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MOLECULAR PHYLOGENETICS AND DIVERGENCE DATING OF BYTTNERIOIDEAE IN BANGLADESH USING *MATK* DNA BARCODE

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Abstract

Byttnerioideae Burnett is an economically and medicinally important subfamily belonging to Malvaceae. A molecular phylogenetic and dating approach was undertaken to elucidate the evolutionary relationships and divergence history of the Byttnerioideae species available in Bangladesh based on the *matK* gene. A multifaceted, algorithm-driven strategy was applied with Maximum-Likelihood (ML), Maximum-Parsimony (MP), and Bayesian Inference (BI) algorithms that resulted in a consistent tree topology for the four tribes, namely as Byttnerieae, Hermannieae, Theobromateae and Lasiopetaleae. All the tribes exhibited monophyletic origin with strong bootstrap and posterior probability support. Byttnerieae, Hermannieae and Theobromateae were found to be more closely related to each other than to Lasiopetaleae. Molecular dating analysis revealed Lasiopetaleae as the oldest tribe, diverging approximately 39.51 million years ago (MYA) in the Bartonian age of the Cenozoic era, while Byttnerieae was identified as the most recent tribe, diverging around 33.24 MYA in the Rupelian age of the same era. These findings would update the phylogenetic relationship of Byttnerioideae and provide valuable insights for the development of the historical biogeography of Byttnerioideae in future endeavors.

Keywords: Byttnerioideae, Molecular phylogenetics, Molecular dating, *matK*, Bayesian inference.

Introduction

Byttnerioideae, one of the nine subfamilies of the angiosperm family Malvaceae, comprises approximately 650 species across 26 genera worldwide. These genera are categorized into four tribes, namely Byttnerieae, Hermannieae, Lasiopetaleae, and Theobromateae. Predominantly distributed in tropical and subtropical regions (Lima *et al*., 2019), Byttnerioideae is represented in Bangladesh by seven taxa belonging to seven genera under three tribes (Ahmed and Rahman, 2024). The characteristic features of the subfamily Byttnerioideae include a 5-lobed calyx, a 5-lobed corolla, numerous stamens united at the base to form a tube-like structure, schizocarpic or capsular fruits and seeds covered with hairs (Ahmed and Rahman, 2024). This subfamily includes numerous economically and medicinally significant species in Bangladesh including *Theobroma*

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cacao L., *Melochia corchorifolia* L., *Abroma augustum* (L.) L. f. and *Kleinhovia hospita* L.

Molecular phylogenetic studies using the chloroplast (cp) genome are crucial for understanding evolutionary relationships, offering high-resolution insights into genetic divergence and species differentiation. The cp genome is particularly valuable due to its conserved structure and maternal inheritance, providing a stable genetic framework for phylogenetic analysis (Guan *et al*., 2024). Among chloroplast genes, *matK* (maturase K) is notable for its exceptional ability to differentiate closely related taxa, owing to its high evolutionary rate and substantial sequence variation, surpassing commonly used genes such as *rbcL* and *ndhF* (Kathriarachchi *et al*., 2005; Müller *et al*., 2006; Li *et al*., 2011; Ahmed *et al*., 2023). The *matK* gene ensures the correct maturation of RNA transcripts, supporting chloroplast functionality and efficiency, which are vital for plant growth and survival (Barthet and Hilu, 2007; Hertel *et al*., 2013). This dual role makes *matK* a powerful tool in evolutionary studies as well as a key component of the chloroplast's genetic machinery (Poovitha *et al*., 2016). While the *ndhF* gene has been used to study floral evolution and molecular phylogenetics within Byttnerioideae, research using the *matK* barcode for phylogenetic reconstruction in this subfamily is lacking (Whitlock *et al*., 2001). Molecular dating using *matK* data facilitates current understanding of evolutionary events within Byttnerioideae. The substantial sequence variation in *matK* enables more accurate estimation of divergence times, allowing reconstruction of detailed timelines of species differentiation and revealing historical biogeographical patterns as well as evolutionary dynamics (Konhar *et al*., 2016; Ahmed *et al*., 2023).

Molecular dating further provides the baseline to enhance our understanding of the mechanisms driving speciation and adaptation in Byttnerioideae species. Knowledge of evolutionary relationships and divergence times can inform breeding programs aimed at enhancing desirable traits, such as disease resistance, yield, and adaptability in Byttnerioideae taxa (Pessoa-Filho *et al*., 2017), potentially leading to the development of more resilient and productive crops. Therefore, molecular dating analysis holds a significant promise in refining classification, guiding conservation efforts, and linking evolutionary developments with geological and climatic shifts (Sauquet, 2013). However, similar to molecular phylogenetic studies, no efforts have yet been made to unveil molecular dating events in Byttnerioideae.

A comprehensive understanding of Byttnerioideae evolution requires an integrated approach that combines molecular phylogenetics and molecular dating. Molecular phylogenetics, particularly when using high-resolution markers such as the *matK* gene,

reconstructs evolutionary relationships, whereas molecular dating places these events within a temporal framework. By employing *matK*-based molecular phylogenetics and molecular dating, we aim to elucidate the evolutionary relationships and estimate divergence times of species in accordance with the geological time scale. This in-depth analysis provides a more detailed understanding of the evolutionary dynamics of Byttnerioideae in Bangladesh.

Materials and methods

Molecular phylogenetic analysis: Gene sequences from various taxa within Byttnerioideae, including outgroups, were retrieved from the NCBI Nucleotide database. Eleven taxa were selected based on the availability of *matK* gene sequences (Table 1). The *matK* sequence for *Ayenia elegans* Ridl. was unavailable in GenBank and could not be retrieved. The obtained sequences were downloaded in FASTA format and aligned using Multiple Sequence Alignment (MSA) on the MAFFT server, specifically employing the E-INS-i method and the BLOSUM62 scoring matrix for amino acid sequences (Katoh *et al*., 2019). Default settings were used for the alignment, and the resulting sequences were saved in FASTA format for further analysis (Tamura *et al.,* 2021). The Models module in MEGA was then used to calculate the transition-transversion bias. Phylogenetic trees were constructed using the Phylogeny module, employing both Maximum Likelihood (ML) and Maximum Parsimony (MP) methods with 1000 bootstrap replicates. The Kimura-2 parameter model was applied, which accounts for both transition and transversion substitutions with uniform rates across sites. Gaps or missing data were handled using partial deletion, with a site coverage cutoff of 95%. Bayesian evolutionary analyses were performed using Mr. Bayes v.3.2.6 (Ronquist *et al*., 2012), employing the General Time Reversible model with 10,000 generations in the Markov Chain Monte Carlo process. Trees were sampled every 10 generations after discarding the first 250 trees as burn-in. Posterior trees were then summarized to infer phylogenetic relationships and estimate associated parameters.

Molecular dating analysis: Molecular dating was conducted using the Clocks module in MEGA v.11, employing the RelTime-ML method (Mello, 2018), starting with matK alignment file and the Maximum Likelihood Tree file in NEWICK format. Outgroup species were then chosen, and the calibration was refined using the TimeTree server to select two calibration nodes based on available taxa and applying uniform distribution constraints (Kumar *et al.,* 2017). The Kimura-2 parameter model was employed for nucleotide substitution, assuming uniform substitution rates throughout the analysis. The

resulting time tree was then visualized using the default Tree Explorer (Srivathsan and Meier, 2012).

Table 1. Taxa investigated in the present study for phylogenetic relationships among Byttnerioideae in Bangladesh.

No.	Taxa	Species codes	Tribe/Family	GenBank accession
Ingroup				
1	*Abroma augustum* (L.) L. f.	Aba	Byttnerieae	HM488448.1
2	*Ayenia grandifolia* (DC.) Christenh. & Byng	Ayg	Byttnerieae	KP093635.1
3	*Commersonia fraseri* J. Gay	Cof	Lasiopetaleae	KM894706.1
4	*Guazuma ulmifolia* Lam.	Guu	Theobromateae	GQ982003.1
5	*Kleinhovia hospita* L.	Klh	Byttnerieae	HM488449.1
6	*Melochia corchorifolia* L.	Mec	Hermannieae	KY607288.1
7	*Rulingia magniflora* F. Muell.	Rum	Lasiopetaleae	HM488451.1
8	*Theobroma cacao* L.	Thc	Theobromateae	GQ982111.1
9	*Waltheria indica* L.	Wai	Hermannieae	OL538011.1
Outgroup				
1	*Daphne mucronata* Royle	Dam	Thymelaeaceae	MZ851783.1
2	*Thymelaea hirsuta* (L.) Endl.	Thh	Thymelaeaceae	OK040774.1

Results and discussion

Molecular phylogenetic analysis of *matK* sequence data revealed distinct patterns among the selected Byttnerioideae taxa, which were retrieved from the NCBI Nucleotide database along with the outgroups using their GenBank accession numbers (Table 1). Following multiple sequence alignment (MSA), transition and transversion sites were analyzed, revealing sequence variability across the *matK* alignment (Table 2).

The transitional substitution rate was 54.75% and the transversional rate was 45.25%, indicating that transitional substitution was predominant over transversional substitution. This finding is consistent with a recent molecular phylogenetics study of the palm family Arecaceae (Ahmed *et al*., 2023). Predominant transitional substitutions can lead to better resolution and more reliable phylogenetic relationships, as transitions are generally less disruptive to protein structure and function (Drummond and Wilke, 2008). Similarly, a DNA barcoding study on *Mentha longifolia*, *Mentha* × *piperita*, and *Lavandula dentata* employing the *ITS*, *ITS2*, *rbcL*, and *trnH* genes found that transition mutations occurred more frequently than transversions (Ahmed, 2018). In addition, *matK* sequences were

used to study the phylogenetic relationships of six *Saraca* L. species (Fabaceae), revealing higher transitional than transversional substitutions (Sil *et al*., 2021). Together, these findings support the use of *matK* gene, with its high rate of transitional substitutions, as a reliable marker for resolving phylogenetic relationships among closely related species.

