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On evolutionary phylogeny of genus *Columba* sp.

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ABSTRACT

The taxonomy of the genus '*Columba*' has been much debated since the early days when taxonomists classified the species of this genus based on morphology, ontology, and vocalizations. Here, apart from the issue of inter-generic relationships of genus *Columba* with other genera, the present study also takes into account the inter-specific relationships with the support of morphology, geographical proximity, plumage coloration, and patterns shaped by evolution, natural and sexual selection over millions of years. Artificial selection based on certain traits within the genus had been considered. Various representatives of genus *Patagioenas*, *Reinwardtoena*, *Turacoena*, *Streptopelia*, *Alectroenas*, and *Leptotila* were taken to construct the phylogenetic tree using mitochondrial sequences. With support of molecular analysis like distance-based methods and maximum likelihood trees, changes in the current taxonomic classification have been recommended with support of distances and comparisons where the two genera *Turacoena* and *Reinwardtoena* have been combined to genus *Columba*. Genus *Aplopelia* has been confirmed as a monotypic genus supported by both molecular and geometric morphometric analysis (GMA). Based on morpho-genetic variations along with inter-specific geographic range proximities and overlaps a new theory of independent evolutionary pattern between Eastern and Western species of the genus *Columba* has been formulated.

Keywords: *Columba*, *Turacoena*, *Reinwardtoena*, *Aplopelia*, phylogeny, evolution

ABBREVIATION

GMA (geometric morphometric analysis), MYA (million years ago), MEGA (Molecular Evolutionary Genetics Analysis), MP (Maximum Parsimony), NNI (Nearest Neighbour Interchange), ♂ (male), ♀ (female)

1. INTRODUCTION

The taxonomic relationships within the genus *Columba* remain elusive even though many studies have been conducted on the topic where some are leading while others are divergent. Ridgway (1916), placed 14 New World Species in ten genera to emphasize their morphological differences. Peters (1937) disagreed and placed fifty-two species in the genus *Columba* (inclusive of Ridgway's genera). Cumley & Irwin (1944) and Irwin & Miller (1961) proposed relationships between New World and Old-World *Columba* (Then; as the same combined genus) based on blood cell antigens. Followed by Miculicz-Radecki's (1949) phylogeny based on plumage pattern and coloration. Boetticher (1954) produced a more extensive phylogeny and placed New World *Columba* species to the Old-World genera. Goodwin (1959) examined the colour pattern of the species based on Peter's (1937) classification and proposed their respective relationships followed by Verheyen (1957) classification based on osteological data. Sibley (1960) & Corbin (1965), (1968) established relationships between the New World and Old World; species. However, according to Johnston (1962), the genus should be split into the 3 genera based on skull osteology, and later Johnston et. al. (2001) recommended the transfer of all New World *Columba* species into a new genus '*Patagioenas*' and eventually placing the Old-world genus into a new genus of its own '*Columba*'. Meanwhile, Johnston & Clayton (2000) showed that species of Old-World *Columba* showed a sister relationship to *Streptopelia*, with species of *Patagioenas* being more distantly related to both groups.

The present study not only dwells on the issue of inter-generic relationships of genus *Columba* with other genera. Various representatives of genus *Patagioenas*, *Reinwardtoena*, *Turacoena*, *Streptopelia*, *Alectroenas*, and *Leptotila* have also been taken into consideration. The maximum likelihood analysis method has been used in consideration with morphology (geometric morphometric analysis has been performed wherever required), geographical proximity and plumage coloration could be used holistically to derive the possible biogeographic histories and subsequent speciation. Artificial selection based on certain traits within the genus is also taken into consideration. Using this, some changes in the current taxonomic classification have been recommended with support of distance-based methods, and compassion has been made concerning morphology, plumage colourations, and geographical proximity data.

2. METHODS

2. 1. Data Collection

Apart from available literature, the study was conducted based on the mitochondrial sequences published in GenBank (Table 1) procured by searching for keywords that included species names and available mitochondrial sequences. The mitochondrial genes evolve at

similar rates at low levels of sequence divergence in birds (Johnson and Sorenson 1998, Johnson and Lanyon 1999).

Table 1. Samples sequenced for cyct b gene, partial cds, mitochondrial genome only.

Genus name	Species name	GenBank Number
<i>Columba</i>	<i>Columba larvata</i>	MH307437
	<i>Aplopelia simplex</i>	MH307439
	<i>Columba larvata principalis</i>	MH307436
	<i>Columba thomensis</i>	MH307444
	<i>Columba malherbii</i>	MH307441
	<i>Columba iriditorques</i>	KT023367
	<i>Columba livia</i>	KF964326
	<i>Columba palumbus</i>	EU481990
	<i>Columba guinea</i>	EU481984
	<i>Columba leuconota</i>	KJ456239
	<i>Columba rupestris</i>	OM401810
	<i>Columba oenas</i>	EU481987
	<i>Columba trocaz</i>	EF012590
	<i>Columba bollii</i>	EU481981
	<i>Columba junoniae</i>	EU481986
	<i>Columba arquatrix</i>	EU481977
	<i>Columba hodgsonii</i>	KJ456238
	<i>Columba vitiensis</i>	GU230687
<i>Streptopelia</i>	<i>Nesoenas mayeri</i>	AF483322
	<i>Streptopelia picturata</i>	MH307541.1
	<i>Streptopelia senegalensis</i>	KF964325
	<i>Streptopelia chinensis</i>	AF182695
<i>Alectroenas</i>	<i>Alectroenas sganzeni</i>	MH307415
<i>Leptotila</i>	<i>Leptotila jamaicensis</i>	AF279706
	<i>Leptotila plumbeiceps</i>	AF279707
	<i>Leptotila megalura</i>	AF483342

