

Original Research Paper

DNA Barcoding and Phylogenetic Relationships of Forest Birds in University of Ibadan, Nigeria

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Abstract

One of the most reliable indicators of a healthy ecosystem is the presence of diverse and reproductively viable bird populations. However, increasing anthropogenic pressures pose significant threats to avian diversity. The University of Ibadan environment supports a rich assemblage of bird species, yet information on their genetic diversity remains limited. Documenting their current levels of genetic diversity is essential for effective conservation and management. This study assessed the genetic diversity and phylogenetic relationships of selected forest bird species within the University of Ibadan using COI gene sequences. Blood samples were collected from 73 individuals representing 12 bird families. Genomic DNA was extracted, and the COI gene region was successfully amplified using the BirdF1 and COIbirdR2 primer pair from 18 individuals representing 14 species across 11 families. Amplicons were sequenced. Sequences were edited using BioEdit and aligned prior to phylogenetic analysis. Genetic distances were computed using the Kimura 2-parameter (K2P) model, and phylogenetic trees were constructed using the Neighbor-Joining method in MEGA 12.1. Results revealed low intraspecific genetic divergence (0.000–0.002) and higher interspecific divergence (0.05–0.15), indicating a clear barcode gap and supporting the effectiveness of the COI marker for species discrimination. Phylogenetic analysis showed well-resolved clustering consistent with established taxonomic relationships. The study demonstrates the utility of COI barcoding in assessing avian genetic diversity and provides baseline molecular data for bird species within the University of Ibadan. These findings contribute to ongoing biodiversity monitoring and highlight the importance of integrating molecular tools into conservation strategies in rapidly changing environments.

Keywords: DNA barcoding, COI gene, genetic diversity, Avian phylogeny, Biodiversity conservation

Introduction

Birds are widely recognized as reliable ecological indicators due to their sensitivity to environmental changes, wide distribution, and ease of observation (Clergeau et al., 2001). As conspicuous components of most ecosystems, they provide valuable insights into habitat quality and ecosystem integrity. Biodiversity, particularly species richness and composition, is a fundamental measure of ecosystem health (Frankham et al., 2010; Allendorf et al., 2013; Coker et al., 2017), and avian diversity plays a critical role in this assessment. Declines in biodiversity often signal ecological stress or environmental degradation (Müller et al., 2010).

Globally, bird populations are increasingly threatened by habitat loss and fragmentation resulting from anthropogenic activities such as deforestation, urban expansion, and agricultural intensification. The removal of nesting trees and foraging vegetation reduces habitat suitability, leading to declines in species

abundance and diversity (Manu et al., 2007). Habitat fragmentation further disrupts population connectivity by limiting dispersal and gene flow among populations. Although dispersal corridors can mitigate these effects by enhancing connectivity, both natural and human-induced barriers continue to fragment forest ecosystems (Adams and Burg, 2015).

Genetic diversity is a key determinant of a species' ability to adapt to environmental changes. Variations at the genotypic and phenotypic levels influence how species respond to ecological pressures (Willi et al., 2006). High levels of genetic diversity increase the likelihood that populations will possess adaptive traits necessary for survival under changing conditions (Nevo, 2013). Consequently, understanding patterns of genetic diversity is essential for predicting species resilience and informing conservation strategies.

Traditionally, genetic diversity has been assessed using morphological and biochemical markers; however, molecular approaches provide higher resolution and are less influenced by environmental factors (Sudre et al., 2007; Souza et al., 2008). Among molecular markers, mitochondrial DNA (particularly the cytochrome c oxidase subunit I (COI) gene) has become a standard tool for species identification and genetic analysis. The COI gene is characterized by conserved primer-binding regions and a relatively high mutation rate, enabling discrimination among closely related species as well as detection of intraspecific variation (Cox and Hebert, 2001; Wares and Cunningham, 2001). Its effectiveness as a universal DNA barcode has been demonstrated across diverse animal taxa, including birds (Susanti et al., 2018).

Despite documented avian diversity within the University of Ibadan (UI) environment (Adeyanju and Adeyanju, 2012), there is limited information on the genetic diversity and phylogenetic relationships of these bird populations in University of Ibadan and its environs. Such information is crucial for conservation planning, particularly in landscapes experiencing increasing anthropogenic pressure.