Table 2. Substitution matrix analysis showing transition/transversion rates of the *matK* sequences after multiple sequence alignment.

DNA bases	A	T	C	G
A	-	*5.02*	*4.92*	**8.15**
T	*4.20*	-	**10.22**	*5.02*
C	*8.62*	**21.44**	-	*3.15*
G	**14.94**	*11.02*	*3.30*	-

Each entry indicates probability of substitution from one base (row) to another base (column). Substitution pattern and rates were estimated under the General Time Reversible model. Rates of different transitional substitutions are shown in **bold** face, while those of transversional substitutions are shown in *italics*.

Of the four tribes of Byttnerioideae, Byttnerieae, Hermannieae, and Theobromateae are represented in Bangladesh, whereas Lasiopetaleae does not occur; however, all four tribes, including Lasiopetaleae, were included in the present study to reconstruct phylogenetic relationships within the subfamily Byttnerioideae. Taxa from the family Thymelaeaceae were chosen as outgroup due to their close resemblance to Malvaceae, as both families belong to the order Malvales (Bredenkamp and Van Wyk, 2001). The Maximum Likelihood (ML) tree showed the monophyletic origin for all four tribes of Byttnerioideae. All nine taxa representing the four tribes exhibited a clear segregation pattern in the phylogenetic tree (Fig. 1). Bootstrap support was higher than 80% for most terminal nodes, confirming the accuracy of the constructed tree.

Monophyletic segregation is crucial for understanding relationships among closely related Byttnerioideae taxa, as it ensures that all members of this subfamily share a common ancestor and include all its descendants. This clear delineation helps accurately reconstruct evolutionary histories and understand the genetic and phenotypic similarities and differences among the studied taxa. Focusing on the monophyletic groups helps avoid misleading conclusions that might arise from convergent evolution or horizontal gene transfer (Chaw *et al*., 2000). The Maximum Parsimony (MP) tree corroborated the topology revealed by the ML tree, exhibiting a similar clustering pattern and a clear segregation of taxa (Fig. 2). Cross-validation using these two approaches is significant, as

the convergence of ML and MP trees indicates that the inferred evolutionary relationships are not artifacts of a specific analytical method but instead reflect true biological patterns.

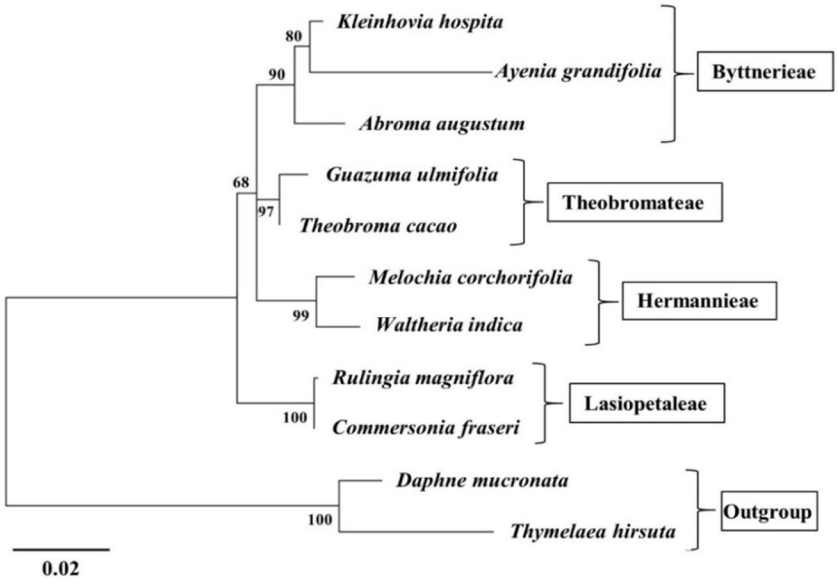

Fig. 1. Maximum-Likelihood tree with 1000 bootstrap replicates showing inter-relationships of Byttnerioideae taxa based on *matK* sequences.

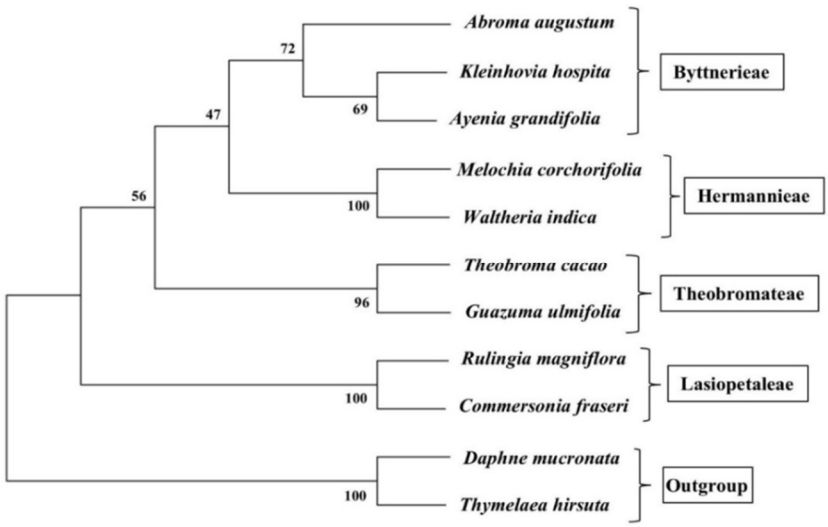

Fig. 2. Maximum-Parsimony tree with 1000 bootstrap replicates showing inter-relationships of Byttnerioideae taxa based on *matK* sequences.

In the MP tree, the tribe Lasiopetaleae, represented by *Rulingia magniflora* and *Commersonia fraseri,* demonstrated a distant relationship from the other three tribes, viz. Byttnerieae, Hermannieae and Theobromateae. Similar to the ML tree, the MP tree also unraveled the monophyletic nature of all four tribes. The genetic distance matrix identified the lowest distance (0.001), indicating maximum similarity between *Rulingia magniflora* and *Commersonia fraseri* (Table 3). In contrast, the highest genetic distance (0.183), indicating minimum similarity was observed between *Melochia corchorifolia* and *Thymelaea hirsuta*

Table 3. Genetic distance matrix showing pairwise distance generated after multiple sequence alignment.

Species	Aba	Ayg	Cof	Dam	Guu	Klh	Mec	Rum	Thc	Thh	Wai
Aba	0										
Ayg	0.057	0									
Cof	0.043	0.073	0								
Dam	0.155	0.179	0.153	0							
Guu	0.033	0.059	0.033	0.149	0						
Klh	0.019	0.043	0.036	0.156	0.026	0					
Mec	0.045	0.075	0.043	0.159	0.034	0.038	0				
Rum	0.045	0.075	0.001	0.153	0.034	0.038	0.045	0			
Thc	0.026	0.055	0.026	0.143	0.006	0.019	0.028	0.028	0		
Thh	0.172	0.174	0.174	0.043	0.170	0.168	0.183	0.174	0.164	0	
Wai	0.045	0.073	0.038	0.155	0.034	0.038	0.019	0.039	0.028	0.176	0

Aba: *Abroma augustum*, Ayg: *Ayenia grandifolia*, Cof: *Commersonia fraseri,* Dam: *Daphne mucronata*, Guu: *Guazuma ulmifolia,* Klh: *Kleinhovia hospita,* Mec: *Melochia corchorifolia,* Rum: *Rulingia magniflora*, Thc: *Theobroma cacao*, Thh: *Thymelaea hirsuta*, Wai: *Waltheria indica.*

Bayesian inference analysis elucidated strong posterior probability support for nearly all nodes. Consistent with the ML and MP trees, the Bayesian tree also supported the overall tree topology and confirmed the monophyletic origin of Byttnerioideae (Fig. 3). Bayesian posterior probability estimation differs somewhat from bootstrap calculation. Bootstrap validation entails resampling the original dataset with replacement to generate multiple pseudo-replicates, reconstructing a phylogenetic tree for each, and determining how frequently each branch appears across these trees. This method provides support values as percentages, indicating the frequency of a branch's occurrence, which can imply confidence but not direct probabilities. In contrast, Bayesian posterior probability uses a model-based approach, employing Markov Chain Monte Carlo (MCMC) simulations to sample trees according to their likelihood and prior information (Chib, 2001). The

posterior probability for each branch is then calculated from the proportion of sampled trees containing that branch, providing a direct probability measure. While bootstrap validation is simpler and widely used, it may overestimate support and is computationally intensive. Bayesian methods, though also computationally demanding and sensitive to model and prior selection, offer a more accurate and probabilistic interpretation of branch support (Efron, 2012).

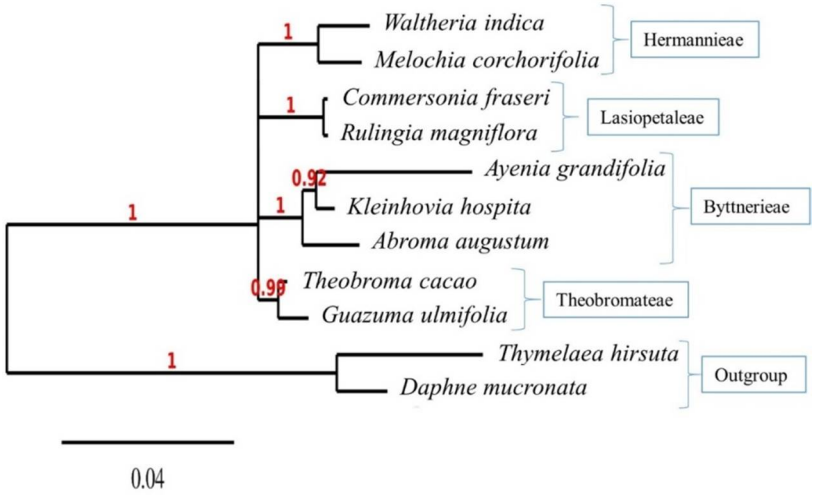

Fig. 3. Bayesian tree showing evolutionary relationships of Byttnerioideae taxa based on *matK* sequences. Posterior probability support has been denoted with red color.

