Phylogenetic analysis of Indian species of genus *Macrophya* Dahlbom (Hymenoptera: Symphyta; Tenthredinidae: Tenthredininae)

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Abstract

Phylogenetic analysis was performed for 14 species of the genus *Macrophya* (Hymenoptera: Tenthredinidae) using the phylogenetic analysis package PAUP, based on 15 of the morphological characters most commonly used for *Macrophya* species identification. Species descriptions were derived primarily from "Indian Sawflies Biodiversity" vol. II (Saini 2007). Parsimony analysis, using equally weighted characters, produced 48 trees. The results are discussed in terms of evolutionary trends or biological maxim that "nature prefer to modify the already existing structures so as to cope with new needs."

Keywords: *Phylogenetic analysis, Macrophya, Evolutionary trends.*

Introduction

The genus *Macrophya* (Hymenoptera: Tenthredinidae) is widely distributed genus with its representatives available in almost all main regions of the globe. With regard to its affinities, it shares most of its characters with *Pachyprotasis* Hartig. Even within *Macrophya* the range of characters is so wide that time to time many of its subgenera were proposed (Malaise, 1945) and because of no distinct boundaries they all got merged (Ross, 1937 ; Gibson, 1980). Today none of its subgenus is considered to be valid (Abe & Smith,1991). The genus *Macrophya* was first described by Dahlbom (1835) as a subgenus of *Tenthredo* Linnaeus, on the basis of body shape, length and form of antenna. He divided this subgenus into two subsections "A" and "B". Hartig (1837) applied names to these two subsections using *T. (Macrophya)* for subsection "B" and *T.(M.) (Pachyprotasis)* for subsection "A". Both of these were later recognised as valid genera by Westwood (1840).

The genus is characterized by venation as in *Pachyprotasis,* but the anal cell may have a cross vein. Malar space mostly shorter than the diameter of an ocellus. The hind legs are strongly built, and the knees reaching and mostly exceeding the apex of the abdomen (Saini, 2007). The larval stages feed on variety of wild herbs, shrubs & trees. Generally adults feed on pollen, flower nectar or leaf juice exuding from wounds caused by strong mandibles. However, many robust species indulge in zoophagy (Cameron,1882; Rohwer,1913; Benson,1938; Malaise,1945; Naito,1988 and Goulet,1996).

The purpose of present study is to trace the long evolutionary history which modified generalizations into specializations of extreme form to suit the circumstances in which subsequently insects dwelled. Parsimony analysis is used to investigate phylogenetic relationships among *Macrophya* species, using data based on morphological characters most commonly used for *Macrophya* identification.

Materials and Methods

Species descriptions were derived primarily from "Indian Sawflies Biodiversity" vol.II (Saini, 2007) and the characters used in the

analysis were those given comparably for all, or almost all, species. *Tenthredo* Linnaeus was also included in the analysis as the outgroup.

Phylogenetic analysis was performed using the package PAUP version 3.1.1. (Swofford,1993). In total 15 morphological characters were used in the phylogenetic analysis. These were :-

1) Clypeus incision (0 = subsquarely incised, 1 = circularly incised, 2 = incised with irregular anterior margin, 3 = incised with truncate bottom, 4 = clypeus triangulary incised).
2) Anterior margin of labrum (0 = rounded, 1 = truncate, 2 = slightly emarginated).
3) Malar space (0 = shorter than diameter of an ocellus, 1 = longer than diamater of an ocellus, 2 = linear, 3 = inconspicuous).
4) Frontal area (0 = below level of eyes , 1 = at level of eyes).
5) Supraantennal tubercles (0 = raised, 1 = indistinct).
6) Median fovea (0 = broad and shallow, 1 = indistinct , 2 = absent).
7) Circumocellar furrow (0 = fine, 1 = distinct, 2 = indistinct).
8) Postocellar furrow (0 = indistinct, 1 = absent, 2 = distinct, 3 = fine).
9) Postocellar area (0 = flat, 1 = subconvex, 2 = raised).
10) Antenna length (0 = two times or more than two times of head width, 1 = antenna length less than two times of head width).
11) Mesoscutellum (0 = raised, 1 = sub convex, 2 = prismatic, 3 = flat, 4 = pulvinate).
12) Mesepisternum (0 = roundly raised, 1 = obtusely raised).
13) Subapical tooth of claw (0 = subapical tooth of claw longer than apical one, 1 = subapical tooth of claw is shorter than   apical one, 2 = subapical tooth is subequal to apical one).

Table-1: Presence or absence data for fifteen characters for 14 species of the genus *Macrophya* as used in the phylogenetic analysis; *Tenthredo* Linnaeus is included as an outgroup.

