



Phylogenetic analysis of Indian species of genus *Himalopsyche* Banks (Trichoptera: Spicipalpia; Rhyacophilidae: Rhyacophilinae)

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Abstract

Phylogenetic analysis was conducted for 19 species of the genus *Himalopsyche* (Trichoptera: Rhyacophilidae) using the phylogenetic analysis package PAUP, based on 12 of the morphological characters most commonly used for *Himalopsyche* species identification. Species descriptions were primarily taken from literature contributed by Morton (1900), Martynov (1930, 1935, 1936), Kimmins (1952) and Schmid (1963, 1966). Parsimony analysis, using equally weighted characters, produced 27 trees and the strict consensus tree derived from these identified two groupings are to be present in all 27 trees. The results are discussed in terms of evolutionary trends or remarkable diversity of genitalic types in the males.

Keywords: *Phylogenetic analysis, Trichoptera, Himalopsyche, Genitalic types.*

Introduction

The small genus *Himalopsyche* originated in the Oriental region and was first described by Banks (1940). All the species occur in Oriental region with exception of *H. phryganea* (Schmid, 1989) which is distributed in North America. So all species except *H. phryganea* are thought to have been designated as endemic Oriental species. From the Oriental region this genus is represented by 38 species out of which 19 are from India alone. Indian species are mainly contributed by Morton (1900), Martynov (1930, 1935, 1936), Kimmins (1952) and Schmid (1963, 1966) to the tune of 1, 3, 2 and 13 species respectively. On the basis of so many morphological affinities this genus is closely related to *Rhyacophila*, of which it seems to be a specialized off shoot.

When viewed from the economic point of view, larvae of this group are important and beneficial components of the trophic dynamics and energy flow in the lakes, rivers and streams they inhabit (Resh and Rosenberg, 1984). This group is considered the most useful and important aquatic organisms for monitoring climatic

changes and are widely used in bio monitoring surveys. Parsimony analysis is used to investigate phylogenetic relationships among *Himalopsyche* species, using data based on morphological characters most commonly used for *Himalopsyche* identification.

Materials and Methods

Species descriptions were derived primarily from literature contributed by Morton (1900), Martynov (1930, 1935, 1936), Kimmins (1952) and Schmid (1963, 1966) and the characters used in the analysis were those given comparably for all, or almost all, species. *Rhyacophila* Pictet 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 12 morphological characters were used in the phylogenetic analysis. These were:-

- 1) Inferior appendage (0= uniarticulated, 1= biarticulated).
- 2) Preanal appendage (0=completely fused with segment X, 1= free from segment X).

- 8) Anal sclerite (0= Anal sclerite with long root invaginated upto half of segment IX, 1 = Anal sclerite with short root not invaginated into segment IX).
- 9) Segment IX (0= quite prominent forms a roof over segment X, 1 = reduced does not form a roof over segment X).
- 10) Paramere (0= absent, 1= present).