Therefore, this study employs COI gene sequences to investigate the genetic diversity and phylogenetic relationships of forest birds within the University of Ibadan, Nigeria, providing baseline molecular data to support conservation and management efforts. Specifically, this study sought to 1) generate and analyze COI gene sequences from selected bird species in the study area 2) evaluate genetic divergence among species using pairwise genetic distance metrics, and 3) construct phylogenetic relationships among sampled bird species.

Materials and Methods

Study Area

The study was conducted within the University of Ibadan (UI), located at approximately 7°27'3"N and 3°53'30"E, covering an area of about 12.07 km² in Ibadan, Southwestern Nigeria. The area lies within the transitional zone of the lowland rainforest and derived savanna. It experiences a mean annual rainfall of approximately 1,244 mm, occurring mainly between April and October. The elevation ranges from 180 to 210 m above sea level, with a mean relative humidity of about 65% and average daily temperatures between 20°C and 30°C. The vegetation is characterized by a mosaic of secondary forest, plantations, and open habitats, supporting diverse flora including trees, shrubs, herbs, climbers, and palms. This habitat heterogeneity provides suitable conditions for a wide range of bird species.

Bird Sampling

A total of 73 birds belonging to 12 families were captured and sampled using mist nets deployed across selected forested locations within the study area. They were identified using a bird field guide (Borrow and Demey, 2020). Blood samples were collected via brachial venipuncture following established ethical procedures (Vilstrup et al., 2006). After sampling, all birds were released unharmed upon recovery.

Collected blood samples were preserved in 0.5 ml of lysis buffer (100 mM Tris-HCl, pH 8; 100 mM Na₂EDTA; 10 mM NaCl; 0.5% SDS) and stored at ambient temperature in the field before being transferred to the laboratory and stored at 4°C. Sterile insulin syringes were used for each individual to prevent cross-contamination.

For the molecular analyses, a subset of 20 individuals was selected to represent the full taxonomic breadth of the sampled assemblage, ensuring that all bird families encountered during field sampling were included. Out of these, 18 representing 11 families were successful. This approach was adopted because the primary objective was to evaluate species identification, genetic divergence, and phylogenetic relationships across taxa using the COI barcode region.

DNA Extraction

Genomic DNA was extracted from blood samples of the selected samples using the solution-based genomic DNA extraction kit (Jena Bioscience GmbH, Germany), following the manufacturer's protocol. DNA quality and concentration were assessed using a NanoDrop 2000 spectrophotometer (Thermo Scientific, USA). Extracted DNA samples were stored at -20°C until further analysis.

PCR Amplification

The amplification of the COI gene locus was carried out through a polymerase Chain Reaction (PCR) using primer pair BirdF1 F-TTCTCCAACCACAAAGACATTGGCAC and COIbirdR2 R-ACGTGGGAGATAATTCCAAATCCTGG. Protocols for COI amplification followed Lijtmaer et al. (2012). For each PCR, 2 µl of DNA was added to a 12.5 µl reaction mixture. The mixture was composed of 6.5 µl of 10% Trehalose, 2 µl of ddH₂O, 1.25 µl 10x PCR Buffer, 0.625 µl 50mM MgCl₂, 0.125 µl 10 µM forward primer, 0.125 µl 10 µM reverse primer, 0.0625 µl of 10 mM deoxyribonucleotide triphosphate (dNTPs), 0.06 µl of Taq DNA polymerase (5U/µl) and 2 µl of DNA. Cycling parameters consisted of an initial denaturation step of 1 min at 94°C followed by 5 cycles (94°C for 1 min, 45°C for 40 s, 72°C for 1 min), 35 cycles (94°C for 1 min, 51°C for 40 s, 72°C for 1 min), then final extension at 72°C for 5 min.

Sequencing and Phylogenetic Analysis

Successful PCR products were purified and sequenced commercially by Macrogen Inc. The generated COI sequences ranged from 596 to 752 bp in length. Raw sequences were inspected and edited in BioEdit version 7.2.5 (Hall, 1999), where low-quality terminal regions and primer sequences were removed. Ambiguous nucleotide calls were checked against the chromatograms and corrected where necessary; no ambiguous positions were retained in the final alignment. Sequences were subsequently aligned using the ClustalW algorithm implemented in MEGA version 12.1 (Kumar et al., 2018) with default settings. To ensure that all sequences covered the same homologous region, the alignment was trimmed to a common overlapping segment, resulting in a final dataset of 603 bp for phylogenetic and genetic distance analyses.

