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Study to Find the Phytogenic Relationship of Spiders from Ten Mixed Agroecosystems of Palakkad

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Abstract: ***Phylogenetic relatedness is a key diversity measure for the analysis and understanding of how species and communities evolve across time and space. A species level phylogenetic tree for spiders were constructed using retrieved COI sequences of 66 species of spiders belongs to 17 family identified from 10 agroecosystems of Palakkad. Phylogram of Araneidae family with 23 specieshave 4 clusters and 6 monophyletic taxa. In theNJ plot of Araneidae family (0.05), Phonognatha graeffei with divergence of 0.174 was found as an out-group species. Argiope keyserlingi was found as internal ancestor (0.075). Phylogenetic tree with 20 species of salticidae family carries 5 cluster with 8 monophyletic taxa. NJ plot of salticidae family at the rate 0.1, Phintella vittate (0.482) showed maximum divergence from the ancestor and seen as outgroup and Menemerus bivittatus (0.131) function as internal ancestor. Phylogram with 66 species of 17 family with available COI sequence showed 4clusters, the first cluster represents orb web spiders. Second cluster formed of species from Araneidae, Salticidae, Theraphosidae, Pholcidae, Oxyopidae, Desidae, Corinnidae family. Third cluster formed of Salticidae family and fourth cluster supports Thomisidae, Lycosidae, Cheiracanthiidae, Sparassidaefamily. NJ plot constructed with 66 species at 0.1 divergence rate in which Menemerus bivittatus (0.138) of Salticidae family was found as outgroup. Nephila pilipes (0.031) ofAraneidae family was found as internal ancestor from which all the spider species evolved. Evolutionary connection between species have no significance from which agroecosystemthe spiders were identified in this study.***

Keywords: Phylogenetic tree, NJ plot, COI sequence, agroecosystem, spider diversity

1. Introduction

Spiders (Order: Araneae) are abundant, generalist predators that play dominant roles in almost every terrestrial ecosystem with more than 51, 461 described species world wide with 4, 239 genera from 130 families [1]. Spiders constitute the seventh largest order in the animal kingdom due to their high diversity and wide predatory preferences [2]. Their abundance and prey regulation in agricultural and natural terrestrial ecosystems helps to consider as model group to assess patterns of ecosystem services [3]-[4]. The voracious feeding habits of spiders make them efficient pest control agents and also serve as key elements in predator prey interactions [4]-[5]. The evolutionary diversification of spiders is attributed to spectacular innovations in silk. A broad higher-level phylogeny of spiders combining molecular data with traditional morphological and behavioural characters to prove the phylogeny to test hypothesis that the spider orb web evolved only once [6]. Scharff et al [7] made a study to describe the phylogeny of the spider family Araneidae based on five genes (28S, 18S, COI, H3 and 16S). Maddison et al [8] reported a new genus *Kelawakaju* Maddison & Ruiz, gen. nov., lineage of bark-dwelling Asian marpissine jumping spiders that represent a dispersal to Eurasia separate from that of the MarpissaMendoza lineage, using four gene regions 28S, Actin 5C, 16SND1, COI. *Atypus karschi* an introduced purse web spider in south eastern Pennsylvania was identified using molecular markers (CO1 sequences) and compared to available data for other atypids and found identical to *A. snetsingeri* native to East Asia [9]. Garrison*et al* [10] studied spider evolutionary relationships using transcriptome-based data set comprising 70 ingroup spider taxa using maximum likelihood and shortcut coalescence-based approaches. Spiders are among the most diverse terrestrial predators but their phylogenetic relationships and diversification dynamics remain poorly understood [11]. Tyagi et al [12] used DNA barcoding for the identification of spiders from India with 101 morphospecies of 72 genera under 21 families, including five endemic species and holotypes of three species. Salticidae evolution was attempted using molecular phylogenetics of gene sequences [13]-[14]-[15]-[16]-[17]. The orb-weaving spiders (Orbiculariae) their taxon sampling, comparative morphology by using new molecular markers orb-weaver evolution was attempted [18]. Li*et al* [19] have done mitochondrial phylogenomics analysis of spiders to date, highlights the usefulness of mitogenomic data not only for providing efficient phylogenetic signals for spider phylogeny, but also for characterizing trait diversification in spider evolution. Jayasree *et al* [20] taxonomically identified 98 species of spiders belonging to 71 genera under 17 families from 10 mixed agroecosystem of Palakkad. This study aims to find out the phytogenic relationship of spiders belonging to 10 agroecosystems of Palakkad Pathiripala, Pattambi, Olavakode Railway colony, Kalipara, Mathur, Puliyaparamb, Nallepilly, Mankara, Ezhakkad and Sreekrishnapuram using COI sequenceavailable from Genbank database.

2. Materials and Method

COI Spider sequences from 10 agroecosystems (Pathiripala, Pattambi, Olavakode Railway colony, Kalipara, Mathur, Puliyaparamb, Nallepilly, Mankara, Ezhakkad and Sreekrishnapuram) available in the database were retrieved. From Araneidae 23 species, salticidae 20 speciesand 23species belonging to 15 other family of Spider lineages were retrieved from previously published transcriptomic and

genomic resources of existing sequence data from NCBI database (https://www. ncbi. nlm. nih. gov/genbank)GenBank collections. Using retrieved COI sequence belonging to 17 family of spiders, multiple sequence alignment was done using clustal X version 2.0 [21] programme. To find the evolutionary relationships between spider among the 10 agroecosystems under study phylogenetic tree was constructed using PhyloDraw and NJ plot [22]. Comparison was done between 17 families identified from the 10 agroecosystems and evolutionary relationship within Araneidae and Salticidae spiders were done separately.

3. Results

3.1 Araneidae family Phylogram

Araneidae family of spider species from selected 10 agroecosystems of Palakkad District with available COI sequence was included in the study (**Table I**). 12 species of spiders reported from Ezhakkad agroecosystem. Phylodraw based analysis of evolutionary relatedness among spider species were conducted by computing phylograms, to unravel their level of phylogenetic closeness and degree of divergence. The result mentions the existence of innumerable counts of sister taxa among clades and independently upon analysis their pair-wise distance, is elucidated in (**Figure1**), phylograms depict the extend of divergence of individual clade, from their rooted ancestral node. The clade with greatest root distance exhibited greater divergence from the nodal ancestor (Figure2), on comparison with its sister taxa. Furthermore, the mono/poly/paraphyletic relatedness among clades is also clearly evident from the tree.

