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RESEARCH PAPER

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Phylogeny of genus *Vipio latrielle* (Hymenoptera: Braconidae) and the placement of *Moneilemae* group of *Vipio* species based on character weighting

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Abstract

The Phylogeny of genus *Vipio* is re-investigated. Characters of *moneilemae* species group were added to data to decide the placement of the *moneilemae* species group in genus *Vipio*. Cladistic analysis were conducted which showed that genus *Vipio* is more closely related to genus *Glyptomorpha* Holmgren than to other glyptomorphine genera. The species *moneilemae* appeared as a sister group of lineage comprising *Mesobracon, Angustibracon, Merinotus, Glydinobracon, Bathyaulax, Euvipio, Odeia, Rhytimorpha, Glyptomorpha* and *Vipio*. In the second stage of analysis successive approximations to character weighting were employed which showed *moneilemae* species group as more closely related to genus *Vipio* than to other genera of tribe Glyptomorphini. The analysis showed that genus *Victoroviella* is more near to glyptomorphines than other tribes of Braconinae.

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Introduction

Genus *Vipio* Latrielle is a member of tribe Glyptomorphini of the subfamily Braconinae. In their revision of the Genus *Vipio* Latrielle, Inayatullah *et al.* (1998) hypothesized the monophyly of the *Vipio* as the presence of two groups of clypeal guard setae which are often twisted apically.

Within Glyptomorphini the Vipio is more closely related to Genus Glyptomorpha than other glyptomorphines. Both genera have short marginal cells: the vein SRI (radius) of the fore wing joins the anterior wing margin well before the apex of the wing. Additionally, the scape is longer dorsally than ventrally and the dorsolateral carina is usually present on T1 (Quicke, 1987). Because of these similarities, many previous workers did not correctly distinguish between these two genera and some Glyptomorpha and Vipio species were incorrectly placed. For a time, Glyptomorpha was even regarded as a junior synonym of Vipio (Muesebeck and Walkley, 1951; Shenefelt, 1978; Marsh, 1979). Quicke (1984) rejected the synonymy and considered Glyptomorpha as a valid genus separate from Vipio based on some consistent morphological differences between the two genera.

Vipio, also, is closely related to *Rhytimorpha* Szepligeti. Both genera have short marginal cells, short r vein (typical of Glyptomorphini) and a basomedial area is present on T2. However, the distinctly postfurcal fore wing vein cu-a, moderately to strongly curved fore wing vein 1-M and the distally expanded second submarginal cell in *Rhytimorpha* make it distinct from *Vipio*.

Phylogeny of the genera of the Braconinae and the position of *Vipio* with in tribe Glyptomorphini has been proposed by Quick (1988). Based on the cladistic analyses of 87 selected genera (including *Vipio* as *Isomecus*), subtribes and tribes in his 4 data sets, Quicke presented some preliminary results. He also suggested that additional taxa and characters needed to be added in order to reach a better

understanding of the taxa, and before anyone made further taxonomic changes. The aim of present study was to add more data and character weighting to Quick (1988) data set 1 and to re-investigate the phylogeny of *Vipio* and to decide the placement of *moneilemae* group of species within tribe Glyptomorphini and subfamily Braconinae by using Hennig 86, computer programme.

Material and methods

A good deal of work has been done on the phylogeny of Braconinae [genus *Vipio* (as *Isomecus*, was included by Quicke (1988)]. In the cladistic analyses, he constructed four data sets and examined a total of 86 characters. Not all, but 59, 38, 30 and 22 of the 86 characters were employed in data sets 1, 2, 3 and 4 respectively. For selection of characters see Quicke (1988).

Quicke's data set 1 was utilized in this study. Data set 1 included 48 tribes, subtribes and genera chosen so as to represent most of the variation within the subfamily Braconinae. He employed 59 characters for the analyses of data set 1 and suggested incorporation of more taxa and data before reaching a conclusion and making taxonomic changes.

In the present study we made five additions/changes in his data set 1. One-Characters of Vipio were added to the Data set 1. Two- Characters for moneilemae species group were also added in the data set 1, because moneilemae species group differs from other Vipio species by the absence of notauli and the silky appearance of the clypeal guard setae but is identical in all other characters. By incorporation of these two taxa the number of taxa was raised to 50, while Quicke analyzed 48 taxa (Table- 1). Three-Character 6 in the Quicke's data set 1 had been incorrectly coded as o for Angustibracon while the actual code according to the description should be 1. Therefore correction for character 6 for Angustibracon was done. Four - Quicke utilized 48 characters for Vipio (as Isomecus Kreichbaumer) in his data set 2. We sought and incorporated 11 more characters for Vipio and moneilemae species group

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to his data set 1 (Table-1). <u>Five</u>: Quicke did not employ characters weighting in his work. In the

present work character weighting was employed in the second stage of analysis.