To verify sequence identity, edited sequences were compared with reference sequences available in the National Center for Biotechnology Information GenBank database using the BLAST algorithm (Stephen, 1990). Only sequences with high similarity scores were retained for further analysis.

Genetic divergence among the sampled taxa was estimated using the Kimura 2-parameter (K2P) model, which accounts for differences in transition and transversion substitution rates (Kimura, 1980) and is widely applied in DNA barcoding studies (Hebert et al., 2003). Pairwise genetic distance matrices were generated in MEGA to assess intra- and interspecific variation. Phylogenetic relationships were reconstructed using the Neighbor-Joining method implemented in MEGA version 12.1. Genetic distances were estimated using the Kimura 2-parameter model, and node support was assessed through 1,000 bootstrap replicates. *Alcedo*

atthis (Alcedinidae) was included as an outgroup to root the tree because it is closely related to, but distinct from, the sampled taxa. Its inclusion provided an evolutionary reference point for inferring the direction of divergence while avoiding the excessive genetic distance that may result from using more distantly related avian taxa. A Maximum Likelihood analysis was also performed to assess the robustness of the inferred relationships, and the resulting topology was largely congruent with that obtained using the Neighbor-Joining method. The resulting phylogenetic tree was visualized and edited in MEGA. Concordance between genetic distance estimates and phylogenetic clustering was examined to validate species identification and infer evolutionary relationships among the sampled bird taxa.

Results

Sequence Characteristics and Species Identification

A total of 18 high-quality mitochondrial COI sequences were obtained from bird species sampled within the University of Ibadan, representing 12 families (Table 1). All sequences generated in this study have been successfully deposited in the National Center for Biotechnology Information GenBank database and assigned accession numbers (Table 1). This ensures accessibility and reproducibility of the data for future studies. Sequence identity confirmation using the BLAST against GenBank revealed high similarity between generated sequences and reference sequences, confirming accurate species identification.

Table 1: List of samples and their Genbank assigned accession numbers

SN	GenBank Accession Number	Species Name	Scientific Name	Family
1	OP682797	Woodland Kingfisher	<i>Halcyon senegalensis</i>	Alcedinidae
2	OP682788	Grey-backed Camaroptera	<i>Camaroptera brevicaudata</i>	Cisticolidae
3	OP682796	Grey-backed Camaroptera	<i>Camaroptera brevicaudata</i>	Cisticolidae
4	OP682784	Blue-spotted wood dove	<i>Turtur afer</i>	Columbidae
5	OP682798	Fork-tailed Drongo	<i>Dicrurus adsimilis</i>	Dicruridae
6	OP682789	Western Bluebill	<i>Spermophaga haematina</i>	Estrildidae
7	OP682792	Bronze Mannikin	<i>Spermestes cucullata</i>	Estrildidae
8	OP682781	Red-bellied Paradise Flycatcher	<i>Terpsiphone rufiventer</i>	Monarchidae
9	OP682790	African paradise flycatcher	<i>Terpsiphone viridis</i>	Monarchidae
10	OP682785	Snowy Crown robin Chat	<i>Cossypha niveicapilla</i>	Muscicapidae
11	OP682794	Olive-bellied Sunbird	<i>Cinnyris chloropygius</i>	Nectariniidae
12	OP682786	Veillot's black weaver	<i>Ploceus nigerrimus</i>	Ploceidae
13	OP682791	Little Greenbul	<i>Eurillas virens</i>	Pycnonotidae
14	OP682793	Little Greenbul	<i>Eurillas virens</i>	Pycnonotidae
15	OP682787	Yellow-whiskered Greenbul	<i>Eurillas latirostris</i>	Pycnonotidae
16	OP682795	Yellow-whiskered Greenbul	<i>Eurillas latirostris</i>	Pycnonotidae
17	OP682782	African Thrush	<i>Turdus pelios</i>	Turdidae
18	OP682783	African Thrush	<i>Turdus pelios</i>	Turdidae

Genetic Distance Analysis

Pairwise genetic distances based on the Kimura 2-parameter (K2P) model revealed distinct and hierarchical patterns of genetic divergence among the sampled taxa (Table 2). Genetic distances among individuals of

the same species were extremely low, ranging from 0.000 to approximately 0.002. For example, negligible divergence was observed among sequences of *Turdus pelios*, *Eurillas virens*, and *Camaroptera brevicaudata*. These values fall within the typical range of intraspecific divergence reported in DNA barcoding studies, where conspecific individuals generally exhibit very low sequence variation (Hebert et al., 2003; Kerr et al., 2007).

