



Revisiting taxonomic problems in the genus *Myrmaplata* Prószyński, 2016 (Araneae: Salticidae)

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Abstract

The genus *Myrmaplata* is a small genus containing five species of ant mimicking jumping spiders, which was earlier part of the genus *Myrmarachne*. It has many taxonomic issues. Present work is an effort to revisit these problems and address them using an integrative approach employing literature survey and phylogenetic studies. In this regard, literature survey concerning this genus as well as some species of the genus *Myrmarachne* was conducted. *Myrmaplata plataleoides* and *Myrmaplata wanlessi* were dealt with in this work. Reports of morpho-variants in case of *Myrmaplata plataleoides* and absence of the report of female in case of *Myrmaplata wanlessi* make these genera a matter of special taxonomic concern. Barcode region of mtCO1 gene was sequenced from both male and female spiders of a recently described melanic morpho-variant of *Myrmaplata plataleoides* for comparison with the typical form. Publicly available barcode region of mtCO1 sequences were retrieved for species of the genus *Myrmaplata* and the genus *Myrmarachne* for phylogenetic studies. Phylogenetic analysis reveals the existence of significant evolutionary divergence in the morpho-variant with respect to the typical form. Previous report of assortative mating in some morpho-variants of this spider and the presence of a significant evolutionary divergence between the melanic morpho-variant and the typical red form as found in the present study suggest that polymorphic mimicry in *Myrmaplata plataleoides* is a magic trait. Literature survey and phylogenetic analysis point towards the possibility of conspecificity between *Myrmaplata wanlessi* and *Myrmarachne lambirensis*. These analyses also suggest removal of *Myrmaplata wanlessi* from the genus *Myrmaplata* and renaming it back as *Myrmarachne wanlessi*. But to confirm its specific identity with more accuracy a through re-examination of its holotype is suggested vis-à-vis the holotype of *Myrmarachne lambirensis*. Need to revisit similar issues associated with the genus *Myrmarachne* in light of integrative taxonomy has also been highlighted.

Keywords: Barcoding, conspecificity, myrmecomorphy, polymorphic mimicry, temporal myrmecomorphy

Introduction

Myrmaplata Prószyński, 2016 [17] is a genus of jumping spiders exhibiting Batesian mimicry with morphological as well as behavioural resemblances towards ants. Only five described species are known from this genus, viz. *Myrmaplata aureonigra* Edmunds & Prószyński, 2003 [9], *Myrmaplata hispidacoxa* Edmunds & Prószyński, 2003 [9], *Myrmaplata plataleoides* O. Pickard-Cambridge, 1869, *Myrmaplata turiformis* Badcock, 1917 and *Myrmaplata wanlessi* Edmunds & Prószyński, 2003 [9] (Caleb 2016 [6]; Prószyński 2016 [17]; Caleb 2020 [5]; Caleb & Shankaran 2022; World Spider Catalog 2022) [4]. All these five species of the genus *Myrmaplata* exhibit similarity in the basic structure of epigyne which is the characteristic feature and the basis of creation of this genus. It is differences in the morphology of the male palp among these species which distinguishes them from one another (Prószyński, 2018) [16]. This genus was carved out of *Myrmarachne* MacLeay, 1839, which is the largest genus of ant mimicking jumping spiders, on the basis of morphological differences in the structure of its copulatory organs (Prószyński 2016 [17]; Yamasaki *et al.* 2018) [25]. This reclassification is entirely morphological and, molecular and phylogenetic studies pertaining to this genus are missing (Ramachandra and Hill, 2018) [18].

Myrmaplata plataleoides, the type species of the genus *Myrmaplata*, is one of the most elusive species of the animal kingdom. Occurrence of morpho-variants makes this species prone to misidentifications (Caleb, 2020 [5], 2016 [6]; Ganesh Kumar, M. & Mohanasundaram, 1998) [10]. Occurrence of

morpho-variants in *Myrmaplata plataleoides* is attributed to its ability to mimic different ant species. Polymorphic mimicry is manifested both in terms of morphological as well as behavioural differences among different morpho-variants (Cushing, 2012) [7]. This spider has been reported to exhibit gradation in its body colouration, displaying different shades of orange, red, brown and black in samples collected from near the colonies of different ant species (Borges *et al.*, 2007) [3]. Different moults of the typical *Myrmaplata plataleoides* individuals has also been reported to mimic different ant species (Bhattacharya, 1938) [2]. Recently an isolated population of a melanic morpho-variant has been identified as *Myrmaplata plataleoides* based on the similarity in its copulatory structures and colour pattern of legs with the type specimen. Although identified as *Myrmaplata plataleoides*, this morpho-variant doesn't mimic *Oecophylla smaragdina* Fabricius, 1775 unlike the typical red individuals and exhibits a unique kind of ant mimicry which has been termed as temporal myrmecomorphy where different moults of the spider mimic different worker sub-castes of *Camponotus compressus* Fabricius, 1787 (Kumar *et al.*, 2022) [12]. Based on differences in behaviour and external appearance like colour, shape of chelicerae and overall body shape, some workers are skeptical to consider it *Myrmaplata plataleoides* and have suggested to consider this recently described morpho-variant population as a different species altogether (Hill and Abhijith, 2022) [11]. Due to these problems, few workers still prefer considering this species to be part of the genus *Myrmarachne* (Ramachandra and Hill, 2018) [18]. All

