MOLECULAR FRONTIERS IN BIODIVERSITY RESEARCH FROM BANGLADESH: A REVIEW

Bioresearch Communications
Volume 12, Issue 1, January 2026

DOI:
doi.org/10.3329/brc.v12i1.86781

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ABSTRACT

Bangladesh harbors a rich and unique biodiversity and is home to numerous threatened species of different categories that are vital for its ecological balance and sustainable development. In recent years, molecular approaches have emerged as powerful tools for studying and conserving this biodiversity and threatened organisms, enabling precise species identification, uncovering cryptic diversity, helping to make informed management strategies. This review aims to synthesize recent advances in molecular taxonomic research on Bangladesh's flora and fauna, with a particular emphasis on the applications of DNA barcoding across marine, freshwater, and terrestrial taxa. The review highlights that, despite the remarkable biodiversity in Bangladesh, only a fraction of these species has been genetically characterized. DNA barcoding initiatives have progressed notably in fishes, arthropods, and fungi, but remain limited for plants and several vertebrate and invertebrate groups, particularly in avian species. This disparity underscores a significant gap between the country's known biodiversity and its molecular-level validation. Moving forward, strengthening molecular databases, integrating advanced genomic tools, and building local research capacity are essential for comprehensive biodiversity assessment, effective monitoring, and informed conservation strategies in Bangladesh.

KEYWORDS: Biodiversity, DNA barcoding, Molecular taxonomy, Bangladesh

RECEIVED: 04 November 2025, ACCEPTED: 26 December 2025

TYPE: Review Article

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Introduction

The unique geographical location coupled with fertile river system and ecosystem makes Bangladesh one of the richest biodiversity nation on earth. Boasting a wide range of both vertebrate and invertebrate species, the region is home to numerous threatened animals (IUCN Bangladesh, 2015a). To conserve this ecosystem and the endangered species, proper documentation and understanding of this rich biodiversity are required, which in turn, demands an accurate and systematic method of species identification.

Taxonomy refers to the identification and classification of all species through scientific method that reveals crucial information on interspecies relation as well as the lineage of the current living species to their possible ancestor species. Gradual and further understanding of the nuanced differences among species led to numerous changes, deviations, and modifications to the taxonomy over time to account for the subtle variations among the species. For the last 250 years, taxonomy has been primarily defined by morphological structures, focusing on the phenotypic traits of individual organisms (Hebert and Gregory, 2005). While morphological identification is a practical approach among species with distinct phenotypical traits, it is a challenging technique for some organisms like shrimp, crabs, and a variety of fishes, due to their diverse larval stages, sexual dimorphism, and plasticity, all of which can be compromised by rough handling (Nicolè *et al.*, 2012; Hillis, 1987). As a result, misidentification is a common phenomenon, and distinguishing them at the genus or species level can be challenging. To address these challenges, DNA barcoding has emerged as a promising alternate method, where it identifies species through a short, universal DNA sequence that provides enough variation to distinguish among species (Hebert *et al.*, 2003). DNA barcoding is widely recognized as a rapid and reliable method for the accurate identification of species, including crustaceans, mollusks, fish, snakes, and other organisms, in various countries such as Bangladesh, Australia, China, Turkey, Malaysia, Vietnam, and India (Murphy and Austin, 2004; Bilgin *et al.*, 2015; Rajkumar *et al.*, 2015; Rahman *et al.*, 2019; Ahmed *et al.*, 2021; Ahmed *et al.*, 2020; Islam *et al.*, 2022; Abdul Halim *et al.*, 2023; Habib *et al.*, 2021a, 2023; Siriwut *et al.*, 2021). Besides DNA barcoding, advanced molecular approaches such as whole-genome sequencing, metabarcoding, environmental DNA (eDNA), and microsatellite analysis are increasingly used for biodiversity monitoring, food safety assessment, and ecosystem health evaluation (Islam *et al.*, 2025; Abraham *et al.*, 2024; Rahman *et al.*, 2024; Wee *et al.*, 2023; Osman *et al.*, 2022). This review aims to provide an up-to-date overview of the advancements in DNA barcoding techniques, their applications, and their impact on taxonomy and biodiversity studies in Bangladesh.