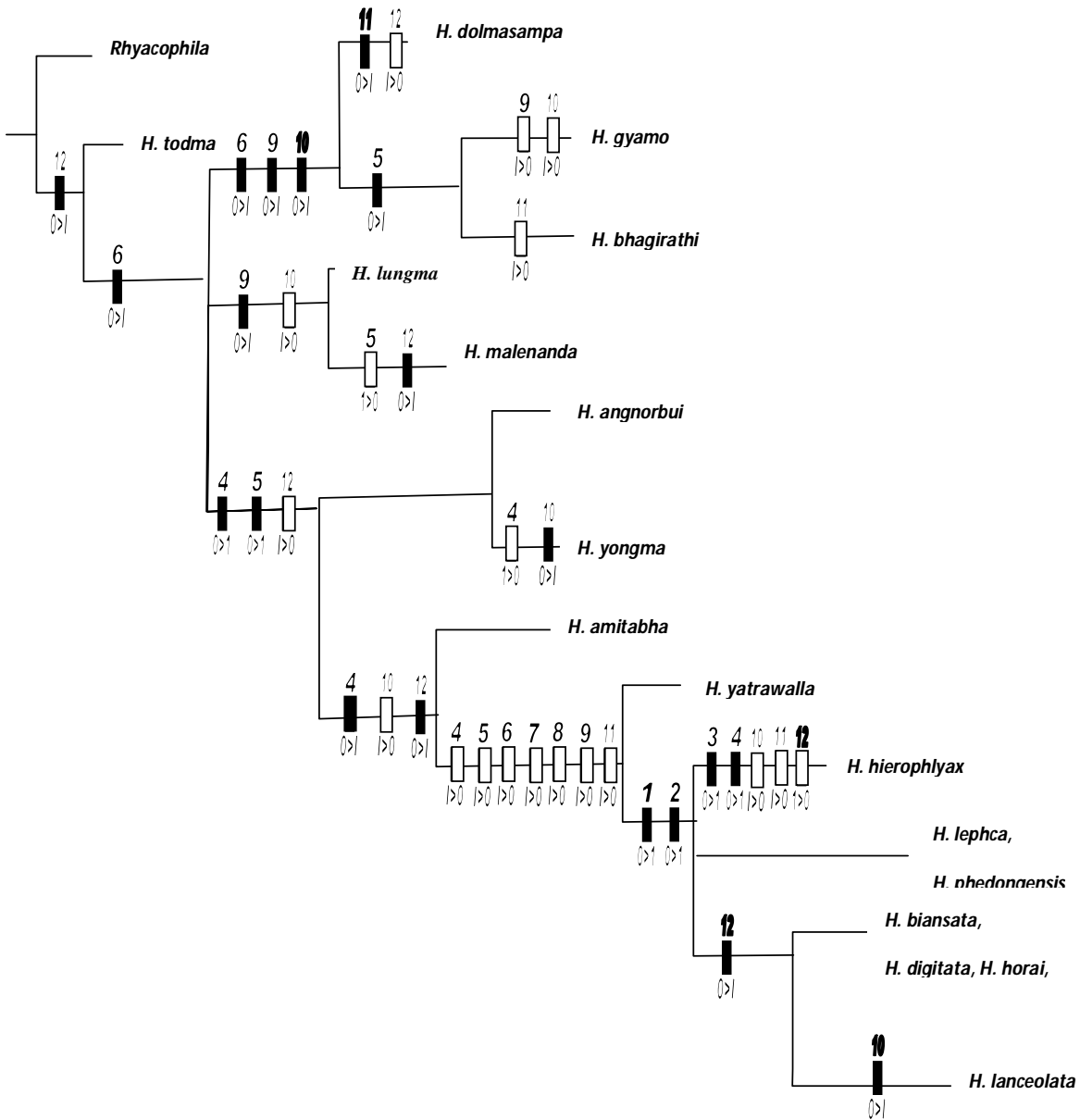


Fig. 1: Strict consensus tree for 19 species of *Himalopsyche* derived from the 27 most parsimonious trees calculated from the data in Table 1; outgroup = *Rhyacophila* Pictet. Character of the ingroup have been optimized by fast transformation as implemented in PAUP. Character numbers are above the hashmarks; state changes are shown below with the respective primitive and derived conditions reported by a '>'. Apomorphy shown by filled hashmarks and plesiomorphy by open hashmarks.

- 11) Scape to pedicel ratio (0= If scape length is less than half of pedicel length, 1= If scape length is more than half of pedicel length).
- 12) IATS : MB : OATS* (0= If MB ratio greater than IATS but smaller than OATS, 1= If MB ratio smaller than IATS but greater than OATS).

* IATS–Inner Apical Tibial spur, MB–Meta basitarsus, OATS–Outer Apical Tibial Spur

Results

Parsimony analysis, using equally weighted characters, produced 27 most parsimonious trees (MPTs). 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 and MAXIMUM LIKELIHOOD methods were used. Parsimony method also known as “Occam’s Razor” after William of Occam, a 14th century English Philosopher who advocated this minimalist problem solving approach of “shaving away” unnecessary complications and the principle of maximum likelihood, is a tree with the highest likelihood and is the best estimate of the true phylogeny. The species *Himalopsyche todma* differs from all other species of *Himalopsyche* by the single character of apically bifidation of anal sclerite (character 6). To further investigate the MPTs the majority rule consensus method was used.

Discussion

In Fig.1 *H. todma* got separated from *Rhyacophila* by character 12 and *H. todma* differed from all other species of *Himalopsyche* due to apically bifidation of anal sclerite. Similarly, all characters are shown in cladogram by which taxa got separated from one another. The derived consensus tree identified two groupings to be present in the cladogram. The first group was

composed of two unique species *H. gyamo* and *H. bhagirathi*. They grouped on the basis of shape of anal sclerite. The second group contained nine species *H. hierophylax*, *H. lepcha*, *H. phedongensis*, *H. biansata*, *H. digitata*, *H. horai*, *H. maitreya*, *H. tibetana* and *H. lanceolata*. They clustered together due to biarticulation of inferior appendage. *H. dolmasampa* got separated from *H. todma* by characters 6, 9 and 10. All characters showed apomorphy. So sign 0>1 showed that there was formation of derived character from ancestral character. *H. gyamo* and *H. bhagirathi* got separated from *H. dolmasampa* by character 5. *H. gyamo* got evolved by characters 9 and 10 and *H. bhagirathi* by character 11. *H. lungma* and *H. malenanda* got separated by characters 9 and 10. Character 9 showed apomorphy and character 10 showed pleisomorphy. *H. malenanda* got evolved due to characters 5 and 12. Character 12 showed maximum evolution. *H. angnorbui* and *H. yongma* got separated from *H. malenanda* by characters 4, 5 and 12. *H. yongma* got evolved by characters 4 and 10. *H. amitabha* got separated from latter by characters 4, 10 and 12. Similarly, *H. yatrwalla* got separated from *H. amitabha* by characters 4, 5, 6, 7, 8, 9 and 11. All the characters showed pleisomorphy. *H. hierophylax* got separated from *H. yatrwalla* due to presence of characters 1 and 12 and got evolved by characters 3, 4, 10, 11 and 12. Only the characters 3 and 4 showed apomorphy. *H. lepcha* and *H. phedongensis* got separated from *H. hierophylax* but they both shared the same characters. *H. biansata*, *H. digitata*, *H. horai*, *H. maitreya* and *H. tibetana* got separated from *H. phedongensis* by character 12 and they all shared the same characters but *H. lanceolata* developed new character 10 and got separated from *H. biansata*, *H. digitata*, *H. horai*, *H. maitreya* and *H. tibetana*. To conclude, this can be said that species of genus *Himalopsyche* Banks exhibit a remarkable diversity of genitalic types in the males.

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