FOVEOLA	19
10	HYDROPHILIDAE	HYDROPHILUS TRIANGULARIS	5

	T 4 A PRIMIT A F	per o per u	1.5
11	LAMPYRIDAE	PTEROPTYX	47
		TENER	
12	MELONIDAE	MYLABRIS	25
		PUSTULATA	
13	ANOBIIDAE	STEGOBIUM	57
		PANECEUM	
14	SCARABAEIDAE	COPRIS FRICATOR	43
		CYCLOCEPHALA	19
		MELANOCEPHLA	
		HOLOTRICHIA	52
		DIOMPHALIA	
		HOLOTRICHIA	31
		CONSANGUINEA	
		HETERONYCHUS	29
		ARATOR	
		ONTHERUS	25
		SULCATOR	_
		ORYCTES	37
		RHYNOCEROUS	37
-		CYCLOCEPHALA	21
		LURIDA	41
		PARASTASIA	16
		MONTROUZIERI	10
		EUETHEOLA	24
		HUMIIS	
		DIPLOTAXIS	31
		LIBERTA	
		PHILLOPHAGA	12
		LATIFORNS	
		APOGONIA	14
		EXPEDITIONIS	
		HELIOCORPRIS	27
		BICEPHALUS	
		ORYCTES	23
	-	NASIORNIS	21
		CATHASSIUS MOLOSSUS	31
		PHYLLOPHAGA	35
		TARSALIS	33
		PHYLLOPHAGA	39
		NEBULOSA	-/
15	TENEBRIONIDAE	TRBOLIUMIUM	68
		CASTANIUM	
	1	1	1

DATA ANALYSIS

Based on the diversity study conducted in Koduvayur gramapanchayat Shannon diversity index was calculated and it was about 3.67. The richness of the beetles under study was 48. The diversity index indicate the maximum diversity of beetles because the index value is not closer to zero. The highest number of species is recorded from the family Scarabaeidae, it contributes 38% of the total beetle population in the study area. The second largest family identified is Chrysomelidae(21%) and the third one is coccinellidae(13%). Family Cerambycidae includes longicorn beetles which contribute 6% of the total beetle population. The remaining families contribute 2% each(Fig.1.).

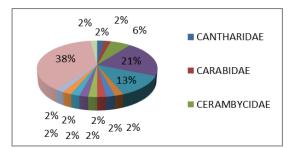


Fig. 1 Diversity of Families of Order Coleoptera in Koduvayur gramapanchayat

PHYLOGENETIC ANALYSIS

Phylogenetic analysis was done to check the evolutionary relationship between the beetles identified from the study area(Fig.2.). The nucleotide sequences were downloaded from the NCBI site. Each species selected from the family and the multiple sequence analysis was conducted using clustal x. Phylodraw is the visualizing tool used to construct phylogenetic tree. The tree represents all the coleopteran families are originated from a single common ancestor. It results the monophyletic origin of coleopteran families. During the course of evolution the node differentiate into two taxa which represents the lineages of the extant taxa. It results in the formation of polyphyletic origin of the current families with respect to the internodes. Among the families Dytiscidae shows lowest root distance (0.086110) (only few changes are occurred in the genetic makeup with respect extant taxa) and it would be the close relative of the common ancestor. Family Hydrophilidae represents recent taxa which shows the highest root distance (0.842630).

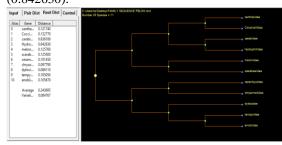


Fig.2.Phylogenetic Analysis in Phylodraw

Scarabeidae is the largest family of coeoptera in the world. The most diverse family of coleoptera reported in this study was Scarabaeidae with 19 species belonging to 13 genera were observed and identified. The similar results are obtained in the preliminary study conducted at Sawanga-Vithoba Lake region in Amaravati district (Varsha *et al.*, 2014). Five species of scarab beetle was reported in the study conducted in the Nagaland (Ghosh et al 2020). The presence of other families like

Chrysomelidae (21%), Coccinellidae (12%),Cerambycidae (7%), Tenebrionidae, Cantharidae, Carabaeidae and Hydrophilidae (4%), and the remaining families (2%) enriches the biodiversity. The phylogenetic analysis conducted during this study reveals that all beetle species are originated from a single common ancestor. This kind of monophyletic origin retains the ancestral features in the new taxa through conserved regions. For example the presence of elytra is the highlighting feature of all the Beetles. It is an ancestral character which is present in all the members of this order with very few exceptions. Elytra is the hard and modified form of the forewings. The hind wings are usually used for flight. But there are lots of intermediate species are formed, which are the ancestors of the end taxa either with monophyletic, polyphyletic or paraphyletic in origin. A molecular phylogenetic analysis of the scarabaeidae (dung beetles) conducted by Monaghan et al., (2007) most of the beetles are evolved from monophyletic origin and some of the members shows the paraphyletic origin. In this study more or less similar result was obtained. Another study was conducted by Martijin et al., (2012) proved that mitochondrial gene in order coleopteran has been conserved for long period of time, and this study supports Elateriformia providing independent support for this lineage and for a single origin of aquatic habits. Phylogenetic studies conducted in the various parts of the world suggest that many of the Beetles are very close to their ancestor, but the modification in the mouth feeding habit, environmental factors ,reproductive strategies all these makes diverse organisms from the ancestor. This will contribute to the richness of the environment.

IV. CONCLUSION

The diversity study conducted during the 5 months of period from October 2021 to may 2022 in Koduvayur gramapanchayat is an attempt to analyse the aspect of biodiversity of beetles. The results highlight that family scarabaeidae contribute 38% of the total beetles identified from the study area. The second and the third position belongs to family chrysomelidae (21%) and Coccinellidae (13%) respectively. A total of 48 species belong to 40 genera of 15 families were identified. The phylogenetic tree constructed at the family level shows that the families are originated from a common ancestor. Among the families Dytiscidae shows lowest root distance (0.086110) and family

Hydrophilidae represents recent taxa which shows the highest root distance (0.842630). The important factor to note that biodiversity studies and a surveys are helpful to check the diversity quantitatively and qualitatively.

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