In the present study, the similar clustering patterns observed in the Bayesian, ML, and MP trees reveal robustness and confidence in the inferred evolutionary relationships of Byttnerioideae. The agreement among multiple analytical methods reduces sensitivity to methodological variation and enhances the overall reliability of the findings. This concordance further helps detect and mitigate method-specific biases, ensuring a more accurate representation of the underlying evolutionary mechanisms of Byttnerioideae. A similar approach was undertaken to understand the phylogenetics of Amaranthaceae using *matK* and *trnK* sequences (Müller and Borsch, 2005), which further supports our protocol. A study using *ndhF* sequences reported that Byttnerieae, Hermannieae, and Lasiopetaleae are more closely related to each other than to Theobromateae in the maximum parsimony (MP) tree (Whitlock *et al*., 2001). Conversely, our investigation using *matK* sequences indicated that Byttnerieae, Hermannieae, and Theobromateae are more closely allied with each other than to Lasiopetaleae in the MP tree. The variation in tree topology between the *ndhF* and *matK* sequences may be attributed to several factors, including gene-specific evolutionary rates, horizontal gene transfer, incomplete lineage

sorting, sampling error, or differing functional constraints. The *ndhF* gene may be evolving under different selective pressures or experiencing more rapid changes compared to the *matK* gene, leading to discrepancies in inferred relationships. Alternatively, the *matK* gene may provide a more accurate reconstruction of overall evolutionary history due to its critical role in cellular functions. Further comprehensive genomic studies are required to resolve these discrepancies.

Molecular dating analysis was performed after estimating pairwise divergent times to establish the nodes (checkpoints) of calibration. Two nodes were selected based on their availability in the TimeTree server, as no additional calibration points were accessible. These nodes represent well-supported relationships within Malvaceae and provide reliable divergence estimates for calibration. The TimeTree server revealed pairwise divergence times for two calibration nodes. The first node, between *Theobroma* and *Guazuma* showed a median divergence time of approximately 18.4 million years ago (MYA). The second node, between *Melochia* and *Waltheria* exhibited a median divergence time of approximately 11.2 MYA (Fig. 4).

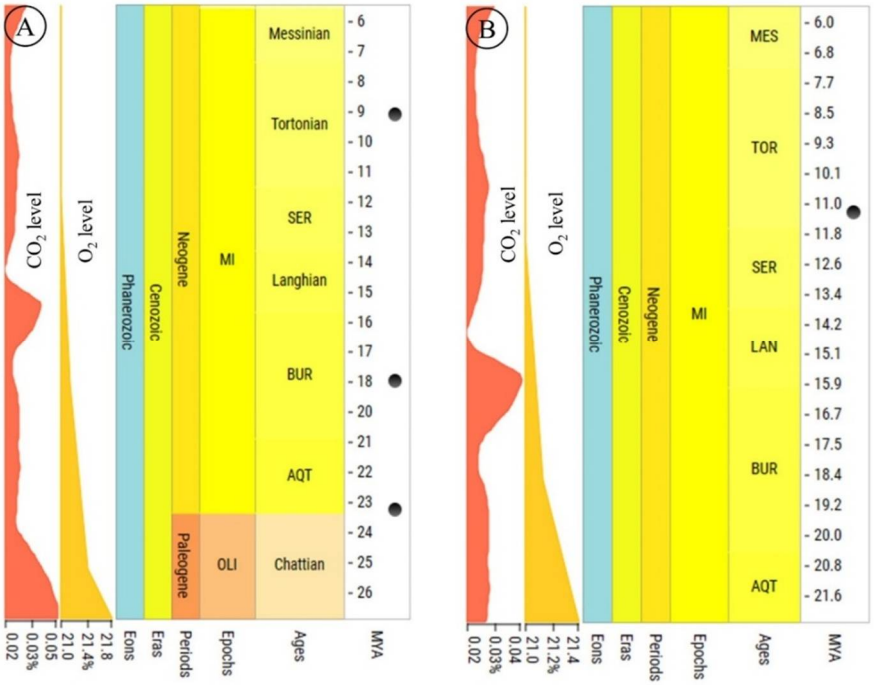

Fig. 4. Pairwise divergent times according to the geological time scales used to calibrate the time tree for molecular dating analysis. A. Divergence between *Theobroma* and *Guazuma*, B. Divergence between *Melochia* and *Waltheria.*

The credibility interval (CI) for the first node ranged from 9.0 to 22.9 MYA, and the adjusted divergence time was 18.0 MYA. The CI for the second node could not be retrieved from the server due to the paucity of available data; therefore, the adjusted divergence time remained 11.2 MYA.

The molecular dating analysis suggested that the divergence of Byttnerioideae began with Lasiopetaleae approximately 39.51 MYA, during the Bartonian age of the Eocene epoch within the Paleogene period of the Cenozoic era (Fig. 5). The Bartonian age (41.2 to 37.8 MYA) was a critical period for angiosperm evolution and diversification. This period witnessed an expansion of tropical and subtropical forests, facilitated by warm and humid climate conditions, which provided diverse habitats for angiosperms to thrive. Moreover, many advanced angiosperm families diversified during this time, resulting in increased richness in trees, shrubs, and herbaceous plants. Additionally, there was a significant advancement in plant-pollinator interactions, with angiosperms developing specialized floral structures and mechanisms to attract insects, birds, and mammals. These evolutionary developments likely played an important role in shaping the existing diversity and complexity of Byttnerioideae (Moraweck *et al.*, 2015).

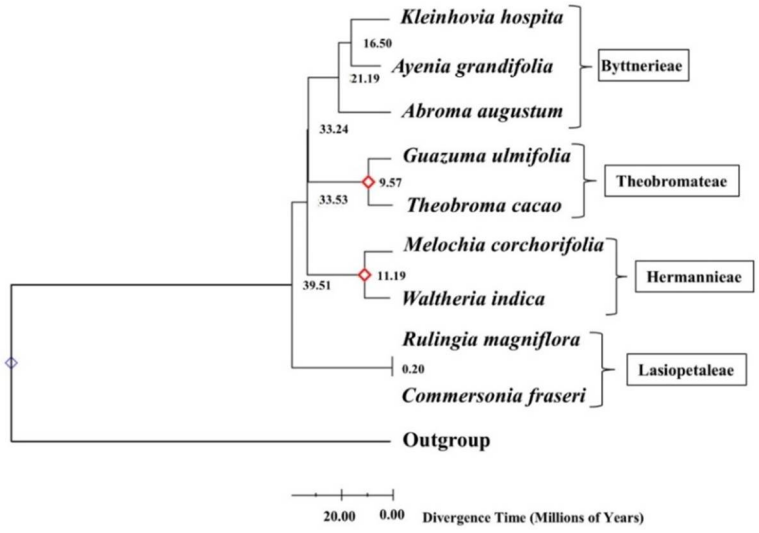

Fig. 5. Molecular dating tree showing divergence time of the four tribes of Byttnerioideae.

Molecular dating analysis further unveiled Lasiopetaleae as the oldest tribe (39.51 MYA), while Byttnerieae was identified as the most recent tribe (33.24 MYA). Except for Lasiopetaleae, all three tribes diverged during the Rupelian age of the Oligocene epoch

within the Paleogene period of the Cenozoic era. The Rupelian age, spanning approximately 33.9 to 28.1 MYA, was marked by significant global cooling and the expansion of Antarctic ice sheets, leading to substantial changes in both marine and terrestrial ecosystems. Marine organisms had to adapt to cooler water, resulting in shifts in species composition and distribution. On land, mammals continued to diversify, evolving new forms and adapting to the cooler climatic conditions. Overall, the Rupelian age represents a critical period of ecological transition, reflecting the broader climatic shifts of the Oligocene epoch (Fornelli *et al.*, 2020).

Conclusion

Molecular phylogenetics and divergence-time analyses were carried out for the first time on Bangladeshi members of Byttnerioideae using the *matK* gene. The study unveiled a higher rate of transitional over transversional substitutions. The reconstructed phylogeny of the four tribes - Byttnerieae, Hermannieae, Theobromateae and Lasiopetaleae, confirmed the monophyletic origin of Byttnerioideae, with all nine taxa exhibiting distinct segregation patterns. Multi-model inference using ML, MP, and Bayesian approaches further corroborated the tree topology and inter-relationships of the species with high bootstrap and posterior probability support. Molecular dating analysis suggested that Lasiopetaleae is the earliest diverging tribe, originating around 39.51 MYA, whereas Byttnerieae represents the most recent lineage, diverging approximately 33.24 MYA. Overall, the findings enrich current understanding of the phylogenetic relationships within Byttnerioideae and provides valuable insights into the evolutionary history of this subfamily in Malvaceae.

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COMPARATIVE STUDY ON THE OCCURRENCE AND INCIDENCE OF INSECT PESTS DUE TO CLIMATE CHANGE IN COASTAL AND HAOR RICE ECOSYSTEM

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Abstract

The survey and assessment were carried out at three coastal and three haor districts of Bangladesh to know the occurrence and incidence of insect pests of rice due to climate change in coastal and haor rice ecosystem during June 2022 to July 2023. The infestations of insect pests in rice ecosystem are changing gradually with time due to changing in climate. Sixteen (16) insect pests of rice and six (6) natural enemies were recorded on rice field of coastal and haor ecosystem. Stem borer, rice leaf roller and Brown plant hopper were one of the major insect pests in coastal and haor rice ecosystems in survey areas. Among three coastal districts, the highest number of stem borer (4.5/30 hills) followed by leaf roller (4.4/30 hills) was observed on boro rice in Khulna followed by Noakhali and the lowest number in Bhola (3.4/30 hills) on T aman rice. Among three haor districts, the highest number of stem borer (3.4/30 hills) in Habigonj followed by Sunamgonj (3.1/30 hills) and the lowest number of stem borer in Kishoregonj (2.9/30 hills). In case of leaf roller, similar trend was also observed on boro rice. Major insect pests of rice is higher in boro season than those of T aman season. Stem borer, rice leaf roller, rice bug and brown plant hopper were one of the major insect pests of rice in coastal and haor rice ecosystems in survey areas. The incidence of 4 major insect pest species of rice crop was higher in coastal rice ecosystem compared to haor rice ecosystem.