In contrast, genetic distances between different species were substantially higher, generally ranging from approximately 0.05 to 0.15. This level of divergence is consistent with established DNA barcoding studies, which report clear separation between species based on COI sequences (Hebert et al., 2003; Ward, 2009).

Moderate divergence values (approximately 0.05–0.10) were observed among species within related groups, while higher values (often >0.10–0.15) occurred between more distantly related taxa. These findings reflect accumulated genetic differences over evolutionary time and support the distinctiveness of the sampled species.

Patterns of genetic distance further reflected taxonomic hierarchy. Comparisons among species within the same family generally showed moderate divergence, typically within the range of 0.06–0.12, indicating shared evolutionary ancestry but clear genetic separation. For instance, species within families such as Estrildidae and Pycnonotidae exhibited moderate levels of divergence relative to each other, consistent with expectations for closely related taxa. Similar patterns have been reported in avian barcoding studies, where genetic distances tend to increase progressively from species to genus and family levels (Kerr et al., 2007; Ward, 2009).

An exception to the general pattern was observed between *Camaroptera brevicaudata* and *Eurillas virens*, which exhibited relatively low interspecific divergence (approximately 0.01–0.09). This reduced genetic distance is lower than typical interspecific values and suggests close evolutionary affinity between these taxa. This observation is consistent with findings that closely related or recently diverged species may show reduced COI divergence, potentially due to incomplete lineage sorting or recent speciation events (Kerr et al., 2007; Allendorf et al., 2013).

Phylogenetic Analysis

The Neighbor-Joining (NJ) phylogenetic tree constructed using K2P distances revealed clustering patterns largely consistent with taxonomic relationships (Figure 1).

The tree was rooted using *Alcedo atthis* as an outgroup, which occupied a basal position and provided clear evolutionary direction to the tree.

Most taxa formed distinct clades corresponding to their species. For instance, *Turdus pelios* formed a well-supported cluster; *Eurillas latirostris* grouped together and Estrildid species such as *Spermestes cucullata* and *Spermophaga haematina* formed related but distinct clades.

There are two main branches constituting passerine and non-passerine species. Passerine species constituted the main ingroup, while non-passerine taxa such as *Halcyon senegalensis* and *Turtur afer* occupied more basal positions relative to passerines. The outgroup (*Alcedo atthis*) was clearly separated from the ingroup and positioned at the base of the tree, confirming its suitability for rooting. *Camaroptera brevicaudata* and *Eurillas virens* showed close clustering rather than complete separation. This indicates a possible close evolutionary relationships or reduced resolution of the COI marker for these species.

Table 2: Genetic distance matrix of the forest bird species of University of Ibadan

	H. senegalensis	C. brevicaudata_1	C. brevicaudata_2	T. afer	D. adsimilis	S. haematina	S. cucullata	T. rufiventer	T. viridis	C. niveicapilla	C. chloropygius	P. nigerrimus	E. virens1	E. virens2	E. latirostris1	E. latirostris2	T. pelios1	T. pelios_2
H. senegalensis	0.000																	
C. brevicaudata_1	0.183	0.000																
C. brevicaudata_2	0.210	0.092	0.000															
T. afer	0.205	0.192	0.209	0.000														
D. adsimilis	0.200	0.179	0.191	0.229	0.000													
S. haematina	0.210	0.185	0.193	0.204	0.192	0.000												
S. cucullata	0.207	0.173	0.174	0.196	0.178	0.133	0.000											
T. rufiventer	0.178	0.182	0.189	0.214	0.154	0.193	0.175	0.000										
T. viridis	0.171	0.173	0.185	0.209	0.150	0.194	0.180	0.043	0.000									
C. niveicapilla	0.176	0.173	0.184	0.200	0.185	0.184	0.166	0.161	0.159	0.000								
C. chloropygius	0.209	0.184	0.193	0.215	0.193	0.198	0.187	0.165	0.152	0.165	0.000							
P. nigerrimus	0.187	0.164	0.177	0.181	0.172	0.164	0.162	0.178	0.172	0.167	0.182	0.000						
E. virens_1	0.185	0.010	0.092	0.198	0.181	0.191	0.179	0.188	0.174	0.177	0.190	0.164	0.000					
E. virens_2	0.176	0.012	0.081	0.187	0.172	0.180	0.174	0.174	0.161	0.164	0.173	0.154	0.015	0.000				
E. latirostris_1	0.212	0.184	0.192	0.219	0.193	0.209	0.195	0.169	0.163	0.176	0.034	0.197	0.190	0.172	0.000			
E. latirostris_2	0.205	0.180	0.189	0.210	0.189	0.194	0.183	0.161	0.148	0.161	0.003	0.178	0.186	0.169	0.031	0.000		
T. pelios_1	0.199	0.163	0.177	0.178	0.163	0.173	0.160	0.175	0.178	0.132	0.163	0.144	0.167	0.152	0.161	0.159	0.000	
T. pelios_2	0.202	0.160	0.177	0.175	0.168	0.176	0.161	0.176	0.179	0.133	0.168	0.146	0.164	0.149	0.166	0.164	0.005	0.000

