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SEARCHING KEY TRAITS FOR FURTHER DESCRIPTION OF PHYTOSEIIDAE MITE FAMILY

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ABSTRACT
The predatory mite family, Phytoseiidae is one of the most explored groups worldwide as biological agents against phytophagous mite pests and small insects *viz* thrips, whiteflies, coccids and pseudo coccids in alternative to application of acracides. In search of key traits of predatory mites for proper identification as the species level classification of Indian phytoseiids is carried out. Our present study considered 171 species along with their 48 morphological characters with MDS. Principal coordinate analysis (PCoA) was carried out using Gower's similarity index and the key traits were retained upon 10 % relaxation provided in the component score matrix. Larger amount of variance (85.5%) explained by 6 major traits with eigen value >1, while length (0.907) and width of dorsal shield (0.504) contributed major variation. Traits like length and width of dorsal shield setae, length ventrianal shield, Ratio R1/s6, Macro setae SgIV and Length of setae s4 is found responsible for major variance in the classification of Phytoseiidae. The key traits can be utilized as importance tools of classification, pest control and predatory phytoseiid mite. This approach can also helps in identification of new species with no time holistic approach.

INTRODUCTION

Biological control of insect pest is a alternative eco-friendly approach to minimized the application of chemical pesticides where predators. The predatory insects and mites help in feed on phytophagous pests and help to keep the population of pest species well below economic threshold level. Phytoseiidae is a family of mites, widely exploited group among all the predatory mites as a potential predatory biological control agent against mite pests thrips (De Moraes, *et al.*, 2004) and they can feed on mites of many families, as well as thrips, whiteflies, nematodes (McMurtry and James 2013). In view of their natural predatory importance family, these mites have also been explored in India, from where many new species have been described since 1960. Apart from these, some Indian worker has also been reviewed on their bio-ecology, predator–prey interactions(Gupta 2003a), and the effects of pesticides on these mites (Srinivasa *et al.*,2014)). Control measures of two spotted spider mite Tetranychus urticae (Koch) on Apples has been reported using mineral oils (Negi and Gupta, 2007). From India, 207 species under 21 genera of eight tribes and three subfamilies arranged as per the classificatory scheme(Chant and McMurtry, 2007). In addition, another 4 species two under *Euseius* and one each under *Neoseiulus* and *Amblyseius* are being described separately by Karmakar and Gupta(In press, 2014) and hence the total now comes to 211 species described (Gupta and Karmakar, 2015). Insect pests of pointed gourd(Trichosanthes dioica Roxb) was reported in West Bengal (Pranab and Jha, 2013). Wide range hosts of phytophagous mites infesting common vegetables(Prasad, 2006).

Rice being the most important staple food crop of world. Small sucking insects and mites cause damage to a greater extent impairing the production system. The phytoseiid predatory mites also play a great role in rice ecosystem by suppressing the population of sucking insects pests. Some of the species of phytoseiidae mites those are utilizing in bio-control programme are *Phytoseiulus persimilis* Athias-Henriot on two spotted spider mite in strawberries, *Galendromus occidentalis* (Nesbitt) on spider mites and eriophyid mites in tree fruits, corn and cotton, *Neoseiulus californicus* (McGregor) on spider mite in rose and *Neoseiulus fallacies* (Garman) on two spotted spider mite in greenhouse plants. Therefore, study of systematic classification and identification of phytoseiid mites would give a better result if it is properly identified and exploit for management of rice pests.

Principal Coordinate Analysis (PCoA) analogous to principal component analysis, Thus output will depend on the nature and behavior of the particular distance measures employed. Principal coordinates analysis begins with a matrix of distances among objects (Pielou, 1984) and technique called classical scaling extent possible, distances retained in a space with a reduced number of dimensions and to similar to psychometrician (Chatfield and Collins 1980, Titus et al., 1984). If the data are quantitative and the distances are squared distances between units in a coordinate space (Euclidean distances), a principal coordinates analysis will produce the same result as well as principal components analysis on the correlation matrix among the attributes (Digby, and Kempton, 1987).

Systematic approach of matrix of Roger's genetic distances was expressed in a two-dimensional graphic space in populations of common mynahs (*Acridotheres tristis*), and the populations in the graph were then connected with a minimum spanning tree according to their distances in the full dimensional space (Baker and Moeed,1987). Another useful analysis using principal coordinates analysis was performed on a matrix of the number of interspecific contacts among 28 species of mosses (Digby and Kempton, 1987).