Key words: Stem borer, leaf roller, BPH, T aman, Boro

Introduction

Rice is considered as the main unique food for most of the Asian and more than 50% of the globe's populations (IRRI, 2006). It is an essential food crop and more than 90% of world production occurs in tropical and semi tropical Asia (FAOSTAT, 2012). For decades rice crops have directly or indirectly played a key role in the livelihood of several billion people. In 2010, 154 million hectares of rice were cultivated worldwide, of

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which 137 million hectares were in Asia, with 48 million hectares harvested in Southeast Asia (FAOSTAT, 2012). In Bangladesh, eighty per cent of agricultural land is dedicated to rice cultivation (DAE, 2010). More than two hundred species of insects are known to be available in rice ecosystems of Bangladesh (Islam and Catling, 2012; Ali *et al*., 2017). Among these 20-33 species are considered as pest which cause yield losses (Ali *et al*., 2021). These insects make a complex food web within the rice ecosystem. In the rice agroecosystem 42 insect species are considered to be pests (Srivastava *et al*., 2004). Minor and major are recognized as status of pest insect species. These pests cause severe damage to rice crops at different growth stages. The degree of damage is dependent on the growing season and surrounding environment (Khaliq *et al*., 2014). The behavior as well as distribution and abundance of Yellow stem borer are influenced by changing in climate in southern Asia due to increasing winter survival rates and the number of generations per year, as well as inducing an earlier appearance in the crops after winter (Patel *et al*., 2017). Elevated winter temperature may not only reduce mortality rates for rice leaf folder and brown plant hopper, but also speed up their development, increasing their potential to accumulate and harm crops in subsequent generations (Kirtani, 1999 and 2007). Altering in climatic factors forced insect pests to move into new ecological niches for survival which is responsible for the invasion of foreign pest in the new habitat as well as threaten for food security (Skendzic *et al*., 2021). Increasing temperature had a positive effect on growth rate of yellow stem borer and the growth rate of yellow stem borer was found to be high at relatively low temperature and abundant rainfall (Ali *et al*., 2020). In addition, higher temperature affected the population dynamics of rice insect pests such as brown plant hopper, *Nilaparvata lugens* (Stal) and rice leaf folder, *Cnaphalocrosis medinalis* (Guen), by lowering the survival rate (Karuppaiah *et al*., 2012). Rice agro-ecosystems have evolved over the last 5,000 years under human management; for this reason human beings are considered to be an integral component. An abundance of insect species are supported through a series of complex interactions that comprise the food web that at its base is maintained by rice (Redfern *et al*., 2015). In this agroecosystem, the food web can serve as a tool to help improve natural ecosystem functions. However, function is dependent upon the continued propagation of predator insect species. Ecosystem function in a healthy rice agroecosystem can be improved through protecting and encouraging those insects that prey on pest species (Allara *et al*., 2012). In conventional pest management strategies the role of predator species is minimized or even eliminated by heavy pesticide application. In China, 889 insect species that prey on pest insects have been identified. These predator insect species account for 64.74% of all naturally occurring enemies of pest species (Lou *et al*., 2013). Increased pesticide use has led to an increase in soil, water and air pollution. These

increases have in turn had an adverse impact on human health and rice quality (Sattar *et al*., 2013). The misuse or excessive use of pesticides can harm plants, livestocks, aquatic organisms, and humans. Jacobsen and Hjelmso (2014) reported that pesticide use has a higher cost to benefit ratio with respect to yields and can have negative impacts on beneficial microbes. One hundred fifty-nine rice insect species are recorded in the rice agroecosystem (Alam, 1977). Among these species, 20–23 species have been found to be most damaging in Bangladesh (Alam, 1977). Farmers often apply pesticides at higher rates and at inappropriate times due to lacking of knowledge relating to insect pest species and insect's life cycle. Farmers are using modern high yielding rice varieties, fertilizers, pesticides, water and other technologies intensively for producing more rice which ultimately changed the ecology and accelerate pest proliferation (Parvin, 2010). A majority of farmers are not concerned with the negative impacts of pesticide use may have on fish, wildlife, humans, soil, and beneficial insect species (Jepson *et al*., 2014). For this reason, previously designated minor insect pests have attained the status of major pests and some major pests have become minor status causing minimum damage and few may be disappeared or extinct from the agro-ecosystem. Hence this study was designed to know the occurrence and incidence of insect pest in coastal and haor rice ecosystem.

Materials and Methods

Survey studies were carried out in the farmers' rice fields of three selected coastal districts such as Khulna, Bhola, Noakhali and three selected haor districts such as Kishoreganj, Habiganj, Sunamganj of Bangladesh to collect data on occurrence and incidence of insect pests of rice and to know the status of insect pests during 2022-23 growing season. Studies were conducted in two locations of each coastal and haor districts. A total 12 upazila viz., Koyra (22.3515^0N and 89.2859^0E), Paikgachha (22.5931^0N and 89.3168^0E) upazila of Khulna district, Bhola sadar (22.6855^0N and 90.6439^0E), Char Fasson (22.1860^0N and 90.7603^0E) upazila of Bhola district, Noakhali sadar (22.8653^0N and 91.0971^0E), Subarnachar (22.6756^0N and 91.1257^0E) upazila of Noakhali district, Itna (24.5278^0N and 91.0958^0E) and Mithamain (24.4196^0N and 91.0634^0E) upazila of Kishoreganj district, Ajmiriganj (24.54890N and 91.23620E) and Baniachong (24.5063^0N and 91.3566^0E) upazila of Habiganj district, Bishwamvapur (25.1209^0N and 91.3135^0E) and Tahirpur (25.0990^0N and 91.1755^0E) upazila of Sunamganj district were selected as study sites for survey. Three rice fields owned by different farmers were selected from each location. Thirty (30) hills of rice plant from each field of each upazila comprising 90 hills of rice plant were selected randomly. A

total 1080 hills of rice plant from 12 locations were observed for taking data on occurrence and incidence of rice insect pests. Data were recorded through observation of individual tillers of rice plant in each location.

Meteorological data: Simultaneously, the meteorological data such as maximum and minimum temperature, relative humidity and rainfall were collected from the meteorological office of study areas. The average minimum and maximum temperature of Sunamganj district were 18 and 31^{0}C, Kishoreganj district were 22 and 32^{0}C, Habiganj district were 17.4 and 36^{0}C, Noakhali district were 20.3 and 32^{0}C, Bhola district were 21 and 23 ^{0}C and Khulna district were 24 and 34ºC.

Statistical analyses: The data obtained were statistically analyzed by using WASP 1.0 (Web Agri Stat Package) software and means were separated by CD (critical difference) values.

Results and Discussion

Occurrence of insect pests in coastal and haor rice ecosystem: The occurrence of insect pests and natural enemies observed in coastal and haor rice ecosystem is presented in Table 1. Sixteen (16) insect pests of rice and six (6) natural enemies were recorded on rice field of coastal and haor ecosystem. Out of 16, six species were under the order Hemiptera, five species were under the order Lepidoptera, two of them were under Orthoptera, two under Diptera and one was under Thysanoptera. Among 16 insect pests, 12 insect pests were found in both coastal and haor rice ecosystem. Three insect pests viz., rice thrips, rice mealybug and whorl maggot were recorded from coastal ecosystem and rice case worm was recorded from haor rice ecosystem in T aman season.

*Incidence of major insect pests in coastal rice ecosystem***:** The mean number of four major insect pests per 30 hills on T aman and boro rice in three coastal districts is presented in Figure 1. Among three coastal districts, the highest number of stem borer (4.5/30 hills) followed by leaf roller (4.4/30 hills) was observed on boro rice in Khulna followed by Noakhali and the lowest number in Bhola (3.4/30 hills) on T aman rice. Likewise, similar trend was also observed in case of brown plant hopper (BPH) (3.1/ 30 hills) and rice bug (2.8/ 30 hills) where BPH was higher than rice bug in boro rice but in T aman, rice bug (2.6/ 30 hills) was higher than BPH (1.6/ 30 hills). From this figure it was found that major insect pests of rice is higher in boro season than those of T aman season.

Table 1. Occurrence of insect pests and natural enemies observed in coastal and haor rice ecosystem.