Transforming classical taxonomy to modern DNA-based identification

The transformation of classical taxonomy into modern DNA-based identification represents a significant milestone in the study of biological diversity. Traditional taxonomy, which depended on morphological and anatomical characteristics, often faced limitations due to phenotypic plasticity, environmental variation, and convergent evolution that obscured true evolutionary relationships (Nicolè *et al.*, 2012). The introduction of molecular tools, particularly DNA barcoding and whole-genome sequencing, has revolutionized species identification by providing precise and reproducible genetic markers. These DNA-based approaches allow scientists to detect minute genetic variations, resolve cryptic species complexes, and construct more accurate phylogenetic relationships (Hebert *et al.*, 2003). Moreover, molecular identification facilitates rapid and reliable classification of organisms across all life forms, including those with incomplete or damaged morphological features. Consequently, the integration of genetic data into taxonomy has transformed it into a more objective and comprehensive discipline, enhancing our understanding of biodiversity, evolution, and conservation biology. This molecular approach not only refines traditional classification systems but also enhances biodiversity assessment, conservation strategies, and evolutionary research.

Current scenario of molecular research in Bangladesh

Molecular research in Bangladesh has gained significant momentum over the past 15 years, with growing interest in genetics, genomics, and molecular ecology. Introduction of DNA barcoding techniques has played a pivotal role in documenting the country's rich biodiversity and supporting conservation initiatives. Early molecular studies in Bangladesh were primarily focused on agricultural crops, fisheries, and infectious diseases, but the scope has since expanded to include diverse taxonomic groups. Several research groups and institutions have initiated barcoding and molecular identification projects on fish, plants, insects, and microorganisms (Ahmed *et al.*, 2019, 2020, 2021a; Rahman *et al.*, 2019; Habib *et al.* 2021, 2023; Islam *et al.*, 2025a,b; Jannat *et al.*, 2024; Meem *et al.*, 2023; Haque *et al.*, 2019). Notably, the Cytochrome c oxidase subunit I (COI) gene has been the most widely employed molecular marker for species identification efforts in the country, while other mitochondrial markers such as 16S rRNA and ND2 have also been utilized across multiple taxa. In addition, advanced molecular approaches including whole-genome sequencing, metabarcoding, environmental DNA (eDNA), and microsatellite analysis have also been applied in biodiversity and taxonomic studies in Bangladesh (Islam *et al.*, 2025; Abraham *et al.*, 2024; Rahman *et al.*, 2024; Islam *et al.*, 2023; Rashid *et al.*, 2020; Rahman *et al.*, 2010; Khan *et al.*, 2009). These foundational efforts have established a robust platform for broader genomic and biotechnological research within the country and emphasize the growing adoption of molecular tools for biodiversity assessment and species authentication.

Barcoding status

Current records indicate approximately 4,255 plant species, 656 fungal species, close to one thousand fish species, around 700 bird species, and more than 500 mollusk species within the country (Shamsi and Alam, 2025; Arfin *et al.*, 2023; Habib and Islam, 2020; Khan, 2018; Shamsi, 2017, 2018; IUCN Bangladesh, 2015a-f; Rahman *et al.*, 2009; Siddiqui *et al.*, 2009; Siddiqui *et al.*, 2007). Despite this impressive diversity, only a portion of these species has been genetically documented through DNA barcoding (Table 1). All molecular data were compiled from NCBI GenBank and relevant peer-reviewed publications from Bangladesh. This disparity highlights a substantial gap between known biodiversity and molecular-level validation.

