



WWJMRD 2017; 3(9): 318-321

www.wwjmr.com

International Journal

Peer Reviewed Journal

Refereed Journal

Indexed Journal

UGC Approved Journal

Impact Factor MJIF: 4.25

e-ISSN: 2454-6615

Naina Khullar

Department of Zoology and
Environmental Sciences,
Punjabi University, Patiala,
India

Devinder Singh

Department of Zoology and
Environmental Sciences,
Punjabi University, Patiala,
India

Chandan Kumar Jha

Department of Human
Genetics, Punjabi University,
Patiala, India

Correspondence:

Naina Khullar

Department of Zoology and
Environmental Sciences,
Punjabi University, Patiala,
India

Calliphoridae: Cladogram Based On Morphological Characters

Naina Khullar, Devinder Singh, Chandan Kumar Jha

Abstract

DNA studies are nowadays predominant in phylogenetics. But morphological approach is still the most widely accepted approach among the taxonomists. In the present study, the author has for the first time tried to construct a cladogram among the calliphorid species based on morphological traits which further stilted the molecular analysis. This analysis was validated through mtDNA studies. Till date, little comprehensive morphological and molecular analysis has been conducted for calliphorids of India.

Keywords: Cladogram, Calliphorids, Apomorphic, Pleisomorphic

Introduction

Calliphorids are immensely valuable insects. Many earlier workers have carried out alpha and beta level of taxonomy on calliphorids but none of them attempted gamma level of taxonomy based on morphological characters. The author has followed Cladistics approach to derive interrelationships among different calliphorid species.

Methodology

The morphological support for this group strongly indicates some of the major autapomorphies. Rognes (1997) tried phylogenetic analysis based on larval and adult morphological traits for 23 monophyletic taxa within Oestroidea based on parsimony. Numerous worthwhile morphological keys are available which can be considered for analysis (e.g. Whitworth, 2006 and Akbarzadeh *et al.*, 2015). A cladogram is a diagram showing relations among different organisms without giving any idea about how ancestors are related and how they have changed over time (Foote, 1996 and Mayr, 2009). A cladogram gets its name from clado (branch or clade) and gamma (trait). A clade is group of organisms descending from most recent common ancestor. Intricate morphological keys are available which need to be studied precisely to evaluate apomorphic and pleisomorphic traits. Apomorphic trait act as a defining trait for a particular species and an autapomorphic trait usually indicates extent of divergence of a species from its closest relation. The cladograms are usually based on synapomorphic traits, while pleisomorphic characters are not diagnostic of a species and so are avoided. Another important point to be considered while constructing a cladogram is that, the same attribute (considered for analysis) may represent an apomorphic trait on one branch and pleisomorphic relative to other branches of a cladogram. In the under mentioned cladogram, some important apomorphic traits have been selected to construct the cladogram. Also to validate the reliability of this cladogram, phylogenetic tree was constructed among the various calliphorid species using MEGA 5 phylogenetic software (figure 2). This analysis was based on *COI* gene fragments.