Phylogram (**Figure1**) shows the relationships and amount of evolution by the branching order and branching length respectively of Araneidae family. Phylogram have 2 main external nodes and the first external node leads 2 internal nodes in that the first internal node carries, a monophyletic taxa with *Argiope pulchella* from (Ezhakkad, Mankara, Sreekrishnapuram)and *Argiope hoiseni (*Olavakode railway colony, Patambi) and 5 species considered as paraphyletic, *Argiope keyserlingi (*Ezhakkad, Pathiripala, Nallepilli), *Argiopeanasuja (*Olavakode railway colony, Patambi), *Argiopeaemula* (Olavakode railway colony, Patambi), *Anepsion depressum* (Ezhakkad, Pathiripala) and *Araneusdiadematus (*Ezhakkad, Patambi). The second Internal node have monophyletic group of *Eviovixia excelsa (*Ezhakkad) *and Phonognatha graeffei (*Ezhakkad, Kalipara, Puliyaparamb), *Bijoaranus mitificus* from Sreekrishnapuram asparaphyletic species and *Araneus ventricosus*found as polyphyletic group from (Mankara, Pathiripala, Nallepilli, Puliyaparamb, Sreekrishnapuram). The second external node leads 2 internal nodes that carries a monophyletic taxon between *Hypsosinga rubens* (Kalipara) and *Hypsosinga pygmaea* (Nallepilli, Patambi) and *Eriovixia laglaizei* as paraphyletic taxon. The last internal node from the second external node has *cyrotophora cicatrosa* from (Ezhakkad) as polyphyletic group. The other inner node carries 2 inner nodes again with a monophyletic taxon between *Neoscona nautica* (Mankara, Puliyaparamb) *and Neoscona adianta (*Ezhakkad, Pathiripala, Nallepilli); *Neoscona crucifera (*Ezhakkad, Pathiripala, Nallepilli) as paraphyletic. The sister taxa from the other inner node have *Cyrtarachne nagasakiensis (*Ezhakkad) *and Parawixia kochi (*Mathur)and *Herennia multipuncta (*Ezhakkad), *Trichonephila inaurata (*Mankara) as monophyletic taxon and *Nephila pilipes (*Ezhakkad, Kalipara, Pathiripala, Nallepilli, Sreekrishnapuram)as paraphyletic. Monophyletic taxon found in Figure1 does not have any significance from which agroecosystem they were collected in study (**TableI**). The NJ plot was done (Figure2) with considering evolutionary divergence at 0.05 rate for spider species of Araneidae family from 10 agroecosystems. *Phonognatha graeffei with* a divergence of0.174 *was* found as an out-group species and Argiope *hoiseni (*0.193), *as* per NJ plot. *Hypsosinga pygmaea (*0.062) *and Hypsosinga rubens (0.071)* was found as monophyletic taxon as per phylodraw and NJ plot.

Table 1: Systematic list of spiders belonging Araneidae family from selected 10 agroecosystems of Palakkad District (COI Sequence available)

No	Species Name	Location
1	*Argiope pulchella*	Ezhakkad, Mankara, Sreekrishnapuram
2	*Argiope anasuja*	Railway colony, Patambi, Sreekrishnapuram
3	*Bijoaraneus mitificus*	Sreekrishnapuram
4	*Eriovixia laglaizei*	Ezhakkad
5	*Araneus diadematus*	EzhakkadPatambi, Sreekrishnapuram
6	*Nephila pilipes*	Ezhakkad, Kalipara, Pathiripala, Nallepilli, Sreekrishnapuram
7	*Anepsion depressum*	Ezhakkad, Pathiripala
8	*Argiope keyserlingi*	Ezhakkad, Pathiripala, Nallepilli
9	*Herennia multipuncta*	Ezhakkad
10	*Cyrtophora cicatrosa*	Ezhakkad
11	*Eriovixia excelsa*	Ezhakkad
12	*Neoscona crucifera*	Ezhakkad, Pathiripala, Nallepilli
13	*Phonognatha graeffei*	Ezhakkad, Kalipara, Puliyaparamb
14	*Neoscona nautica*	Mankara, Puliyaparamb
15	*Araneus ventricosus*	Mankara, Pathiripala, Nallepilli, Puliyaparamb, Sreekrishnapuram
16	*Hypsosinga rubens*	Kalipara
17	*Hypsosinga pygmaea*	Nallepilli, Patambi
18	*Argiope aemula*	Olavakode railway colony, Patambi
19	*Trichonephila inaurata*	Mankara

20	*Neoscona adianta*	Ezhakkad, Pathiripala, Nallepilli
21	*Argiope hoiseni*	Olavakode railway colony, Patambi
22	*Cyrtarachne nagasakiensis*	Ezhakkad
23	*Parawixia kochi*	Mathur