	<i>Leptotila verreauxi</i>	AY443662
	<i>Leptotila cassini</i>	AY443661
	<i>Leptotila rufaxilla</i>	AF182698
<i>Patagioenas</i>	<i>Patagioenas picazuro</i>	KT023368
	<i>Columba speciosa</i>	AF279711.1
	<i>Columba squamosa</i>	AY443657

For most of the species cyt b gene, partial cds have been taken. But in certain species such as *Reinwardtoena reinwardtii*, *Columba pulchricollis*, *Columba vitiensis*, and *Turacoena manadensis*, cytochrome c oxidase subunit I (COI) gene, partial cds have been used where distance-based methods have been taken into consideration (Table 2).

Table 2. Samples sequenced for cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial genome only.

Genus name	Species name	GenBank Number
<i>Reinwardtoena</i>	<i>Reinwardtoena reinwardtii</i>	KU194393.1
<i>Turacoena</i>	<i>Turacoena manadensis</i>	EF373394.1
<i>Columba</i>	<i>Columba vitiensis</i>	GU230686.1
<i>Columba</i>	<i>Columba iriditorques</i>	KT023317.1

The time period (in mya) of columbid species of genus *Columba*, *Rienwardtoena*, and *Turacoena* has been procured from the OneZoom Tree of Life Explorer website (Wong, Rosindell 2022), which is mentioned in Table 3.

Table 3. Time period (in mya) of columbiform species of genus *Columba*, *Rienwardtoena*, and *Turacoena*.

Species Name	Time period (mya)
<i>Columba larvata</i>	12.70
<i>Columba polleni</i>	8.68
<i>Columba oenas</i>	6.53
<i>Rienwardtoena</i> genus (First sp. <i>R reinwardtsi</i>)	6.53

<i>Columba oliviae</i>	6.22
<i>Columba albitorques</i>	5.89
<i>Columba palumboides</i>	5.65
<i>Columba pulchricollis</i>	5.11
<i>Columba pallidiceps</i>	4.78
<i>Columba unicincta</i>	4.50
<i>Columba delegorguei</i>	4.35
<i>Columba arquatrix</i> and <i>Columba iriditorques</i>	4.07
<i>Turacoena</i> genus	3.68
<i>Columba bollii</i> and <i>Columba palumbus</i>	3.02
<i>Columba albinucha</i> and <i>Columba thomensis</i>	2.98
<i>Columba eversmanni</i>	2.78
<i>Columba guinea</i> and <i>Columba hodgsonii</i>	2.66
<i>Columba elphinstonii</i> , <i>Columba punicea</i> and <i>Columba junoniae</i>	2.58
<i>Columba torringtoni</i>	2.54
<i>Columba vitiensis</i> and <i>Columba janthina</i>	2.30
<i>Columba trocaz</i> and <i>Columba argentina</i>	2.20
<i>Columba albinucha</i> , <i>Columba leucomela</i> and <i>Columba leuconota</i>	2.15
<i>Columba sjostedti</i> and <i>Columba malherbii</i>	1.90
<i>Columba rupestris</i> and <i>Colombia livia</i>	1.43

Source:

<https://www.onezoom.org/life/@Columba=938415?otthome=%40Columba%3D938415#x779,y581,w0.6334>

2. 2. Data Analysis

MEGA 11 was used for all phylogenetic analyses. Initially, the sequences were aligned by MUSCLE and afterward, a maximum likelihood with Nearest Neighbour Interchange (NNI), bootstrapping also of 1000 replicates was done using the Tamura-Nei model. For distance measurement between genera *Columba*, *Turacoena*, and *Reinwardtoena*, the Maximum Composite Likelihood model was used where Transition+Traversion substitutions were done.

The resultant matrix was analyzed for minimum distance. GMA has been performed using tpsUtil ver.1.83, tpsDig2 ver.2.31, and MorphoJ 1.07a for *Aplopelia larvata*, *Columba pollenii*, *Columba hodgsonii*, *Columba thomensis* and *Columba arquatrix*. Where landmarking was performed on beaks of *Aplopelia larvata* and *Columba pollenii* and cere of *Columba hodgsonii*, *Columba thomensis*, *Columba arquatrix* using tpsUtil ver.1.83 and tpsDig2 ver.2.31, based on the specimens from *markmybird.org*. Principal axes were aligned and procrustes fit was performed for all these species. Covariance matrixes were generated followed by PCA (Principal Component Analysis) using MorphoJ 1.07a.

