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Abundance and Phylogeny of lepidopteran species in and around Karamadai area Coimbatore district Tamil Nadu South India

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Abstract

Lepidoptera are a diverse and charismatic group of insects that have received significant taxonomic and systematic attention. Lepidoptera are members of natural shrub-grassland communities. The documented butterflies were belonging to the family Papilionidae, Nymphalidae, Lycaenidae, Hesperidae during the study period May 2018 to April 2019 by using transect counting method in Karamadai area. Totally 2,280 individuals belonging to 43 species of butterflies were documented in three different study area namely Human altered area, Agriculture area and scrub jungle area and the diversity of species were calculated by using Shannon–Weiner index. A comprehensive phylogeny is constructed to examine the origins and species diversity for Papilionidae, Nymphalidae, Lycaenidae, Hesperidae, since the phylogeny is the proposition, universally accepted in the scientific community, that plants or animals of different species descended from common ancestors. The habitat place major role for the abundance of the lepidopteron diversity.

Keywords: Abundance, lepidoptera, phylogeny, Karamadai, Shannon-weiner index

Introduction

Butterflies are a large group of insects, belonging to the order “Lepidoptera”. This refers to the characteristic feature that distinguishes them from most other insects. The butterfly diversity is high in the tropics compared to temperate regions of the world ^[1]. Although only a quarter of India’s butterfly diversity is represented in the Western Ghats, it has the characteristic of high alpha diversity of butterflies in certain locations ^[2]. 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 it is represented by phylogenetic trees which graphically explain the evolutionary history related to the species of interest. The COI appears to process a great range of phylogenetic signals, showing fast rate of nucleotide substitution that not only enable the discrimination of cryptic species, but also can reveal phylogeographic structure within a species ^[3]. Keeping this in view present study was conducted.

Materials and Methods

The study area is located in the Coimbatore district, the state of Tamilnadu, India. The study was conducted from May 2018 to April 2019 in Karamadai area and the area is situated approximately between 11.27 ° N and 76.97 ° E. It also rises to a height of 353 meters or 1158 feet above the mean sea level. Encompassing with 203 villages. The survey was made in all the villages by transect method in different plots like human altered area, Agriculture area and scrub jungle area.

The COI nucleotide sequences of each species were retrieved from National Center for biotechnology information. Multiple sequences of the retrieved sequences from were performed using CLUSTALW with default parameters in MEGA 5.0 ^[4]. By using CLUSTALW program distance matrix by pair wise sequence divergence was calculated and for constructing the combined phylogenetic tree for lepidoteran species. The multiple sequence output from CLUSTALW was saved and executed in MEGA5.0 to generate Neighbor-joining tree using bootstrapping analysis.

Results and Discussion

The survey was done and totally 2,280 Lepidoptera species were surveyed. The total individuals were belonging to 43 species of butterflies were documented in three different study area namely Human altered area, Agriculture area and scrub jungle area. The species were belonging to the family Papilionidae, Nymphalidae, Lycaenidae, Hesperidae during the study period (Fig. 1). The phylogenetic results provides a high support for Nymphalidae and the relationships among other three families in order Lepidoptera (Fig. 2) and the

(table 1) shows the retrieved sequence of butterflies. Agricultural sites had significantly more butterflies than non-agricultural sites [5]. But in case of this study the species abundance shows very high scrub forest, following that the species abundance is more in agriculture area and the human altered area shows low abundance. Butterflies have traditionally been viewed as an excellent group of bioindicators, mainly due to complexity of ecological management required by many species [6, 7].