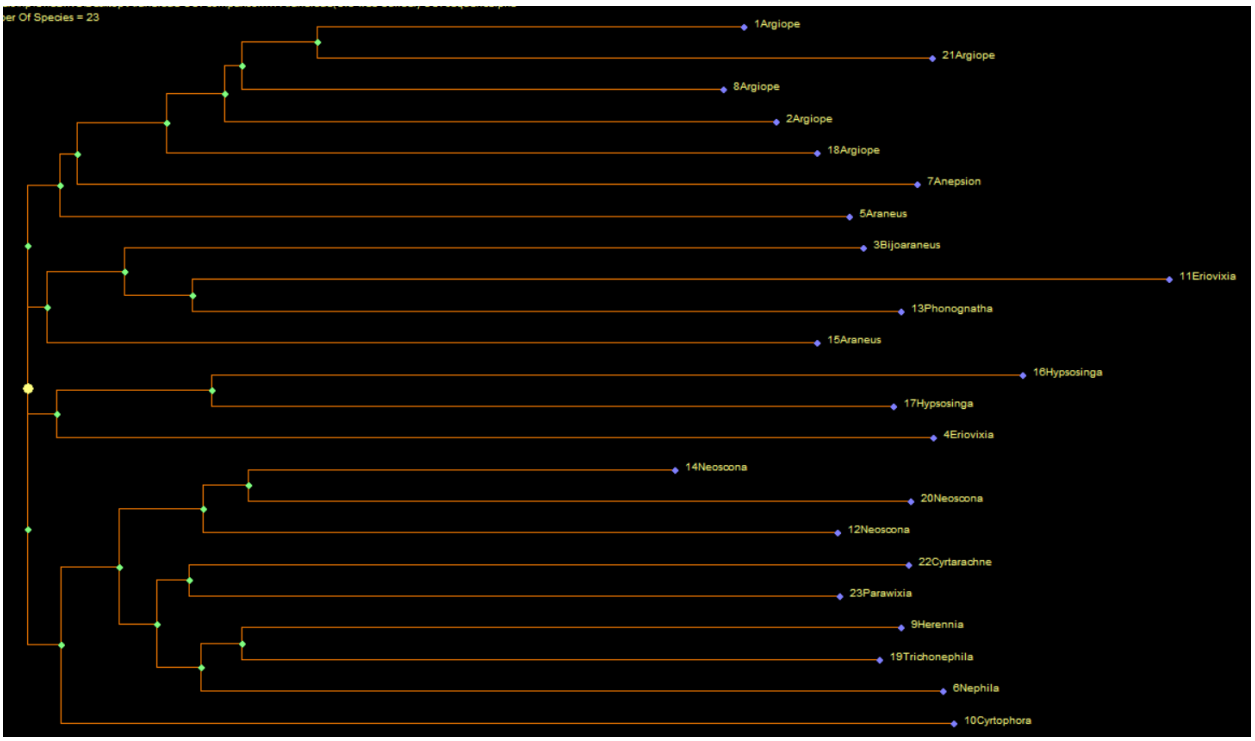

Figure 1: Phylogram of Araneidae family from 10 agroecosystems of Palakkad

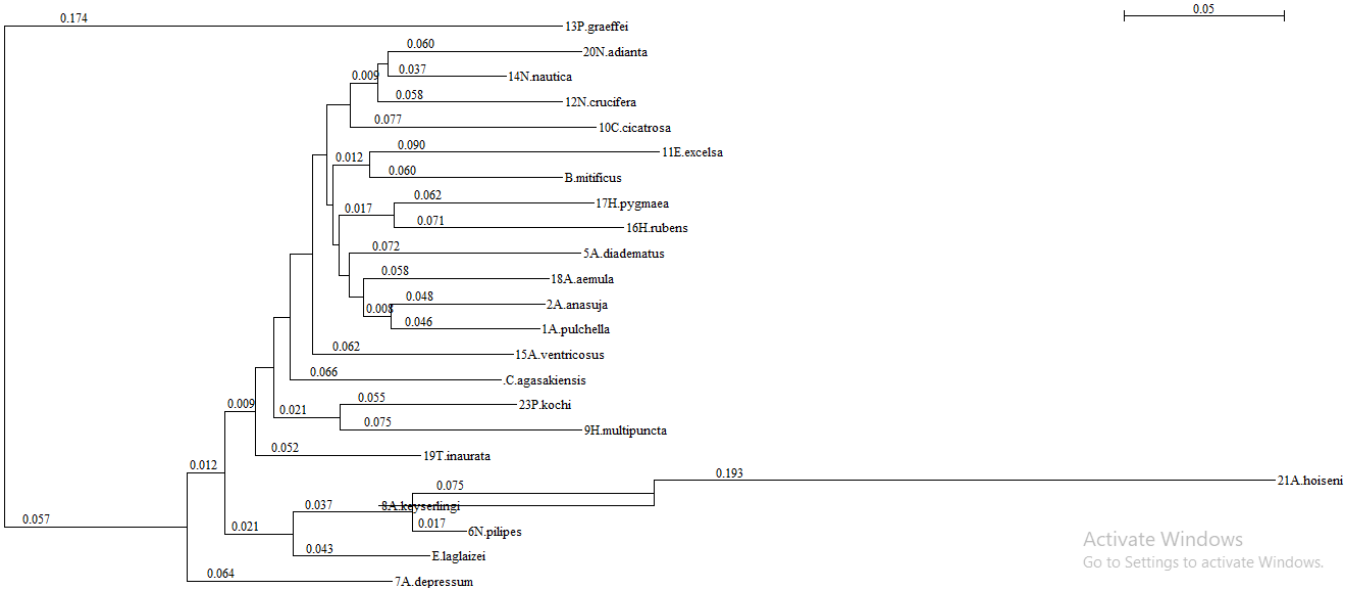

Figure 2: NJ plot prediction of Araneidae family phylogenetic connection among 10 agroecosystems of Palakkad.

3.2 Salticidae family Phylogram

Salticidae family of spider species from selected 10 agroecosystems of Palakkad District with available COI sequence were included in the study (**Table. II**). In the Phylogram of Salticidae family (**Figure2**) 3 external nodes was prominent and the first external node leads 2 internal nodes. The first internal node have two monophyletic taxa, between *Myrmaplata plataleoides (*Ezhakkad)and *Phlegra fasciata* (Kalipara, Pathiripala, Nallepilli); *Cosmophasis umbratical* (Kalipara) *and Menemerus bivittatus* (Ezhakkad, Olavakode railway colony, Sreekrishnapuram), paraphyletic taxa of *Myrmaplata plataleoides (*Sreekrishnapuram) and *Phintella vittata* (Ezhakkad) and one polyphyletic taxa *Hasarius adansoni* from (Nallepilli, Olavakode railway colony, Sreekrishnapuram). Second internal node forms another monophyletic taxa between *Telamonia dimidiate (*Ezhakkad, Sreekrishnapuram) and *Carrhotus viduus* (Olavakode railway colony).

The second external node has two internal nodes and the first internal node bifurcate into two inner nodes again with

monophyletic taxa between *Hyllus semicupreus* (Ezhakkad, Puliyaparamb) and *Chrysilla volupe* (Sreekrishnapuram); *Menemerus semilimbatu (*Olavakode railway colony*)* and *Stenaelurillus lesserti* (Ezhakkad); *Phintella vittata* (Ezhakkad, Sreekrishnapuram)and *Epocilla aurantiaca (*Ezhakkad). *Hentzia mitrata (*Mankara) and *Phidippus sp*. (Ezhkkad) function as monophyletic group from which paraphyletic taxon of *Rhene flavigera* (Sreekrishnapuram) was found. The 3rd external node from which a monophyletic taxon of *Plexippus paykulli* (*Sreekrishnapuram*, Ezhakkad, Mankara, Pathiripala, Nallepilli, Olavakode railway colony, Patambi)and *Plexippus sp. (Sreekrishnapuram*, Ezhakkad, Mankara, Pathiripala, Nallepilli, Olavakode railway colony, Patambi) was found. Here also place of collection was not significant. NJ plot of salticidae family (Figure 4) shows the divergence between species at the rate 0.1. *Phintella vittate (*0.482) from Ezhakkad *and Sreekrishnapuram* showed maximum divergence from the ancestor and seen as out group. *Menemerus bivittatus (*Ezhakkad, Olavakode railway colony, Sreekrishnapuram) was found as internal ancestor with 0.131 divergence from which other species have evolved. The other species which shows divergence are *Cosmophasis umbratical (0.145), Phlegra fasciata* (0.120), *Myrmaplata plataleoides (*0.118), *Menemerus bivittatus* (0.131).

Table II: Systematic list of spiders belonging Salticidae family from selected 10 agroecosystems of Palakkad District (COI Sequence available)

No	Species Name	Location
1	*Hyllus semicupreus*	Ezhakkad, Puliyaparamb
2	*Rhene flavigera*	Sreekrishnapuram
3	*Plexippus paykulli*	Sreekrishnapuram, Ezhakkad, Mankara, PathiripalaNallepilli, Olavakode railway colony, Patambi
4	*Telamonia dimidiata*	Ezhakkad, Sreekrishnapuram
5	*Phintella vittata*	Ezhakkad, Sreekrishnapuram
6	*Myrmaplata plataleoides*	Sreekrishnapuram
7	*Asemonea sichuanensis*	Ezhakkad
8	*Plexippus sp.*	Sreekrishnapuram, Ezhakkad, Mankara, Pathiripala, Nallepilli, Olavakode railway colony Patambi
9	*Phintella vittata*	Ezhakkad
10	*Chrysilla volupe*	Sreekrishnapuram
11	*Menemerus bivittatus*	Ezhakkad, Railway colony, Sreekrishnapuram
12	*Epocilla aurantiaca*	Ezhakkad
13	*Stenaelurillus lesserti*	Ezhakkad
14	*Phidippus sp.*	Ezhakkad
15	*Hentzia mitrata*	Mankara
16	*Cosmophasis umbratica*	Kalipara
17	*Phlegra fasciata*	Kalipara, Pathiripala, Nallepilli
18	*Hasarius adansoni*	Nallepilli, Railway colony, Sreekrishnapuram
19	*Menemerus semilimbatus*	Railway colony
20	*Carrhotus viduus*	Railway colony