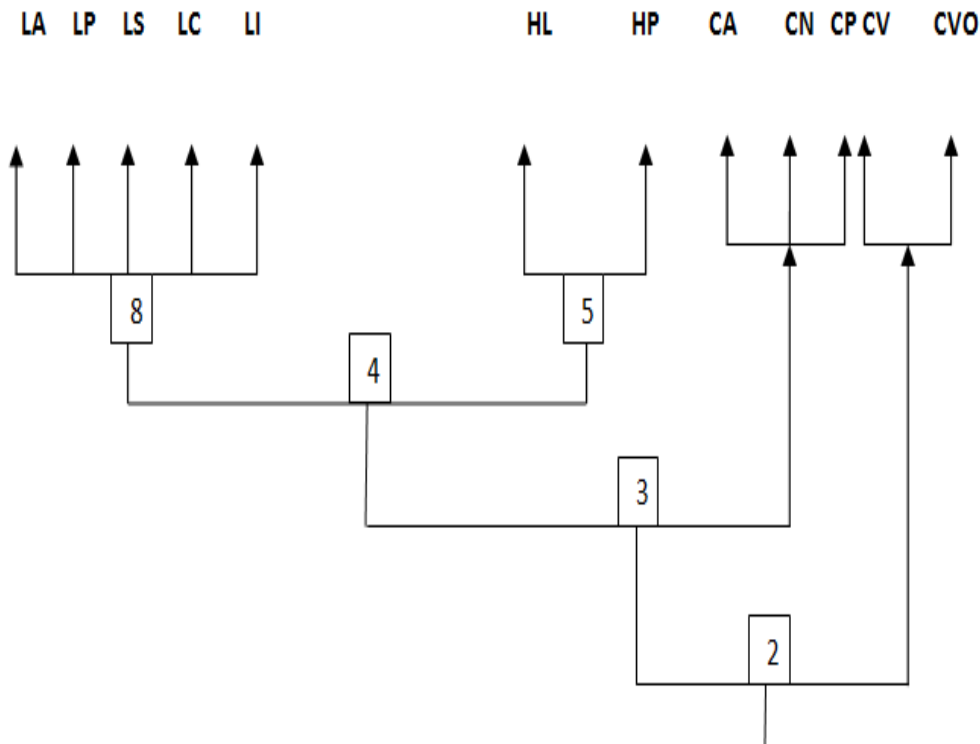


Fig. 1: Caldogram based on morphological attributes (here CV-Calliphora vicina, CVO-Calliphora vomitoria, CP-Chrysomya pinguis, CN-Chrysomya nigripes, CA- Chrysomya albiceps, LP-Lucilia porphyrina, LA-Lucilia ampullacea, LS-Lucilia sericata, LC-Lucilia cuprina, HL-Hemipyrellia ligurriens, and HP-Hemipyrellia pulchra)

Table 1: Data table showing morphological traits possessed by different calliphorid species (here CV-Calliphora vicina, CVO-Calliphora vomitoria, CP-Chrysomya pinguis, CN- Chrysomya nigripes, CA- Chrysomya albiceps, LP-Lucilia porphyrina, LA-Lucilia ampullacea, LS-Lucilia sericata, LC-Lucilia cuprina, HL-Hemipyrellia ligurriens, and HP-Hemipyrellia pulchra). The morphological traits (considered in the above table) (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22) are mentioned below. The table indicates whether the characteristic is present or not.

	CV	CVO	CP	CN	CA	LP	LA	LS	LC	LI	HL	HP
1	√	√	√	√	√	√	√	√	√	√	√	√
2	X	X	√	√	√	√	√	√	√	√	√	√
3	X	X	√	√	√	X	X	X	X	X	X	X
4	X	X	X	X	X	√	√	√	√	√	√	√
5	X	X	X	X	X	X	X	X	X	X	√	√
6	X	X	X	X	X	X	X	X	X	X	√	X
7	X	X	X	X	X	X	X	X	X	X	X	√
8	X	X	X	X	X	√	√	√	√	√	X	X
9	X	X	X	X	X	X	X	√	X	X	X	X
10	X	X	X	X	X	X	X	X	√	X	X	X
11	X	X	X	X	X	X	√	X	X	X	X	X
12	X	X	X	X	X	√	X	X	X	X	X	X
13	X	X	X	X	X	X	X	X	X	√	X	X
14	X	X	√	X	X	X	X	X	X	X	X	X
15	X	X	X	√	X	X	X	X	X	X	X	X
16	X	X	X	X	√	X	X	X	X	X	X	X
17	√	X	X	X	X	X	X	X	X	X	X	X
18	X	√	X	X	X	X	X	X	X	X	X	X
19	√	√	√	√	√	√	√	√	√	√	√	√
20	√	√	√	√	√	√	√	√	√	√	√	√
21	√	√	√	√	√	√	√	√	√	√	√	√
22	√	√	√	√	√	√	√	√	√	√	√	√

Morphological Traits

- Sharply bent wing vein M and bristles on meron (Characteristic of all Calliphoridae)
- Metallic lustre (Characteristic of Luciliinae and Chrysoyminae; absent in Calliphorinae)
- Hair on stem vein (Characteristic of Chrysoyminae)
- Bare dorsal lower calypter (Characteristic of Luciliinae)
- Katergite with long hairs (Characteristic of Hemipyrellia)
- Katergite with long hairs and third antennal segment dark (Characteristic of Hemipyrellia ligurriens).
- Katergite with long hairs and third antennal segment dark (Characteristic of Hemipyrellia pulchra).