3. RESULT

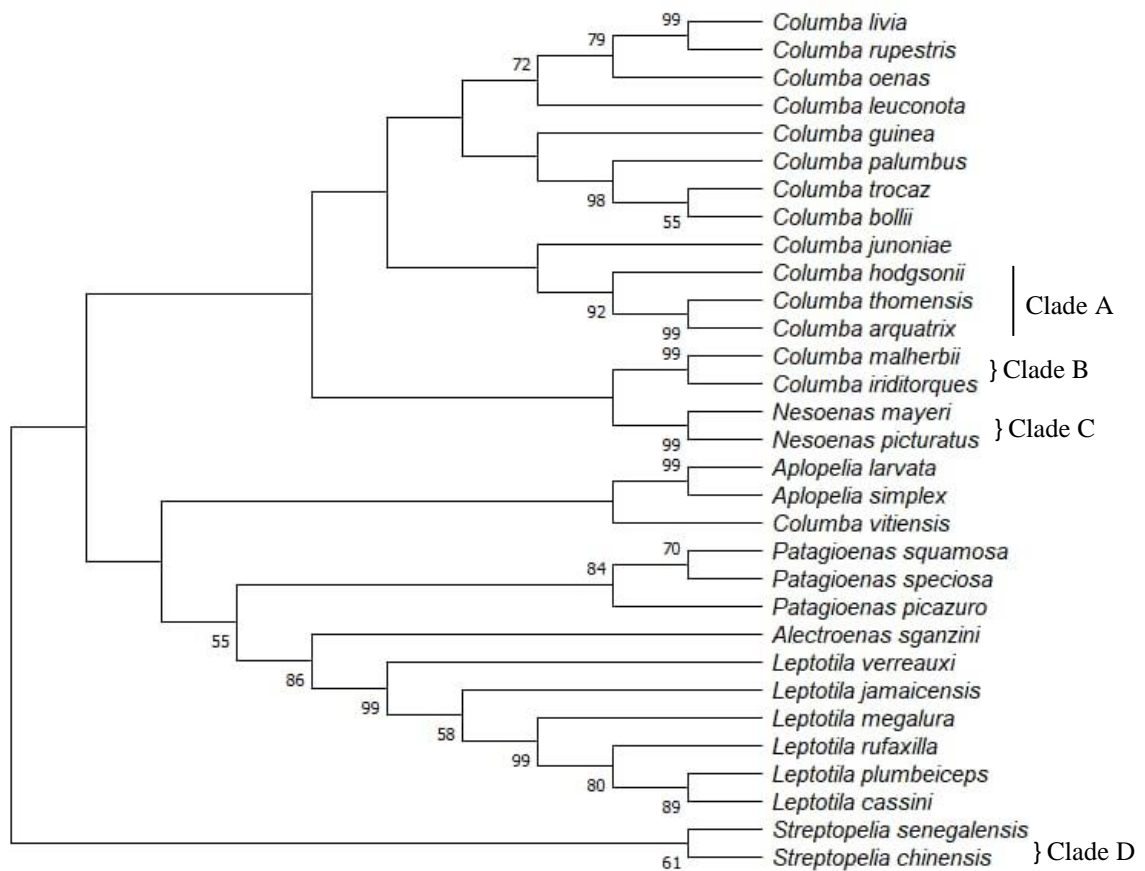


Fig. 1. Phylogeny resulting from Maximum Likelihood analysis of *cyct b*, partial *cds* mitochondrial genome with % bootstrap support on branches: $\geq 50\%$ based on 1000 iterations. Unlabelled nodes received $\leq 50\%$ bootstrap support. The indicated taxa are referred to in the text.

A phylogenetic tree was constructed using maximum likelihood analysis (Figure 1) based on *cyct b*, partial *cds* mitochondrial genome with % bootstrap support on branches: $\geq 50\%$ based

on 1000 iterations where an inter-specific relationship and probable ancestral relationships between genera as in *Columba* and *Streptopelia* have been observed. Also, the resulting data on analyzing the matrix of distances between the above-mentioned genera (Table 4) is plotted in Table 5. Variance% vs PC plot for *Aplopelia larvata* and *Columba pollenii* along with PC scores of cere size and shape were retrieved as a result of morphological analysis.

Table 4. Matrix of relative distances between the genera *Reinwardtoena*, *Turacoena* and *Columba*

	<i>Reinwardtoena reinwardti</i>	<i>Turacoena manadensis</i>	<i>Columba vitiensis</i>	<i>Columba iriditorques</i>
<i>Reinwardtoena reinwardti</i>				
<i>Turacoena manadensis</i>	0.673			
<i>Columba vitiensis</i>	0.732	0.128		
<i>Columba iriditorques</i>	0.138	0.640	0.652	

Table 5. The resultant minimum distance obtained and thus suggesting a relation between *Columba* and genus *Reinwardtoena* and *Turacoena* respectively.