these issues make it necessary to study morpho-variants too at par with the type specimen in order to address and solve the taxonomic problems associated with this species.

Therefore, in present study, an integrative approach has been employed to study taxonomy of *Myrmaplata plataleoides* as well as the genus *Myrmaplata* as a whole. Literature survey involving all previous literature and datasets pertaining to these taxa as well as some of the species of the genus *Myrmarachne* has been carried out. DNA barcode region of the mtCO1 gene was sequenced from the recently described melanic morpho-variant of *Myrmaplata plataleoides* (Kumar *et al.*, 2022) ^[12], which was used for comparison with the DNA barcode of typical red individual. Phylogenetic analysis was carried out using this mtCO1 sequence along with the publically available mtCO1 sequences of other *Myrmaplata* species and the members of the genus *Myrmarachne*. It should be noted that for most of these species only mtCO1 DNA sequences are publically available. Other genomic sequence information is not available for most of these species. Therefore, phylogenetic studies were conducted using mtCO1 DNA sequences only. Based on the inputs from the literature survey and phylogenetic analysis, in present work, some of the most important taxonomic problems associated with the genus *Myrmaplata* have been addressed in the light of integrative taxonomy.

Materials and methods

Sample used for the study

A female and a male specimen of the recently described melanic morpho-variant of *Myrmaplata plataleoides*

(Kumar *et al.*, 2022 ^[12], voucher number MPMVF03 and MPMVM04, Zoology Museum, University Department of Zoology, Vinoba Bhave University, Hazaribag) were used for the present study. These specimens were stored in 70% ethanol for preservation. The habitus and the previously studied (Kumar *et al.*, 2022) ^[12] microscopic slides of the reproductive structures of both the male and the female spiders were photographed using a Leica (Wetzlar, Germany) DFC 425C digital camera mounted over a Leica M205FA stereozoom automontage microscope (Figure 1).

DNA extraction, PCR amplification and DNA sequencing

DNA was extracted from the legs of the ethanol preserved specimens of the male and the female spider using QIAGEN QIAmp DNA Investigator Kit according to the manufacturer's protocol. The extracted DNA was quantified using a Thermo Scientific NanoDrop 2000 Spectrophotometer and stored at -20°C for future use. PCR was conducted to amplify the barcode region of mitochondrial cytochrome oxidase subunit I (mtCOI) gene. Table 1 contains details of the respective forward and reverse primers used for the amplification and sequencing of these gene segments. After PCR, amplicons were run on a 2% agarose gel containing ethidium bromide for visualization of amplicons under UV light using the gel documentation system. After detection on gel, sequencing of the PCR product was conducted. Sequencing of mtCO1 amplicon was conducted for both the male and the female spiders. The resulting chromatograms were visualized and analyzed using FinchTV 1.4.0 (Geospiza Inc.).

Table 1: Details of primers used for PCR and sequencing

S. No.	Genomic Region	Primer Pair	Primer Sequences (5'-3')	References
1.	CO1	FORWARD	GGTCAACAAATCATAAAGATATTGG	Folmer <i>et al.</i> , 1994
2.	CO1	REVERSE	TAAACTTCAGGGTGACCAAAAAATCA	Folmer <i>et al.</i> , 1994

Sequence submission

All the raw chromatogram files (.ab1 format files) and the raw sequence files (.fasta format files) were submitted to Barcode of Life Data System (BOLD) database (Ratnasingham and Hebert, 2007) ^[19]. Processed sequence files of mtCO1 gene (.fasta format files) were submitted to National Center for Biotechnology Information (NCBI)-GenBank. During processing terminal regions of the DNA sequence were trimmed and the regions aligning with the

Reference sequence (BOLD ID- GBCH11719-13) were retained. Submission details of respective sequences are summarized in Table 2. Voucher IDs of both the specimens were also registered with BOLD database and GenBank while sequence submission. The submitted sequences, voucher IDs and its barcodes are clustered under the BOLD BIN (Barcode Index Number) registry ID: ADS9399 (<http://dx.doi.org/10.5883/BOLD:ADS9399>).