Species	Character number														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
M. andreasi Saini and Vasu	1	0	2	1	1	0	0	0	1	1	0	1	0	1	4
M. brancuccii Muche	1	1	3	1	1	2	1	1	0	1	0	1	0	1	1
M. formosana Rohwer	1	1	0	1	0	1	0	3	1	1	0	0	2	1	4
M. gopeshwari Saini *et al.*	1	1	0	0	0	0	1	0	0	0	2	1	0	0	1
M. khasiana Saini *et al.*	0	1	3	0	0	0	1	0	1	1	0	1	0	1	1
M. maculicornis Cameron	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
M. manganensis Saini *et al.*	4	2	0	1	0	1	0	3	0	1	0	1	0	1	2
M. naga Saini and Vasu	1	0	1	1	1	1	1	2	1	0	4	1	0	1	4
M. planata Mocsary	2	0	0	0	0	1	2	0	1	0	2	1	0	1	2
M. pompilina Malaise	0	0	1	0	0	1	0	1	1	0	1	0	0	1	0
M. pseudoplanata Saini *et al.*	3	0	0	0	1	0	1	2	0	0	3	1	0	1	3
M. regia Forsius	0	1	0	0	1	2	0	1	2	1	0	0	0	1	0
M. rufipodus Saini *et al.*	1	1	0	1	0	1	1	1	0	0	1	0	0	1	1
M. verticalis Konow	1	1	0	0	0	2	1	1	0	1	0	1	1	1	0
Tenthredo Linnaeus	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0

14) Metabasitarsus (0 = as long as following joints combined, 1 = longer than following joints combined).

15) Wing appearance (0 = clear, 1 = hyaline, 2 = yellowish hyaline, 3 = dusky hyaline, 4 = smoky hyaline).
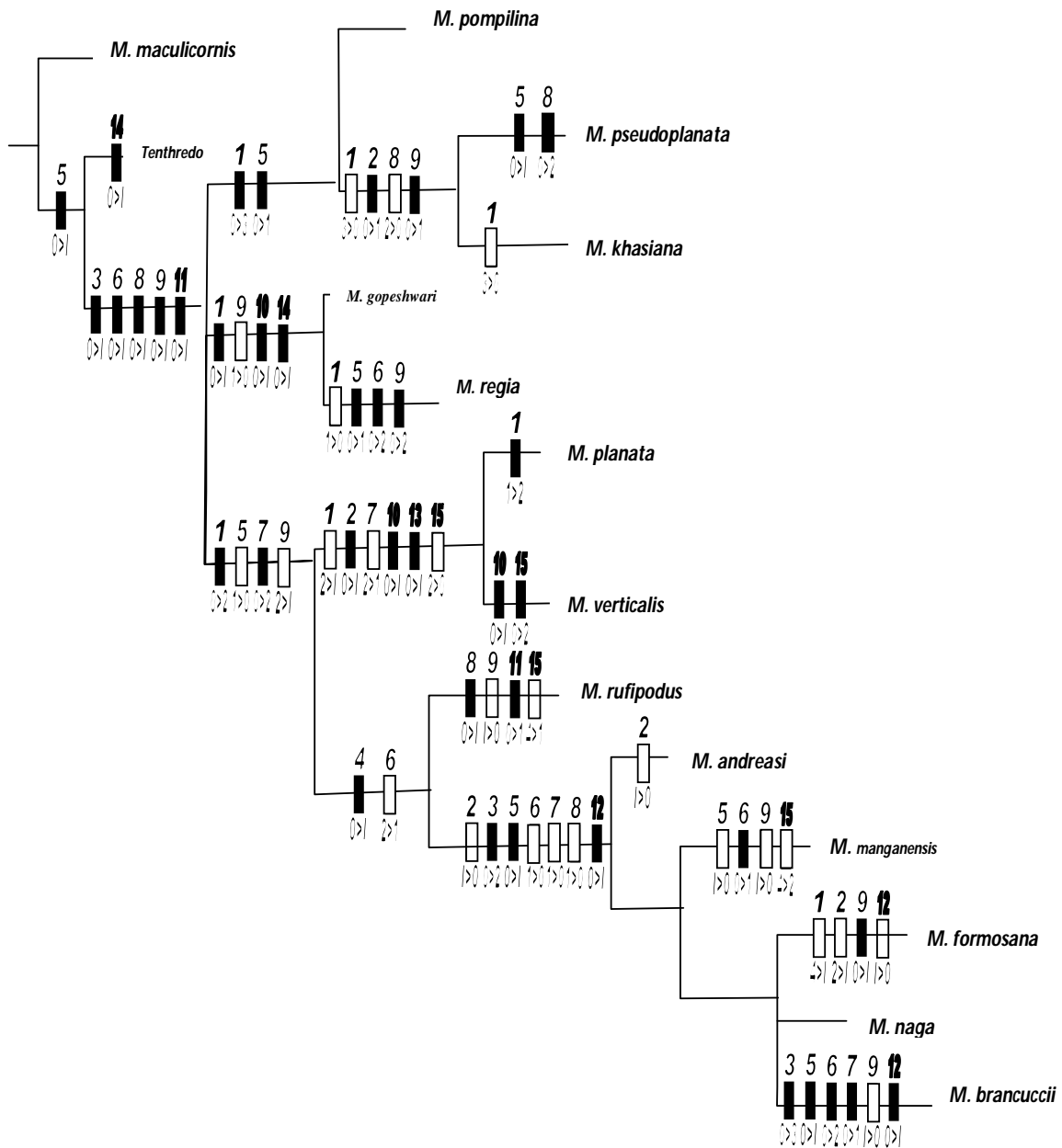