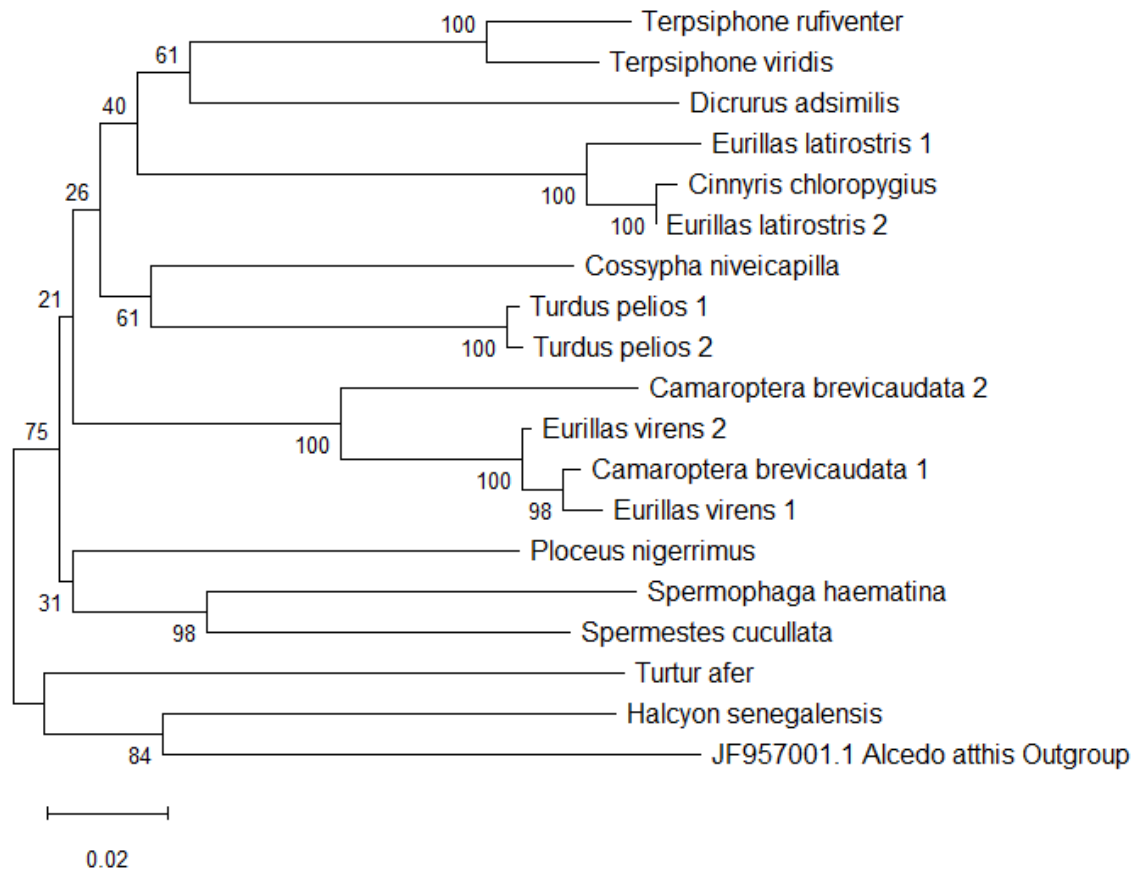


Figure 1: Neighbor-Joining (NJ) phylogenetic tree showing the relationships among COI haplotypes of forest birds from University of Ibadan, Nigeria. Values shown at internal nodes represent bootstrap percentages obtained from 1,000 pseudoreplicates and indicate the statistical support for each branch. Branch lengths are proportional to the number of nucleotide substitutions per site. *Alcedo atthis* was used to root the tree.