Table 2: Details of the DNA sequences submitted to online repositories

S.No.	Genomic Region	Voucher ID	BOLD Process ID	Gen Bank Accession Number	Sex of the sample
1.	mtCO1	MPMVM04	MPMV002-22	OQ127703	Male
2.	mtCO1	MPMVF03	MPMV001-22	OQ121835	Female

Literature survey

Literature survey was conducted for all described species of the genus *Myrmaplata* and some species of the genus *Myrmarachne* using resources available on World Spider Catalog, 2022. The criteria that which species of the genus *Myrmarachne* is selected for the literature survey is based on the availability of its barcode sequence information on the BOLD database. Digital illustrations and the images of each described species of the genus *Myrmaplata* and some species of the genus *Myrmarachne* were analyzed carefully apart from their published written descriptions. The genus

Myrmarachne was studied along with the genus *Myrmaplata* because the genus *Myrmaplata* was part of the genus *Myrmarachne* previously and it was thought that studying the genus *Myrmarachne* could yield important cues for addressing the taxonomic problems associated with the genus *Myrmaplata*. Barcode sequences of the mtCO1 gene for the genus *Myrmaplata* and the genus *Myrmarachne* were retrieved from BOLD database (Table 3). It should be noted that out of the five described species of the genus *Myrmaplata*, barcode sequence information is only available for *Myrmaplata plataleoides* and *Myrmaplata wanlessi*. Out

of the barcode sequence information of all the species of the genus *Myrmarachne*, only those sequences were considered for further studies which are continuous in nature and show significant (>230 base pairs) alignment with one another and also with the sequences of both the species of the genus *Myrmaplata*. This is also the selection criteria of the species

of the genus *Myrmarachne* used to conduct literature survey as mentioned earlier. Comparative analysis was done based on the available morphological and molecular data. Both morphological and molecular cues were used to assess taxonomic issues concerned with the genus *Myrmaplata*.

Table 3: Details of the retrieved mtCO1 DNA sequences used for phylogenetic studies

S.No.	Species	BOLD ID	Remarks
1.	<i>Myrmaplata plataleoides</i>	GBCH11719-13	Reference sequence
2.	<i>Myrmaplata wanlessi</i>	GACS5651-19	
3.	<i>Myrmarachne formicaria</i>	ARAEU136-12	
4.	<i>Myrmarachne melanotarsa</i>	GACO3865-19	
5.	<i>Myrmarachne melanocephala</i>	GACO3867-19	
6.	<i>Myrmarachne tristis</i>	GACO3868-19	
7.	<i>Myrmarachne helensmithae</i>	GACS1082-19	
8.	<i>Myrmarachne smaragdina</i>	GACS1086-19	
9.	<i>Myrmarachne macaulayi</i>	GACS1088-19	
10.	<i>Myrmarachne luctuosa</i>	GACS1091-19	
11.	<i>Myrmarachne zabkai</i>	GACS1114-19	
12.	<i>Myrmarachne japonica</i>	GACS5234-19	
13.	<i>Myrmarachne assimilis</i>	GACS5632-19	
14.	<i>Myrmarachne cornuta</i>	GACS5634-19	
15.	<i>Myrmarachne endoi</i>	GACS5638-19	
16.	<i>Myrmarachne lambirensis</i>	GACS5647-19	
17.	<i>Myrmarachne foenisex</i>	GBCH11720-13	
18.	<i>Myrmarachne evidens</i>	GBCH11721-13	
19.	<i>Myrmarachne nigella</i>	GBMNC10586-20	
20.	<i>Viciria praemandibularis</i>	GBMNC10735-20	Outgroup sequence

Multiple sequence alignment

The sequenced genomic regions were verified using NCBI-BLAST (NCBI-Basic Local Alignment Search Tool) (Wheeler *et al.*, 2007) [22]. All the mtCO1 sequences retrieved and acquired in the present study were then aligned using CLUSTAL W (Thompson *et al.*, 1994) [20] multiple alignment tool. The resulting alignments were highlighted to display conserved sites and differences in individual nitrogenous bases using Jalview 2.11.2.0 (Waterhouse *et al.*, 2009) [21].

Construction of the phylogenetic tree

All the mtCO1 sequences were realigned using MEGA-X software (Kumar *et al.*, 2018) [13]. After performing alignments, as standard practice, the non-aligning terminal extensions were trimmed from each sequences in order to construct a more accurate phylogenetic tree. A combined distance matrix for all the sequences were generated using MEGA-X (Supplementary File 1). Distance matrix provides respective genetic distances between each pair of DNA sequences. Genetic distance is a measure of evolutionary divergence. The matrix was graphically converted into a heat map using Heatmapper (Babicki *et al.*, 2016) [1]. Selection of appropriate model for phylogenetic tree construction was done using MEGA-X. Models with the lowest BIC scores (Bayesian Information Criterion) are considered to describe the substitution pattern the best. Therefore, TN93+G (Tamura-Nei with Gamma Distribution) model was selected for tree construction because for the given sequences this model has the lowest BIC score (Supplementary File 2). *Viciria praemandibularis* van Hasselt, 1893 mtCO1 sequence was used as the outgroup. A maximum likelihood (ML) tree was generated for analysis using TN93+G model at a bootstrap value of

10,000. Such a stringent bootstrap value was used due to small size of the DNA sequences used in the present study.