Bacteria

Although 584,820 bacterial sequences exist in databases, most are from global sequencing pipelines rather than native species identification. Local bacterial barcoding and genome sequencing initiatives remain limited. The lack of detailed taxonomic breakdown indicates that bacterial barcoding in Bangladesh is still in its infancy. Furthermore, most bacterial barcodes originate from environmental metagenomic studies rather than species-level characterizations. This highlights the need for targeted studies focusing on medically, industrially, and ecologically important bacterial taxa endemic to Bangladesh.

Animal Diversity

Chordates

Among chordates, barcoding progress varies considerably between groups. Mammals (127 species recorded) have about 70 species (55.12%) barcoded, reflecting moderate molecular coverage. Many of these sequences are derived from endangered and economically important species, showing a research focus on conservation and forensic applications.

Birds, with 690 species (Khan, 2018), exhibit a much lower barcoding rate (5.65%), suggesting that avian molecular profiling in Bangladesh remains limited. Given the country's importance along the East Asian Australasian Flyway, this represents a critical gap in genetic data for migratory and resident species.

For reptiles (167 species) and amphibians (63 species), barcode coverage is 26.95% and 46.77%, respectively. The relatively higher amphibian coverage reflects recent integrative taxonomic efforts aimed at resolving cryptic species and new records in the Chittagong Hill Tracts and Sylhet regions.

Fish diversity, encompassing both freshwater and marine habitats, shows the most comprehensive barcode coverage among chordates. Out of 909 recorded species, 664 species (73.05%) have barcode data (Figure 1). This progress reflects not only the strategic value of DNA barcoding in strengthening national biodiversity documentation, but also the pioneering scientific leadership of researchers such as Ahmed *et al.* (2019, 2020, 2021a), Rahman *et al.* (2019), and Habib *et al.* (2021, 2023). Their sustained efforts have been instrumental in advancing molecular biodiversity research and establishing DNA barcoding as a core tool for species identification and conservation in Bangladesh. Similarly, sharks and rays (81 species) show a relatively high coverage of 59.26%, reflecting the growing concern for elasmobranch conservation in the Bay of Bengal.

Table 1. Summary of taxonomic groups and DNA barcoding status of biodiversity, including total species recorded, DNA sequence availability, barcoded species count, and coverage percentage across major taxa from Bangladesh.

Division	Sub-division	Sub-group	Total Recorded Species	Total DNA Sequences Available	No. of Barcoded Species	Barcode Coverage (%)
Animals	Chordates	Mammals	$127^{(1)}$	17700	70	55.12
		Birds	$690^{(2-3)}$	937	39	5.65
		Reptiles	$167^{(4)}$	386	45	26.95
		Amphibia	$63^{(4-6)}$	559	29	46.77
		Fishes	$909^{(7-13)}$	4534	664	73.05
		Sharks and Rays	$81^{(7,9,10,14)}$	265	48	59.26
	Arthropods	Butterflies and Moths	$421^{(15,44)}$	325	223	52.97
		Mosquitoes	$115^{(16)}$	145	20	17.39
		Crustaceans		1047		
		Crabs	$79^{(17-28)}$	250	50	63.29
		Shrimps	$66^{(26,28-31)}$	763	42	65.63
		Lobster and Mantis shrimp	$17^{(26,28,32-36)}$	34	10	58.82
	Mollusk	Gastropods	$318^{(37-38)}$	690	42	13.21
		Bivalves	$148^{(37-38)}$	294	23	15.54
		Cephalopods	$12^{(37, 39)}$	59	8	66.67
Fungi			$656^{(40-42)}$	3996	314	47.87
Plants			$4255^{(43)}$	46305	297	6.98
Protists			-	1777	88	
Bacteria			-	584820		

