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Molecular Phylogeny and DNA Barcoding of the Genus *Arhopala* Boisduval, 1832 (Lepidoptera: Lycaenidae) from Northwest India

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ABSTRACT

The genus *Arhopala* (Lycaenidae: Theclinae) is one of the most diverse groups of butterflies in the Oriental region, yet molecular data for Indian species remain limited. In this study, we sequenced the mitochondrial Cytochrome Oxidase I (COI) gene from five species collected in Northwestern India: *Arhopala amantes* (Hewitson, 1862), *A. rama* (Kollar, 1844), *A. ganesa* (Moore, 1858), *A. dodonaea* (Moore, 1858) and *Surendra quercetorum* (Moore, 1858) (Outgroup), generating seven new COI sequences. Maximum Likelihood phylogenetic analyses were conducted using 54 sequences encompassing 49 *Arhopala* species and relevant outgroups. The results confirmed the monophyly of the *Centaurus, Eumolphus, Epimuta*, and *Rama* groups, whereas the *Amphimuta* and *Muta* subgroups were polyphyletic. Genetic divergence among *Arhopala* species ranged from 0.6% to 13.3%, with intergeneric divergence from outgroups up to 13.5%, supporting the utility of COI barcoding for species delineation. This study provides the first molecular records for these species in India, establishes DNA barcodes, clarifies their phylogenetic positions, and contributes to the understanding of evolutionary relationships within *Arhopala*.

Keywords: Oakblues, Cytochrome c oxidase I, Divergence, Arhopalini, Theclinae.

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INTRODUCTION

The tribe Arhopalini (Lycaenidae: Theclinae), commonly known as "oakblues," is an ecologically significant group of butterflies that contribute to pollination and ecosystem functioning. Globally, the tribe comprises approximately 250 species across 9 genera (Vane-Wright & de Jong, 2003), with the genus *Arhopala* Boisduval, 1832, being the most diverse, containing nearly 200 species distributed throughout the Oriental and Australian regions, with a slight extension into the Palaearctic (Megens et al., 2004). Its range extends from the Palaearctic transition in Afghanistan in the west to the Solomon Islands in the east (Tennent, 2002). In India, Arhopalini is represented by 9 genera and 72 species, including 47 species of *Arhopala* (Smetacek, 2025).

The genus *Arhopala* occurs from Sri Lanka to Japan and from southern Nepal through the Archipelago to Northern Australia. Many species are further divided into subspecies or forms, often corresponding to geographic regions and likely reflecting ecotypic variation (Evans, 1957; Eliot, 1963; D'Abrera, 1986, 1990; Corbet & Pendlebury, 1992; Parsons, 1998). *Arhopala* exhibits considerable ecological diversity. Species vary in host plant preferences, ranging from oligophagy to polyphagy, and maintain specialized interactions with ants, including obligatory myrmecophily and rare carnivory, as in *A. wildei* (Fiedler, 1991; Maschwitz et al., 1984; King & Ring, 1996). Despite this ecological diversity, morphological variation is remarkably conserved. Males typically have lustrous blue to violet-blue dorsal surfaces, while females display broader and irregular black margins; ventral surfaces are generally cryptic brown. Definitive identification usually requires a combination of wing maculation and genitalic characters due to limited interspecific variation (Corbet, 1946; D'Abrera, 1986).

Historically, the classification of *Arhopala* has been challenging. Early taxonomists, such as Corbet (1941), Evans (1957), and Eliot (1963, 1973), attempted to divide the genus into species groups and subgroups based on combinations of wing and genitalia morphology. Major recognized species groups include *Centaurus, Eumolphus, Camdeo, Epimuta, Amphimuta, Agelastus*, along with several smaller or monotypic groups. Eliot (1973) also defined sections such as *Flos*, *Semanga*, and *Surendra*, though the boundaries of these groups often remain ambiguous. Morphology alone has proven insufficient to resolve the phylogenetic relationships among these groups due to homoplasy and overlapping characters, leaving many inter-group relationships unresolved.

DNA barcoding, based on the mitochondrial Cytochrome Oxidase I (COI) gene, provides a standardized approach for accurate species identification, detection of cryptic taxa, and clarification of morphological ambiguities (Hebert et al., 2003; Hebert & Gregory, 2005). Previous molecular investigations, such as Megens et al. (2004), utilized both mitochondrial and nuclear genetic markers to elucidate phylogenetic relationships within *Arhopala*, revealing that while several species groups including *Centaurus, Eumolphus, Camdeo*, and *Epimuta* are monophyletic, other groups such as *Amphimuta* are not, and the genus as a whole shows some incongruence with previous morphological classifications. These findings underscore the complexity of *Arhopala* phylogeny and highlight the need for additional molecular data, particularly for Indian taxa. In contrast, the present study focuses exclusively on COI sequences to generate molecular data for Indian *Arhopala* species and evaluate their phylogenetic positions.

Specifically, we aim to establish DNA barcodes and explore evolutionary relationships for five species: *Arhopala amantes* (Hewitson, 1862), *A. dodonaea* (Moore, 1858), *A. ganesa* (Moore, 1858), *A. rama* (Kollar, 1844), and *Surendra quercetorum* (Moore, 1858), thereby contributing novel genetic data to aid taxonomic resolution and inform conservation efforts.

MATERIALS AND METHODS

Specimen Collection, Preservation, and Identification

Butterflies were collected from six different locations in Northwestern India using a sweeping net from 2022-2024 (Figure 1). Species identification was carried out by examining wing colour patterns and shapes, with reference to relevant literature (Varshney & Smetacek, 2015; Kehimkar, 2016). To confirm taxonomic identity, genitalic dissections were performed following Robinson (1976), with anatomical nomenclature standardized according to Klots (1970). Specimens were preserved in alcohol and stored at -20°C in the Department of Zoology and Environmental Sciences, Punjabi University, Patiala, India. Geospatial data and distribution patterns were visualized and mapped using QGIS software.

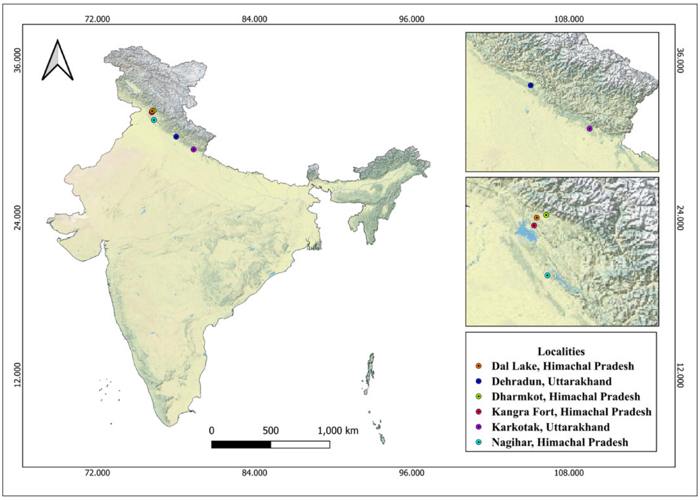

Figure 1. Google satellite map illustrating butterfly sampling localities generated using QGIS software.