Results and discussion

The melanic morpho-variant of *Myrmaplata plataleoides* is genetically similar to the typical red type

NCBI-BLAST result of the mtCO1 sequences of both sexes of the melanic morpho-variant of *Myrmaplata plataleoides* shows both of these sequences to be most similar (98.88% identity with 80% query cover for female and 99.82% identity with 82% query cover for male) to the mtCO1 sequence of the typical *Myrmaplata plataleoides*. In the top ten hits of the NCBI-BLAST results, mtCO1 sequence of the typical *Myrmaplata plataleoides* appears at the top of the pairwise alignment results clearly indicating identity of the morpho-variant (Supplementary Files 3, 4). the melanic morpho-variant of *Myrmaplata plataleoides* is genetically similar (not identical) to the typical red type.

The melanic morpho-variant population of *Myrmaplata plataleoides* exhibits significant divergence from the typical red type: magic traits in action

Multiple sequence alignment result shows the region of differences between the the mtCO1 sequences of both sexes of the melanic morpho-variant of *Myrmaplata plataleoides* and the mtCO1 sequence of the typical *Myrmaplata plataleoides* (Figure 2A). In case of the mtCO1 sequences of both sexes of the melanic morpho-variant, adenine is present in place of guanine at 88th and 121st positions, guanine is present in place of adenine at 104th, 160th and 202nd positions, and thymine is present in place of adenine at 127th position. Therefore, there are five transitions and one transversion in the mtCO1 sequences of both sexes of the melanic morpho-variant with respect to the mtCO1 sequence of the typical *Myrmaplata plataleoides* taken as a

reference. These changes account for significant evolutionary divergence. Branch support values of 41% was recovered for the divergence of the melanic morpho-variant individuals with respect to the typical red type in the maximum likelihood tree and the neighbour joining tree respectively. Both sexes of the morpho-variant cluster together with high branch support values (99%) for both the trees (Figure 3). The estimates of evolutionary divergence between the mtCO1 sequences of both sexes of the melanic morpho-variant and the mtCO1 sequence of the reference comes around 3.84% (which is more than 3.5%) (Figure 2B, Supplementary File 1). According to the 3.5% divergence rule (De Barro *et al.*, 2010)^[8], this morpho-variant qualifies to be considered as a new species by a narrow margin but due to existence of identical reproductive structures and non-availability of more genomic information pertaining to this species and its other morpho-variants, it was not considered a new species altogether. Also, a recent report documented maximum 4.2% intraspecific genetic divergence among some spiders (Oh *et al.*, 2022)^[14]. Therefore, it is not a different species. There are many significant differences though. Although this melanic morpho-variant exhibits similarities in its reproductive structures and colour pattern of legs with the typical red type, it differs in its body colour, shape of chelicerae and overall form (Figure 1). The one-half of the paturon of the male in the morpho-variant is inflated whereas in typical *Myrmaplata plataleoides* male, only the distal two-third of each paturon is inflated. Also it exhibits numerous behavioural differences with respect to the typical form (Kumar *et al.*, 2022)^[12]. Therefore, based on the molecular data along with the behavioural and morphological differences with respect to the typical red type, it was found that this black coloured morpho-variant exhibits significant evolutionary divergence with respect to the typical red type and is in the process of becoming a new species in future. In their study, Borges *et al.* (2007)^[3] provided evidence for the presence of assortative mating to some extent among some morpho-variants of *M. plataleoides*. In their study, Kumar *et al.* (2022)^[12] demonstrated the existence of numerous unique morphological and behavioural traits within a geographically isolated population of a melanic morpho-variant of *M. plataleoides*. These traits were not observed in the typical red form, as mentioned earlier. Instead of the shared presence of reproductive components, molecular analyses utilising the mtCO1 gene have uncovered a discernible level of evolutionary difference (3.84%) between the conventional red form and the melanic morpho-variant. These preliminary results indicate that there is a potential for divergence among morpho-variant populations within a species. Therefore, polymorphic mimicry in *M. plataleoides* is a magic trait.