Superscript numbers next to species counts indicate the chronological numbers of following citations: 1. IUCN Bangladesh (2015f), 2. Khan (2018), 3. Shome *et al.*, (2023), 4. IUCN Bangladesh (2015b), 5. Rahman *et al.*, (2022), 6. Al-Razi *et al.*, (2020), 7. Habib and Islam (2020), 8. Rahman *et al.*, (2019), 9. Ahmed *et al.*, (2021a), 10. Rahman *et al.*, (2009), 11. IUCN Bangladesh (2015c), 12. Siddiqui *et al.*, (2009), 13. Ahmed *et al.*, (2020), 14. Haque *et al.*, (2019), 15. IUCN Bangladesh (2015d), 16. Bashar *et al.*, (2020), 17. Chowdhury *et al.*, (2020), 18. Ahmed *et al.*, (2021b), 19. Akash *et al.*, (2020), 20. Antu *et al.*, (2024), 21. Shashi *et al.*, (2023), 22. Sarkar *et al.*, (2024), 23. Habib *et al.*, (2021b), 24. Barua *et al.*, (2021), 25. Haque *et al.*, (2024), 26. Ahmed *et al.*, (2008), 27. Alam *et al.*, (2020), 28. IUCN Bangladesh (2015e), 29. Hossain (2013), 30. Datta *et al.*, (2024), 31. Ahmed *et al.*, (2021c), 32. Ahmed *et al.*, (2022), 33. Ahmed *et al.*, (2023), 34. Ahmed *et al.*, (2024), 35. Tabassum and Akash (2022). 36. Habib *et al.*, (2025), 37. Siddiqui *et al.*, (2007), 38. Antu *et al.*, (2023), 39. Arfin *et al.*, (2023), 40. Shamsi (2017), 41. Shamsi (2018), 42. Shamsi and Alam (2025), 43. IUCN Bangladesh (2024), 44. Hossain (2023). *Percentage of barcoded species represents the proportion of documented species with available molecular barcode data in public databases (https://www.ncbi.nlm.nih.gov/nuccore, as of 31 October 2025)*