DNA Extraction

For DNA extraction, the thoracic muscles and legs of the butterflies were used, employing the Qiagen DNA extraction kit. The quality and integrity of the extracted DNA were evaluated using agarose gel electrophoresis.

PCR Amplification

The mitochondrial CO1 gene was amplified *via* PCR, following the protocol outlined by Gaikwad et al. (2012). The primers used for PCR amplification were LCO-1490 (Forward primer: 5' GGTCAACAAATCATAAAGATATTGG 3', 25 bp) and HCO-2198 (Reverse primer: 5' TAAACTTCAGGGTGACCAAAAAATCA 3', 26 bp), as described by Folmer et al. (1994). The PCR reaction was carried out with a total volume of 30 µl, consisting of 2.5 µl of forward primer, 2.5 µl of reverse primer, 15 µl of master mix, 5 µl of nuclease-free water, 2 µl of Bovine Serum Albumin and 3 µl of DNA template. The PCR protocol included an initial heated lid setting at 112°C and a hot start at 94°C for 1 minute. The amplification consisted of 35 cycles with denaturation at 94°C for 1 minute, annealing at 45°C for 1 minute and 30 seconds, and elongation at 72°C for 1 minute. The final extension was performed at 72°C for 5 minutes. The amplified PCR products were run in 1% agarose gel stained and visualized under UV light in BioRad Gel Documentation System.

Sequencing and accession numbers

The amplified products were sent for sequencing to a commercial service provider (Biologia, New Delhi) using the Sanger dideoxy sequencing method. The highest-quality sequences were selected based on the chromatogram peak analysis. These sequences were manually aligned and trimmed using the Clustal W algorithm in MEGA X version 12. To identify conspecific sequences, the sequences were compared using the NCBI BLAST search tool. A total of seven COI gene sequences, representing five butterfly species, were deposited in the NCBI GenBank database and the corresponding accession numbers were acquired if available.

Genetic variations and Phylogenetic analysis

A total of 54 sequences were included in this study, of which 50 sequences belonged to the genus *Arhopala*, representing 22 distinct species groups. Additionally, species from the *Flos* (Apidanus group), *Semanga*, and *Surendra* sections were incorporated. COI sequences from 47 GenBank entries (Basset et al., 2011; Braby et al., 2020; Espeland et al., 2015; Hebert et al., 2013; Megens et al., 2004; Nakabayashi & Ohshima, 2024; Schröder & Stradomsky, 2016; Ueda et al., 2012; Wilson, Sing, & Sofian-Azirun, 2013; Zhang, Cong, Shen, Song, & Grishin, 2023) for *Arhopala* (including *Flos anniella*) and *Semanga* were incorporated.

Sequences were aligned using Clustal W in MEGA X version 12 (Kumar et al., 2024) and manually inspected for accuracy. Phylogenetic analyses were performed using Maximum Likelihood (ML) with the GTR + G + I model. In Northwest India, specimens representing four species of *Arhopala* and one species of *Surendra* were collected, generating seven new COI sequences. Interspecific and intergeneric genetic distances were calculated using the K2P model.

The study primarily focused on the genus *Arhopala* (including *Flos*), with *Semanga superba* and *Surendra quercetorum* used as outgroups. A detailed list of all species used in the phylogenetic analysis, including accession numbers, voucher numbers, collection sites, and NCBI references, is provided in Table 1.

Table 1. List of species with GenBank accession numbers, voucher names, localities and references used for phylogenetic and distance analyses.