Myrmaplata wanlessi* is genetically more closely related to *Myrmarachne lambirensis* than *Myrmaplata plataleoides

In the phylogenetic tree, *Myrmaplata wanlessi* does not cluster with *Myrmaplata plataleoides*. Rather, it gets segregated with *Myrmarachne lambirensis* Yamasaki and Ahmad, 2013^[24] separately. Looking at the distance matrix reveals a lesser genetic distance between *Myrmaplata wanlessi* and *Myrmarachne lambirensis* than the same between *Myrmaplata wanlessi* and *Myrmaplata plataleoides* (Figure 1B, Supplementary File 1). Phylogenetic analysis

questions the present taxonomic position of *Myrmaplata wanlessi*.

Literature survey and molecular data suggests removal of *Myrmaplata wanlessi* from the genus *Myrmaplata*

The finding of the phylogenetic analysis regarding *Myrmaplata wanlessi* was followed by literature survey. Careful analysis of the descriptions and illustrations of *Myrmaplata wanlessi* and *Myrmarachne lambirensis* reveals striking morphological similarities between them (Figure 4). It should be noted that the taxonomic description of *Myrmaplata wanlessi* is based on the male spider. It was originally described as *Myrmarachne wanlessi* (Edmunds, M. & Prószyński, 2003)^[9]. Later it was renamed as *Myrmaplata wanlessi* (Prószyński, 2016)^[17]. Female spider for this taxa has never been discovered. *Myrmarachne lambirensis* was discovered 10 years after *Myrmaplata wanlessi* was described (Yamasaki and Ahmad, 2013)^[24]. Here, both male and female spiders were described. Structure of epigyne is the basis of separation of genus *Myrmaplata* from the genus *Myrmarachne*. But in case of *Myrmaplata wanlessi*, female is missing. The male reproductive structure (palp) is also almost identical in *Myrmaplata wanlessi* and *Myrmarachne lambirensis*. Female of *Myrmarachne lambirensis* has a reproductive structure typical of the genus *Myrmarachne*. *Myrmarachne lambirensis* was differentiated from *Myrmaplata wanlessi* by minor morphological differences. The striking morphological similarities coupled with molecular findings make the present taxonomic status of *Myrmaplata wanlessi* questionable. Both literature survey-based analysis and phylogenetic data point towards the possibility of conspecificity between *Myrmaplata wanlessi* and *Myrmarachne lambirensis*. These findings further suggest removal of *Myrmaplata wanlessi* from the genus *Myrmaplata*. Although it is suggested to place *Myrmaplata wanlessi* back to the genus *Myrmarachne* and to restore its previous name, i.e., *Myrmarachne wanlessi*, as a necessary taxonomic correction, a thorough re-examination of the holotypes of *Myrmaplata wanlessi* and *Myrmarachne lambirensis* is suggested to confirm the specific identity of these taxa with more accuracy.

Present study also calls for review of the genus *Myrmarachne*

Although concerned with the genus *Myrmaplata*, present study also reveals various issues concerned with the taxonomy of the genus *Myrmarachne*. On one hand, in case of *Myrmaplata plataleoides*, occurrence of various morpho-variants is attributed to polymorphic mimicry and instead of having many morphological differences these morpho-variants are not considered different species due to identical reproductive structures and molecular similarities in terms of mtCO1 sequence, on the other hand many different species of the genus *Myrmarachne* have been described based on minor morphological differences irrespective of the fact that they exhibit almost identical reproductive structures and molecular signature in terms of mtCO1 sequence. As apparent the phylogenetic tree, *Myrmarachne smaragdina* Ceccarelli, 2010, *Myrmarachne helensmithae* Pekár, 2017^[15] and *Myrmarachne macaulayi* Pekár, 2017 appear to be conspecific as they have same mtCO1 signature and morphological similarities, but these have been described as different species based on minor morphological differences (Pekár *et al.*, 2017)^[15]. Genetic relatedness

among *Myrmarachne melanocephala* MacLeay, 1839 and *Myrmaplata platalaeoides* as apparent from the phylogenetic tree calls for further analysis of their evolutionary

relationship and taxonomic positions. Therefore, taxonomic issues associated with the genus *Myrmarachne* also needs to be revisited using integrative taxonomic approaches.