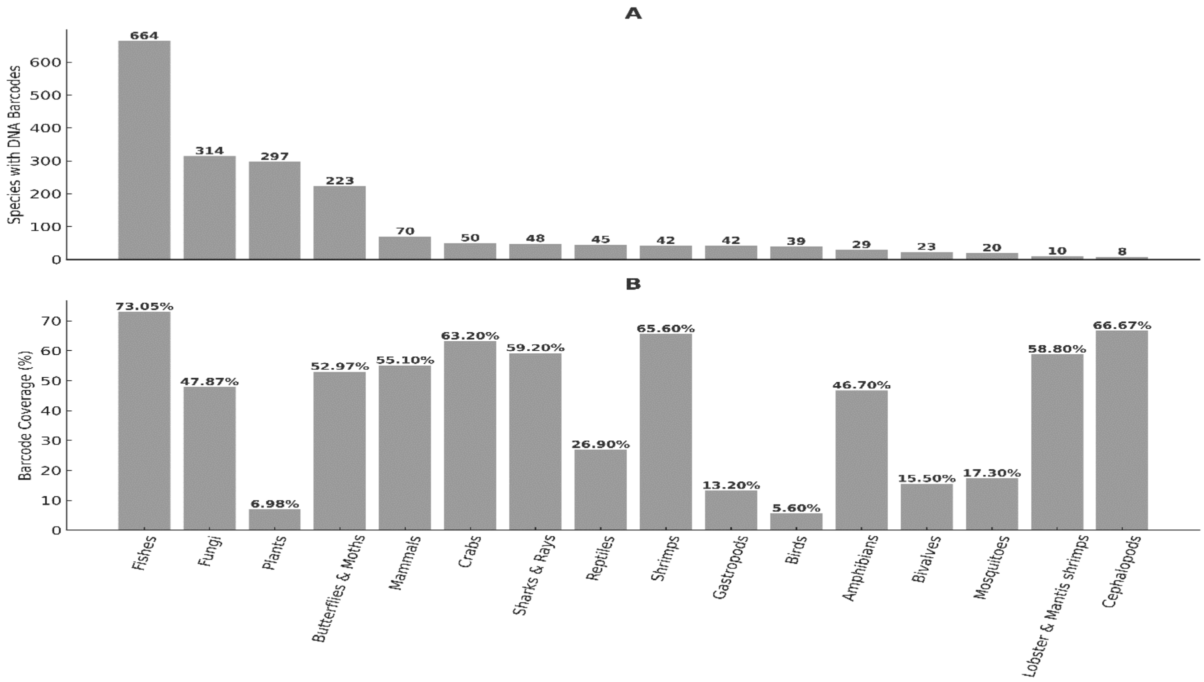

Figure 1. Comparison of DNA barcoding status across major taxonomic groups in Bangladesh. (A) Total number of species with DNA barcodes by taxonomic group. (B) Percentage of species barcoded within each group.

Arthropods

Arthropods represent the largest animal phylum in Bangladesh, exhibiting remarkable diversity across several taxonomic groups. Within this phylum, butterflies and moths constitute one of the most studied groups. Their documented richness has increased from 305 species (IUCN Bangladesh, 2015d) to 421 species in recent updates (Hossain, 2023), reflecting significant progress in taxonomic assessment. Out of these, 223 species have been successfully barcoded, accounting for approximately 52.97% of the known butterfly and moth fauna in the country. This substantial molecular documentation highlights the relatively advanced barcoding progress within Lepidoptera compared to many other arthropod groups in Bangladesh, although further effort remains essential to achieve complete coverage. Conversely, mosquitoes (115 species) show a low barcoding rate (17.39%), despite their relevance to public health. This highlights a pressing need for species-level molecular characterization to support vector surveillance programs.

Within crustaceans, molecular data are gradually expanding. Crabs (79 species), shrimps (66 species), and lobsters and mantis shrimps (17 species) exhibit barcode coverage of 63.29%, 65.63%, and 58.82%, respectively. This reflects the economic importance of these taxa in fisheries and aquaculture research. Significant molecular research on this group has been contributed by Ahmed *et al.* (2021b,c, 2022), Barua *et al.* (2021), and Sarkar *et al.* (2024), who collectively advanced species documentation and DNA barcoding efforts in Bangladesh.

Mollusks

The molluscan fauna of Bangladesh remains comparatively underrepresented in molecular databases. Out of 318 gastropod and 148 bivalve species reported (Siddiqui *et al.*, 2007), only 13.21% and 15.54% are barcoded, respectively (Mahjabin *et al.*, 2023; Sultana *et al.*, 2021). In contrast, cephalopods show a markedly higher coverage of 66.67% that mostly done by Arfin *et al.* (2023), likely due to their commercial and ecological significance in marine ecosystems. This disparity underscores uneven research emphasis among molluscan subgroups.

Fungi

Fungal diversity, comprising 656 recorded species (Shamsi, 2017, 2028 & 2025), exhibits moderate barcode representation, with 314 species (47.87%) having sequence data. The relatively high number of fungal barcodes (3996 sequences) reflects recent progress in documenting phytopathogenic and saprophytic species, especially those associated with agricultural ecosystems. Nevertheless, a large fraction of the country's fungal flora particularly endophytic and marine fungi remains uncharacterized at the molecular level.

Plants

Bangladesh harbors approximately 4,255 plant species (IUCN Bangladesh, 2024), yet only 297 species (6.98%) have DNA barcode records. Despite the availability of over 46,000 sequences, these data represent a narrow taxonomic scope, mostly focusing on medicinal, mangrove, and crop-related plants. Expanding barcode coverage to endemic and threatened plant taxa is essential for effective biodiversity conservation, ecological monitoring, and sustainable resource management.

Protists

Protists remain the least studied group, with 1777 barcode sequences corresponding to 88 species. Given their ecological significance in nutrient cycling and aquatic ecosystems, this taxonomic gap highlights a major frontier for future barcoding initiatives in Bangladesh.