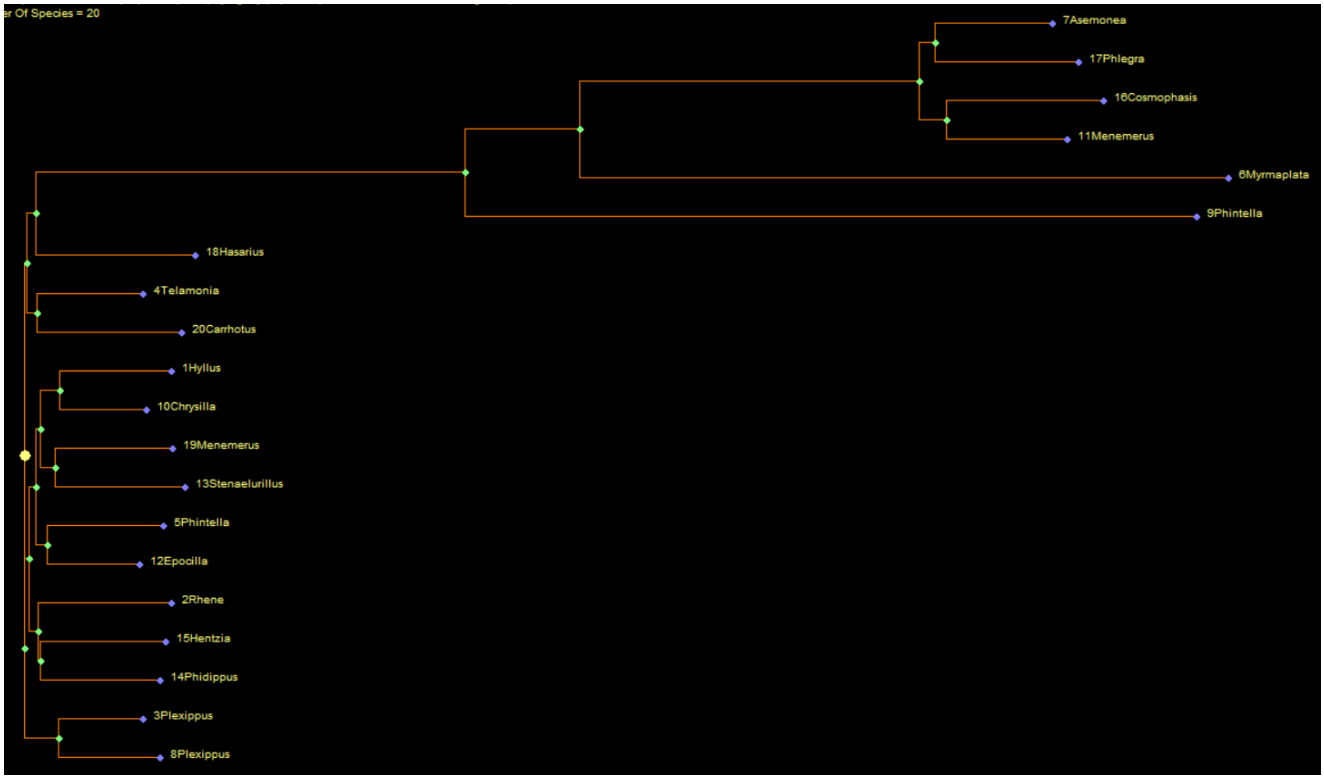

Figure 3: Phylogram of Salticidaefamily of spiders from10 agroecosystems of Palakkad

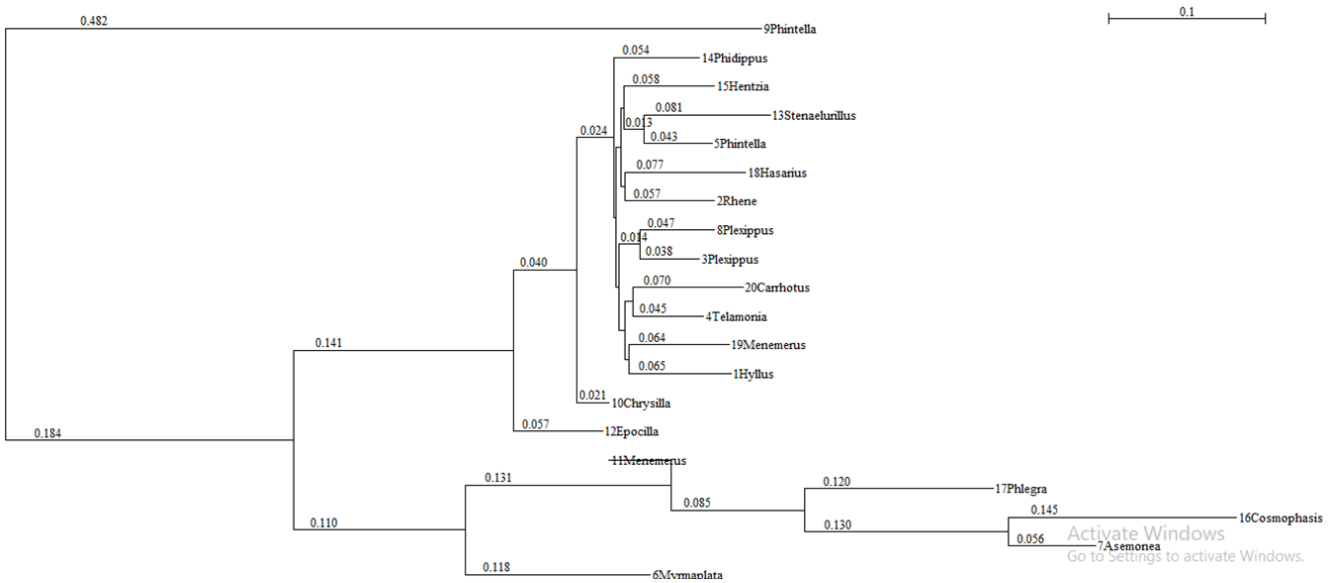

Figure 4: NJ plot of Salticidae family of spiders from 10 agroecosystems of Palakkad.

3.3 Phylogram all species from ten agroecosystems of Palakkad

Comparison between 66 species of spiders from 10 agroecosystems belonging to 17 family with available COI sequence were tabulated (**TableIII**). The phylogram (**Figure5**) represents spider evolution among 66 species belongs to 17 family of spiders, have 4 external nodes and each carries 2 internal nodes each. The first internal node represents a cluster of orb web spiders (Araneidae and Tetragnathidae). The first internal node carries three nodes (sister taxa) again of which the first node represents monophyletic taxa between Argiope *pulchella* and *Argiope hoiseni*, *Argiope aemula*, *Argiope anasuja*, *Araneus diadematus*, *Cyrtophora cicatrosa* found as paraphyletic. *Bijoaraneus mitificus* and *Eriovixia excelsa* forms monophyletic taxon and *Anepsion depressum* as polyphyletic. The inner node from which produces two nodes again with a monophyletic taxon between *Hypsosinga rubens* and *Hypsosinga pygmaea* whereas *Parawixia kochi*, *Cyrtarachne nagasakiensis* as parahyletic to this clade. The other inner node carries two monophyletic taxa between *Neoscona nautica* and *Neoscona adianta* where as *Neoscona crucifera* as paraphyletic; *Herennia multipuncta* and *Trichonephila inaurata* forms another clade. All these spiders belongs to Araneidae family. The first inner node from the external node bears one monophyletic taxa between *Tetragnatha sp.* and *Tylorida ventralis* both belongs to Tetragnathidae family and *Opadometa fastigata*, *Leucauge venusta* as paraphyletic and *Phonognatha graeffei*, *Theridion promiscuum* as polyphyletic belongs to Theridiidae. In the phylogram Araneidae was found to be evolved from Tetragnathidae and both together forms orb web spider cluster.