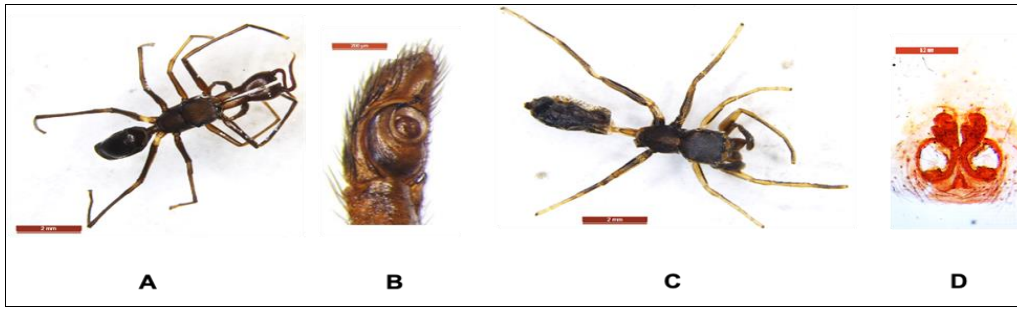


Fig 1: The recently described melanic morpho-variant of *Myrmaplata platalaeoides* used in the present study. (A) Male spider in dorsal view (scale bar 2 mm). (B) Right palp of Male spider in ventral view (scale bar 0.2 mm). (C) Female spider in dorsal view (scale bar 2 mm). (D) Stained squash preparation of epigyne of the female spider (scale bar 0.2 mm).

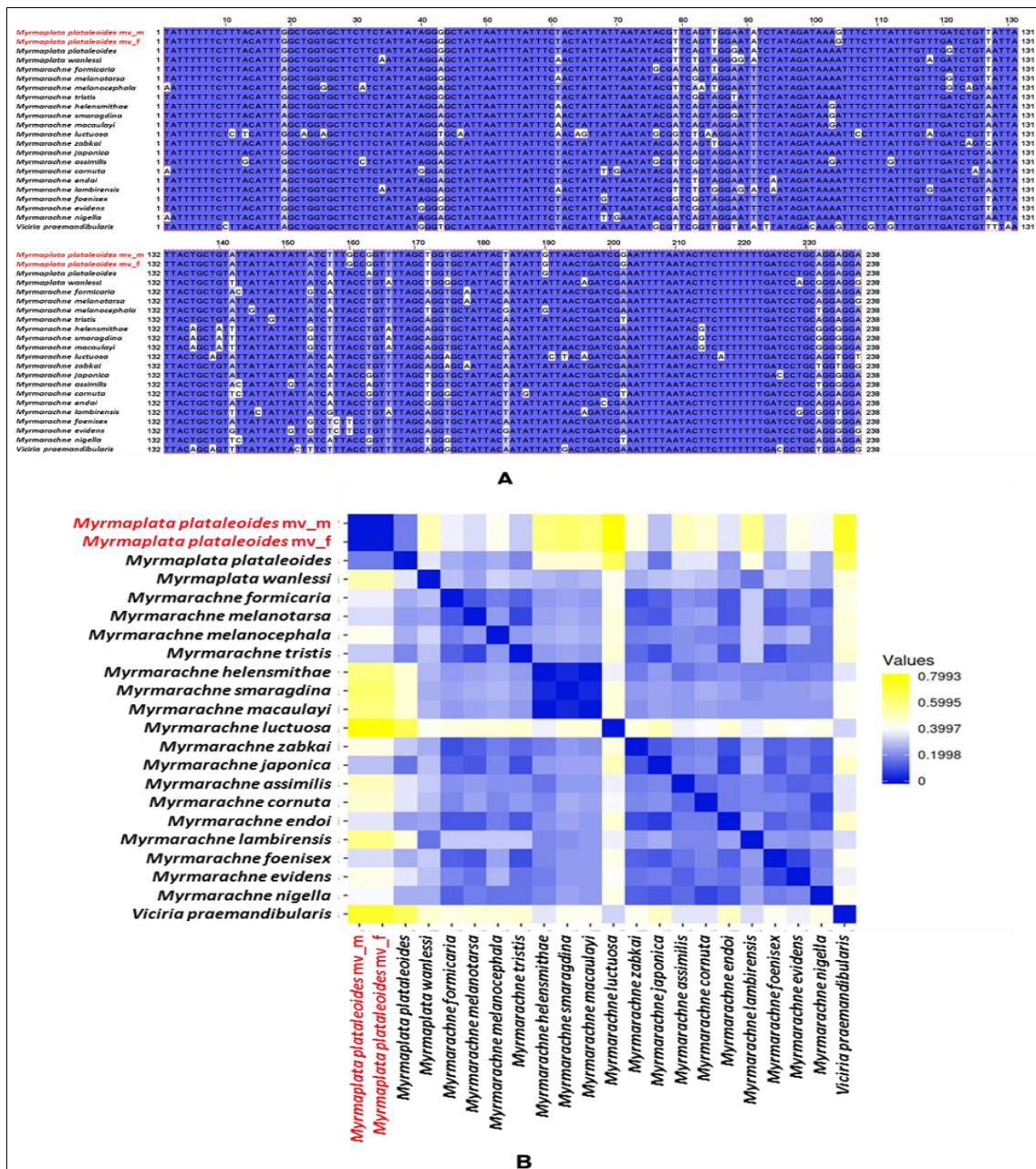


Fig 2: mtCO1 sequence analysis. (A) Multiple sequence alignment of the mtCO1 DNA sequences of both sexes of the melanic morpho-variant of *Myrmaplata platalaeoides* with publically available mtCO1 DNA sequences of the species of genus *Myrmaplata* and *Myrmarachne*. (B) Graphical representation of the combined distance matrix for all the mtCO1 sequences used in the present study. mv_m= morpho-variant male, mv_f= morpho-variant female.