Temporal Trends in DNA Sequence Generation and Molecular Research Output from Bangladesh

The temporal distribution of DNA sequence submissions from Bangladesh since 2010 showcases a significant acceleration in molecular biodiversity research capacity (Figure 2). Prior to this period, the majority of sequencing efforts involving Bangladeshi biodiversity were conducted by international research groups, utilizing specimens collected either directly from the country or through contributions from Bangladeshi collaborators. This early phase reflects limited domestic laboratory facilities and technical expertise for molecular work. From 2010 onward, molecular research capacity in Bangladesh began to strengthen, marked by gradual growth between 2010-2013 as local laboratories, DNA barcoding initiatives, and trained personnel increasingly emerged. A dramatic surge in 2015 corresponds to enhanced institutional engagement, academic–international collaborations, and targeted sequencing programs particularly in fisheries, crustaceans, and microbial research. Subsequent fluctuations represent varying project cycles, funding phases, and emerging genomic technologies. The steep rise observed in 2024-2025 indicates renewed momentum driven by expanded next-generation sequencing (NGS) facilities, environmental DNA (eDNA) adoption, and broader taxonomic coverage, demonstrating Bangladesh's transition from foundational barcoding efforts to advanced genomic and metagenomics research.

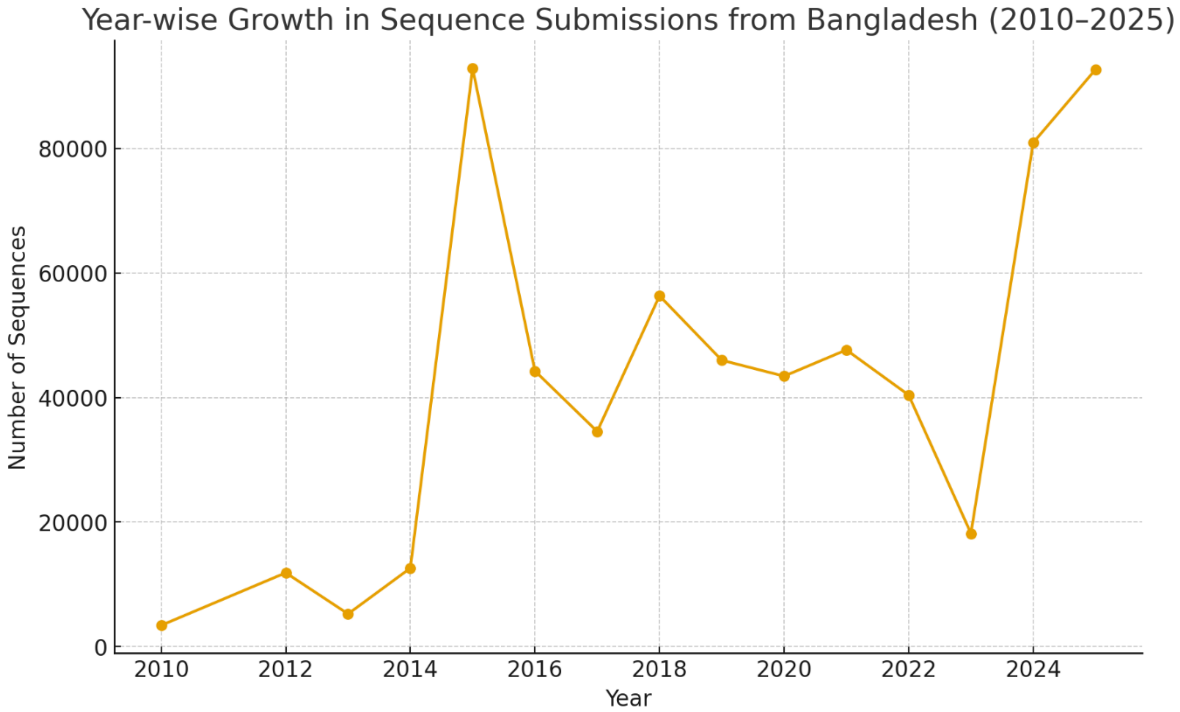

Figure 2. Year-wise DNA sequence submission trends from Bangladesh (2010–2025)