Fig. 1: Strict consensus tree for 14 species of *Macrophya* derived from the 48 most parsimonious trees calculated from the data in Table 1 ; outgroup = *Tenthredo* Linnaeus. Character of the ingroup have been optimized by fast transformation as implemented in PAUP. Character numbers are above the hashmarks; state changes are shown below with the respective primitive and derived conditions reported by a '>'. Apomorphy shown by filled hashmarks and pleisomorphy by open hashmarks.

Results

Parsimony analysis, using equally weighted characters, produced 48 most parsimonious trees (MPTs). Exact analysis by implicit enumeration (the 'i.e.' command of PAUP, which finds almost – parsimonious solutions) of the data in Table 1 resulted in formation of many cladograms which differed only at some places due to presence of more evolutionary events. Successive weighting was applied as a check of the reliability of the results. The main objective of phylogenetics is to correctly reconstruct the evolutionary history based on the observed character divergence between organisms. For estimating phylogenetic trees the most widely used PARSIMONY method (which hold the shortest tree to be the best estimate of the phylogeny) was used. Parsimony method is also called "Occam's Razor" after William of Occam, a 14th Century English philosopher who advocated this minimalist problem solving approach of "shaving away" unnecessary complications. The principle of maximum parsimony is to search for a tree that requires the smallest number of evolutionary changes to explain the differences observed among the OTU under study. As discussed by Goloboff (1991) the term parsimony is still regarded in two different ways by cladists:

1) as the principle of seeking the cladogram with the greatest explanatory power, given the weights the character deserve.

2) as the principle of seeking the cladogram with minimum length under equal weights.

Discussion

In Fig.1 *M. maculicornis* is separated from *Tenthredo* by character five and there occurs formation of derived or apomorphic character. Similarly, all characters shown in cladogram by which taxa are separated from one another and if there occurs formation of apomorphy then that character is shown by filled hashmarks and pleisomorphy by open hashmarks in the cladogram.

Tenthredo got separated from all other taxa by characters 3, 6, 8, 9 and 11 and there occurs formation of derived character and *M. pompilina*

got separated from the latter by character 1 and character 5. Character 1 and character 5 both show apomorphy. So, sign 0>3 or 0>1 shows that there is formation of a derived character from the ancestral character. *M. pseudoplanata* and *M. khasiana* got separated from *M. pompilina* by characters 1, 2, 8 and 9. Similarly, *M. pseudoplanata* got evolved by character 5 and 8 and *M. khasiana* by character 1. *M. gopeshwari* and *M. regia* got separated by characters 1, 9, 10 and 14 and *M. regia* evolved due to characters 1, 5, 6 and 9. *M. planata*, *M. verticalis*, *M. rufipodus*, *M. andreasi*, *M. manganensis*, *M. formosana*, *M. naga* and *M. brancuccii* got separated from all above taxa by characters 1, 5, 7 and 9. *M. planata* and *M. verticalis* again separated from another by characters 1, 2, 7, 10, 13 and 15. The both taxa also got separated by some characters. *M. planata* by character 1 and *M. verticalis* by characters 10 and 15. *M. rufipodus*, *M. andreasi*, *M. manganensis*, *M. formosana*, *M. naga* and *M. brancuccii* got separated from *M. planata* and *M. verticalis* by characters 4 and 6. *M. rufipodus* got evolved due to character 8, 9, 11 and 15 and similarly, all other taxa got separated from other taxa due to presence of new characters present in them. So, extremely specialized forms descended by gradual changes leads to accumulation of certain appropriate features which represents body organization acquired to become complex so as to meet requirements which also underlies the biological maxim.

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