8. Bare katergite (Characteristic of *Lucilia*)
9. Bare katergite with yellow basicosta and 6-8 hairs on posterior slope of humeral callus (Characteristic of *Lucilia sericata*)
10. Bare katergite with yellow basicosta and 0-4 hairs on posterior slope of humeral callus (Characteristic of *Lucilia cuprina*)
11. Bare katergite with basicosta brown and white calypter (Characteristic of *Lucilia ampullacea*)
12. Bare katergite with basicosta brown and brown calypter (Characteristic of *Lucilia porphyrina*)
13. Bare katergite with lower white calypter and no marginal bands on III and IV abdominal segments (Characteristic of *Lucilia illustris*)
14. Post gena with black hair and hairs on stem vein (Characteristic of *Chrysomya pinguis*)
15. Hairs on V tergite and hair on stem vein (Characteristic of *Chrysomya nigripes*)
16. Proepimeral setae and hair on stem vein (Characteristic of *Chrysomya albiceps*)
17. Three pairs of post sutural acrostichial setae and genal dilation yellow-red (Characteristic of *Calliphora vicina*)
18. Three pairs of post sutural acrostichial setae and genal dilation black (Characteristic of *Calliphora vomitoria*)
19. Row of bristles on meron (Characteristic of

Calliphoridae)

20. Plumose (hairy) arista (Characteristic of Calliphoridae)
21. Having two notopleural bristles and a hindmost posthumeral bristle located lateral to pre-sutural bristle (Characteristic of Calliphoridae)
22. Presence of haltere (Characteristic of Diptera)

Discussion

Here the traits 1, 19, 20, 21, 22 are pleisomorphic traits, thus, were not considered in the cladogram. Trait 2 is a synapomorphic trait which is shared by members of the two sub families namely Luciliinae and Chrysomyinae, while trait 3 stands out to be an autapomorphic trait in case Chrysomyinae. Again, trait 4 is autapomorphic to the sub family Luciliinae but synapomorphic to the members of the sub family Luciliinae. Similarly, trait 5 and 8 are characteristic of the genus *Hemipyrellia* and *Lucilia* respectively so are considered as autapomorphic traits respectively, but but synapomorphic to their respective members. Rest of the traits are characteristic to the respective species, thus, all of these represent autapomorphic traits specific to each species. The observations from the cladogram (figure1) were further supported by phylogenetic tree relationships derived using mtDNA.