Distance between <i>Reinwardtoena reinwardti</i> and <i>Columba iriditorques</i>	0.138
Distance between <i>Turacoena manadensis</i> and <i>Columba vitiensis</i>	0.128

4. DISCUSSION

4. 1. Inter-generic Relationships

The phylogeny hereby presented doesn't support any monophyly between Clade A comprising *Columba* species *Columba hodgsonii*, *Columba arquatrix*, and *Columba thomensis* with Clade D comprising *Streptopelia senegalensis* and *Streptopelia chinensis*. But monophily has been found in Clade B comprising of genus *Columba* comprising of *Columba malhdbii* and *Columba iriditorques* with Clade C comprising a monotypic genus *Neosenas* (Species: *Neosenas mayeri*) along with *Streptopelia* species: *Streptopelia picturata*. Since *Neosenas mayeri* was reclassified based on phylogenetic analysis as presented in Johnson et al (2001). To resolve the uncertainty of the monophyly of genus *Streptopelia* concerning the old-world *Columba* as proposed in the manuscript (Johnson, K. P., de Kort, S., et al (2001)), a reconsideration regarding reclassification has to be considered or a presumed case of hybrid speciation might have taken place thereby requiring further investigation on the matter.

Also, the phylogeny shows no correspondence between the genus *Columba* and the genus *Leptotila* thus contradicting the hypothesis given by Corbin (Corbin, K. W. (1968) about the

possibility of the genus *Streptopelia* and *Leptotila* being evolved from the Old-World genus *Columba*.

But the evolutionary relationship of the genus of Old-World *Columba* with the species of New World *Columba* as mentioned by Goodwin (Goodwin, D. (1959)) and supported by Corbin (Corbin, K. W. (1968)) has to be clarified. Based on data by Johnson et. al. (Johnson, K. P., de Kort, S., et. al. (2001)), the species of New World *Columba* are recommended to be transferred to a different genus altogether of “*Patagioenas*”. So, what might explain the similarity between the songs and the similarity of morphology between the species (some of them) of the genus *Patagioenas* and *Columba*?

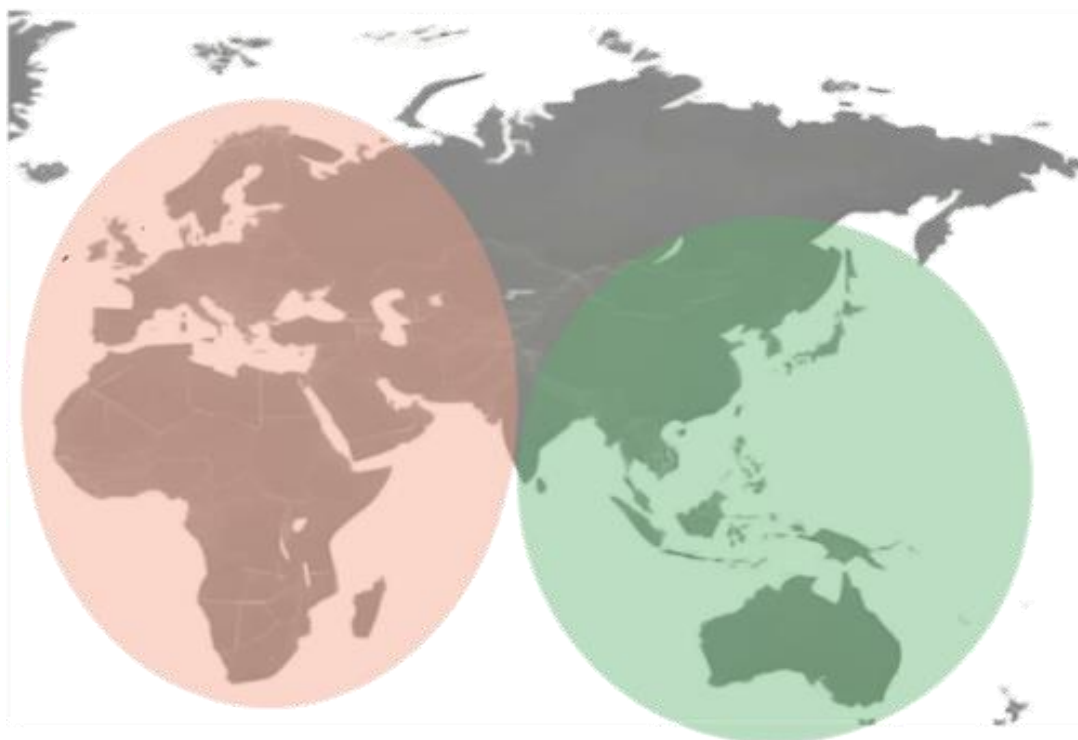


Fig. 2. The diagram depicts, a minimum regional distribution of species of genus *Columba* where there's an independent evolutionary pattern between Eastern (green) & Western (red) species of genus *Columba* based on the facts mentioned above. Where western species include *Columba polleni*, *Columba thiriouxi*, *Columba oenas*, *Columba arquatrix*, *Columba thomensis*, *Columba hodgsonii*, *Columba bollii*, *Columba trocaz*, *Columba albitorques*, *Columba junoniae*, *Columba olivae*, *Columba delegorguei*, *Columba sjostedti*, *Columba uncinata*, *Columba iriditorques*, *Columba malherbii*, *Columba rupestris*, *Columba livia*, *Columba guinea*, *Columba leuconota*, *Columba congi* & *C. albinucha* and eastern species include *Columba vitiensis*, *Columba janthina*, *Columba jouyi*, *Columba versicolor*, *Columba pallidiceps*, *Columba leucomela*, *Columba palumboides*, *Columba argentina*, *Columba punicia*, *Columba torringtoni*, *Columba elphinstonii*, *Columba pulchricollis*, *Reinwardtoena reinwardti*, *Reinwardtoena browni*, *Reinwardtoena crassirostris*, *Turacoena manadensis*, *Turacoena sulaensis* and *Turacoena modesta*. All data is based on the distribution of species that have been retrieved from eBird database (<https://ebird.org/explore>).