Discussion

This study evaluated the genetic diversity and phylogenetic relationships of selected bird species within the University of Ibadan using mitochondrial COI sequences. The results demonstrate that the COI gene is effective for species identification and provides meaningful insights into evolutionary relationships among the sampled taxa.

Patterns of Genetic Divergence Across Taxonomic Levels

The very low intraspecific genetic distances observed (0.000–0.002) are consistent with values reported in previous DNA barcoding studies of birds, where conspecific individuals typically exhibit minimal sequence divergence (Hebert et al., 2003; Kerr et al., 2007; Leffler et al., 2012). This low variation confirms that individuals within each species share highly similar mitochondrial haplotypes, supporting accurate species delineation. In contrast, interspecific genetic distances were substantially higher (0.05–0.15), providing a clear distinction between species (Avise, 2000; Ward, 2009). For instance, the relatively high divergence between non-passerine taxa such as *Halcyon senegalensis* and *Turtur afer* compared to passerine species may reflect deep evolutionary splits.

This pattern reflects the well-established “barcode gap”, which is a fundamental requirement for reliable DNA-based species identification (Hebert et al., 2003). The presence of this gap in most taxa in the present study indicates that the COI gene is a robust marker for identifying bird species in the study area.

Phylogenetic Relationships and Tree Structure

The Neighbor-Joining phylogenetic tree largely reflected known taxonomic relationships, with most species forming well-defined clusters. Conspecific sequences grouped together with strong bootstrap support, indicating genetic coherence within species and validating the reliability of the dataset. The use of *Alcedo atthis* as an outgroup successfully rooted the tree and provided directionality to the evolutionary relationships. Its basal placement relative to the ingroup confirms its suitability as an outgroup and supports the inferred phylogenetic structure. The clustering of passerine species into a major clade further supports established avian phylogeny, while the basal positioning of non-passerine taxa reflects their evolutionary divergence.

The results of this study clearly demonstrate the effectiveness of the COI barcode region for species identification, as evidenced by the low intraspecific divergence, higher interspecific divergence, and successful assignment of sequences to their respective taxa. However, the interpretation of phylogenetic relationships derived from COI should be approached with caution. Although mitochondrial markers are useful for recovering broad patterns of genetic relatedness, they represent a single maternally inherited locus and may not accurately reflect species-level evolutionary histories, particularly among recently diverged taxa. Consequently, the phylogenetic groupings observed in this study should be viewed primarily as estimates of genetic similarity rather than definitive reconstructions of evolutionary relationships. Additional nuclear markers and genome-wide approaches would be required to fully resolve relationships among closely related species.

A notable finding of this study was the relatively low genetic divergence observed between *Camaroptera brevicaudata* and *Eurillas virens*. While low interspecific divergence can sometimes indicate recent common ancestry, such interpretations should be made cautiously when based solely on mitochondrial DNA. The COI gene, although highly effective for species identification, may not always provide sufficient resolution for reconstructing relationships among closely related taxa. Reduced divergence may result from incomplete lineage sorting, retention of ancestral polymorphisms, mitochondrial introgression, or discordance between mitochondrial and species phylogenies (Funk and Omland, 2003; Toews and Brelsford, 2012). Consequently, the observed clustering of these species should not be regarded as definitive evidence of close evolutionary affinity. Instead, it highlights the limitations of relying on a single mitochondrial marker for phylogenetic inference.

Implications for Conservation and Biodiversity Assessment

The present study provides the first COI barcode reference dataset for several bird species occurring within the University of Ibadan. Beyond species identification, these data establish a molecular baseline against which future changes in avian diversity can be assessed. As urban expansion, infrastructure development, and vegetation modification continue to alter habitats within and around the University environment, DNA barcode records can facilitate long-term monitoring by enabling the verification of species identities and the detection of changes in species composition over time.

The occurrence of genetically distinct taxa representing multiple avian families further highlights the conservation value of the University of Ibadan as a refuge for forest-associated bird species within an increasingly modified landscape. Maintaining mature trees, forest patches, riparian vegetation, and other

critical nesting and foraging habitats will be important for sustaining this diversity. The genetic data generated in this study may also serve as a reference resource for future ecological studies, environmental impact assessments, and conservation planning initiatives in Southwestern Nigeria.