Primitive	0?00000000000000000000?00?0002100?2??00??0 11?01?11001302
Adeshini	0?020000000000011201101000?00?2001101002111001000000?000
Alienoclypeus	1?0010000000000000000000000000000000000
Angustibracon	100011001000110000100000000000000000000
Aphrastobracon	010210001020000200000000002100020100100001300?101?010103302
Archibracon	000010001000002000100001000010000100100?10010010010102302
Aspidobrcon	0?02000000000011120100100110001001001010??111000001000?000
Atanycolus	0?01110010000020000000001100020010010013?001001010103001
Bathyaulax	0000100010000000100000100110110021000000
Bracon	0101000000000101?10000000100020010010100200?0010000001000
Calcaribracon	1100001000000000000000000021000?201111110010000200100003000
Callibracon	00001000?0000000000000000021000200000000
Calobracon	1100110010200102000100000121000200001000012000000
Campyloneurus	0000100011100000020001000110002000001000??0111011011102101
Cervellus	000010001000000100000001000020001000001100100
Chaoilta	100111001000001000000000000000000000000
Coeloides	??0200000000000200200000001000200100100022001001
Compso	1100100010210001000001200002100100000330000000110012011
braconoides	
Cratobracon	100010001000000002000200010000200000000
Cyanopterus	110010000000000000000000000000000000000
Cyclaulax	1101110010210001000000001210002101?0100000000
Digonogastera	000010001000000100100000011000100000000
Euurobracon	100000000000000000000000000000000000000
Euvipio	00001000100100100100000100110100020000022001001
Fraterar	000010001100000100000000000000000000000
Gammabracon	010210001020000100100000020000200100000123021201101?011001
Gluptomorpha	1010002010000000002001001000111110000000
51 1	
Hemibracon	1001110010000020000000002100021010000003?01110100101?3111
Hybogaster	?00000010000010000000000000000000000000
Iphiaulax	00001000100000010000000011100020002000001100100
Lasiophous	1101100000100100000000001110001000010002100100
Leptobracon	01001000?0000000011000000100002100200000010000000
Megabracon	000110000000001000100000001000110000000
Merinotus	1000100011200002001000000000001100200001130000012011?1?00?
Mesobrac	110000001000000002010000000001001210000011011

<i>Mollibra</i> con	010000000000000000000000000000000000000
Moneilemae	100000111010001000000000000101000000000
Myosoma	1100000000000000000010002101001010000000
Nesaulax	0102100011200001001000000210002000001000330011011011013302
Odesia	0002100010010020010010001103000200000120000010001
Pachybracon	0100000110000200100000001000200000101002011101001110?00?
Plaxopsi	1100000010000000010000001100020001000001100100
Psittaci	?00200000000000000000000000000000000000
Rhadinobrcon	1010100010200002000000000001102100200001230000011011012001
Rhamnura	0000000001000100010000000001100210000??0000010000?12001
Rhytimorpha	0?0110001010000100100000000111100000000
Stigmatobracon	0?00000100000000000001100001000110000000
Victoroviella	1011100000000000000000011111200?001001??0000010010?0??0?
Vipio	000000111000001000200100000011120010000110001110101101
Virgulibrcon	000000000000000000000000000000000000000
Zaglyptobracon	010010001110000100000000110001100100000??001001

After incorporating the above changes the combined data (Table 1) were re-analyzed using Hennig 86, a computer programme (Ferris, 86). The options used were "bb" and "mhennig" followed by "nelsen". In the second stage of re-analyses successive approximation to character weighting was employed to see if character weighting would alter the position of *Vipio* or *moneilemae* species group on the cladogram.

Results and discussion

Quicke's data set 1 was re-analyzed for the exact phylogenic position of genus Vipio Latrielle on the basis of character weighting. The re-analysis generated 16 trees with a minimum length of 443 and consistency index of 19. From the 16 trees, a nelson consensus tree was constructed and the following results were obtained. The species moneilemae appeared as a sister group of lineage comprising Mesobracon, Angustibracon, Merinotus, Glydinobracon, Bathyaulax, Euvipio, Odeia, Rhytimorpha, Glyptomorpha and Vipio. Vipio appeared as a sister group of Glyptomorpha, and both appeared as sister group of Rhytimorpha (Fig. 1). The rest of the cladoram was similar to that of Quicke's Fig. 2 for position of the tribe Glyptomorphini. It differed, however, in the positioning of genera within Glyptomorphini.