Such as the comparable similarity of the vocalizations of *Columba palumbus* and *Patagioenas picazaro* or the comparable plumage morphology of *Columba punicea* and *Patagioenas leucopcephala*; which needs to be further resolved.

A novel finding in the study was the very close intergeneric relationship between the two genera *Columba* and *Reinwardtoena* based on the distance calculated between *Columba pulchricollis* and *Reinwardtoena reinwardti*. Secondly, similar data is obtained for the relationship between *Columba* and the genus *Turacoena* where the sequence of *Columba vitiensis* and *Turacoena manadensis* has been used and the overall minimum distance can be inferred from Table 5. The relationship between *Reinwardtoena reinwardti* and *Columba pulchricollis* is well supported in light of morphological evidence like a bluish-grey head and pink feet in common. Still, the former has comparatively fewer ornamental features than *Columba pulchricollis* with a purplish upper neck with iridescent bluish-grey green markings. On the other hand, *Columba vitiensis* and *Turacoena manadensis* are more morphologically similar (to an extent) like the presence of white throat and cheeks, neck with iridescence, and purplish-red orbital skin. Based on data mentioned in Table 3, *Reinwardtoena reinwardti* originated at 6.53 mya suggesting to be the common ancestor of not only *Columba pulchricollis* but presumably also of *Columba palumboides*, and *Columba pallidiceps* which originated at 5.11, 5.65, and 4.78 mya respectively based on the morphological evidence, it might be the common ancestor of *Columba leucomela* which originated at 2.13 mya. Based on the facts mentioned above, *Columba palumboides* and *Columba argentina* might be related, which will be discussed later.

Turacoena manadensis originated at 3.08 mya. So, it could be the common ancestor of *Columba vitiensis* and its subspecies along with *Columba palumbus* which originated at 2.3 mya and 3.02 mya respectively, thus subsequently might have resulted in the speciation of *Columba janthina* as postulated by Stresemann (1934) suggesting New Guinea as place of origin of *Columba janthina*; hence suggesting an “independent evolutionary pattern between Eastern and Western species of genus *Columba*.” All claims are also well supported with distribution* and morphology*.

4. 2. Taxonomic implication

Since *Reinwardtoena reinwardti* and *Columba pulchricollis* are both closely related along with *Turacoena manadensis* and *Columba vitiensis* on the support of the data mentioned and given the close geographic proximity, it is recommended to transfer the genus *Reinwardtoena* (Bonaparte, 1854) and genus *Tuarcoena* (Bonaparte, 1854) to genus *Columba* (Linnaeus, 1758).

*All data on both distribution and morphology were retrieved from Birds of the World, Cornell Lab of Ornithology website:
(<https://birdsoftheworld.org/bow/species/columb2/cur/introduction#genusColumba>)

4. 2. 1. Inter-specific Relationships

Based on Fig. 1 and 2 *Aplopelia larvata* should be placed in a separate monotypic genus of *Aplopelia* as initially given by C. L. Bonaparte devoid of genus *Columba* as given by C. J. Temminck (Temminck, 1809). The above is also supported by beak structures and the variance% vs PC plot as a result of GMA.