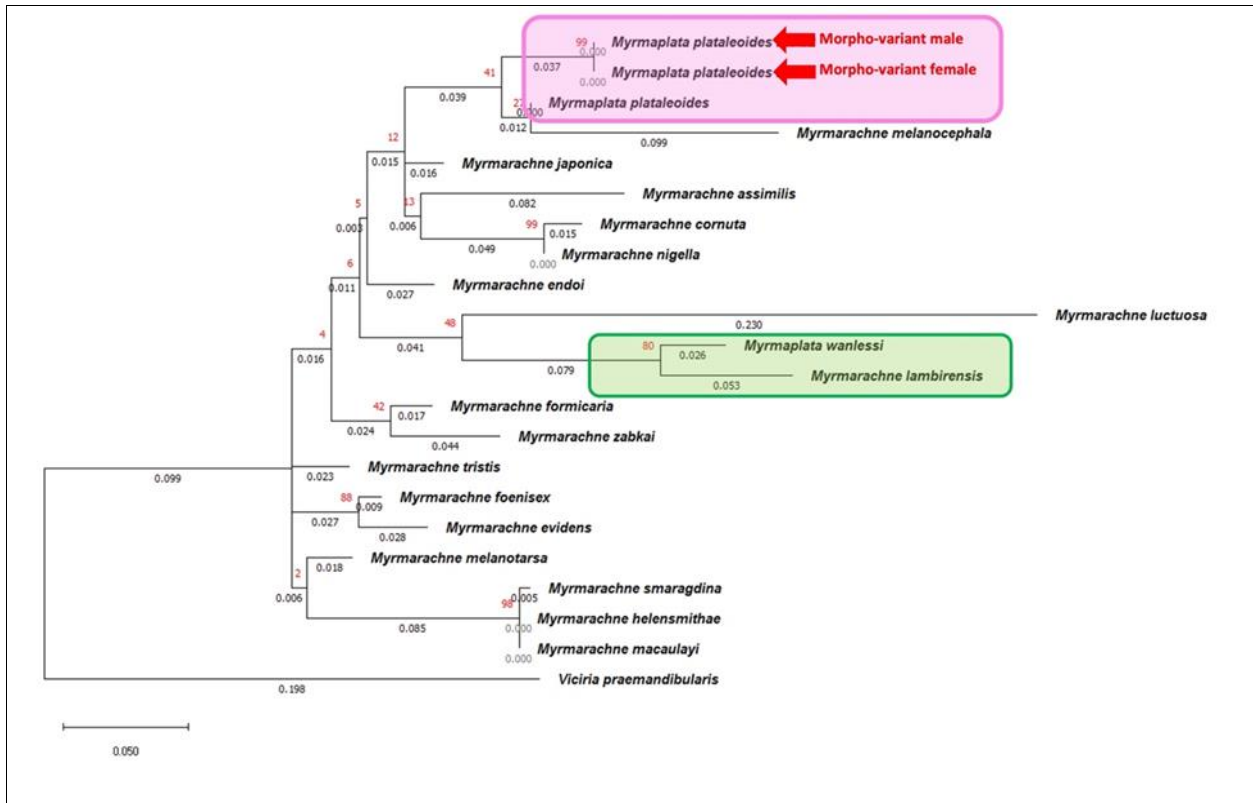


Fig 3: Phylogenetic tree based on mtCO1 sequences of different species of the genus *Myrmaplata* and *Myrmarachne*. A phylogenetic tree constructed using maximum likelihood method. Numbers above branches are bootstrap percentages, below branches are branch lengths.