Rice ecosystem	Insect pests	Scientific name	Family	Order
Coastal & haor	Stem borer	*Scirpophaga incertulas*	Crambidae	Lepidoptera
Coastal & haor	Brown plant hopper	*Nilaparvata lugens*	Delphacidae	Hemiptera
Coastal & haor	Rice leaf roller	*Cnaphalocrosis medinalis*	Pyralidae	Lepidoptera
Coastal & haor	Green rice leafhopper	*Nephotettix nigropictus* *N. virescence* *Recilia dorsalis*	Cicadellidae	Hemiptera
Coastal & haor	Short horned grasshopper	*Oxya velox* *O. chinensis*	Acrididae	Orthoptera
Coastal & haor	Long horned grasshopper	*Conocephalus longipennis*	Tettigoniidae	Orthoptera
Coastal & haor	Rice bug	*Leptocorisa acuta*	Coreidae	Hemiptera
Coastal & haor	White backed planthopper	*Sogatella furcifera*	Delphacidae	Hemiptera
Coastal & haor	Rice gall midge	*Orseolia oryzae*	Cecidomyiidae	Diptera
Coastal	Rice thrips	*Stenchaetothrips biformis*	Thripidae	Thysanoptera
Coastal & haor	Rice ear cutting caterpillar	*Mythimna separata*	Noctuidae	Lepidoptera
Haor	Rice caseworm	*Nymphula depunctalis*	Pyralidae	Lepidoptera
Coastal	Small brown planthopper	*Laodelphax striatellus*	Delphacidae	Hemiptera
Coastal	Rice mealybug	*Brevennia rehi*	Pseudococcidae	Hemiptera
Coastal & haor	Swarming caterpillar	*Spodoptera mauritia*	Noctuidae	Lepidoptera
Natutal enemies				
Coastal & haor	Spiders	Species was not identified		
Coastal & haor	Dragonfly	Species was not identified	Libellulidae	Odonata
Coastal & haor	Carabid beetle	Species was not identified	Carabidae	Coleoptera
Coastal & haor	Mirid bug	Species was not identified	Miridae	Hemiptera
Coastal & haor	Lady bird beetle	Species was not identified	Coccinellidae	Coleoptera
Coastal & haor	Damselfly	Species was not identified	Coenagrionidae	Odonata

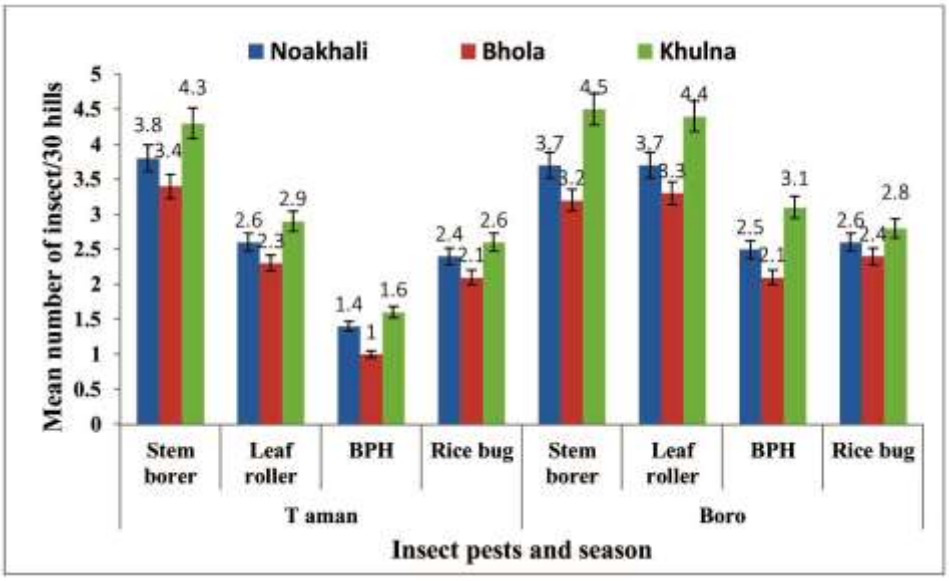

Fig. 1. Mean number of major insect pests at T aman and boro season in coastal rice ecosystem during July 2022 to June 2023

*Incidence of major insect pests in haor rice ecosystem***:** The mean number of four major insect pests per 30 hills on T aman and boro rice in three haor districts is presented in Fig. 2. Among three haor districts, the highest number of stem borer (3.4/30 hills) in Habigonj followed by Sunamgonj (3.1/ 30 hills) and the lowest number of stem borer in Kishoregonj (2.9/30 hills). In case of leaf roller, similar trend was also observed on boro rice. The number of brown plant hopper (BPH) (2.4/ 30 hills) and rice bug (2.4/ 30 hills) were identical on boro rice in Habigonj which was followed by Sunamgonj and Kishoregonj. In T aman rice, the highest number of stem borer (2.7-3.1) was recoreded in three coastal districts followed by leaf roller (1.9-2.4) while the lowest number of BPH (1-1.2) was recorded in Habigonj and Sunamgonj districts followed by rice bug (1.5-2.1). No BPH was recorded on T aman in Kishoregonj district. From this figure it was evident that major insect pests of rice is higher in boro season than those of T aman season.

*Major insect pests on T aman in haor and coastal rice ecosystem***:** The incidence of four major insect pest species on T aman in haor and coastal rice ecosystem is presented in Fig. 3. The incidence of stem borer was maximum in Khulna district followed by Noakhali and Bhola while the lowest incidence was observed in Kishoregonj followed by Sunamgonj and Habigong. In case of leaf roller and rice bug, similar trend was also

found. The incidence of BPH was maximum in Khulna district followed by Noakhali and Habigonj while the lowest incidence was observed in Sunamgonj followed by Habigong. No BPH was found in Kishoregonj. The incidence of 4 major insect pest species of rice crop was higher in coastal rice ecosystem compared to haor rice ecosystem.

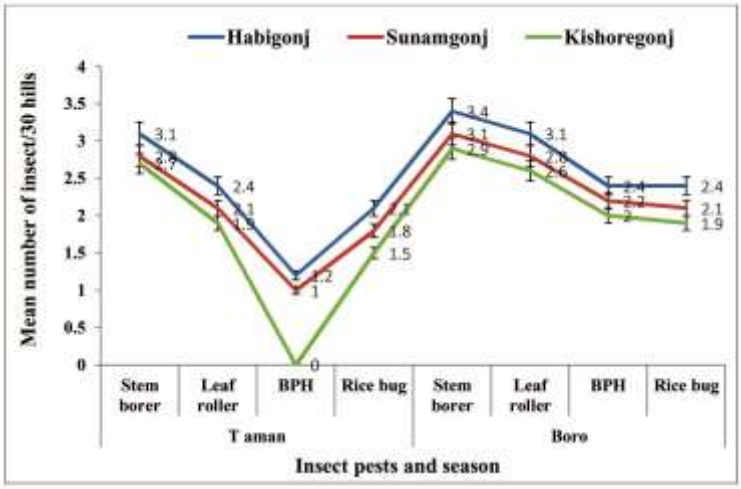

Fig. 2. Mean number of major insect pests at T aman and boro season in haor rice ecosystem during July 2022 to June 2023

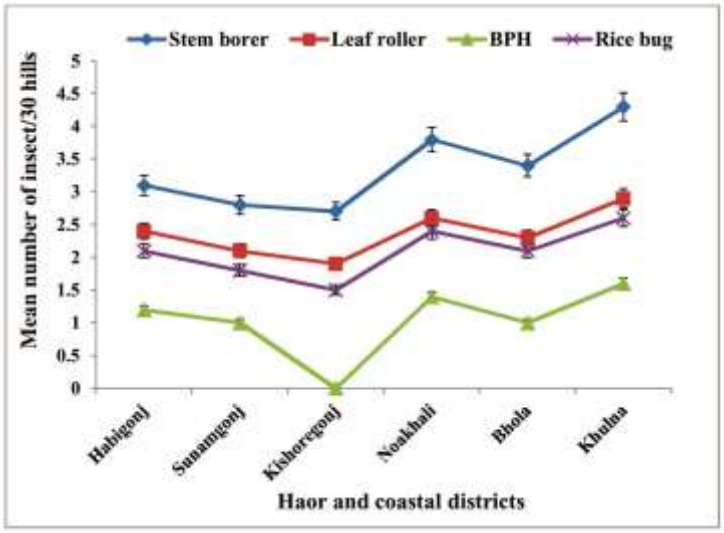

Fig. 3. Comparison of major insect pests on T aman rice in haor and coastal rice ecosystem

*Major insect pests on boro in haor and coastal rice ecosystem***:** The incidence of four major insect pest species on boro in haor and coastal rice ecosystem is presented in Fig. 4. The incidence of stem borer and leaf roller was maximum in Khulna district followed by Noakhali and Bhola while the lowest incidence was observed in Kishoregonj followed by Sunamgonj and Habigong. In case of rice bug, similar trend was also observed. The incidence of BPH was maximum in Khulna district followed by Noakhali and Habigonj while the lowest incidence was observed in Kishoregonj followed by Bhola and Sunamgonj.

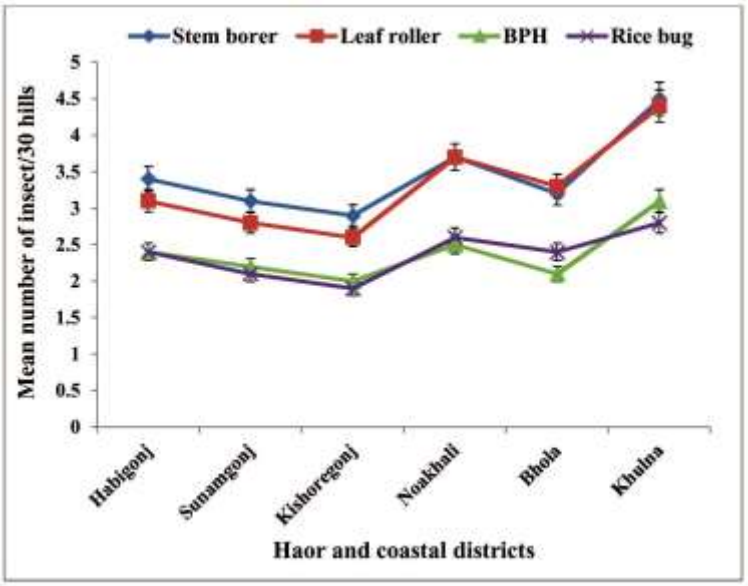

Fig. 4. Comparison of major insect pests on boro rice in haor and coastal rice ecosystem