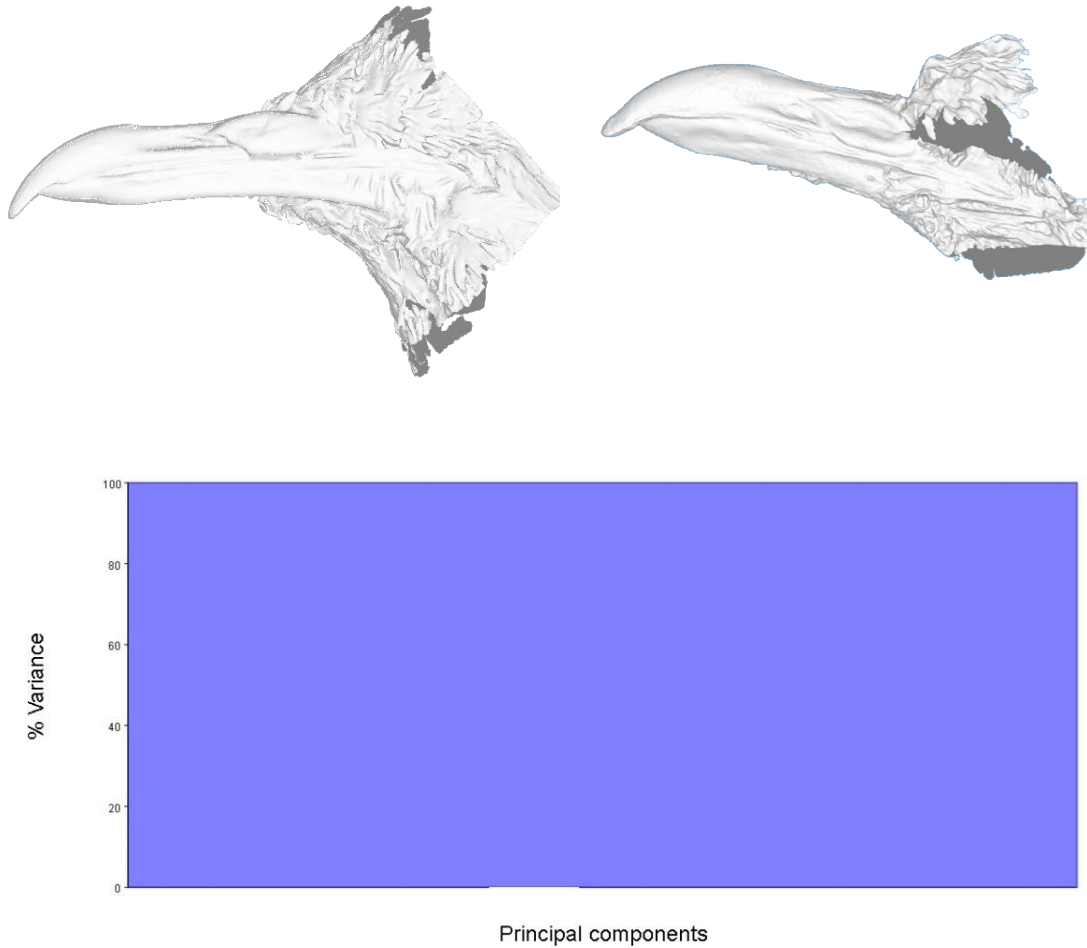


Fig. 3. The beak morphology of *Columba larvata* (Left) and *Columba pollenii* (Right) (Procured from markmybird.org) where the Variance % vs PC plot shows a variance in beak shape of 100%.

Source: https://www.markmybird.org/gallery/abeillia_abeillei/1169

One hypothesis I put forward is that the last recent ancestor of *Columba pollenii* (which I name for the present case as “x”) would also be the last ancestor of the extinct *Columba thiriouxi* living in the close geographical proximity to the islands of Comoros & Mauritius respectively (which needs to be further verified). It probably flew to the nearby island of Comoros crossing the Mozambique Channel, where some might have settled at new unexploited Miocene forests of subsidiary islands and might have flown further to Madagascar through an evolutionary bridge (Bassias, Yannis. (2016)) and went further to Mauritius and speciated accordingly.

Aplopelia larvata simplex has a huge plumage variation within the species i.e. ♂ are grey washed with vinaceous on the breast, brownish-black glossed with purple on the back whereas ♀ are brownishly glossed with vinaceous on the breast, head, and shoulders, whitish on the abdomen and deep brown. Based on the specimens collected by Jose’ G. Correa, now in the American Museum of Natural History, which were adult ♂ in breeding condition were exactly

similar to the ♀ of species and are bigger than the grey phase ♂ of the species above mentioned. It is also evident from the wing lengths mentioned in his manuscript.

♂ (Brown phase) : 152 – 160

♂ (Grey phase) : 145 – 157

♀ (Grey phase) : 145 – 152

In some ♂ underparts are intermediate while in others underparts are grey below and brown above. Immature of grey face have darker more purplish colour anterior (Amadon, D., & Correia, J. G. (1953)). So, it may be quite possible that the common ancestor “x” might have undergone müllerian mimicry with the plumage of immature-intermediate *Aplopelia* subspecies (brown face ♂ as later described in the text) that were more beneficial to blend in with the surrounding afro-tropical forests. Amadon D (Amadon, D., & Correia, J. G. (1953)) it is also mentioned that, ♂ of grey face of *Aplopelia l simplex* is similar to *Aplopelia l jaxoni* which inhabits the west coast area. Based on two ♂ specimens of *Aplopelia jaxoni* collected by Dr. James P. Chapin on Ruwenzori, Uganda is much more vinaceous less greyish than the other. The third ♂ of *Aplopelia jaxoni* collected by him which is of vinaceous type. (All three specimens mentioned are now in American Museum of Nature History) could justify the possibility of the hypothesis regarding the speciation of *Columba pollenii* (Fig. 3).