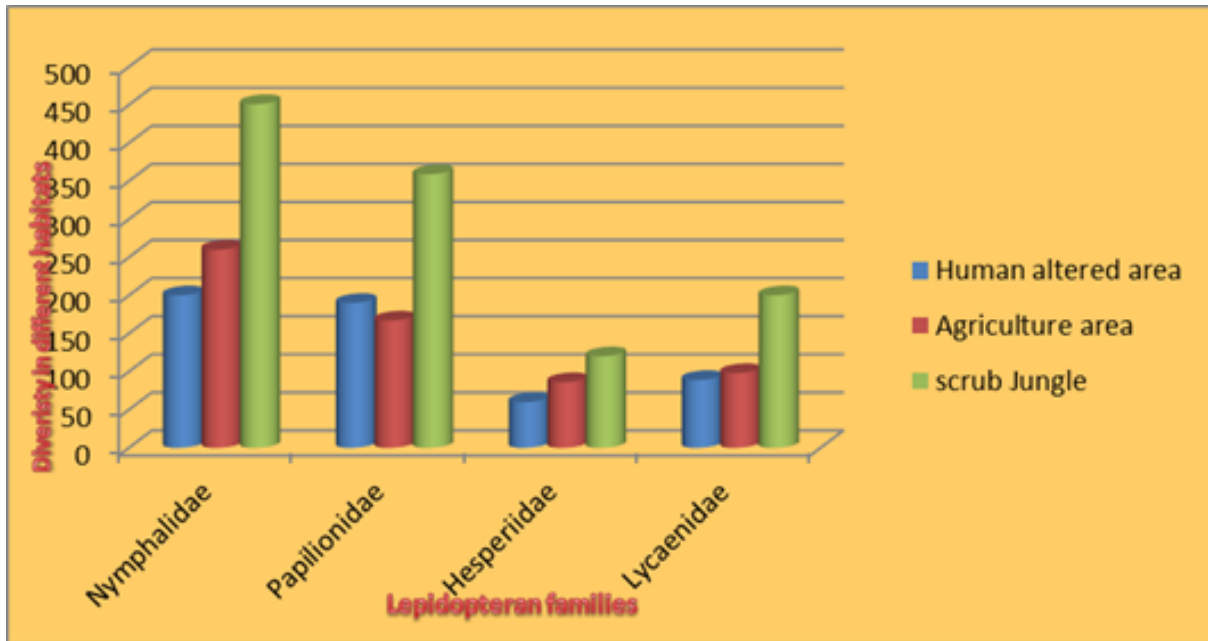


Fig 1: Shows the Abundance of Lepidopteran

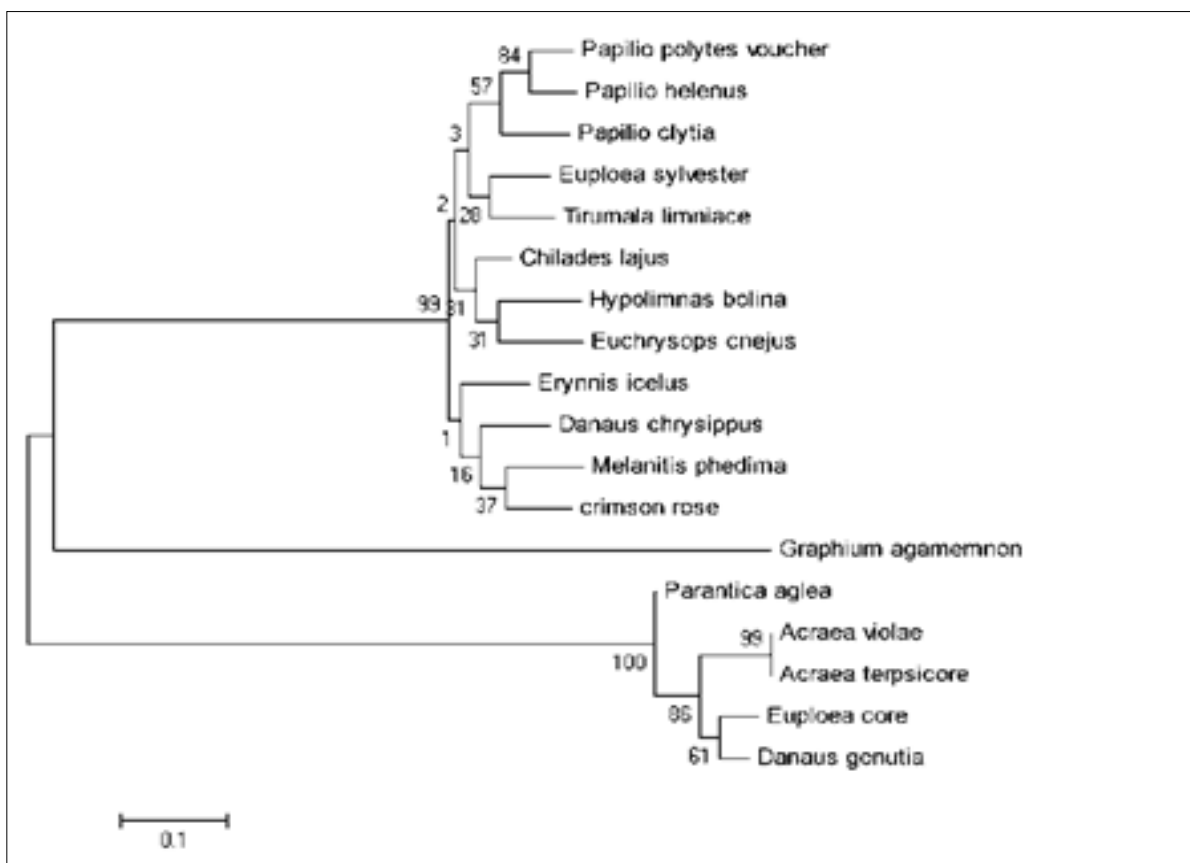


Fig 2: Shows the Cladogram of Lepidoptera species

Table 1: Retrieved sequence of Butterflies

S. No	Family	Species Name	Gene	Genbank Accession No	Sequence length (bp)
1	Nymphalidae	<i>Euploea Sylvester</i>	COI	KC306721.1	600
2	Nymphalidae	<i>Acraea violae</i>	COI	JX226067.1	610
3	Nymphalidae	<i>Euploea core</i>	COI	KC306729.1	470
4	Nymphalidae	<i>Danaus genutia</i>	COI	KC306724.1	429
5	Nymphalidae	<i>Danaus chrysippus</i>	COI	AF394193.2	676
6	Nymphalidae	<i>Parantica aglea</i>	COI	KC306718.1	645
7	Nymphalidae	<i>Tirumala limniace</i>	COI	KC306727.1	616
8	Nymphalidae	<i>Melanitis phedima</i>	COI	HQ962147.1	658
9	Nymphalidae	<i>Acraea terpsicore</i>	COI	JQ614099.1	658
10	Nymphalidae	<i>Hypolimnas bolina</i>	COI	GU091500.1	627
11	Hesperiidae	<i>Erynnis icelus</i>	COI	GU088761.1	579
12	Papilionidae	<i>Graphium agamemnon</i>	COI	AB377325.1	707
13	Papilionidae	<i>Papilio polytes</i>	COI	HQ962338.1	658
14	Papilionidae	<i>crimson rose (Atrophaneura hector)</i>	COI	JX261944.1	631
15	Papilionidae	<i>Papilio helenus</i>	COI	EU792497.1	688
16	Papilionidae	<i>Papilio clytia</i>	COI	HM246468.1	661
17	Lycaenidae	<i>Chilades lajus</i>	COI	GQ128946.1	2238
18	Lycaenidae	<i>Euchrysops cnejus</i>	COI	GQ129020.1	2238

The phylogenetic tree shows that the origin of the cladogram was from *Papilio polytes* and *Papilio helenus*, and the both species were present in same clades. The total divergence of the species from *Papilio polytes* and *Papilio helenus* extended up to *Graphium agamemnon*. The origin of the another branch was *Parantica aglea* and extended upto *Euploea core* and *Danus genutia*. This phylogenetic tree reveals the evolutionary relationship between the families of Nymphalidae, Hesperiidae, Papilionidae and Lycaenidae.

Conclusion

The purpose of present investigation is to understand the butterfly diversity and to number of individual's diversity and species richness in Karamadai area in Coimbatore district and the CO1 is a conserved gene and therefore they can be used for the butterfly species. If a particular gene is not altered by the environmental influences, it is then proved to be an ideal gene for tracing the evolutionary studies and species identification which was determined from phylogenetic analysis. We have to take necessary action to conserve the species in karamadai region especially for Lepidoptera.

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