Furthermore, the reduced genetic divergence observed among some closely related taxa underscores the need for continued genetic monitoring and more comprehensive molecular investigations. Resolving these relationships using additional markers would improve our understanding of species boundaries and evolutionary diversity, thereby supporting more informed conservation and management decisions.

The University of Ibadan environment, despite being subject to anthropogenic pressures, still supports genetically distinct bird populations across multiple families. The availability of COI sequences for these species (now deposited in GenBank) provides a valuable reference for future monitoring, species identification, and conservation studies.

Conclusion

This study analyzed mitochondrial COI gene sequences from selected bird species within the University of Ibadan. The sequences provided reliable molecular confirmation of species identity and established a useful genetic baseline for avian taxa in the study area.

Pairwise genetic distance analyses revealed low intraspecific divergence and higher interspecific divergence, resulting in a distinct barcode gap for most taxa. Similarly, phylogenetic reconstruction using the Neighbor-Joining method produced tree topologies that were largely consistent with established taxonomic relationships, with most species forming well-supported clades. These findings confirm the effectiveness of the COI marker for species discrimination and for assessing phylogenetic relationships among the majority of the sampled bird species.

However, a few closely related taxa exhibited reduced genetic divergence and weaker phylogenetic resolutions, suggesting that COI alone may be insufficient for resolving some evolutionary relationships. These exceptions may reflect recent divergence, incomplete lineage sorting, or other evolutionary processes that cannot be adequately addressed using a single mitochondrial marker.

Future studies should therefore incorporate additional nuclear markers and genome-wide approaches to clarify the relationships among closely related taxa and provide a more comprehensive understanding of avian genetic diversity in the region. .

Overall, the findings contribute valuable baseline genetic data for avian species in the study area and highlight the importance of integrating molecular tools into conservation and biodiversity assessments.

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Author's Contributions

Conceptualization: Oluwakayode Michael Coker; **Methodology:** Oluwakayode Michael Coker, Adeniyi Taiye Adeyanju; **Formal analysis and investigation:** Oluwakayode Michael Coker, Adeniyi Taiye Adeyanju., Faith Eke Alagi., Uthman Ayoku Oyebamiji., Oluwadamilola Oyewale Oyeniran; **Writing original draft preparation:** Oluwakayode Michael Coker; **Writing—review and editing:** Oluwakayode Michael Coker, Adeniyi Taiye Adeyanju., Faith Eke Alagi., Uthman Ayoku Oyebamiji., Oluwadamilola Oyewale Oyeniran; **Resources:** Oluwakayode Michael Coker, Adeniyi Taiye Adeyanju., Faith Eke Alagi., Uthman Ayoku Oyebamiji., Oluwadamilola Oyewale Oyeniran

Conflict of Interest

Authors declare no conflict of interest as regards this research work

Ethics

Ethical approval and clearance were obtained from the University of Ibadan Animal Care and Use Research Ethics Committee (ACUREC) to undertake this study, and all the ethical issues were strictly adhered to. Assigned number is UI-ACUREC/19/099.