S No.	Species Group	Name of the Species	Voucher Name	GenBank Accession	Place	References
1	*Abseus* group	*Arhopala abseus* Hewitson, 1862	MWT-93-E051	AY235896	Malaysia	Megens *et al*., 2004
2	*Agelastus* group	*Arhopala labuana* Bethune-Baker, 1896	HJM97240522	AY235872	Malaysia	Megens *et al*., 2004
3	*Agelastus* group	*Arhopala barami* Bethune-Baker, 1903	HJM9725054	AY235875	Indonesia	Megens *et al*., 2004
4	*Agelastus* group	*Arhopala alaconia* Hewitson, 1869	HJM97280512	AY235876	Indonesia	Megens *et al*., 2004
5	*Agesias* group	*Arhopala agesias* (Hewitson, 1862)	UMKL-JJW0405	KF226296	Malaysia	Wilson *et al*., 2013
6	*Agesias* group	*Arhopala kinabala* Druce, 1895	Tadahiro Okubo:A34	AB576399	Malaysia	Ueda *et al*., 2012
7	*Alitaeus* group	*Arhopala denta* Evans, 1957	HJM9728051	AY235885	Indonesia	Megens *et al*., 2004
8	*Amphimuta* group	*Arhopala amphimuta* (C. & R. Felder, 1860)	Yasuo Seki:AR13	AB576404	Malaysia	Ueda *et al*., 2012
9	*Amphimuta* group	*Arhopala muta* Hewitson, 1862	NP-95-Z297	AY235889	Malaysia	Megens *et al*., 2004
10	*Amphimuta* group	*Arhopala antimuta* Felder, 1865	NP 95-Y312	AY235894	Malaysia	Megens *et al*., 2004
11	*Amphimuta* group	*Arhopala dajagaka* Bethune-Baker, 1896	Tadahiro Okubo:A28	AB576393	Malaysia	Ueda *et al*., 2012
12	*Amphimuta* group	*Arhopala major* (Staudinger, 1889)	Yasuo Seki:AR14	AB576405	Malaysia	Ueda *et al*., 2012
13	*Amphimuta* group	*Arhopala metamuta* (Hewitson, 1863)	DL_09_X149	MT165275	USA	Braby *et al*., 2020
14	*Amphimuta* group	*Arhopala moolaiana* (Moore, 1878)	Yasuo Seki:AR07	AB576402	Malaysia	Ueda *et al*., 2012
15	*Amphimuta* group	*Arhopala zylda* Corbet, 1941	Tadahiro Okubo:A15	AB576380	Malaysia	Ueda *et al*., 2012
16	*Anthelus* group	*Arhopala achelous* Hewitson, 1862	HJM240528	AY235901	Malaysia	Megens *et al*., 2004
17	*Anthelus* group	*Arhopala anthelus* Westwood, 1851	NP-95-Z316	AY235890	Malaysia	Megens *et al*., 2004
18	*Aurea* group	*Arhopala aurea* Hewitson, 1862	DC97733	AY235892	Indonesia	Megens *et al*., 2004
19	*Camdeo* group	*Arhopala wildei* Miskin, 1891	11ANIC-05844	KF393403	Australia	Hebert *et al*., 2013
20	*Camdeo* group	*Arhopala hellada* Fruhstorfer, 1914	MWT-93-E050 c	AY235868	Malaysia	Megens *et al*., 2004
21	*Camdeo* group	*Arhopala opalina* Moore, 1884	MWT-93-C071	AY235867	Malaysia	Megens *et al*., 2004
22	*Centaurus* group	*Arhopala adherbal* Grose-Smith, 1902	USNM:ENT:00705181	HQ570820	Canada	Basset *et al*., 2011
23	*Centaurus* group	*Arhopala aexone* (Hewitson, 1863)	USNM:ENT:00705065	HQ570720	Papua New Guinea	Basset *et al*., 2011
24	*Centaurus* group	*Arhopala centaurus* (Fabricius, 1775)	11ANIC-05847	KF393136	Australia	Hebert *et al*., 2013
25	*Centaurus* group	*Arhopala madytus* Fruhstorfer, 1914	11ANIC-05853	KF394739	Australia	Hebert *et al*., 2013
26	*Centaurus* group	*Arhopala pseudocentaurus* Fruhstorfer, 1914	Tadahiro Okubo:A39	AB576401	Malaysia	Ueda *et al*., 2012
27	*Centaurus* group	*Arhopala amantes* (Hewitson, 1862)	DT21	PQ676249	India	Present study
28	*Centaurus* group	*Arhopala micale* Blanchard, 1853	11ANIC-05858	KF392557	Australia	Hebert *et al*., 2013
29	*Cleander* group	*Arhopala phaenops* C. & R. Felder, 1865	UMKL-JJW0412	KF226304	Malaysia	Wilson *et al*., 2013
30	*Cleander* group	*Arhopala ace* De Nice'ville, 1892	NP 95-Y261	AY235888	Malaysia	Megens *et al*., 2004
31	*Cleander* group	*Arhopala agrata* De Nice'ville, 1890	MWT93-E068	AY235887	Malaysia	Megens *et al*., 2004
32	*Cleander* group	*Arhopala silhetensis* Hewitson, 1862	HJM97240523	AY235891	Indonesia	Megens *et al*., 2004
33	*Cleander* group	*Arhopala zambra* Swinhoe, 1911	UMKL-JJW0438	KF226305	Malaysia	Wilson *et al*., 2013
34	*Democritus* group	*Arhopala democritus* Fabricius, 1793	HJM97240526	AY235884	Indonesia	Megens *et al*., 2004
35	*Epimuta* group	*Arhopala epimuta* Moore, 1857	HJM27055	AY235878	Indonesia	Megens *et al*., 2004
36	*Epimuta* group	*Arhopala atosia* Hewitson, 1863	HJM 97270523	AY235902	Indonesia	Megens *et al*., 2004
37	*Eumolphus* group	*Arhopala bazalus* (Hewitson, 1862)	YT-049	OP443323	Japan	Nakabayashi and Ohshima, 2024
38	*Eumolphus* group	*Arhopala critala* (Felder, 1860)	USNM:ENT:00705053	HQ570709	Papua New Guinea	Basset *et al*., 2011
39	*Eumolphus* group	*Arhopala eumolphus* Cramer, 1780	NP-95-Y311	PQ818050	Vietnam	Zhang *et al*., 2023
40	*Eumolphus* group	*Arhopala horsfieldi* Pagenstecher, 1890	NP 95-Y249	AY235886	Malaysia	Megens *et al*., 2004
41	*Ganesa* group	*Arhopala ganesa* (Moore, 1858)	DT7	OQ457070	India	Present study
42	*Ganesa* group	*Arhopala paraganesa* De Nice'ville, 1882	MWT93-D026	AY235882	Indonesia	Megens *et al*., 2004
43	*Hercules* group	*Arhopala hercules* (Hewitson, 1862)	ILL_251	KU189180	Indonesia	Schröder and Stradomsky, 2016
44	*Oenea* group	*Arhopala allata* (Staudinger, 1889)	UMKL-JJW0437	KF226297	Malaysia	Wilson *et al*., 2013
45	*Rama* group	*Arhopala rama* (Kollar, 1844)	DT24	PQ676266	India	Present study
46	*Rama* group	*Arhopala rama* (Kollar, 1844)	DT25	PV076737	India	Present study
47	*Rama* group	*Arhopala japonica* (Murray, 1875)	YT-261	OP443358	Japan	Nakabayashi and Ohshima, 2024
48	*Rama* group	*Arhopala dodonaea* (Moore, 1858)	DT9	PQ676328	India	Present study
49	*Thamyras* group	*Arhopala thamyras* (Linnaeus, 1758)	USNM:ENT:00705231	HQ570865	Canada	Basset *et al*., 2011
50	*Thamyras* group	*Arhopala helianthes* Grose-Smith, 1902	USNM:ENT:00705120	HQ570769	Canada	Basset *et al*., 2011

Table continued

S No.	Species Group	Name of the Species	Voucher Name	GenBank Accession	Place	References
51	*Apidanus* group	*Flos anniella* Hewitson, 1862	DC 977714	AY235898	Indonesia	Megens *et al*., 2004
52	*Semanga* section	*Semanga superba* (Druce, 1873)	MWT93D002	KT286525	USA	Espeland *et al*., 2015
53	*Surendra* section	*Surendra quercetorum* (Moore, 1858)	DT41	PV076869	India	Present study
54	*Surendra* section	*Surendra quercetorum* (Moore, 1858)	DT8	OQ435907	India	Present study

RESULTS AND DISCUSSION

Molecular Data

In this study, a total of seven COI gene sequences, each over 600 bp, were successfully amplified and sequenced, representing five distinct butterfly species collected from Northwestern India. Among these, four species belong to the genus *Arhopala* (*A. amantes, A. dodonaea, A. ganesa* and *A. rama*), while one species, *Surendra quercetorum*, is from the genus *Surendra* (Outgroup). These sequences have been submitted to GenBank, adding to the molecular database for Theclinae butterflies. They also adhere to the BOLD criteria, which define sequences longer than 500 bp as standard DNA barcodes (Ratnasingham & Hebert, 2007). To our knowledge, this is the first study providing molecular data for these species from India. The obtained genetic data provides new insights into the regions biodiversity and contributes valuable information to the understanding of these species' genetic characteristics.