There may be some species of Phytoseiidae which can act as good predators against soft bodied insects and plant feeding mite species in rice. The species those are already identified can be exploited and utilized in the rice field. Keeping, this in view our present investigation 171 species of Phytoseiidae along with the 48 morphological characters were considered and applied principal coordinates analysis (PCoA) to plot the 171 species on the Euclidean space for exploiting the selected traits of effective biological control agents and identification of Phyotseiidae family against plant feeding mites and other harmful organisms.

MATERIALS AND METHODS

Data base

Data base for the present studies was collected from different literatures and books (Gupta, 2003, Chant and Murtry, 2007). Data for present in-depth investigation were collected and considered from 171 Phytoseiidae mite species with their 48 morphological characters by microscopic measurement in different scale (Nominal, Ordinal, Ratio and Interval). Binary characters of present and absence were coded as 1 and 0 respectively and setae length were measured in micrometer (μm).

Gower's Distance

A similarity coefficient measures the resemblance between two individuals based on either or both of two logically distinct kinds of information pertaining to v variables and allowing for possible missing information. In taxonomy, where similarity coefficients are often used, this may be the only kind of information used to build up a taxonomic classification. The taxonomist has the problem of deciding whether a character occurring in one group of organisms also occurs in another group; this is the so-called homology problem. A missing character should not be confused with missing information because it is known that the character definitely does not exist. Missing information can occur, for example, with incomplete fossil material or with poor descriptions in the literature, from which the existence or otherwise of a character cannot be inferred. When the characters used are measured in different scale then most of the distance measures can not be used therefore the distance which accept all the measurement is Gower's distance method(Gower and Legendre, 1986).

Principal Coordinate Analysis (PCoA)

Principal coordinate analysis is another ordination method, somewhat similar to PCA. The PC finds the eigen values and eigen vectors of matrix containing the distance between all data points. The Gower measure will normally be used instead of Euclidean distance. We assumed that ordinates receiving high eigen values best represent variation in the system. Therefore, not only the PCo's with eigen values ≥ 1 (Kaiser, 1960) but all the positive eigen values based upon expert opinion were used to accommodate more number of distinct traits as MDS (Minimum Data Sets, Andrews., *et al.*,2002). Additionally, those explain ≥ 58% of the variability in the species of Phytosiidae family were included.

Key traits selection

Eigen vectors along coordinate axis were chosen for the further analysis and ordinate axis with eigen value up to 0.009 (6 ordinate axis) were selected. The maximum absolute value was identified within each PCo and given a 10% relaxation for choosing key indicator variables within that range. The traits which are falling in that range of relaxation (10%) those were given the priority and linear relation between those traits was further studied using Pearson's correlation coefficient (r). Traits which exhibit significant correlation within the chosen ordinate axis and with the maximum ordinate score, were eliminated. This method was repeated for all PCos that explain ≥58% of the variability

RESULTS AND DISCUSSION

Perusal from the Table 1., revealed that, using Gower's similarity index (Gower, 1986) 171 species of Phytoseidae was subjected to the PCoA based on the morphological dicharacters with MDS. The studied Data base contained both qualitative as well as quantitative therefore distance measure Gower is considered and it was appropriate because nature of mixed data. When the data base used in the analysis are measured in different scale (Mixed data) then most of the distance measures can't be used and in that situation Gower's similarity could be used.

Taxonomical morphological characters like Arrangement of teeth, Fusion of peritrematal shield with dorsal shield, Notch near s4, Waist at level of R1, Presence of z3, Presence of s6, Fusion of ventral and anal shield, Bifurcation of atrium, Extension of peritreme, Chaetotaxy genu II, Chaetotaxy genu III and Macrosetae on leg IV were of qualitative in nature and the rest 36 characters were of quantitative in nature. Dorsal shield was longer (322.21) than width (192.16) and exhibited better variation lesser than Z5 setae among 171 species of phytoseiidae. Setae s4 also produced better variance among species and other characters also produced better variation in the classification of phytoseiidae. Morphological characters used in the analysis may not all the characters responsible for the separations of the species but some of the key traits which actually separate the species in to different groups. There may be some of the characters responsible for maximum variation are highly correlated those characters may not bring better results in the taxonomic studies.