Benefits of expanding DNA barcoding

DNA barcoding has evolved beyond its original concept and has become a versatile tool with many applications in different scientific fields (Hajibabaei *et al.*, 2007). Various applications of DNA barcoding contribute to a better understanding of biodiversity and facilitate accurate species identification including-

***Biodiversity assessment and conservation**:* Bangladesh has an immense but poorly cataloged biodiversity. DNA barcoding can provide a rapid and accurate inventory of species, which is essential for effective conservation and management strategies (Datta *et al.*, 2020; Ananya *et al.*, 2025; Naznin *et al.*, 2020; Rahman *et al.*, 2019). This is particularly important in biodiversity-rich areas like the Sundarbans mangrove forest (Habib *et al.*, 2021a).

***Wildlife forensics**:* Barcoding can be used to identify illegally traded animal parts, such as shark fins, aiding in law enforcement and the protection of endangered species (Islam *et al.*, 2022; Haque *et al.*, 2019).

***Combating food fraud**:* The mislabeling and adulteration of food products, especially fish and herbal medicines, are common issues. Barcoding provides a reliable method for authentication, ensuring product quality and consumer safety (Afrin *et al.*, 2024; Smriti *et al.*, 2017).

***Blue economy development**:* With a large maritime area, Bangladesh can use DNA barcoding to identify and characterize potential marine organisms, which supports the sustainable development of its marine economic activities (Akter *et al.*, 2023; Ahmed *et al.*, 2021a; Habib *et al.*, 2023)

***Agricultural pest management**:* Rapid and accurate identification of pests and invasive species helps farmers and researchers implement targeted control measures and prevent crop failures (Khatun *et al.*, 2024; Aslam *et al.*, 2019; Douglas *et al.*, 2018).

Challenges and Future Prospects

The overall barcode coverage across major taxonomic groups reveals a pronounced imbalance. Animal taxa, particularly fishes and selected invertebrates, exhibit substantial progress, while microorganisms, plants, and protists remain grossly underrepresented. The high sequence-to-species ratios observed in some groups (e.g., plants, fungi) indicate that although sequencing efforts exist, taxonomic resolution and verification are often incomplete. Challenges include limited taxonomic expertise, inadequate funding for molecular research, and fragmented data sharing among institutions. Furthermore, the lack of national coordination between biodiversity inventories and barcoding repositories has slowed integration into global databases such as BOLD and GenBank.

Advancing molecular biodiversity research in Bangladesh requires establishing a national barcoding consortium and prioritizing key sectors such as fisheries, agriculture, and medicinal plants. The consortium emphasizes coordinated participation among universities, research institutes, government agencies, and natural history collections. Its core activities include standardized specimen collection, integration of DNA barcoding with advanced molecular approaches such as eDNA and metabarcoding, rigorous data validation and curation, and systematic submission of verified records to international databases. Building skilled human resources through training in taxonomy, molecular biology, and bioinformatics will be essential. Sustained support from national and international funding sources is crucial for expanding sequencing efforts and developing robust reference libraries.

Conclusion

Bangladesh's strategic biogeographic position endows it with exceptional biological richness, yet molecular exploration of this diversity remains fragmented. DNA barcoding initiatives have advanced notably in fishes, arthropods, and fungi, but remain limited for plants, protists, and several invertebrate groups. Strengthening national genomic infrastructure and fostering data integration across research institutions are essential to bridge these taxonomic and molecular gaps. Future research should embrace integrative molecular approaches; combining DNA barcoding, environmental DNA, and genomic tools to enhance species discovery, ecological monitoring, and conservation planning. By uniting traditional taxonomy with molecular frontiers, Bangladesh can transform its biodiversity research landscape, contributing robustly to global initiatives in species documentation, evolutionary biology, and sustainable ecosystem management.

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