Genetic Divergence (Table 2)

The genetic divergence within the genus *Arhopala* ranged from 0.6% to 13.3%, aligning with the findings of Wiemers & Fiedler (2007), who reported interspecific divergences ranging from 0.4% to 12.4%. In particular, *Arhopala amantes* exhibited minimal genetic divergence (1.2%, 1.4% and 1.9%) from closely related species like *Arhopala centaurus*, *A. micale* and *A. madytus*, while showing a significantly higher divergence of 8.6% from *Arhopala abseus*. *Arhopala dodonaea* demonstrated moderate divergence, with a genetic distance of 1.9% from *Arhopala japonica* and the highest divergence of 8.6% from *Arhopala abseus*.

Similarly, *Arhopala ganesa* showed a divergence of 2.4% from *Arhopala paraganesa* and 7.1% from *Arhopala zylda*, *A. anthelus* and *A. ace*, whereas *Arhopala rama* exhibited a 2.0% divergence from *Arhopala japonica* and the greatest divergence of 9.0% from *A. abseus*.

In contrast, the genetic divergence between species of *Arhopala* and the outgroups *Semanga* and *Surendra* ranged from 9.0% to 12.5% and 8.6% to 13.5%, respectively indicating a considerable phylogenetic separation between these groups.

Interestingly, *Semanga superba* and *Surendra quercetorum*, were traditionally placed within the Arhopalini tribe (Eliot, 1973; Kawahara et al., 2023), however more recent studies have placed them in the newly established tribe Surendrini, based on nuclear genome protein-coding regions (Zhang et al., 2023). This reclassification contrasts with the findings of Zhang et al. (2023), who placed *Semanga* and *Surendra* together within the tribe Surendrini as a single, well-supported clade based on nuclear genome data, highlighting the complexity of phylogenetic relationships within these taxa.

Phylogenetic analysis

In Maximum Likelihood (ML) analyses (Fig. 2), the phylogenetic tree was rooted with *Surendra quercetorum* and *Semanga superba* as the designated outgroups. This rooting provides a clear evolutionary framework for the Arhopala ingroup, revealing the several key patterns:

Arhopala ganesa (Clade 1) and *Arhopala bazalus* (Clade 2) resolved as the earliest diverging lineages. Clade 3, representing a distinct subgroup with close evolutionary affinity, features *Arhopala metamuta* grouping with *A. phaenops* and *A. silhetensis* (51% support). Similarly, the clustering of *A. silhetensis*, *A. phaenops*, and *A. zambra* was recovered with moderate support. In Clade 4, a highly robust association was confirmed within the *rama* species group; *A. rama* samples achieved 100% bootstrap support, while the broader group including *A. dodonaea* and *A. japonica* recovered with 77-86% statistical support. Clade 5 was divided into two major lineages: one comprising *A. allata*, *A. zylda*, *A. major*, *A. dajagaka*, *A. agesias*, *A. amphimuta*, and *A. moolaiana*, while the second includes the *centaurus* group, where *A. amantes* clustered within centaurus group. Clade 6 emerged as a taxonomically diverse lineage, with *Flos anniella* deep within the *Arhopala* cluster. This clade also included a stable terminal cluster containing *A. muta*, *A. ace*, *A. anthelus*, *A. atosia*, and *A. epimuta*, with the *A. epimuta* and *A. atosia* pair exhibiting high bootstrap support of 96%. Furthermore, the *Camdeo group* was significantly clarified, with *Arhopala wildei* and *A. critala* resolved as sister taxa with 99% support, the highest observed for this grouping, justifying the inclusion of *A. critala* within this group. While *A. thamyras* and *A. helianthes* maintain a perfect 100% bootstrap support (*Thamyras group*), whereas species such as *A. opalina*, *A. hellada*, *A. alaconia*, *A. labuana*, *A. barami*, *A. aurea*, and *A. agrata* resolved as independent single clades, with *A. antimuta* and *A. paraganesa* clustering together with low support.

The molecular data suggested that the *Amphimuta group* is polyphyletic, as its members were recovered across multiple, distantly related clades. Within the subgroup *Amphimuta*, *Arhopala amphimuta* recovered as sister to *A. agesias* (*Agesias group*) with robust support (96%), while *A. zylda* associated with the *A. allata* cluster (51%). These findings contrast with the monophyletic recovery of the subgroup reported by Megens et al. (2004).

Similarly, the *Muta* and *Perimuta* subgroups exhibited significant taxonomic displacement; *A. muta* clustered with the *Democritus group*, whereas *A. metamuta* was associated with members of the *Cleander group* (*A. silhetensis*, *A. phaenops* and *A. zambra*). Furthermore, *A. antimuta* showed an affinity for *A. paraganesa* (*Ganesa group*) lineage, albeit with low nodal support.

The *Centaurus group* was recovered as a monophyletic lineage, showing high congruence with the systematic findings of Megens et al. (2004). All constituent members of the group formed a well-supported clade, within which Arhopala amantes the species of the current study was nested. This stable and consistent placement of *A. amantes* within this cluster confirms its correct taxonomic positioning and reinforces the molecular integrity of the *Centaurus group*.

The phylogenetic analyses conducted in this study recovered the *eumolphus* and *epimuta* groups with high degrees of nodal support, largely corroborating the findings of Megens et al. (2004). Within the *eumolphus* group, *Arhopala eumolphus* and *A. horsfieldi* formed a robust clade (92%), although *A. bazalus* remained phylogenetically distinct and failed to cluster with these congeners. Furthermore, members of the epimuta group, *A. epimuta* and *A. atosia*, showed a close sister-group relationship with strong bootstrap value (93%).

Within the *camdeo* group, *Arhopala opalina* and *A. hellada* were recovered as distinct clades, in contrast to Megens et al. (2004), who reported monophyly for this group. In comparison, the relationship between Arhopala wildei and *A. critala* (*eumolphus* group) was strongly supported (88%) across analyses.

Within the *agelastus* species group, the relationships between Arhopala barami, *A. labuana* and *A. alaconia* remain partially unresolved, mirroring the taxonomic ambiguity noted by both Eliot (1963) and Megens et al. (2004). While our findings generally support their classification as a group of closely related species, the internal topology lacked resolution. the specific interspecific boundaries within the agelastus group require further genomic clarification.

Within the *Alitaeus group*, *A. denta* associated with *Flos anniella* and *A. Achelous.* This lack of nodal support mirrors the weak affinity between *A. denta* and *A. democritus* noted by Megens et al. (2004), suggesting its current taxonomic position is tenuous and necessitates further genomic resolution.

Consistent with Eliot (1972) classification of the *Cleander group* into "large" and "small" species complexes, our results reveal substantial phylogenetic heterogeneity and partially unresolved relationships. While Megens et al. (2004) reported ambiguity in the placement of the "large" taxa, our analyses recovered a cohesive cluster comprising *Arhopala silhetensis*, *A. zambra*, and *A. phaenops* with moderate bootstrap support. In contrast, the "small" species exhibited lower stability: *A. ace* clustered with *A. anthelus* with weak support, and *A. agrata* showed methodological discordance, forming a single clade.