Results from the Table 2., revealed that, twenty four PCos were extracted with positive eigen values and coordinates explaining ≥ 0.58% variation were retained upon giving 10 %

Table 1: Morphological characters considered for the ordination of Phytoseiidae family

Characters	Mean	SD	Max	Min	range	Variance
No. of teeth on movable digit	1.51	1.15	4.00	0.00	4.00	1.31
No. of teeth on fixed digit	4.52	2.40	10.50	0.00	10.50	5.74
Arrangement of teeth	0.12	0.33	1.00	0.00	1.00	0.11
Fusion of peritrematal shield with dorsal shield	0.98	0.13	1.00	0.00	1.00	0.02
Length dorsal shield	322.21	42.45	504.00	200.00	304.00	1801.94
Width dorsal shield	192.16	41.17	307.00	114.00	193.00	1695.24
Notch near s4	0.04	0.20	1.00	0.00	1.00	0.04
Waist at level of R1	0.01	0.08	1.00	0.00	1.00	0.01
No. of dorsal shield setae	16.64	1.31	19.00	10.00	9.00	1.73
Presence of z3	0.39	0.49	1.00	0.00	1.00	0.24
Presence of s6	0.39	0.49	1.00	0.00	1.00	0.24
j1	23.14	7.92	51.00	1.00	50.00	62.79
j3	32.24	18.09	90.00	1.00	89.00	327.10
j4	10.36	7.72	58.00	1.00	57.00	59.58
j5	12.24	9.94	69.50	0.00	69.50	98.87
j6	13.43	10.98	72.00	0.00	72.00	120.53
J2	15.32	14.24	76.00	0.00	76.00	202.90
J5	6.71	2.93	16.50	1.00	15.50	8.59
z2	14.46	9.42	69.00	1.00	68.00	88.80
z3	10.42	15.44	74.00	0.00	74.00	238.28
z4	17.97	11.53	73.00	1.00	72.00	132.96
z5	10.56	7.42	45.00	1.00	44.00	55.02
Z1	9.07	14.29	82.00	0.00	82.00	204.08
Z4	54.85	35.44	195.00	1.00	194.00	1255.84
Z5	86.72	73.58	528.00	1.00	527.00	5413.99
s4	57.48	40.68	210.00	1.00	209.00	1654.75
s6	18.72	28.18	97.00	0.00	97.00	793.88
S2	19.29	18.23	85.00	0.00	85.00	332.43
S4	16.60	14.93	60.00	0.00	60.00	223.03
S5	13.96	14.45	103.00	0.00	103.00	208.67
r3	23.97	13.07	58.00	6.00	52.00	170.82
R1	17.07	9.72	67.00	0.00	67.00	94.57
s4:Z1	2.65	5.41	41.00	0.00	41.00	29.27
s4:S2	3.83	17.66	201.00	0.00	201.00	312.01
Ratio R1/s6	0.13	0.30	1.20	0.00	1.20	0.09
Fusion of ventral and anal shield	1.02	0.13	2.00	1.00	1.00	0.02
Length of Ventrianal Shield	98.60	21.52	157.00	0.00	157.00	463.01
Width of Ventrianal Shield	74.97	28.14	224.00	0.00	224.00	791.69
Ratio of length/width of VS	1.36	0.38	2.58	0.00	2.58	0.14
No. of preanal setae	3.22	0.41	4.00	3.00	1.00	0.17
Bi furcation /vaculation of atrium/major duct	1.02	0.13	2.00	1.00	1.00	0.02
Extension of peritreme	2.78	2.40	12.00	1.00	11.00	5.77
Chaetotaxy genu II	1.22	0.93	7.00	1.00	6.00	0.86
Chaetotaxy genu III	2.96	2.71	12.00	1.00	11.00	7.36
Macrosetae on leg IV	0.96	0.20	1.00	0.00	1.00	0.04
Macro setae SgIV	38.39	38.67	264.00	0.00	264.00	1495.17
Sti IV	36.07	26.85	201.00	0.00	201.00	720.88
St IV	47.53	22.09	160.00	0.00	160.00	487.82

relaxation within each PCo to choose possible key traits which contributes maximum variation in the Phytoseiidae family. Out of 24 positive coordinates, 6 coordinates were chosen, whereas PCo1 was responsible for the maximum variation of 85.510% followed by PCo2 (2.987), PCo3 (2.146), PCo4 (1.146), PCo5 (1.020) and PCo6 (0.583).

Eigen value for PCo1 was more as compared to other 5 ordinate axes. Among 48 morphological characters 6 traits were extracted viz., Length and width of dorsal shield setae, Length ventrianal shield, Ratio R1/s6, Macro setae SgIV and Length of setae s4 (All quantitative characters measured in micrometer (μm). Component score matrix was considered for indexing whereas the maximum absolute value of the score matrix within the principal coordinates was chosen. Highest score within the principal coordinates were provided 10 % relaxation to incorporate more possible traits which brings maximum variation. When more than one factor was retained under a single PCo, correlation coefficients were employed to determine if the variables could be considered redundant and, therefore, eliminated from the MDS (Andrews *et al.,* 2001). If the highly weighted factors were not correlated (assumed $p > 0.05$) then each was considered important, and thus, retained in the MDS. Among well correlated variables, the variable with the highest factor loading (absolute value) was

Table 2: Variance explained by each principal coordinates and factor loadings of the key traits with MDS