The second internal node of 1st external node bears 2 more inner nodes, one monophyletic taxon between *Plesiophrictussp.* and *Chilobrachyssp* belongs to *Theraphosidae; Scytodes thoracica* as paraphyletic taxa of Pholcidae. *Pholcus phalangioides* and *Holocnemuspluchei* belongs toPholcidae forms another monophyletic taxa. *Heteropoda venatoria* seen as polyphyletic taxa. From one inner node evolve a group of spiders with *Phlegra fasciata* and *Menemerus bivittatus* as monophyletic taxa belongs to Salticidae ; *Nephila pilipes* and *Argiope keyserlingi* both belongs to Araneidae and *Eriovixia laglaizei* of Araneidae as paraphyletic.

The 3rd external node gives numerous inner nodes and sister taxa and forms a cluster of Salticidae family with monophyletic taxa of between *Myrmaplata plataleoides and Hasarius adansoni; Plexippus paykulli and Plexippus sp.* . From the next inner node arises monophyletic taxa of *Chrysilla volupe and Menemerus semilimbatus: Stenaelurillus lesserti* as paraphyletic taxa to this and one polyphyletic taxa arises from this node *Epocilla aurantiaca* and bears another monophyletic taxa between *Hyllus semicupreus and Phintella vittate*. Another inner node results another monophyletic taxa between *Phidippus sp.* and *Hentzia mitrata* to which *Rhene flavigeram* was found as paraphyletic. Another inner node holds *Telamonia dimidiata* and *Carrhotus viduus. Callilepis nocturna* found as polyphyletic to the above node. The first inner node from the external node holds one monophyletic taxon between *Philodromus aureolus* and and *Tibellus maritimus* of Philodromidae family. The last cluster arises from the 4th external node supports *Thomisus onustus and Oxytate virens* of Thomisidae family, *Lycosa godeffroyi* (Lycosidae), *Oxyopes sunandae (*Thomisidae), *Cheiracanthium sp.* (Cheiracanthiidae) as paraphyletic and *Olios argelasius* (Theraphosidae) polyphyletic taxon.

Rooted tree (Figure6) from phylodraw indicates orb web family cluster with Araneidae and Tetragnathidae with least root distance from the ancestor on one side and salticidae family cluster on the other side of the ancestor. Another cluster formed between *Thomisus onustus* and *Oxytate virens* of Thomisidae family, *Dolomedes tenebrosus (*Pisauridae*), Lycosa godeffroyi (*Lycosidae), *Oxyopes sunandae* (Thomisidae)and *Cheiracanthium sp. (*cheracanthidae) family forms a cluster near from the ancestor. The 3rd cluster diverged from ancestor with 2 monophyletic taxon *Plesiophrictussp. (0.138)* and *Chilobrachyssp* (0.136)of (Theraphosidae) family; *Pholcus*

phalangioides (0.129) and *Holocnemuspluchei* (0.138) of Pholcidae, *Scytodes thoracica* (0.129) and *Heteropoda venatoria* (0.075)of Pholcidae as paraphyletic.

Phintella vittate of salticidae family was found as the maximum divergent species with root distance of 0.521. The divergent cluster 4th with *2* monophyletic taxon *Phlegra fasciata* (0.51080) and *Menemerus bivittatus* (0.517)34 of Salticidae family and *Nephila pilipes* (0.5173) and *Argiope keyserlingi* (0.5075) of Araneidae family was found. *Badumna insignis* of Desidae (0.47), *Castianeira sp* (0.467). of Corinnidae family, *Cosmophasis umbratical* (0.45) and *Asemonea sichuanensis* (0.44) of salticidae was found as paraphyletic.

In the NJ plot of all species was constructed at 0.1 divergence rate and *Menemerus bivittatus* ofSalticidae family was found as outgroup. From which emergences a clades with *Badumna insignis of* Desidae family *and Castianeira sp. of* Corinnidae familyand another between *Cosmophasis umbratical* and *Asemonea sichuanensis* of Salticidae family. *Nephila pilipes (*0.031) of Araneidae family was found as internal ancestor from which all the spider species evolved. *Phintella vittate (*0.182) of Salticidae family and *Phonognatha graeffei* (0.182) Araneidae family was found with maximum divergence rate from ancestor. The evolution of araneidae family and salticidae and how other family of spiders evolved from the ancestor was clearly evident in the study and agroecosystem from which collected was insignificant in this study.

The phylogram prediction represents 1st cluster (**TableIV**) Orbweb spiders (Araneidae and Tetragnathidae) together forms 6 monophyletic taxa, 2nd cluster 4 monophyletic taxa, 3rd cluster (Salticidae) 7 monophyletic taxa and the 4th cluster with 1 monophyletic taxon.

Table III: Comparison between 17 spider family selected from 10 agroecosystems of Palakkad

No	Species Name	Family	Location
1	*Argiope pulchella*	Araneidae	Ezhakkad, Mankara, Sreekrishnapuram
2	*Argiope anasuja*	Araneidae	Railway colony, Patambi, Sreekrishnapuram
3	*Bijoaraneus mitificus*	Araneidae	Sreekrishnapuram
4	*Eriovixia laglaizei*	Araneidae	Ezhakkad
5	*Araneus diadematus*	Araneidae	Ezhakkad Patambi, Sreekrishnapuram
6	*Nephila pilipes*	Araneidae	Ezhakkad, Kalipara, Pathiripala, Nallepilli, Sreekrishnapuram
7	*Anepsion depressum*	Araneidae	Ezhakkad, Pathiripala
8	*Argiope keyserlingi*	Araneidae	Ezhakkad, Pathiripala, Nallepilli
9	*Herennia multipuncta*	Araneidae	Ezhakkad
10	*Cyrtophora cicatrosa*	Araneidae	Ezhakkad
11	*Eriovixia excelsa*	Araneidae	Ezhakkad
12	*Neoscona crucifera*	Araneidae	Ezhakkad, Pathiripala, Nallepilli
13	*Phonognatha graeffei*	Araneidae	Ezhakkad, Kalipara, Puliyaparamb
14	*Neoscona nautica*	Araneidae	Mankara, Puliyaparamb
15	*Araneus ventricosus*	Araneidae	Mankara, Pathiripala, Nallepilli, Puliyaparamb, Sreekrishnapuram
16	*Hypsosinga rubens*	Araneidae	Kalipara
17	*Hypsosinga pygmaea*	Araneidae	Nallepilli, Patambi
18	*Argiope aemula*	Araneidae	Olavakode railway colony, Patambi
19	*Trichonephila inaurata*	Araneidae	Mankara
20	*Neoscona adianta*	Araneidae	Ezhakkad, Pathiripala, Nallepilli
21	*Argiope hoiseni*	Araneidae	Olavakode railway colony, Patambi
22	*Cyrtarachne nagasakiensis*	Araneidae	Ezhakkad
23	*Parawixia kochi*	Araneidae	Mathur
24	*Hyllus semicupreus*	Salticidae	Ezhakkad, Puliyaparamb
25	*Rhene flavigera*	Salticidae	Sreekrishnapuram
26	*Plexippus paykulli*	Salticidae	Sreekrishnapuram, Ezhakkad, Mankara, Pathiripala Nallepilli, Olavakode railway colony, Patambi
27	*Telamonia dimidiata*	Salticidae	Ezhakkad, Sreekrishnapuram
28	*Phintella vittata*	Salticidae	Ezhakkad, Sreekrishnapuram
29	*Myrmaplata plataleoides*	Salticidae	Sreekrishnapuram
30	*Asemonea sichuanensis*	Salticidae	Ezhakkad
31	*Plexippus sp.*	Salticidae	Sreekrishnapuram, Ezhakkad, Mankara, Pathiripala, Nallepilli, Railway colony, atambi
32	*Phintella vittata*	Salticidae	Ezhakkad
33	*Chrysilla volupe*	Salticidae	Sreekrishnapuram
34	*Menemerus bivittatus*	Salticidae	Ezhakkad, Railway colony, Sreekrishnapuram
35	*Epocilla aurantiaca*	Salticidae	Ezhakkad
36	*Stenaelurillus lesserti*	Salticidae	Ezhakkad
37	*Phidippus sp.*	Salticidae	Ezhakkad
38	*Hentzia mitrata*	Salticidae	Mankara
39	*Cosmophasis umbratica*	Salticidae	Kalipara
40	*Phlegra fasciata*	Salticidae	Kalipara, Pathiripala, Nallepilli
41	*Hasarius adansoni*	Salticidae	Nallepilli, Railway colony, Sreekrishnapuram
42	*Menemerus semilimbatus*	Salticidae	Railway colony
43	*Carrhotus viduus*	Salticidae	Railway colony
44	*Tetragnatha sp.*	Tetragnathidae	Pattambi