Consistent with the discrepancies noted by Corbet (1941), Evans (1957), and Eliot (1963), our molecular phylogeny failed to recover a sister-group relationship between *Arhopala anthelus* and *A. achelous*. All such associations, However, were characterized by low bootstrap support, suggesting that the morphological grouping of these species is not supported by current COI data and likely reflects a need for more robust genomic sampling to clarify their true phylogenetic affinities.

While Megens et al. (2004) recovered *Arhopala abseus* as sister to *Flos* based on shared wing venation, our molecular analysis failed to corroborate this relationship. We observed significant topological instability with low bootstrap support: *Flos anniella* clustered with *A. achelous*. These results suggest that morphological synapomorphies, such as the shortened ninth forewing vein, may be homoplasious or that current COI data lacks the resolution to confirm this lineage.

A highly robust association was confirmed within the *rama* species group, with *Arhopala rama* samples achieving 100% bootstrap support across all analyses. Furthermore, the broader clade encompassing *A. dodonaea* and *A. japonica* was recovered with significant statistical support, 58-88% in the analysis. Although *A. dodonaea* and *A. japonica* have historically lacked formal group assignments, their consistent phylogenetic clustering with *A. rama* strongly suggests their inclusion within the *rama* group.

COI gene provides reliable resolution for species-level identification and DNA barcoding but it has limited power to resolve deeper phylogenetic relationships within *Arhopala*. Accordingly, observations regarding the paraphyly of the genus, the polyphyly of the *Amphimuta* group, and the placement of certain species groups should be interpreted as preliminary hypotheses, requiring confirmation through multilocus or phylogenomic analyses, ideally integrated with morphological evidence.

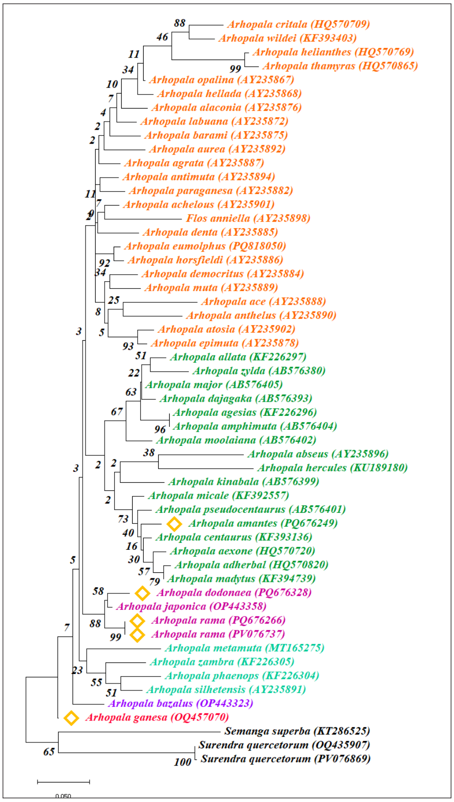

Figure 2. Phylogenetic trees inferred using Maximum Likelihood (ML) method with the General Time Reversible (GTR) model of nucleotide substitution, and the tree with the highest log likelihood (-4,167.01) is shown. The percentage of replicate trees in which the associated taxa clustered together (1,000 bootstrap replicates) is indicated next to the branches. The evolutionary rate variation among sites was modelled using a discrete Gamma distribution (+G, 5 categories, parameter = 0.5695), with 53.99% of sites invariant (+I). The analysis included 54 nucleotide sequences, resulting in a final dataset of 590 positions. Evolutionary analyses were conducted using MEGA X version 12.

CONCLUSION

This study provides the first molecular assessment of selected Indian *Arhopala* species using COI sequences. Maximum Likelihood analyses recovered well-supported phylogenetic relationships for key species groups, including *Centaurus, Eumolphus, Epimuta,* and *Rama*. The analyses also suggest that the *Amphimuta* and *Muta* subgroups may be polyphyletic; however, these observations should be considered preliminary, as COI alone provides limited resolution for deeper phylogenetic relationships. Pairwise genetic divergences confirm species-level differentiation and support the utility of COI for DNA barcoding. Overall, the results provide valuable molecular resources to address taxonomic ambiguities and inform conservation strategies for Indian *Arhopala*. Future studies incorporating multiple loci or phylogenomic data, ideally combined with morphological evidence, are needed to validate the placement of species with low bootstrap support and complex evolutionary histories.

Table 2. Pairwise genetic divergence among *Arhopala* species based on COI sequences.