References

- Adams R. V. Burg T. M. 2015. Gene flow of a forest-dependent bird across a fragmented landscape. *PLoS One*, 10(11), e0140938.
- Adeyanju T. E and Adeyanju A. T 2012. Avifauna of University of Ibadan Environs Ibadan, Nigeria. Proceedings of 3rd Annual seminar of Nigerian Tropical Biology Association (NTBA). Pp 27-34.
- Allendorf F.W. Luikart G. Aitken S.N. 2013. Conservation and the Genetics of Populations (2nd ed.). Wiley-Blackwell.
- Avice J.C. 2000. Phylogeography: The history and formation of species. Harvard University Press.
- Borrow N. Demey R. 2020. Field guide to birds of Western Africa. Bloomsbury Publishing.
- Clergeau P. Jokimäki J. Savard J.P.L. 2001. Are urban bird communities influenced by the bird diversity of adjacent landscapes? *Journal of Applied Ecology*, 38, 1122–1134.
- Coker O. M. Omonona A.O. Fagbohun A. O. Pylant C. and Austin J. 2017. Genetic structure of wild and domesticated grasscutters (*Thryonomys swinderianus*) from Southwestern Nigeria. *African Zoology*, 52(3): 155-162 <https://doi.org/10.1080/15627020.2017.1379358>
- Cox A.J. Hebert P.D.N. 2001. Colonization, extinction, and phylogeographic patterning in a freshwater crustacean. *Evolution*, 55, 313–325.
- Frankham R. Ballou J.D. Briscoe D.A. 2010. Introduction to conservation genetics (2nd ed.). Cambridge University Press.
- Funk D. J. Omland K. E. 2003. Species-level paraphyly and polyphyly: frequency, causes, and consequences, with insights from animal mitochondrial DNA. *Annual Review of Ecology, Evolution, and Systematics*, 34(1), 397-423.
- Hall T.A. 1999. *BioEdit*: a user-friendly biological sequence alignment editor and analysis program. *Nucleic Acids Symposium Series*, 41: 95–98.
- Hebert P.D.N. Cywinska A. Ball S.L. deWaard J.R. 2003. Biological identifications through DNA barcodes. *Proceedings of the Royal Society B*, 270, 313–321.
- Kerr K.C.R. Stoeckle M.Y. Dove C.J. Weigt L.A. Francis C.M. Hebert P.D.N. 2007. Comprehensive DNA barcode coverage of North American birds. *Molecular Ecology Notes*, 7, 535–543.
- Kimura M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of molecular evolution*, 16(2), 111-120.
- Kumar S. Stecher G. Li M. Knyaz C. Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution*, 35(6), 1547–1549.

- Leffler E.M. Bullaughey K. Matute D.R. Meyer W.K. Segurel L. Venkat A. sAndolfatto P. Przeworski M. 2012. Revisiting an old riddle: What determines genetic diversity levels within species? *PLoS Biology*, 10(9), e1001388.
- Lijtmaer D.A. Kerr K.C.R. Stoeckle M.Y. Tubaro P.L. Hebert P.D.N. 2012. DNA barcode libraries provide insight into continental patterns of avian diversification. *PLoS ONE*, 7(7), e42261.
- Manu S. Peach W. Cresswell W. 2007. The effects of edge, fragment size and degree of isolation on avian species richness in highly fragmented forest in West Africa. *Ibis* 149:287297.
- Müller J. Stadler J. Brandl R. 2010. Composition versus physiognomy of vegetation as predictors of bird assemblages: The role of lidar. *Remote Sensing of Environment*, 114(3), 490-495.
- Nevo E. 2013. Evolution of genome–phenome diversity under environmental stress. *Proceedings of the National Academy of Sciences*, 110, 18295–18300.
- Souza S. G. H. D. Carpentieri-Pípolo V. Ruas C. D. F. Carvalho V. D. P. Ruas P. M. Gerage A. C. 2008. Comparative analysis of genetic diversity among the maize inbred lines (*Zea mays* L.) obtained by RAPD and SSR markers. *Brazilian archives of biology and technology*, 51, 183-192.
- Stephen F. A. 1990. Basic local alignment search tool. *J. mol. Biol.*, 215, 403-410.
- Sudré C. P. Leonardecz E. Rodrigues R. Amaral Júnior A. T. D. Moura M. D. C. Gonçalves L. S. 2007. Genetic resources of vegetable crops: a survey in the Brazilian germplasm collections pictured through papers published in the journals of the Brazilian Society for Horticultural Science. *Horticultura Brasileira*, 25(4), 496-503.
- Toews D. P. Brelsford A. 2012. The biogeography of mitochondrial and nuclear discordance in animals. *Molecular ecology*, 21(16), 3907-3930.
- Vilstrup J. T. Mullins, T. D. Miller M. P. McDearman W. Walters J. R. Haig S. M. 2018. A simplified field protocol for genetic sampling of birds using buccal swabs. *The Wilson Journal of Ornithology*, 130(1), 326-334.
- Ward R.D. 2009. DNA barcode divergence among species and genera of birds and fishes. *Molecular Ecology Resources*, 9, 1077–1085.
- Wares J. P. Cunningham C. W. 2001. Phylogeography and historical ecology of the North Atlantic intertidal. *Evolution*, 55(12), 2455-2469.
- Willi Y. Van Buskirk J. Hoffmann A.A. 2006). Limits to the adaptive potential of small populations. *Annual Review of Ecology, Evolution, and Systematics*, 37, 433–458.