Principal Coordinates	PCo1	PCo2	PCo3	PCo4	PCo5	PCo6
Eigen value	1.385	0.048	0.035	0.019	0.017	0.009
Per cent	85.510	2.987	2.146	1.146	1.020	0.583
Characters						
Length dorsal shield	0.907	0.068	-0.012	-0.036	-0.019	0.014
Ratio R1/s6	-0.092	0.044	-0.005	-0.002	-0.016	-0.001
Length VS	0.239	-0.052	0.087	0.042	-0.015	-0.034
Macro setae SgIV	0.028	-0.033	0.030	-0.074	-0.010	-0.021
Width dorsal shield	0.504	0.024	-0.012	0.027	0.064	-0.022
s4	0.099	-0.013	-0.046	0.016	-0.037	-0.036

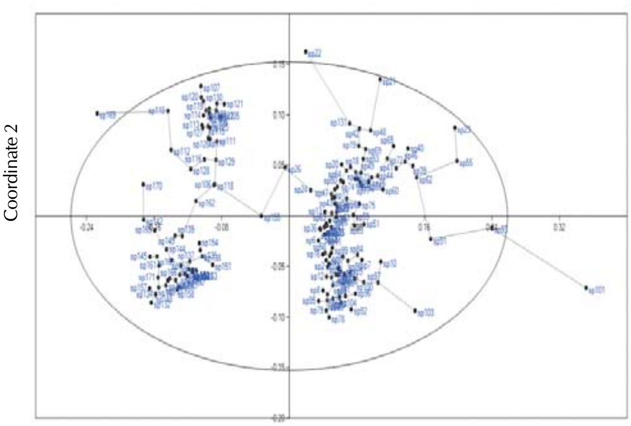

Figure 1: Species ordination of Phytoseiidae mite family using PCoA at 95 % Confidence Interval

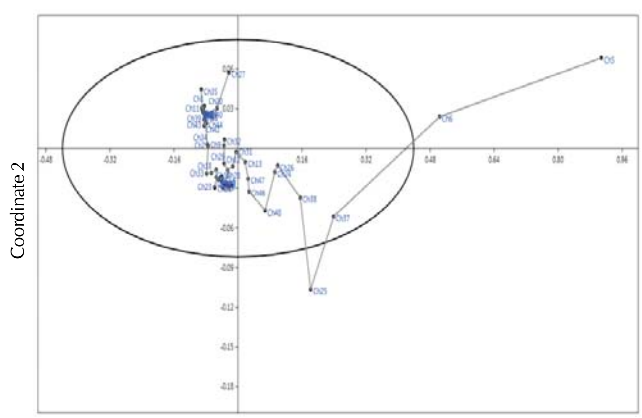

Figure 2: Morphological character ordination of Phytoseiidae mite family using PCoA at 95 % confidence interval

chosen for the MDS.

Among the mentioned characters in the Table 2, length and width of dorsal shield found highly weighted factors (0.907 and 0.504 respectively) and length of ventrianal shield provided better loadings (0.239) within PCo1. Factors loadings for Macro setae SgIV, s4 found less whereas the trait ratio of R1/s6 was associated with the negative score but these traits were associated with less factor loadings due to less eigen value for the coordinates.

Scores were plotted against coordinate 1 by the coordinate 2 (Figure 1) for the 171 species based on 48 morphological traits. From Fig 1 one can found 3 major groups of Phytoseidae (Chant and McMurtry, 2007), the group which distributed in the right side of plot (two quadrants) were Amblyseiinae, top left side group was Phytoseiinae and left bottom group was Typhlodrominae. Species 160 (*Typhlodromus Anthoseius orissaensis*), 169 (*Typhlodromus Anthoseius zafari*) and 170 (*Typhlodromus confuses*) were approaching Phytoseiinae group. Apart from these three species other species are well represented in their respective groups. Plot for the considered traits revealed that, Ch5 (Length of dorsal shield) and Ch6 (Width of dorsal shield) respectively represented on the ordination axis found as significant traits (at 95 % confidence interval) as compared to other 46 traits considered in the analysis (Figure 2).

Summary and Conclusion.

The morphometric characters used in the analysis is found fit for the ordination purpose . Gower's similarity was found fit for the ordination. General Taxonomic study needs huge man power, time for the collection of species specimens, measurement . Dimension reduction can generate idea of number of clusters based on the similarity measures used in the coordinate analysis (Mixture of cluster analysis and PCA). Therefore, key traits like Length width of dorsal shield setae, Length ventrianal shield, Ratio R1/s6, Macro setae SgIV and Length of setae s4 could be used in the classification of Phytoseiidae than considering more number of morphological characters to save time, space and money.

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