The findings of the present study revealed that different species of insect pest were affecting the rice crop which was supported by Paramasiva *et al*. (2024) who stated that over one hundred insect pest species consume rice. Twenty of these species were significant pests that seriously harm the economy. The brown planthopper, *Nilaparvata lugens* (Stal), rice yellow stem borer *Scirpophaga incertulas* (Walker), leaf folder, *Cnapalocrocis medinalis* (Linnaeus), gall midge (GM), *Orseolia oryzae* (Wood-Mason), panicle mite, and *Steneotarsonemus spinki* were the main insect pests of recent years that have regional significance. Among these pests, leaf folder, rice stem borer and brown

plant hopper were very important economically to cause great losses in yield of rice (Barley and Butter, 2008). BPH was a severe pest in rice crop, which was harming to rice plant with heavy damage (Madhuri *et al*., 2017). The rice leaf folder, *Cnaphalocrocis medinalis*, was shown in several lab experiments to be affected by high temperatures in terms of growth rate, reproduction rate, survival, adult longevity, population size, and sexual behavior (Liao *et al*., 2014). Though there were several possible reasons for the abundance/shifts in insect pests viz., growing varieties lacking resistance to major pests, extensive cultivation of high yielding varieties, intensified rice cultivation throughout the year providing niches for pest multiplication, imbalance use of fertilizers and indiscriminate use of insecticides, harmful cultural practices, evolution of biotypes, changes in temperatures or rainfall patterns had profound influence on pest scenario of rice crop. Majority of the researchers opined that the infestation of BPH increased due to the miss use and overuses of nitrogenous fertilizers which favours to excrete more honeydew by BPH (Rashid *et al*., 2017), the plants become more vulnerable to BPH by using more amount of nitrogen. Along with the rice production using modern rice varieties, the insects/pests attack was also increased and loss of rice was continuously going on. These attacks always demanded more care for the rice plant (Horgan *et al*., 2018). Due to the insects/ pests at the global level the rice yield has decreased (Horgan *et al*., 2007). A tropical monsoon climate of Bangladesh was characterized by wide seasonal variations in rainfall, high temperatures, and high humidity which influenced the multiplication of pest. Haq *et al.* (2008) observed a decline in the number of *S. incertulas* during the past thirty years, which could be attributed to mortality brought on by increased rainfall and temperatures. Global warming might theoretically lead to an increase in the number of generations of rice insect pests and their potential to do harm, although this isn't necessarily the case. It is undoubtedly a significant impact in the population rise, even though many other causes might also be involved (Paramasiva *et al.*, 2024).

Conclusion

Sixteen (16) insect pests of rice and six (6) natural enemies were recorded on rice field of coastal and haor ecosystem. Major insect pests of rice is higher in boro season than those of T aman season. Stem borer, rice leaf roller, rice bug and brown plant hopper were one of the major insect pests of rice in coastal and haor rice ecosystems in survey areas. The incidence of 4 major insect pest species of rice crop was higher in coastal rice ecosystem compared to haor rice ecosystem.

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TEMPORAL VARIATION AND HETEROGENEITY OF AVIFAUNA IN THE BANGLADESH NATIONAL MUSEUM PREMISES

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Abstract

The study on temporal variation and heterogeneity of avifauna was carried out in the Bangladesh national museum premises during May 2018 to April 2019 employing Strip Transect Sampling technique. A total of 46 species of birds belonging to 11 orders, 26 families and 40 genera were recorded. Of which, 21 species were passerines and 25 non-passerines, 40 were resident and 6 migratory. Family Ardeidae and Sturnidae constituted the highest number of species (n=4, 8.7%of total). Only a single species were recorded from each of the 13 families. The maximum numbers (33%) of species were locally rare. Insectivorous birds were the highest (n=18,39.13% of total) than the other type of birds (piscivorous, frugivorous, omnivorous, granivorous, scavengers, nectarivorous and carnivorous). The highest number of species were (36.22%) recorded during winter than the other two seasons and the species heterogeneity was negatively correlated with temperature ($y = -0.011x + 1.118$, $R^2 = 0.262$) and precipitation ($y = -0.000x + 0.835$, $R^2 = 0.048$) of the study area. The Euclidean distance between the recorded birds in monsoon and winter are much closer than summer. One third of the recorded birds (31.11% of total) used the tree holes, bank of the pond, tree canopies and roof top of the main building of the Bangladesh National Museum for breeding purposes. Altogether 63 tree species (n=556 individuals) of 34 families were recorded in the premises, all of which were used by birds for different purposes. Of the total species of trees, 60% of trees were used for roosting, 30% for feeding and 11% for nesting by birds.

Keywords: Bird diversity, Passerine, Non-passerine, Resident, Migratory, Birds and plant interaction

Introduction

Bird diversity is considered to be a great indicator of healthy environment and it's occupying a wide range of habitats (Islam *et al.*, 2014). It can be sensitive to environmental change and are belong to near or at the top of the food chain (Khan and Ahsan, 2015). It can, therefore, be excellent barometers of the health of the environment and of the sustainability of human progress (Khan and Ahsan, 2015).They are potentials pollinators and bio-indicators (Amat and Green, 2010). Globally about 10,500 species of

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birds are recorded of which, 13% are threatened (IUCN Bangladesh, 2015). Bangladesh is harbours about 690 species of birds, of which 337 residents, 208 winter visitors, 12 summer visitors, 14 passage visitors and 119 vagrants (Khan, 2018). But due to excessive anthropogenic activities and lack of proper conservation measures 19 species of birds have extirpated from Bangladesh (IUCN Bangladesh, 2015). At present Dhaka is being an overpopulated city with a very limited range of habitats for wildlife (Kabir *et al.*, 2010).

Every county of a country should have a list of birds, because they are important biological components of all ecosystems (Ahsan and Khanom, 2005). This research was an attempted to find out the scientific data on temporal variation and avifaunal species diversity, local status and some other aspects of birds of Bangladesh National Museum (BNM) premises. Except this area, sporadically some studies have been done on birds of the different part of the capital city of Dhaka. Chowdhury *et al.* (2014) and Banu *et al.* (2016) studied on seasonal occurrence and checklist of avifauna in Dhaka University campus. The study on avifauna of the national botanical garden of Bangladesh, Dhaka was done by Islam *et al.* (2014). Status and diversity of birds in the Ramna park, Dhaka was noted by Rajia *et al.* (2015). Mohsanin and Khan recorded the status and seasonal occurrence of the birds in Jahangirnager University Campus, Bangladesh (Mohsanin, 2009). The study on diversity of avifauna in Sher-e-Bangla Agricultural University Campus was done by Shovon *et al.* (2014). Diversity and population of avifauna of two urban sites in Dhaka city was recorded by Sarker *et al*. (2009). Capital city of Dhaka is highly diversified with bird species. Bangladesh National Museum campus is surrounding by diversified plant species of Dhaka University Campus and Ramna Park. Hence, an attempt was taken to find out the temporal variation and bird species diversity of the Bangladesh National Museum area. This study should provide baseline information to take in-depth research plan in future.

The objectives of this study were to: (1) find out the diversity of bird species, (2) know the present status with abundance of passerine, non-passerine, resident and migratory bird species, (3) find out the temporal variation and (4) to examine the interaction of birds with tree species in this area.

Materials and Methods

Study site: The study was carried out at the Bangladesh National Museum (BNM) premises, Shahbag, Dhaka, Bangladesh from May 2018 to April 2019. Bangladesh National Museum is a national institute, focused on collection, preservation, research and

interpretative display of historical documents, archaeological artefacts, decorative arts, ethnological materials and specimens of natural heritage of Bangladesh. The museum is located at Shahbag in Dhaka city (Fig. 1) occupying 8.63 acres land, with a magnificent building. The geographical position of the study area is 23°44′15″ N latitude and 90°23′40.2″E longitude.

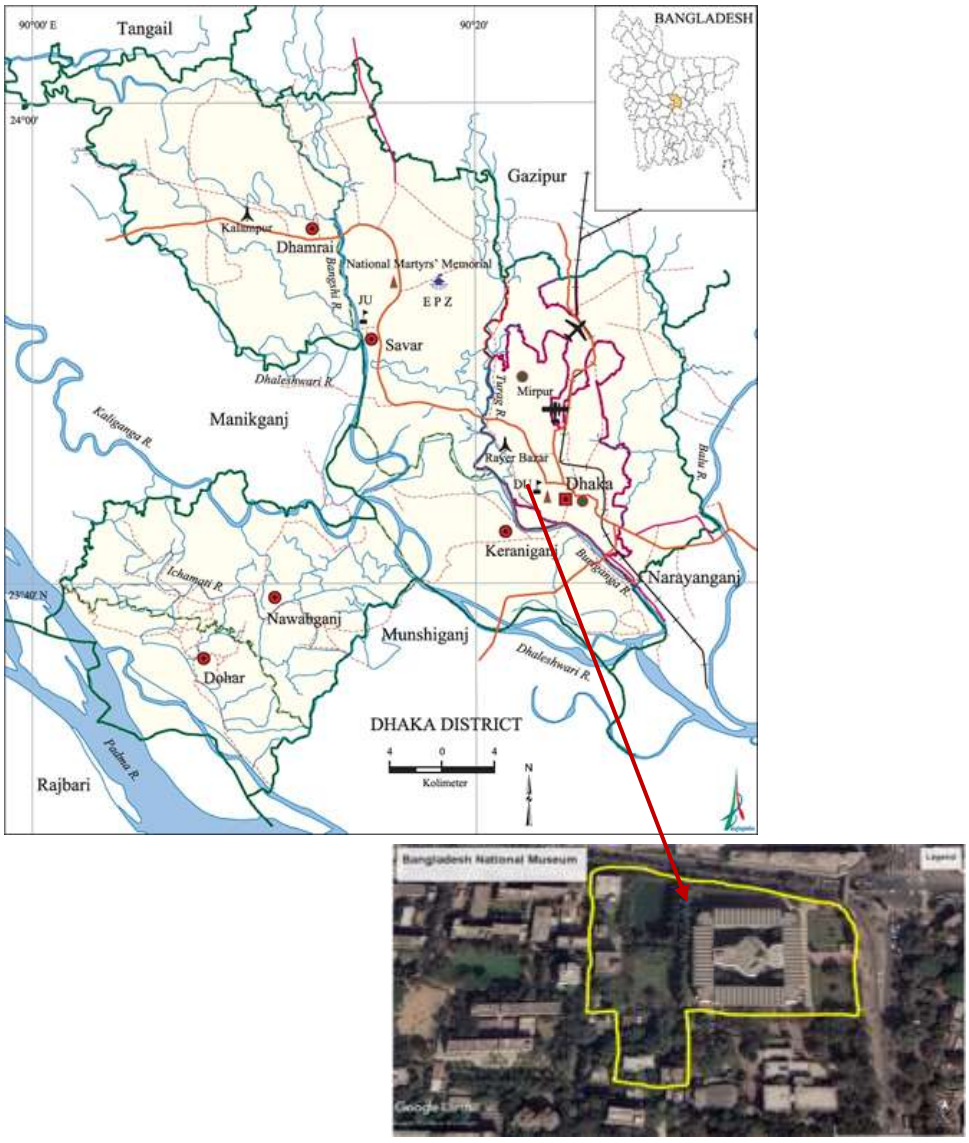

Fig. 1. Map of the study area (map source: Banglapedia 2009 and Google Earth).