In Figure 1, the relationship of *Columba arquatrix*, is well established with *Columba hodgsonii* and has a monophily. On evaluation, the species based on zoogeography is a dilemma and how this *Columba* species closely related to *Columba thomensis* and *Columba arquatrix* ended up in the oriental region while other of its relatives is in the afro-tropical region. One hypothesis, I put forward for the problem based on time period is that an ancestral species moved to the Palaearctic via the Mediterranean region (Pereira, S.L et. al,2007) where some started living near the Tethys. The uplift of the Himalayas from 10 mya resulted in a significant environmental change some got away towards the Palaearctic regions as far as Europe and those that got trapped in the forming Himalayas independently evolved according to the changing climate to *Columba hodgsonii* at 2.66 mya and those groups that got separated evolved long before *Columba hodgsonii*'s speciation at 6.53 mya to *Columba oenas* which is evident by beak structure, where cere' size of *Columba hodgsonii*'s is much enlarged than other two species which may help filter both snow and dust particles and would help to warm the incoming air during breathing in a cold environment living in an altitude range of 1800 – 4000 m. For comparison of cere sizes, GMA was performed and the resulting PC score plot is hereby presented. (Fig. 4).

Based on Fig. 1 and 2, *Columba bollii* and *Columba trocaz* are also very related which can be inferred by its geographical locations and morphology but *Columba junoniae* is not closely related to the above species mentioned. Since plumage colourations are similar and also based on geographical proximity shows some sort of convergence between *C. junoniae* and *Columba bollii*. The difference between the two species can be inferred by their vocalizations and also from the absence of dark bands on the tail as in *Columba junoniae* and based on the phylogeny. The earlier claims of *Columba junoniae* being closer to *Columba palumbus* don't support as told by Goodwin (Goodwin, D. (1959)).

In support of timeline, morphology, and geographical proximity, *Columba oenas* is the probable ancestor to *Columba olivae* (originated at 6.22 mya) and *Columba evermanni*

(originated at 2.78 mya) as mentioned by Goodwin (Goodwin, D. (1959), Pereira, S.L et.al, (2007)). Based on geographical proximity, *Columba oliviae* seems to be the closest ancestor to *Columba albitorques*. Based on beak structure, a considerable elongation of the middle portion of the beak of *Columba oliviae*, *Columba albitorques*, and *Columba eversmanni* has been noticed as mentioned by Ryeland (Ryeland, J., et al (2017)) for being a thermo regulatory method that, birds with relatively larger bills are more prone to heat loss and keep body temperature relatively low from the environmental temperature. Upon considering the geographical range of *Columba oliviae*, *Columba eversmanni*, and *Columba albitorques* overlap arid steppe highlands where temperatures rise considerably high. Goodwin (1959) also proposes the loss of the black wing bar and pale brown colouration of *Columba oliviae* to camouflage to its environment along with the similarity of bowing display, tail pattern and black marking of *Columba albitorques* to *Columba oenas* suggests a common ancestry.