45	*Leucauge venusta*	Tetragnathidae	Ezhakkad, Mankara, Railway colony (Palakkad
46	*Tylorida ventralis*	Tetragnathidae	Sreekrishnapuram
47	*Opadometa fastigata*	Tetragnathidae	Ezhakkad
48	*Theridion promiscuum*	Theridiidae	Puliyaparamb
49	*Thomisus onustus*	Thomisidae	Ezhakkad
50	*Oxytate virens*	Thomisidae	Ezhakkad
51	*Oxyopes sunandae*	Thomisidae	Ezhakkad
52	*Pholcus phalangioides*	Oxyopidae	Ezhakkad, Puliyaparamb
53	*Scytodes thoracica*	Pholcidae	Ezhakkad, Mankara, Kalipara, Pathiripala Nallepilli, Puliyaparamb, Sreekrishnapuram, Patambi
54	*Heteropoda venatoria*	Pholcidae	Ezhakkad, Mathur, Pathiripala, Nallepilli Railway colony, Patambi
55	*Cheiracanthium sp.*	Cheiracanthiidae	Ezhakkad
56	*Castianeira sp.*	Corinnidae	Ezhakkad
57	*Dolomedes tenebrosus*	Pisauridae	Ehakkad
58	*Callilepis nocturna*	Gnaphosidae	Ezhakkad
59	*Philodromus aureolus*	Philodromidae	Mathur, Puliyaparamb, Patambi
60	*Badumna insignis*	Desidae	Sreekrishnapuram
61	*Lycosa godeffroyi*	Lycosidae	Nallepilli
62	*Holocnemuspluchei*	Pholcidae	Ezhakkad, Mathur, Pathiripala, Nallepilli Olavakode railway colony, Patambi
63	*Olios argelasius*	Sparassidae	Sreekrishnapuram
64	*Plesiophrictussp.*	Theraphosidae	sreekrishnapuram
65	*Chilobrachyssp*	Theraphosidae	Sreekrishnapuram
66	*Tibellus maritimus*	Philodromidae	Ezhakkad

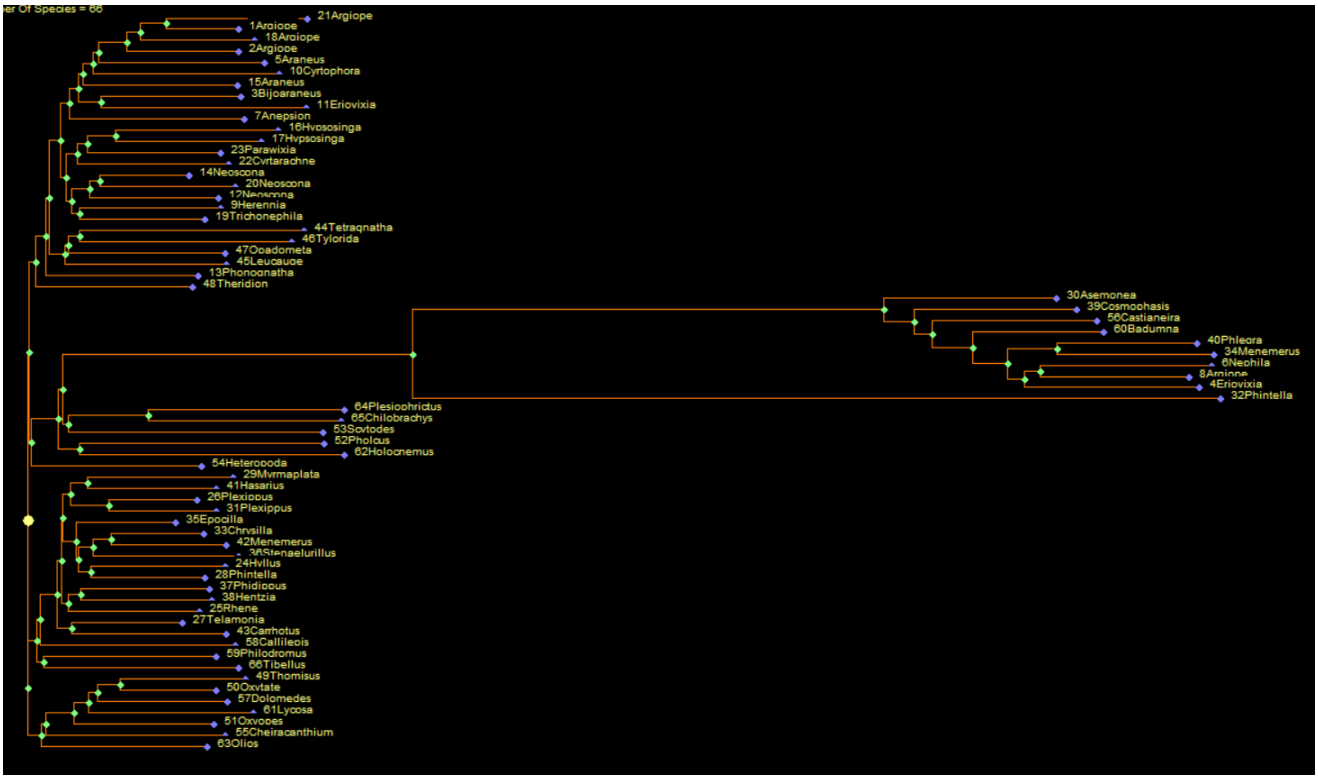

Figure 5: Phylogram showing evolutionary relationship between spiders belonging to 17 family.