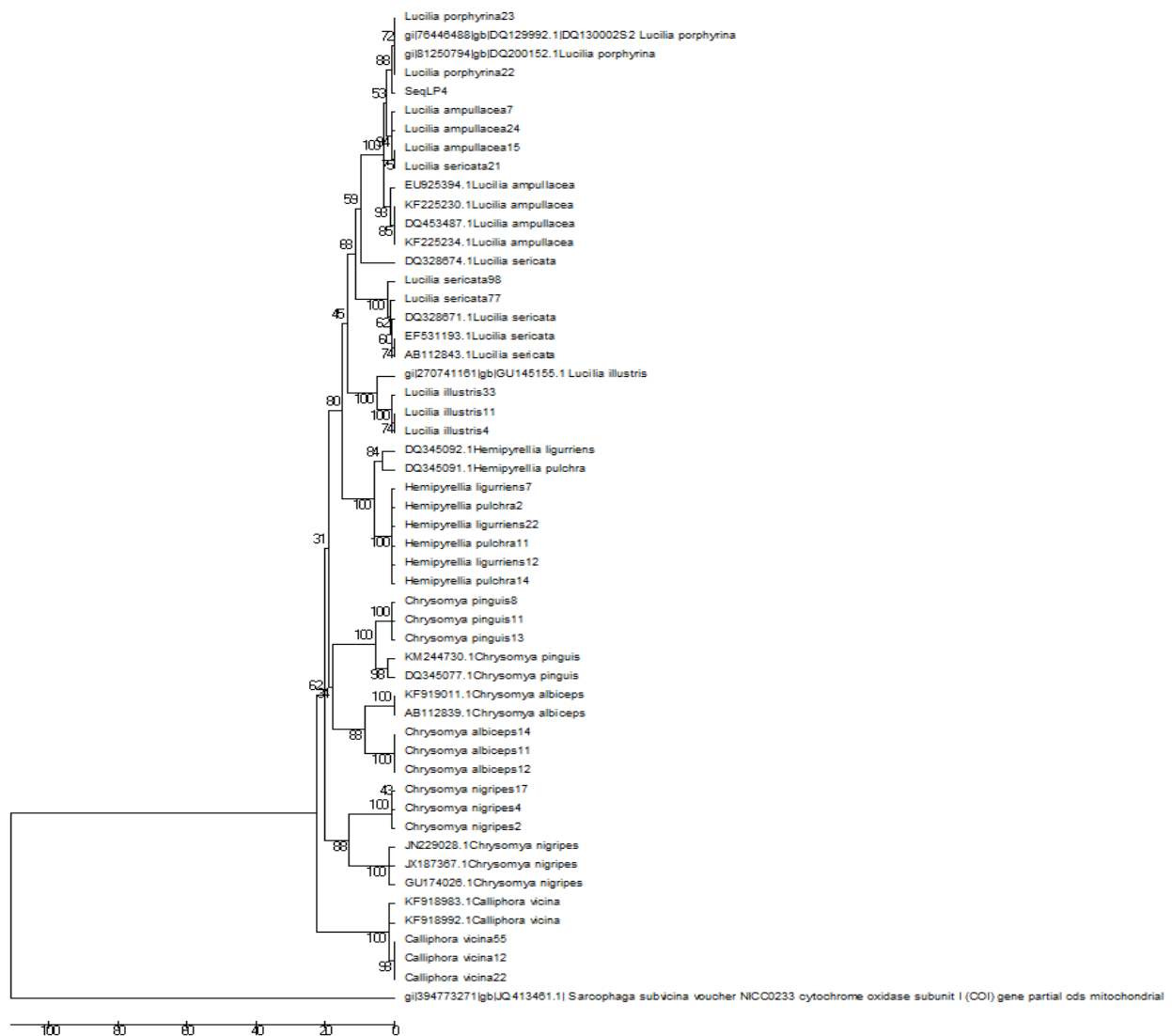


Fig. 2: The evolutionary history was inferred using the UPGMA method. Evolutionary analyses were conducted in MEGA5.

Conclusion

Both the approaches (molecular and morphological) clearly separated the three subfamilies in the trees (represented by different branches). Also, the various species rightly got allotted to their respective genera and subfamilies. Thus, the interrelationships derived between different species based on morphological attributes aggrandized the morphotaxonomy from alpha to gamma level.

Acknowledgements

This study was funded by Innovation in Science Pursuit for Inspired Research (INSPIRE), an innovative programme sponsored and managed by the Department of Science & Technology, New Delhi.

Disclosure

The authors are not conversant of any memberships, financial holdings, affiliations that could raise a conflict of interest.

References

1. Akbarzadeh, K., Wallman, J.F., Sulakova, H. and Szpila, K. 2015. Species identification of Middle Eastern blowflies (Diptera: Calliphoridae) of forensic importance. *Parasitol. Res.*, **114**(4): 1463-1472.
2. Foote, M. 1996. On the Probability of Ancestors in the Fossil Record. *Paleobiology*, **22** (2): 141-51.
3. Mayr, E. 2009. Cladistic analysis or cladistic classification? *J.Zool. Syst.Evol. Res.*, **12**: 94.
4. Rognes, K. 1997. The Calliphoridae (blowflies) (Diptera: Oestroidea) are not a monophyletic group. *Cladistics*, **13**: 27-66.
5. Whitworth, T. 2006. Keys to the genera and species of blow flies (Diptera: Calliphoridae) of America north of Mexico. *Proc. Entomol. Soc. Wash.*, **108**(3):689-725.