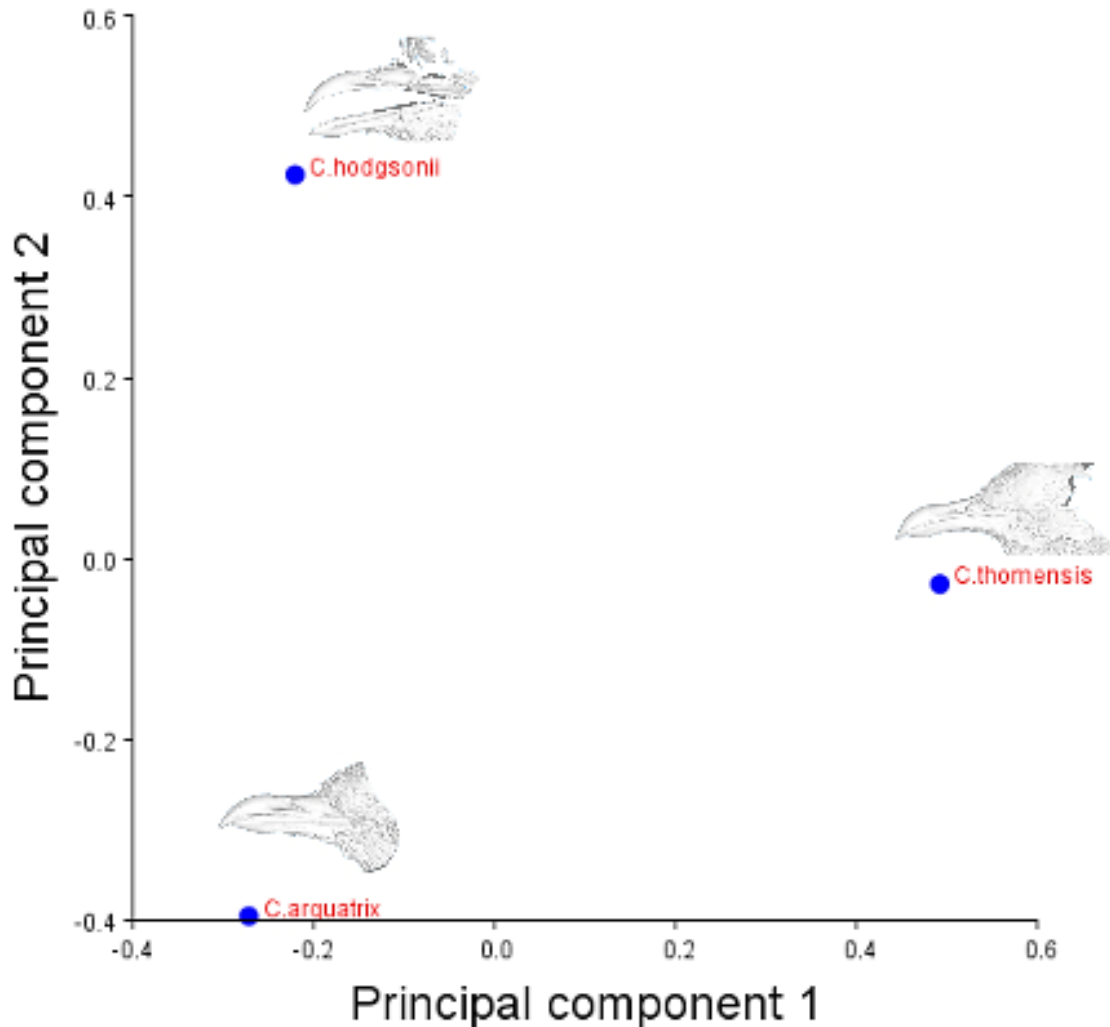


Fig. 4. The figure shows a huge variation in cere sizes of *Columba thomensis*, *Columba arquatrix*, and *Columba hodgsonni* thus complementing the facts mentioned above.

Based on intergeneric relationships, *Columba reinwardti* radiated to Indonesian islands enveloping the geographical range of another Columbiform, *Ducula bicolor*. The *Columba* sp. *reinwardti* started mimicking *Ducula bicolor* and started living in close proximity to the species (LI, Y. D. (2009)) and speciated to *Columba argentina* long after radiation and speciation of the ancestral form (which gave rise to *Columba argentina* 2.2 mya) to *Columba palmoides* 5.65 mya in the nearby island of Andaman in the Bay of Bengal can be inferred from plumage colouration (to some extent) also explained by timeline and geographical range proximity.

Due to geographical proximation and plumage coloration; presumably, *Columba punicia* might also be the result of radiation and subsequent evolution from *Columba reinwardtii* to Southeast Asian countries like Cambodia, Laos, Vietnam, Burma, Bangladesh, and the Indian subcontinent; Which flew further southwards the Indian subcontinent (as records exist (Jayakar, S. D. (1967), Kumar, T. S. et. al. (2010), Mooney, HF (1934)) and may have sympatrically evolved to *Columba elphinstonii* in response to the humid-tropical climate of Western Ghats at 2.58 mya or consider *Columba pulchricollis* as the probable ancestor to the *Columba elphinstonii* and hence *Columba torringtoni* as Goodwin (1959) anticipated based on plumage colour pattern. Either way, we can say that *Columba elphinstonii* and *Columba torringtoni* are closely related to *Columba reinwardti*.

4. 2. 2. Artificial Selection

“Sister / anagenic relationship” of *Columba livia* and *Columba rupestris* with the extinct *Columba congi* as mentioned by Shen et. al. (2021) based on the Pleistocene fossil from Zhoukoudian, Beijing, China; is one such evidence for the southward movement of the species. Human selection has paved the way for current *Columba* evolution to its various nominate forms showing a multitude of diversity from gigantism to dwarfism, elongated to shortened bills, naked to feathered tarsi, supremacy tail feathers, hypertrophied nose and eye ceres, frontal and occipital Ceres, iris colour and presence or absence of orbital rings, sexual dichromatic, head crests and much more (Baptista, L. F., et al (2009), Donegan, Thomas. (2016)). All these characters were selected by man for entertainment purposes and were also highly valued for their beauty. Due to artificial selection by man, the vocalizations have also varied from 1 breed to another. On thinking of the fact, pigeon breeds like fantails, tumblers, owls, pouters, homers, rollers, etc. have been a creation of man and all are just derivations of crosses of *Columba livia* with different breeds. Charles Darwin famously mentioned in his manuscript “On the Origin of Species” in the chapter on “Variation under Domestication” (Darwin, C., & Beer, G. (1996)): “Altogether at least a score of pigeons might be chosen, which if shown to an ornithologist, and he were told that they were wild birds, would certainly, I think, be ranked by him as well as defined species. Moreover, I do not believe that any ornithologist would place the English carrier, the short-faced tumbler, the runt, the barb, pouter, and fantail in the same genus; more especially as in each of these breeds several truly inherited sub-breeds or species as he might have called them, could be shown to him”

5. CONCLUSIONS

This comprehensive investigation of possible taxonomic relationships between species of genus *Columba* with other genera of family Columbidae namely *Streptopelia*, *Leptotila*,

Aplopelia, *Patagioenas*, *Turacoena* and *Reinwardtoena* has been conducted in accordance with the genetic evidence and previously published research, taking into consideration the morphology and geographic distribution. This approach led to the inclusion of the genera *Reinwardtoena* and *Turacoena* into the genus *Columba*. Based on phylogenetic tree and distance measurements, a hypothesis regarding the evolution of species of genus *Columba* has been formulated, taking care of morphological and zoogeographical similarities and differences where further investigation is required. The paper also discusses genus *Columba*'s interspecific relationships and their possible radiation patterns resulting in the diversity we see today.

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