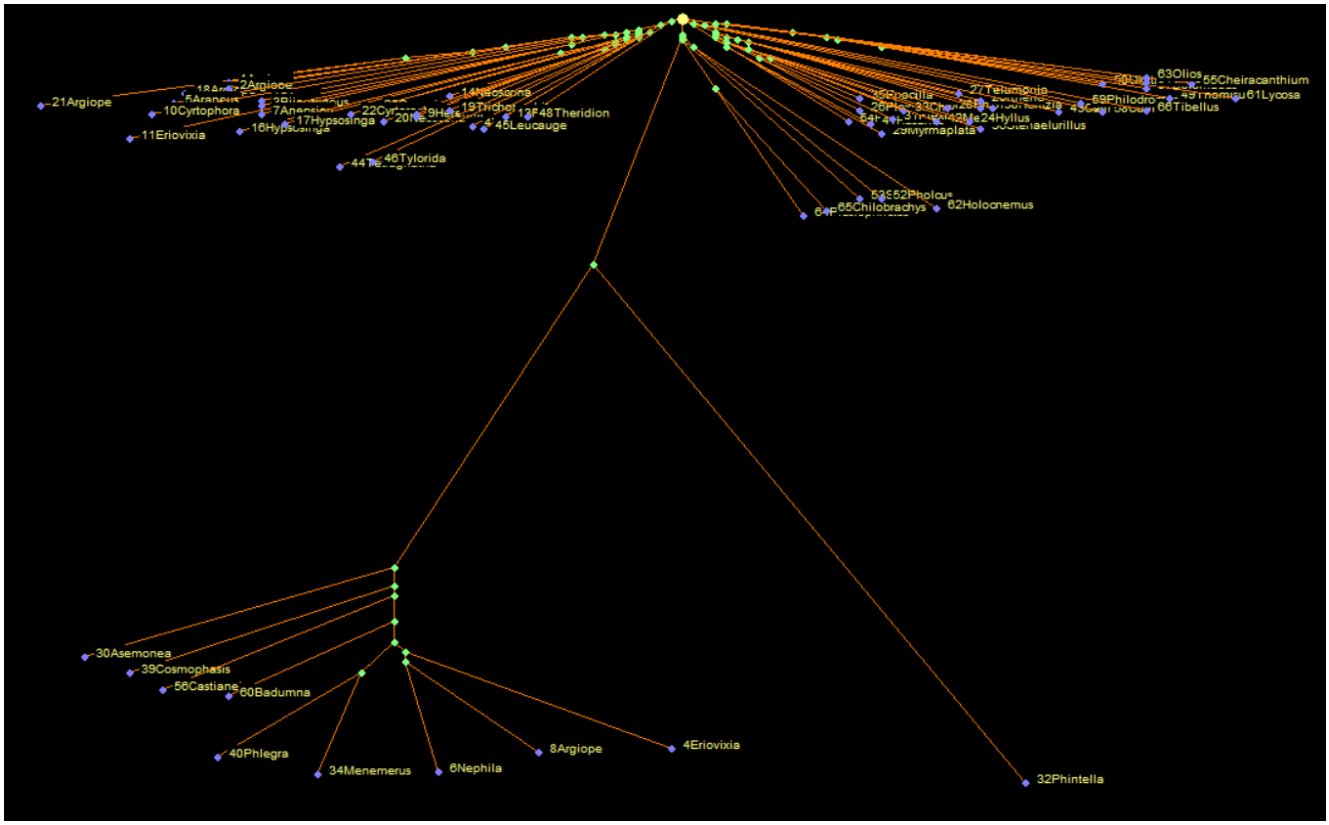

Figure 6: Rooted tree showing the evolution of spider species from 17 family members.

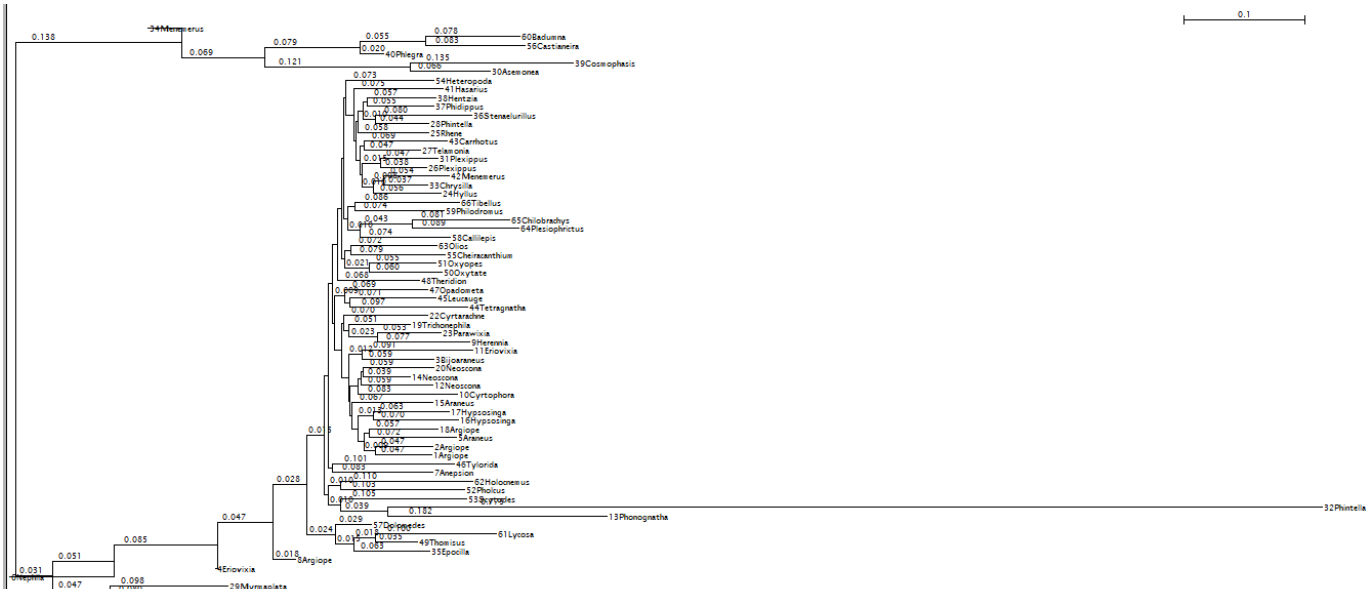

Figure 7: NJ plot showing the evolution of 66 spider species

Table IV: Monophyletic taxa found in the phylogram from 66 species from 10 agroecosystems

Cluster	Taxa	Species	Distance	Family
1st cluster Orb web spider	Monophyletic	*Argiope pulchella*	0.122	Araneidae
		Argiope hoiseni	0.091	Araneidae
	Monophyletic	*Bijoaraneus mitificus*	0.093	Araneidae
		Eriovixia excelsa	0.121	Araneidae
	Monophyletic	*Hypsosinga rubens*	0.109	Araneidae
		Hypsosinga pygmaea	0.101	Araneidae
	Monophyletic	*Neoscona nautica*	0.070	Araneidae
		Neoscona adianta	0.090	Araneidae
	Monophyletic	*Herennia multipuncta*	0.084	Araneidae
		Trichonephila inaurata	0.077	Araneidae
	Monophyletic	*Tetragnatha sp.*	0.120	Tetragnathidae
		Tylorida ventralis	0.115	Tetragnathidae