S. No.	Name of the Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1	*Arhopala abseus* (AY235896)																						
2	*Arhopala ace* (AY235888)	8,1																					
3	*Arhopala achelous* (AY235901)	7,1	4,9																				
4	*Arhopala adherbal* (HQ570820)	8,6	7,3	4,7																			
5	*Arhopala aexone* (HQ570720)	8,4	7,7	5,3	2,1																		
6	*Arhopala agesias* (KF226296)	10,5	9	5,6	5,4	6,2																	
7	*Arhopala agrata* (AY235887)	6,6	5,7	3,5	5,8	5,8	6,7																
8	*Arhopala alaconia* (AY235876)	6,6	5,7	3,1	4,7	4,9	6,4	3,6															
9	*Arhopala allata* (KF226297)	9,2	8	5,2	6	6	3,1	5,2	5,4														
10	*Arhopala amantes* (PQ676249)	8,6	7,1	4,4	2,9	2,8	5,1	5,6	5,1	4,8													
11	*Arhopala amphimuta* (AB576404)	11,1	9	4,3	5,6	6,1	0	5,8	5,3	1,8	4,8												
12	*Arhopala anthelus* (AY235890)	7,7	6,4	5,7	6,7	6,7	8,2	6,2	6,2	7	6,6	7,9											
13	*Arhopala antimuta* (AY235894)	6,7	6	3,3	5,6	5,8	6,9	3,3	4	5,4	5,3	6,1	5,6										
14	*Arhopala atosia* (AY235902)	6	5,8	3,7	6,4	6,7	7,3	4,6	4,9	6,4	5,8	6,6	6,6	4,2									
15	*Arhopala aurea* (AY235892)	7,9	7,4	4,2	7,1	7,1	7,5	3,8	5,3	6	6,7	6,9	7,5	4,7	5,3								
16	*Arhopala barami* (AY235875)	7,1	6,6	3,7	5,3	4,9	6,7	4	3,6	6	5,3	5,8	6	4,5	5,8	4,2							
17	*Arhopala bazalus* (OP443323)	7,5	7,1	4	4,5	5,6	5,5	4,4	4	4,8	5,3	4,6	6,9	4,5	5,5	4,9	4,9						
18	*Arhopala centaurus* (KF393136)	7,3	6,4	4,4	1,9	1,4	5,1	4	4	5,1	1,2	4,4	5,3	4,9	5,3	6	4,6	4,6					
19	*Arhopala critala* (HQ570709)	10,7	9,2	7,1	6,6	6,9	7,3	7,7	6,7	7,8	6,4	7,1	9,6	8	9	8,4	7,7	6,2	6,9				
20	*Arhopala dajagaka* (AB576393)	10,8	9,8	5,1	6,1	6,3	2,1	5,6	6,1	2,6	5,3	2,1	8,4	6,3	7,1	6,1	5,6	5,1	5,1	7,9			
21	*Arhopala democritus* (AY235884)	6,9	6,8	3,5	6,2	6,7	7,1	4,4	4,2	6,2	6,4	6,3	5,5	4,2	4,7	5,3	4,7	4,9	4,9	9,4	6,3		
22	*Arhopala denta* (AY235885)	6,7	6	4,2	6	6,6	7,9	3,8	4	6,2	5,8	7,4	6,4	4,2	5,3	5,3	4,9	4,9	5,5	8,2	7,1	4,4	
23	*Arhopala dodonaea* (PQ676328)	8,6	7,3	4,6	6,9	7,1	7,1	5,3	5,6	5,2	5,8	6,4	6,9	4,4	5,8	6,4	6,6	4,7	6	7,1	6,6	5,7	6
24	*Arhopala epimuta* (AY235878)	5,8	6	4	6,4	6,9	7,3	3,8	4,9	6,6	6,4	6,6	5,8	4,2	1,9	5,6	5,6	5,6	5,5	8,8	7,1	4,4	4,9
25	*Arhopala eumolphus* (PQ818050)	6,4	5,8	3,1	5,1	5,6	6,4	3,5	3,1	5,2	5,8	5,3	6	3,1	4	4,9	4,4	3,3	5,1	7,3	6,1	3,8	3,8
26	*Arhopala ganesa* (OQ457070)	6,7	7,1	3,8	5,3	6	6	4,2	4,4	5,2	5,8	4,8	7,1	3,3	4,2	5,3	5,4	2,8	5,1	6,7	5,1	4,9	4,7
27	*Arhopala helianthes* (HQ570769)	9	8,4	6,9	5,3	5,8	8,4	6,6	5,8	7,8	6,2	8,4	7,9	6,7	8,2	8,6	6,7	6,4	5,3	6,4	8,9	8,4	6,5
28	*Arhopala hellada* (AY235868)	7,1	6,2	4,2	4,9	5,1	7,1	4	3,5	6,2	4,7	6,3	6,2	3,6	5,6	5,3	4,2	5,3	4,6	5,6	6,1	5,8	4,9
29	*Arhopala hercules* (KU189180)	8	9,7	7,6	7,8	7,8	8,7	6,9	7,1	8	7,8	8,5	9,7	8,5	7,6	7,8	7,6	7,1	8,3	8,2	8,5	8	7,3
30	*Arhopala horsfieldi* (AY235886)	6,7	6	3,3	5,6	6,2	6,6	3,3	3,3	5,4	6	5,6	6,6	3,5	4,4	4,7	4,9	3,5	5,3	7,9	5,8	4	4,4
31	*Arhopala japonica* (OP443358)	7,5	6,8	4,2	5,8	6	6,6	4,2	4,9	4,7	5,3	5,3	6,2	3,3	4,9	5,6	5,5	4,4	4,9	6,7	5,1	5,1	5,3
32	*Arhopala kinabala* (AB576399)	9,2	8,2	6,1	5,8	5,6	5,6	7,4	6,3	7,5	6,1	5,6	9,7	7,4	7,4	8,1	6,3	6,3	5,1	8,1	6,3	7,6	7,9
33	*Arhopala labuana* (AY235872)	7,7	5,8	2,2	4,7	4,7	5,5	4	2,9	5	3,8	4,1	5,6	4,2	4,9	4,4	3,5	4,2	4	6,2	4,3	4,7	4,7
34	*Arhopala madytus* (KF394739)	8	6,4	4,4	0,6	1,4	4,9	4,4	4,2	5,5	1,9	4,4	5,3	5,3	6	6,4	4,6	4,4	1,7	6,9	5,1	5,1	6
35	*Arhopala major* (AB576405)	10,8	9,2	4,3	5,6	5,8	0,9	5,3	5,3	1,6	4,8	0,9	8,4	6,1	6,6	6,4	5,3	4,6	4,4	7,1	1,2	6,9	7,4
36	*Arhopala metamuta* (MT165275)	10,2	9,4	6,6	7,5	7,9	8,5	7,7	7,9	7,8	6,8	9	9,4	6	7,5	8,1	8,5	6	6	9,2	8,7	7,7	7,7
37	*Arhopala micale* (KF392557)	7,3	6,2	3,8	2,5	1,9	4,9	3,8	4	4,9	1,4	4,4	5,3	5,1	5,1	5,3	4,2	4,2	1,9	6,4	5,1	5,1	5,3
38	*Arhopala moolaiana* (AB576402)	10,8	7,9	4,6	6,3	6,6	3,6	5,8	6,6	4,5	5,6	3,6	9,5	6,1	6,6	7,9	7,1	6,1	5,1	8,1	4,3	7,4	7,6
39	*Arhopala muta* (AY235889)	7,3	5,5	3,3	6,2	6,4	6,6	3,3	4,4	5,4	5,6	5,6	6,2	4,2	4,4	4,7	5,3	4,5	4,2	8,2	6,3	3,7	5,3
40	*Arhopala opalina* (AY235867)	7,1	5,8	4,2	4,7	5,1	7,1	3,8	3,3	6,2	4,9	6,3	6	4,2	5,3	5,1	4	5,1	4,9	4,5	6,6	5,8	4,7
41	*Arhopala paraganesa* (AY235882)	5,6	6	3,5	5,8	6,2	7,1	3,8	4	6	6	6,4	5,8	2,8	3,1	5,3	4,7	4,2	5,5	7,9	6,6	4,6	4,4
42	*Arhopala phaenops* (KF226304)	8,4	7,5	5,6	7,3	8,2	8,8	6,7	6,7	7,8	8,1	8,4	8,5	6	6,7	7,3	7,3	5,5	7,1	8,8	9	7,1	6,9
43	*Arhopala pseudocentaurus* (AB576401)	9,5	8,7	4,8	2,9	3,6	5,3	5,8	5,8	7	2,9	5,3	7,9	5,6	7,1	6,6	5,6	5,3	1,6	6,6	5,3	7,1	6,9
44	*Arhopala rama* (PQ676266)	9	6,8	4,6	5,3	6,2	5,9	4,9	5,3	4,8	4,9	4,3	6,8	4,4	5,7	6,3	6,1	4,5	5,1	6,8	4,8	5,1	6,1
45	*Arhopala rama* (PV076737)	9	6,8	4,6	5,3	6,2	5,9	4,9	5,3	4,8	4,9	4,3	6,8	4,4	5,7	6,3	6,1	4,5	5,1	6,8	4,8	5,1	6,1
46	*Arhopala silhetensis* (AY235891)	6,7	6,2	4,2	6,7	7,1	8,3	4,9	5,1	7,2	7,1	7,9	6,8	4,2	4,7	5,1	4,7	5,3	6	9,2	7,9	4,9	5,5
47	*Arhopala thamyras* (HQ570865)	9,6	8,4	6,7	6	6,4	8,8	7,5	6,4	8,4	6,2	8,7	8,2	7,3	8,2	8,6	7,1	6,4	6	6,2	9,2	9,2	7,1
48	*Arhopala wildei* (KF393403)	10,7	8,8	7,3	6,2	6,7	7,1	7,5	6,6	7,6	5,8	6,6	9,4	7,7	8,4	8,3	7,1	6,4	6,4	3,5	7,4	9,2	8,4
49	*Arhopala zambra* (KF226305)	9,3	8,9	6,8	7,9	8,3	7,8	7,2	7	7,2	8,1	6,7	9,3	6,6	6,8	8	8	6,4	7,5	8,3	7,2	7,4	7,2
50	*Arhopala zylda* (AB576380)	13,3	10,1	7,1	7,9	8,1	3,8	6,9	7,6	3,1	6,6	3,8	9,7	6,9	8,9	8	7,4	6,3	6,1	7,9	4,4	9	8,7
51	*Flos anniella* (AY235898)	7,1	7,3	4,9	6,9	7,1	8,1	6,2	5,1	7,2	6,9	7,6	7,9	6,2	6,2	6,9	6,2	6,6	6,6	9,4	8,1	6,6	6,6
52	*Semanga superba* (KT286525)	11,5	10,4	10,2	9,8	10	10,8	10,2	10,6	10,5	10	10,8	10,4	9	10,4	10,4	10	9,4	9,4	12,3	10,3	10,6	10,7
53	*Surendra quercetorum* (OQ435907)	12,1	12,9	10,9	10,1	10,3	10,2	10,2	11,9	10,2	10,2	10,3	11,7	10,3	11,7	11,5	12,3	9,8	10,5	10,5	11,1	11,7	11,5
54	*Surendra quercetorum* (PV076869)	12,6	13,5	11,3	10,7	10,9	10,5	10,5	12,4	10,6	10,9	10,5	12,2	10,7	12,2	12	12,9	10,3	11	10,9	11,4	12,2	12