Fig. 1. Cladogram showing relationship of *Vipio* and moneilemae species group with other braconines before employing character weighting.

In a second stage of the re-analysis, successive approximations to character weighting (Farris, 1969) were employed to see if character weighting would alter the position of *Vipio* or *moneilemae*. After the eighth iteration, 100 trees with a minimum length of 228 and consistency index of 72 were obtained. A nelson consensus tree then was constructed and the position of taxa as they appeared on the cladogram

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(Fig. 2) was as follows. The species, *moneilemae*, appeared as sister group of *Vipio*. *Vipio* (+ *moneilemae*) appeared as a sister group of *Glyptomorpha*. All the three taxa (*moneilemae* + *Vipio* and *Glyptomorpha* appeared as sister group of *Rhytimorpha*.



Fig. 2. Cladogram showing relationship of *Vipio* and moneilemae species group with other braconines after employing character weighting.

Quicke (1988) analysis shows genus *Victoroviella* as a sister group of Bathyaulacini + Glyptomorphinae which he states as reasonable (see Quicke Fig. 2). He further states that additional characters will have to be found before *Victoroviella* is placed with certainty. Our analysis, after employing character weighting, shows *Victoroviella* as more closely related to Glyptomorphini than Bathyaulacini as shown in Fig. 2.

To summarize, in the cladogram generated (Fig. 1 and 2), *Vipio* appeared in close association with other genera of the tribe Glyptomorphini. Based on this new analysis, *Vipio* is more closely related to *Glyptomorpha* than to other members of the tribe Glyptomorphini of the subfamily Braconinae. Within Glyptomorphini *moneilemae* species group appeared as more closely related to *Vipio* than other glyptomorphine genera which justify its placement in *Vipio*.

Phylogenetic Position of Vipio within the Braconinae

In his cladistic analyses, Quicke (1988) utilized four data sets and examined a total of 86 characters. Not all, but 59, 38, 30 and 22 characters were employed in data set 1, 2, 3 and 4 respectively. Quicke's data set 1 included 48 tribes, subtribes and genera chosen so as to represent most of the variation within the subfamily. Data set 2 included 34 genera of Bathylaucini and Glyptomorphini, together with a number of potentially related taxonomic groupings. In data set 3, a reduced subset of data was analyzed, and in the 4th data set, 21 genera belonging to the tribe Braconini, including the *Plesiobracon* group were analyzed.

Quicke included the prominent member of the tribe Glyptomorphini, *Glyptomorpha* Holmgern, in date set 1. In the second data set, *Vipio* (as *Isomecus* Kriechbaumer) was added. In data set 3 and 4 other braconines were added.

In the Quicke's analyses of the data set 1, *Glyptomorpha* Holmgren + *Rhytimorpha* Szepligeti were shown to be the sister group of *Angustibracon* Quicke. These three genera (*Angustibracon*, *Glyptomorpha*, *Rhytimorpha*) + (*Merinotus* + *Rhydinobracon*) [Glyptomorphini] were shown to be the sister group of *Odesia* [Bathyaulacini]. In his analyses of data set 2, again Bathylaucini and Glyptomirphini were shown to be sister groups. Within the Glyptomorphini, the *Glyptomorpha*+ *Teraturus* combination appeared as sister group of *Vipio* (see Quicke, 1988, Fig. 2).

In the Quicke's data analysis *Angustibracon* was shown to be the sister group of *Glyptomorpha* + *Rhytimorpha*. In our analysis of data set 1 *Vipio* appeared as sister group of *Glyptomorpha* when data for *Vipio* was incorporated into the Quicke's data set 1. This change in the position of *Angustibracon* occurred because of character 6, which was incorrectly coded for the genus. In his analysis of the second data set, Quicke included mostly genera of the tribe Glyptomorphini. *Vipio* (as

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Isomecus Kreichbaumer) was shown to be a sister group of *Glyptomorpha* + *Teraturus*. Since *Teraturus* has been regarded as a subgenus of *Glyptomorpha* (Sarhan and Quicke, 1989), therefore it can be said that according to Quicke, and the present re-analysis, *Vipio* is more closely related to *Glyptomorpha* than to other glyptomorphine genera. The study showed *Victoroviella* closely related to glyptomorphine genera. Our analysis also showed the *moneilemae* group of species, though a little different from other *Vipio* species, is more closely related to *Vipio* than other glyptomorphines and therefore belong to genus *Vipio*.

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