PG hospital on the north and Dhaka University campus practically limit the southern and western boundaries of the study area. The Shahbag police station is on the eastern side of the national museum campus.

Dhaka experiences a hot, wet and humid tropical climate. The city has a distinct monsoonal season. The average high temperature for Dhaka ranges from 26°C in January to approximately 36.3°C in April. Similarly, the average low temperature oscillates from 15.3°C in January to 27.3°C in June (Fig. 2). Rainfall is significantly less frequent between October and April, with monthly averages not exceeding 10mm. Conversely, May to September is the wettest months, with an average of 100mm to 134mm of rain per month (Fig. 2). Cold weather is unusual in and around Dhaka.

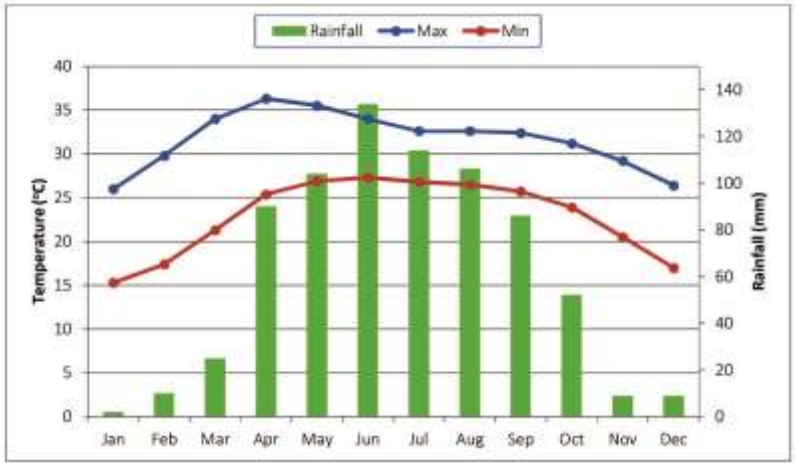

Fig. 2.Graphs show monthlyweather averages over the year in Dhaka city (Data source: www.weather-atlas.com).

Materials used: For clear observation of bird a pair of binoculars (Bushnell 10 x 40X) was used from a safe distance. Sometimes, telescope (Swarovski ATS 80 HD with 20 x 60X) was used on roof top of officer's building number 2 to observe the bird from a long distance. Nikon (D3200) camera with 70–300 mm lens used to take photographs of birds and tree species. Garmin (etrex 10) GPS machine used to measure the length of each transect and also to record latitude and longitude of start and end point of each transect. Weather station (Acurite 5 in 1) used to record the temperature, relative humidity and precipitation of the study area.

Data collection: The study area was inspected twice a week during day time. Sometimes night survey (from sunset to 2100 hr) was done to record nocturnal species from their sound call. A total of 96 days, 672 hours (7 hrs/day) were spent for this study. The observation was done during 0600 – 1000 hr and 1500 – 1800 hr. The time schedule was fluctuated depending on the seasonal day length variation. Most of the birds are diurnally active and data were collected through direct field observations. The survey was conducted through simple Strip Transect Sampling technique (Buckland *et al*., 2001). In total 6 transects were used to count the bird species. Each transect was repeated 3 to 4 times in a day. The total length of transects were 1,023.9 m (Table 1). Sometimes ad libitum data were also recorded to count the bird species.

All bird species were identified following Grimmette *et al*. (1999) and Halder (2010). The local status of the bird species was assessed based on the percentage of occurrence during observations (Emrose, 2024): Very Common (VC) – a species seen during 76 to 100% of the visits; Common (C) – a species seen during 51 to 75% of the visits; Fairly Common (FC) – a species seen during 26 to 50 % of the visits; and Rare (R) – a species seen single or in small number of occasions, i.e. up to 25% of the visits.

Table 1.Transects no, length and GPS coordinate.

Transect no.	Location	Length (m)	GPS	
			Start point	End point
1	Taltala gate to BNM substation	142	23°44′13″N 90°23′43″E	23°44′13″N 90°23′37″E
2	In between Officer's building number 2 and 3 to Agrani bank gate	226	23°44′11″N 90°23′37″E	23°44′17″N 90°23′36″E
3	North – west – south side of officer's building 2	76.4	23°44′12″N 90°23′37″E	23°44′11″N 90°23′37″E
4	East – north – west side of BNM main building	292	23°44′13″N 90°23′41″E	23°44′13″N 90°23′38″E
5	Taltala gate – shahbagh foot over – Agrani bank gate	246	23°44′13″N 90°23′43″E	23°44′17″N 90°23′36″E
6	South side of pond	41.5	23°44′15″N 90°23′37″E	23°44′15″N 90°23′36″E
	Total =	**1,023.9**		

Data analysis: All data were computerized and analysedby SPSS (version 19) software. Pearson two-tailed test performed to determine the correlation coefficient between number of bird species with monthly temperature and precipitation of the area. The temporal changes were analysed by comparing seasons. The hierarchical cluster analysis was done to find out the Euclidean distance between the numbers of bird species based on their diet and also to find out the temporal variation of bird diversity.

Results and Discussion

Heterogeneity of avifauna: During the study period, a total of 46 species of birds recorded belonging to 11 orders, 26 families and 40 genera (Table 2). Among the recorded species, 21species were passerine and 25 non-passerines (Fig. 3); 40 resident and 6 migratory (Fig. 4) (Plate 1). Whereas Shome *et al.* (2022), Banu *et al.* (2016) and Chowdhury *et al.* (2014) recorded 70, 54 and 78 species, respectively from the Dhaka University campus and 65 species were reported by Islam *et al.* (2014) from the National Botanical garden. Rajia *et al*. (2015) found 50 species from Ramna park. Shovon *et al*. (2014) and Sarker *et al*. (2009) recorded 60 and 27 species from Sher-e-Bangla Agricultural University campus and Uttara (sector 7 and 9), respectively.

Plate 1. Recorded migratory bird species in BNM premises: (a) Brown Shrike, (b) Taiga Flycatcher, (c) Blyth's Leaf Warbler, (d) Clamorous Reed Warbler. (Photo credit:Author)

Table 2. Recorded avifaunal species in the Bangladesh National Museum (BNM) premises during May 2018 to April 2019.

Scientific name	English common name	Resident/ Migratory	LS	CS (IUCN Bangladesh 2015)	GS
Order: Columbiformes					
Family: Columbidae					
Columba livia	Rock Dove	R	C	LC	LC
Spilopelia chinensis	Eastern Spotted Dove	R	FC	LC	LC
Order: Caprimulgiformes					
Family: Caprimulgidae					
Caprimulgus macrurus	Large-tailed Nightjar	R	Ra	LC	LC
Family: Apodidae					
Cypsiurus balasiensis	Asian Palm Swift	R	FC	LC	LC
Apus nipalensis	House Swift	R	Ra	LC	LC
Order: Cuculiformes					
Family: Cuculidae					
Eudynamys scolopaceus	Western Koel (Asian Koel)	R	C	LC	LC
Cacomantis merulinus	Plaintive Cuckoo	R	Ra	LC	LC
Order: Pelecaniformes					
Family: Ardeidae					
Butorides striata	Green-backed (Striated) Heron	R	Ra	LC	LC
Ardeola grayii	Indian Pond Heron	R	FC	LC	LC
Egretta garzetta	Little Egret	R	Ra	LC	LC
Ixobrychus cinnamomeus	Cinnamon bittern	R	Ra	LC	LC
Order: Suliformes					
Family: Phalacrocoracidae					
Microcarbo (Phalacrocorax) niger	Little Cormorant	R	Ra	LC	LC
Order: Strigiformes					
Family: Tytonidae					
Tyto alba	Common Barn Owl	R	FC	LC	LC
Family: Strigidae					
Athene brama	Spotted Owlet	R	FC	LC	LC
Order: Accipitriformes					
Family: Accipitridae					
Milvus migrans	Black Kite	R	C	LC	LC
Order: Coraciiformes					
Family: Meropidae					
Merops orientalis	Asian Green Bea-eater	R	FC	LC	LC
Family: Alcedinidae					
Alcedo atthis	Common Kingfisher	R	C	LC	LC
Family:Dalcelonidae					
Halcyon smyrnensis	White-breasted Kingfisher	R	VC	LC	LC
Pelargopsis capensis	Stork-billed Kingfisher	R	Ra	LC	LC
Order: Piciformes					
Family: Megalaimidae					
Psilopogon haemacephalus	Coppersmith Barbet	R	VC	LC	LC