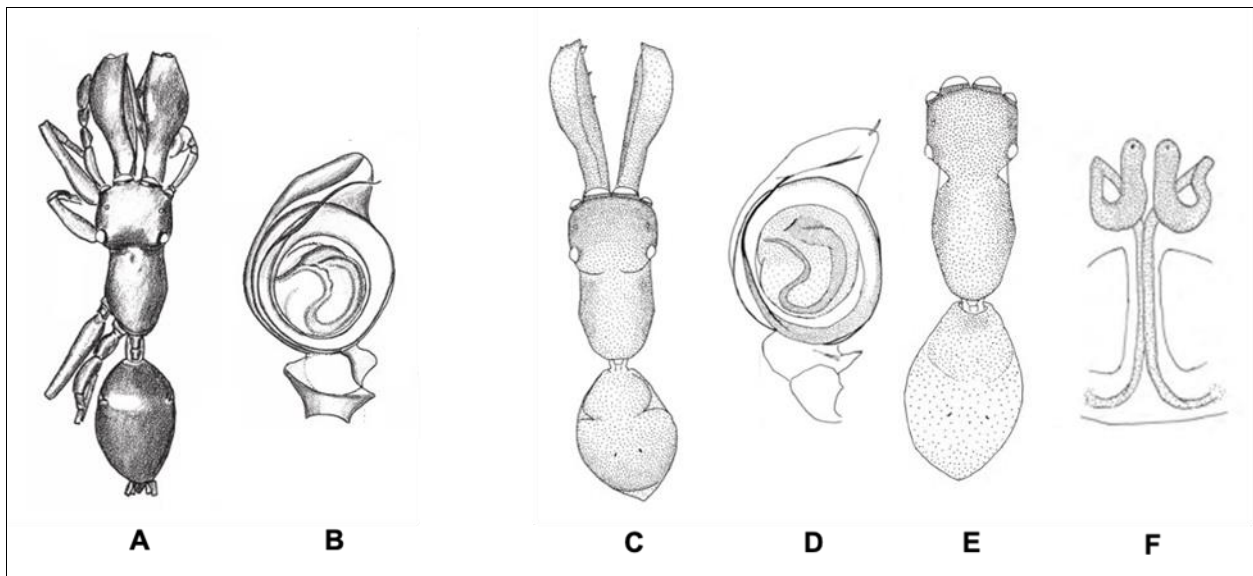


Fig 4: Morphological comparison between *Myrmaplata wanlessi* (= *Myrmarachne wanlessi*) and *Myrmarachne lambirensis*. A-B. *Myrmaplata wanlessi* (= *Myrmarachne wanlessi*) adult male. (A) Habitus, dorsal view; (B) Left palpal organ, ventral view. C-D. *Myrmarachne lambirensis* adult male. (C) Habitus, dorsal view; (D) Palp, ventral view. E-F. *Myrmarachne lambirensis* adult female. (E) Habitus, dorsal view; (F) Internal structure of epigyne, ventral view. Images A-B reproduced from Edmunds, M. & Prószyński, 2003 [9] by permission of the ©Magnolia Press (copyright 2022). Images C-F reproduced from Yamasaki & Ahmad, 2013 [24] by permission of the ©British Arachnological Society (copyright 2022).

Conclusions

Present work is an effort to address important taxonomic issues concerned with the genus *Myrmaplata*. Barcode region of mtCO1 gene was sequenced for both sexes of a melanic morpho-variant of *Myrmaplata plataleoides* and it was compared with the existing sequence of the typical form. The existence of assortative mating in certain morpho-variants of this spider as per a previous report, along with the observed evolutionary divergence between the melanic

morpho-variant and the typical red form in this study, indicate that polymorphic mimicry in *Myrmaplata plataleoides* is a magic trait. Apart from establishing significant evolutionary divergence in the recently described melanic morpho-variant of *Myrmaplata plataleoides* using an integrative approach involving literature survey and phylogenetic studies, present work also suggests removal of *Myrmaplata wanlessi* from the genus *Myrmaplata* and renaming back as *Myrmarachne wanlessi*. Chances of

conspicuity between *Myrmaplata wanlessi* and *Myrmarachne lambirensis* has been highlighted using various evidences. Thorough re-examination of the holotypes of these species is suggested to confirm the validity of these assumptions with more accuracy. Even if *Myrmaplata wanlessi* and *Myrmarachne lambirensis* are not conspecific, *Myrmaplata wanlessi* certainly does not belong to the genus *Myrmaplata*. Present work also raises concerns over the taxonomic status of different species of another genus *Myrmarachne*. In this regard, a more holistic and thorough study employing an integrated approach needs to be conducted.

Supplementary data

All supplementary data files are uploaded on Zenodo and are publicly available on following link:

<https://zenodo.org/doi/10.5281/zenodo.8374334>

Supplementary file 1: Estimates of Evolutionary Divergence between Sequences

Supplementary file 2: Maximum Likelihood fits of 24 different nucleotide substitution models

Supplementary file 3: Summary of top ten BLAST hits for mtCO1 sequence of the female melanic morpho-variant of *Myrmaplata plataleoides*

Supplementary file 4: Summary of top ten BLAST hits for mtCO1 sequence of the male melanic morpho-variant of *Myrmaplata plataleoides*

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Conflict of interests

The authors declare that there are no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Author's contributions

RK, BKG and AKS conceived the research problem and study design. RK collected data, performed all analyses and wrote the first draft of the manuscript. BKG and AK supervised this study and approved the final manuscript before submission.

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