Table continued

S. No.	Name of the Species	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44
1	*Arhopala abseus* (AY235896)																						
2	*Arhopala ace* (AY235888)																						
3	*Arhopala achelous* (AY235901)																						
4	*Arhopala adherbal* (HQ570820)																						
5	*Arhopala aexone* (HQ570720)																						
6	*Arhopala agesias* (KF226296)																						
7	*Arhopala agrata* (AY235887)																						
8	*Arhopala alaconia* (AY235876)																						
9	*Arhopala allata* (KF226297)																						
10	*Arhopala amantes* (PQ676249)																						
11	*Arhopala amphimuta* (AB576404)																						
12	*Arhopala anthelus* (AY235890)																						
13	*Arhopala antimuta* (AY235894)																						
14	*Arhopala atosia* (AY235902)																						
15	*Arhopala aurea* (AY235892)																						
16	*Arhopala barami* (AY235875)																						
17	*Arhopala bazalus* (OP443323)																						
18	*Arhopala centaurus* (KF393136)																						
19	*Arhopala critala* (HQ570709)																						
20	*Arhopala dajagaka* (AB576393)																						
21	*Arhopala democritus* (AY235884)																						
22	*Arhopala denta* (AY235885)																						
23	*Arhopala dodonaea* (PQ676328)																						
24	*Arhopala epimuta* (AY235878)	6,2																					
25	*Arhopala eumolphus* (PQ818050)	4,9	4,2																				
26	*Arhopala ganesa* (OQ457070)	4	4,5	3,1																			
27	*Arhopala helianthes* (HQ570769)	7,5	7,3	6,7	6,4																		
28	*Arhopala hellada* (AY235868)	6	5,4	4,5	4,7	5,3																	
29	*Arhopala hercules* (KU189180)	8	7,8	7,3	6,9	9,4	7,8																
30	*Arhopala horsfieldi* (AY235886)	5,1	4,2	1,2	3,5	7,1	4,5	7,8															
31	*Arhopala japonica* (OP443358)	1,9	5,3	4,2	3,3	6,7	4,9	6,7	4,4														
32	*Arhopala kinabala* (AB576399)	7,6	7,4	7,1	6,1	8,9	7,4	8,8	7,9	6,6													
33	*Arhopala labuana* (AY235872)	5,5	5,1	4	4,7	5,8	2,9	8,5	3,8	5,1	6,3												
34	*Arhopala madytus* (KF394739)	6,4	6	4,9	5,3	5,3	4,9	7,8	5,5	5,3	5,4	4,4											
35	*Arhopala major* (AB576405)	5,8	7,1	5,3	4,8	8,4	6,3	8,5	5,6	4,8	5,6	4,1	4,4										
36	*Arhopala metamuta* (MT165275)	6,6	8,7	6,4	6	7,7	8,8	9,9	7	6,4	8,7	7,5	7,1	8,4									
37	*Arhopala micale* (KF392557)	5,7	4,9	4,9	5,1	5,7	4,2	7,3	5,3	4,6	4,7	3,8	2,3	4,4	7,1								
38	*Arhopala moolaiana* (AB576402)	5,9	7,1	6,3	5,8	9,7	7,6	9,5	6,1	4,8	6,3	5,3	5,1	3,1	9	5,1							
39	*Arhopala muta* (AY235889)	5,1	4,5	3,7	4,5	8,6	5,8	7,4	3,8	4,9	8,1	3,8	4,4	6,1	6,9	4,2	5,6						
40	*Arhopala opalina* (AY235867)	6	5,1	4,2	4,9	5,3	1,5	7,6	4,7	4,9	7,4	3,1	4,9	6,3	9	4,4	7,6	5,6					
41	*Arhopala paraganesa* (AY235882)	5,3	3,8	2,4	2,4	6,9	4	7,6	3,1	4,2	8,1	4,4	5,7	6,3	6,6	5,5	6,3	4,2	3,8				
42	*Arhopala phaenops* (KF226304)	6,8	6,7	5,6	5,1	7,1	7,1	9,9	6,2	6,2	9,2	6,6	7,1	8,4	7,5	6,9	8,4	6,6	7,7	5,8			
43	*Arhopala pseudocentaurus* (AB576401)	6,9	6,8	6,9	5,8	6,3	5,3	7,8	7,1	5,3	5,3	4,6	1,5	5,3	8,2	2,2	6,1	7,1	5,3	7,1	8,7		
44	*Arhopala rama* (PQ676266)	2,7	5,9	4,9	4	6,4	5,3	8	5,1	2	6,2	5,1	5,1	4,3	6,7	5,3	4,6	4,9	5,3	5,3	6,4	5,1	
45	*Arhopala rama* (PV076737)	2,7	5,9	4,9	4	6,4	5,3	8	5,1	2	6,2	5,1	5,1	4,3	6,7	5,3	4,6	4,9	5,3	5,3	6,4	5,1	0
46	*Arhopala silhetensis* (AY235891)	6	5,1	4,4	4,2	6,9	5,4	9,2	4,6	5,1	8,4	5,1	6,6	7,9	7	6,6	8,4	4,9	5,4	3,8	3,8	7,6	5,7
47	*Arhopala thamyras* (HQ570865)	7,7	7,7	7,1	6,4	1,4	6,2	9,4	7,5	7,1	8,9	5,4	6	8,7	7,9	6	9,7	8,2	5,8	6,9	7,5	7,1	7
48	*Arhopala wildei* (KF393403)	7,1	8,2	7,3	6,9	6,4	5,3	8,5	7,9	6,2	8,1	6,4	6,2	6,6	9,6	6	7,9	8,6	4,2	6,9	9,4	6,1	6,2
49	*Arhopala zambra* (KF226305)	6,5	7,2	6,1	4,8	7,8	7,9	9,2	6,8	5,9	8	7,4	8	7	6,9	7,8	7,5	7,4	7,6	6,1	5,4	7,7	5,7
50	*Arhopala zylda* (AB576380)	7,1	8,9	7,6	7,1	9,7	7,1	9,5	7,4	6,1	8,1	6,9	6,1	3,3	10,3	6,1	6,1	8,4	7,1	8,7	10,8	7,6	4,8
51	*Flos anniella* (AY235898)	8,2	6	5,4	7,1	7,9	6,4	9,2	5,6	7,5	9,2	5,6	6,6	7,6	9,4	6,2	8,4	6,4	6	5,6	7,9	8,1	7,4
52	*Semanga superba* (KT286525)	10,6	10	10,2	9,4	11,1	10,5	13	10,8	10	10	10,4	9,4	10,8	12,3	9,6	11,1	10,8	10,3	10	10,5	9,7	10,6
53	*Surendra quercetorum* (OQ435907)	10,5	11,3	10,5	8,6	10,3	10,9	12,3	10,9	10,2	12,2	11,3	10,5	10,3	11,4	10,5	11,9	10,9	10,9	10,7	11,3	10,8	9,9
54	*Surendra quercetorum* (PV076869)	11,1	11,8	10,9	8,8	10,7	11,3	12,9	11,3	10,3	12,4	11,8	11,2	10,5	11,8	11,2	12,2	11,3	11,3	11,1	12	11,1	10,3