2nd cluster	Monophyletic	*Phlegra fasciata*	0.510	Salticidae
		Menemerus bivittatus	0.518	Salticidae
	Monophyletic	*Nephila pilipes*	0.517	Araneidae
		Argiope keyserlingi	0.507	Araneidae
	Monophyletic	*Plesiophrictussp.*	0.138	Theraphosidae
		Chilobrachyssp	0.136	Theraphosidae
	Monophyletic	*Pholcus phalangioides*	0.129	Oxyopidae
		Holocnemuspluchei	0.138	Pholcidae
3rd cluster Salticidae	Monophyletic	*Myrmaplata plataleoides*	0.089	Salticidae
		Hasarius adansoni	0.082	Salticidae
	Monophyletic	*Plexippus paykulli*	0.073	Salticidae
		Plexippus sp.	0.082	Salticidae
	Monophyletic	*Chrysilla volupe*	0.077	Salticidae
		Menemerus semilimbatus	0.086	Salticidae
	Monophyletic	*Hyllus semicupreus*	0.086	Salticidae
		Phintella vittata	0.077	Salticidae
	Monophyletic	*Phidippus sp.*	0.079	Salticidae
		Hentzia mitrata	0.080	Salticidae
	Monophyletic	*Telamonia dimidiata*	0.067	Salticidae
		Carrhotus viduus	0.086	Salticidae
	Monophyletic	*Philodromus aureolus*	0.082	Philodromidae
		Tibellus maritimus	0.092	Philodromidae
4th Cluster	Monophyletic	*Thomisus onustus*	0.095	Thomisidae
		Oxytate virens	0.082	Thomisidae

4. Discussion

Spiders are exceptionally diverse and abundant in terrestrial ecosystems and evolutionary diversification of spiders is not coupled with major trophic shifts. All spiders are predators of arthropods, and spiders are dominant consumers at intermediate trophic levels [23]-[24]. Spiders are massively abundant generalist arthropod predators that are found in nearly every ecosystem on the planet. In our study Araneidae was found to be largest family with 6 monophyletic taxa from 23 species and 20 species of Salticidae with 7 monophyletic taxa. In the studies of Scharff et al [7] Araneidae was found as the most speciose family of spiders at a global scale after Salticidae and Linyphiidae. In another study [25] reported that orb web evolved earlier phylogenetically than previously thought, only to be subsequently lost at least three times independently during the Cretaceous. In our observation also *Nephila pilipes (*0.031)of Araneidae family was found as internal ancestor from which all the spider species evolved. Blackledge et al. [26] in his study portrays the orbicularian relationships and monophyly using DNA sequences from six genes (COI, 16S rRNA, 18S rRNA, 28S rRNA, histone H3, and *wingless*)and morphological and behavioral characters.

In this study Figure 5 & 7 shows the evolutionary relationship of Araneidaeand Tetragnathidae family clades originate from a common ancestor, and both are orb-weaving spiders. Álvarez-Padilla andGustavo Hormiga [27] carried out a phylogenetic analysis using morphological and DNA sequence data selecting 47 taxa including 25 tetragnathids, 11 araneids and four nephilids and created an orb weaving spider atlas. A new phylogeny of the spider family Araneidae based on five genes (28S, 18S, COI, H3 and 16S) for 158 taxa and found 25 out groups and 133 araneid ingroups representing the subfamilies Zygiellinae Simon, 1929, Nephilinae Simon, 1894, and the typical araneids and described as “ARA Clade” [7]. In this study Araneidae was the dominant and diverse spider family with 23 species (**Table I**) with 6 monophyletic taxa (**Figure1**) and in Figure5describes an ARA clade. *Argiope pulchella* collected from Ezhakkad and Mankara form a monophyletic taxa with Argiope*hoiseni* fromRailway colony and Patambi agroecosystem**.** *Eviovixia excelsa (*Ezhakkad) and *Phonognatha graeffei (*Ezhakkad, Kalipara, Puliyaparamb) forms another monophyletic taxon. *Neoscona nautical (*Mankara, Puliyaparamb**)**and *Neoscona adianta (*Ezhakkad, Pathiripala, Nallepilli)falls under monophyletic taxa, *Cyrtarachne nagasakiensis (*Ezhakkad) and *Parawixia kochi* (Mathur); *Herennia multipuncta (*Ezhakkad) and *Trichonephila inaurata (*Mankara)falls under another monophyletic group. In this study also *Araneus ventricosus* found as polyphyletic (**Figure1**) as in the study of Scharff et al [7].

Berger et al [28] in their study examined the genetic basis of secondary web loss within web-building spiders (Araneoidea) of the lineage of spiders in the genus Tetragnatha (Tetragnathidae) that has diverged into two clades associated with the relatively recent (5 mya) colonization of, and subsequent adaptive radiation within, the Hawaiian Islands. In the study also most of the Araneidae species evolved from Tetragnathidae (Figure6 & 7). Hill and Richman [29] in their study describes the origin of Salticidae dionychan clades, which include Philodromidae, Thomisidae, Miturgidae, Anyphaenidae, Gnaphosidae and related groups. In this study as per phylodraw (Figure3 & 6)Salticidae forms a cluster with 7 monophyletic taxa. Jumping spiders are diverse in morphology, behaviour and predatory ecology [30], which makes them attractive model organisms for examining questions of evolutionary phenomena. Spider relationships based on phylogenomic analyses was done to explain high level groupings such as Opisthothele, Mygalomorphae, Atypoidina, Avicularoidea, Theraphosoidina, Araneomorphae, Entelegynae, Araneoidea, the RTA clade, Dionycha and the Lycosoidea in another study [10]. Spiders are divided into two major infraorders, the Araneomorphae

and Mygalomorphae and Araneomorphs comprise Orbiculariae, the orb-weaving spiders [31]. Salticidae are another family with a well-resolved phylogenetic backbone, based on morphological and molecular analyses [32]-[33]-[34]-[35]. In this study *Holocnemuspluchei* (Pholcidae) and *Pholcus phalangioides (*Oxyopidae) *forms a clade* (Figure6). Pholcid systematics were attempted and support the division of Pholcidae into five subfamilies: Ninetinae, Arteminae, Modisiminae, Smeringopinae, and Pholcinae [36]. Morphological and molecular data have greatly contributed to advances in the phylogeny and evolutionary dynamics of spiders using mitochondrial phylogenomics analysis on 78 mitochondrial genomes (mitogenomes) representing 29 families; of these, 23 species from eight families were newly generated [37].

The monophyletic origin of orb web spiders was proved in a molecular phylogenetic study despite conspicuous differences in the silk used to spin different types of orbs [38] which gives an important of understanding both web evolution and spider diversification.

Macías-Hernández et al [39] have carried out a phylogenetic analysis of two biogeographical regions (Iberian Peninsula and Macaronesia) with a taxon-rich backbone matrix of Genbank sequences and a topological constraint derived from recent phylogenomic studies. In the study spiders identified from 10 agroecosystems were compared and found that spider evolution has absolutely no relation between place of origin. Our phylogenomic analyses represent the largest assessment of spider phylogeny to date using COI data from Palakkad and found the lineage of spiders from Araneidae and the orb web spiders has found successful.

5. Conclusion

Phylogram constructed with 66 species selected from 10 agroecosystem belongs to 17 family contains 4 clusters, the first cluster represents orb web spiders which connectsAraneidae and Tetragnathidae. The orb web spiders descend fromTheridiidae. Second cluster includes few monophyletic taxa of Araneidae, Salticidae which descend from Theraphosidae, Pholcidae, Oxyopidae, Desidae, Corinnidaefamily. Third cluster formed of Salticidae family and few species of Gnaphosidae and Philodromidae. Fourth cluster starts from Sparassidae and end with monophyletic taxa of Thomisidae, other family (Pisauridae, Cheiracanthiidae, Lycosidae)seen as para and polyphyletic taxon. *Nephila pilipes* (0.031) of Araneidae family was found as internal ancestor from which all the spider species evolvedand agroecosystem from which collected was insignificant in this study.

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