Table continued

S. No.	Name of the Species	45	46	47	48	49	50	51	52	53	54
1	*Arhopala abseus* (AY235896)										
2	*Arhopala ace* (AY235888)										
3	*Arhopala achelous* (AY235901)										
4	*Arhopala adherbal* (HQ570820)										
5	*Arhopala aexone* (HQ570720)										
6	*Arhopala agesias* (KF226296)										
7	*Arhopala agrata* (AY235887)										
8	*Arhopala alaconia* (AY235876)										
9	*Arhopala allata* (KF226297)										
10	*Arhopala amantes* (PQ676249)										
11	*Arhopala amphimuta* (AB576404)										
12	*Arhopala anthelus* (AY235890)										
13	*Arhopala antimuta* (AY235894)										
14	*Arhopala atosia* (AY235902)										
15	*Arhopala aurea* (AY235892)										
16	*Arhopala barami* (AY235875)										
17	*Arhopala bazalus* (OP443323)										
18	*Arhopala centaurus* (KF393136)										
19	*Arhopala critala* (HQ570709)										
20	*Arhopala dajagaka* (AB576393)										
21	*Arhopala democritus* (AY235884)										
22	*Arhopala denta* (AY235885)										
23	*Arhopala dodonaea* (PQ676328)										
24	*Arhopala epimuta* (AY235878)										
25	*Arhopala eumolphus* (PQ818050)										
26	*Arhopala ganesa* (OQ457070)										
27	*Arhopala helianthes* (HQ570769)										
28	*Arhopala hellada* (AY235868)										
29	*Arhopala hercules* (KU189180)										
30	*Arhopala horsfieldi* (AY235886)										
31	*Arhopala japonica* (OP443358)										
32	*Arhopala kinabala* (AB576399)										
33	*Arhopala labuana* (AY235872)										
34	*Arhopala madytus* (KF394739)										
35	*Arhopala major* (AB576405)										
36	*Arhopala metamuta* (MT165275)										
37	*Arhopala micale* (KF392557)										
38	*Arhopala moolaiana* (AB576402)										
39	*Arhopala muta* (AY235889)										
40	*Arhopala opalina* (AY235867)										
41	*Arhopala paraganesa* (AY235882)										
42	*Arhopala phaenops* (KF226304)										
43	*Arhopala pseudocentaurus* (AB576401)										
44	*Arhopala rama* (PQ676266)										
45	*Arhopala rama* (PV076737)										
46	*Arhopala silhetensis* (AY235891)	5,7									
47	*Arhopala thamyras* (HQ570865)	7	7,3								
48	*Arhopala wildei* (KF393403)	6,2	8,6	6,6							
49	*Arhopala zambra* (KF226305)	5,7	5	7,9	8,5						
50	*Arhopala zylda* (AB576380)	4,8	10,3	10	7,4	9,1					
51	*Flos anniella* (AY235898)	7,4	6,7	8,2	8,6	9,7	8,9				
52	*Semanga superba* (KT286525)	10,6	9,6	11,5	11,5	11,3	11,6	12,5			
53	*Surendra quercetorum* (OQ435907)	9,9	12,1	10,3	11,1	10,3	11,9	12,7	12,1		
54	*Surendra quercetorum* (PV076869)	10,3	12,6	10,7	11,6	10,4	12,2	13,3	12,7	0,2	

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