Family: Picidae					
Dinopium benghalense	Black-rumped Flameback	R	C	LC	LC
Micropternus brachyurus	Rufous Woodpecker	R	Ra	LC	LC
Dendrocopos macei	Fulvous-breasted Woodpecker	R	FC	LC	LC
Order: Psittaciformes					
Family: Psittacidae					
Psittacula krameri	Rose-ringed Parakeet	R	VC	LC	LC
Psittacula alexandri	Red-breasted Parakeet	R	Ra	LC	NT
Order: Passeriformes					
Family: Lanidae					
Lanius cristatus	Brown Shrike	M	Ra	LC	LC
Family: Oriolidae					
Oriolus xanthornus	Black-hooded Oriole	R	C	LC	LC
Family: Dicruridae					
Dicrurus macrocercus	Black Drongo	R	C	LC	LC
Family: Corvidae					
Dendrocitta vagabunda	Rufous Tree-pie	R	FC	LC	LC
Corvus splendens	House Crow	R	VC	LC	LC
Corvus levaillantii	Jungle Crow	R	C	LC	LC
Family: Pycnonotidae					
Pycnonotus cafer	Red-vented Bulbul	R	VC	LC	LC
Family: Sylvidae					
Orthotomus sutorius	Common Tailorbird	R	VC	LC	LC
Acrocephalus dumetorum	Blyth's Leaf Warbler	M	Ra	LC	LC
Acrocephalus stentoreus	Clamorous Reed Warbler	M	Ra	LC	LC
Family: Sturnidae					
Sturnus contra	Asian Pied Starling	R	VC	LC	LC
Sturnus malabaricus	Chestnut-tailed Starling	R	VC	LC	LC
Acridotheres fuscus	Jungle Myna	R	C	LC	LC
Acridotheres tristis	Common Myna	R	VC	LC	LC
Family: Muscicapidae					
Ficedula albicilla	Taiga Flycatcher	M	Ra	LC	LC
Copsychus saularis	Oriental Magpie Robin	R	VC	LC	LC
Family: Nectarinidae					
Nectarinia zeylonica	Purple-rumped Sunbird	R	C	LC	LC
Nectarinia asiatica	Purple Sunbird	R	C	LC	LC
Family: Passeridae					
Passer domesticus	House Sparrow	R	C	LC	LC
Dendronanthus indicus	Forest Wagtail	M	Ra	LC	LC
Family: Motacilidae					
Motacilla alba	White Wagtail	M	FC	LC	LC

Note: LS - Local Status, CS - Country Status, GS - Global Status, R - Resident, M - Migratory, VC - Very Common, C - Common, FC - Fairly Common, Ra - Rare, LC - Least Concern, NT - Near Threatened

Number of bird species according to the order: The significant number of species (45.7%) and generae (40%) were recorded from the Order Passeriformes and the minimum number of species (2.2%) and generae (2.5%) recorded from Suliformes and Accipitriformes, respectively.

Passerine birds: Among the Order Passeriformes, family Sturnidae comprised the highest number of species (8.7% of the total and 19.1% of the passerines). Five generae consisted (*Corvus, Acrocephalus, Sturnus, Acridotheres* and *Nectarinia*) the maximum number of species (two, i.e. 4.5% of the total and 9.5% of the passerine species). Thirteen (8 Non-passerines and 5 Passerines) of the 26 recorded families contained single species.

Non-passerine birds: In case of non-passerine, Family Ardeidae consisted of the highest number of genera (four, i.e. 10% of the total and 16.7% of the non-passerines) and species (four, i.e. 8.7% of the total and 16% of the non-passerines) (Table 2). *Psittacula* consisted of the maximum number of species (two, i.e. 4.4% of the total and 8% of the non-passerines).

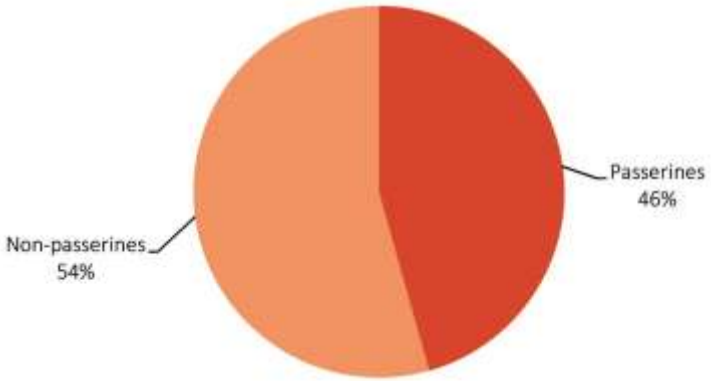

Fig. 3. Percentage of passerine and non-passerine species.

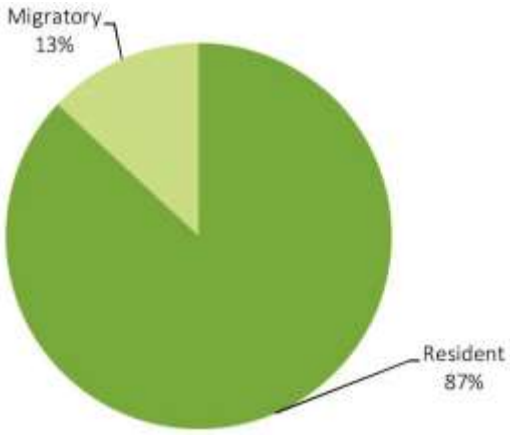

Fig. 4. Percentage of resident and migratory species.

Local status of the recorded bird species: During the study period the maximum number of species (15) were locally rare, 12 species were common, 10 very common and 9 species were fairly common (Fig. 5). Among the passerine species 7 were very common, 7 common, 5 rare and 2 fairly common and in non-passerine 10 rare, 7 fairly common, 5 common and 3 very common species recorded.

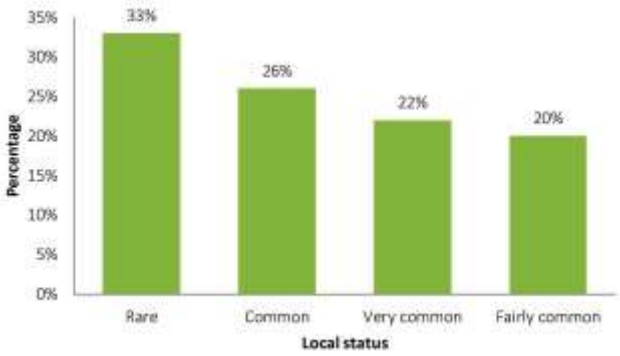

Fig. 5. Local status of the recorded species.

Bird species based on their food habit: Among the recorded species, the highest numbers of birds (18 species) were insectivorous than the other types of birds (piscivorous, frugivorous, omnivorous, granivorous, scavengers, nectarivorous and carnivorous) (Fig. 6).

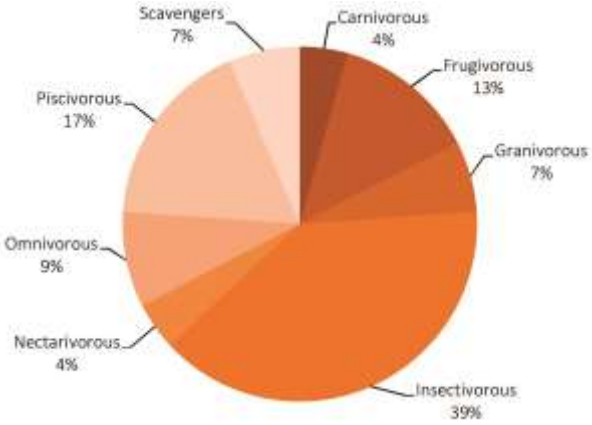

Fig. 6. Bird species based on their food habit.

Temporal variation: This study reported that the maximum numbers of bird species (36.22%) were recorded during winter due to abundance of migratory species than the other two seasons (monsoon, summer) (Fig. 7). Shome *et al.* (2022) also found the highest species diversity in winter.

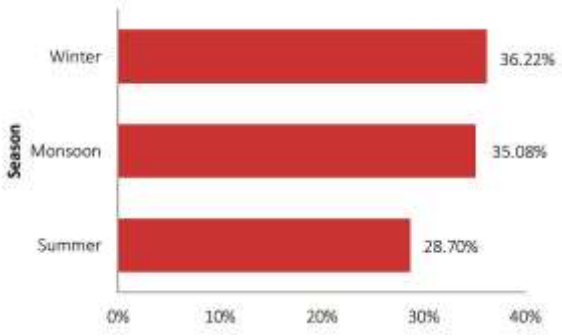

Fig. 7. Temporal variation of bird species in the BNM premises.

From hierarchical cluster analysis it is revealed that the Euclidean distance between the recorded birds in monsoon and winter are much closer than summer (Fig. 8). That means the recorded birds in winter and monsoon is more similar.

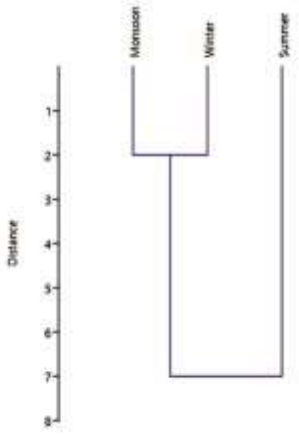

Fig. 8. Euclidean distance between the number of birds in different seasons.

Heterogeneity of birds in relation to temperature and precipitation: The bird species heterogeneity was negatively correlated with temperature ($y = -0.011x + 1.118$, $R^2 = 0.262$) and precipitation ($y = -0.000x + 0.835$, $R^2 = 0.048$) in this area (Fig. 9). That means, the highest number of species were recorded when the temperature was low and minimum precipitation recorded.

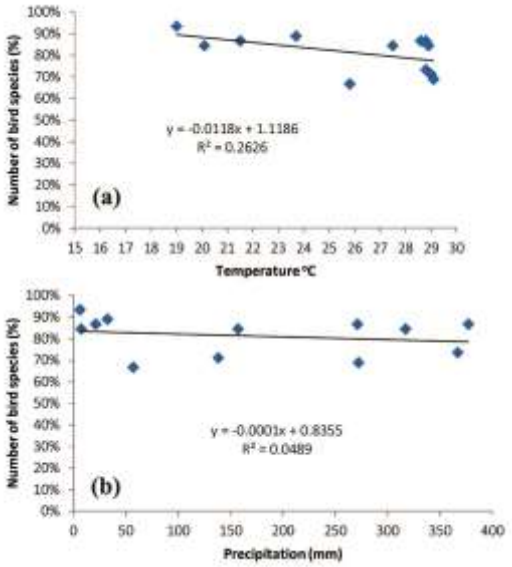

Fig. 9. Relationship of bird species diversity with temperature (a) and rainfall (b) of the study area.

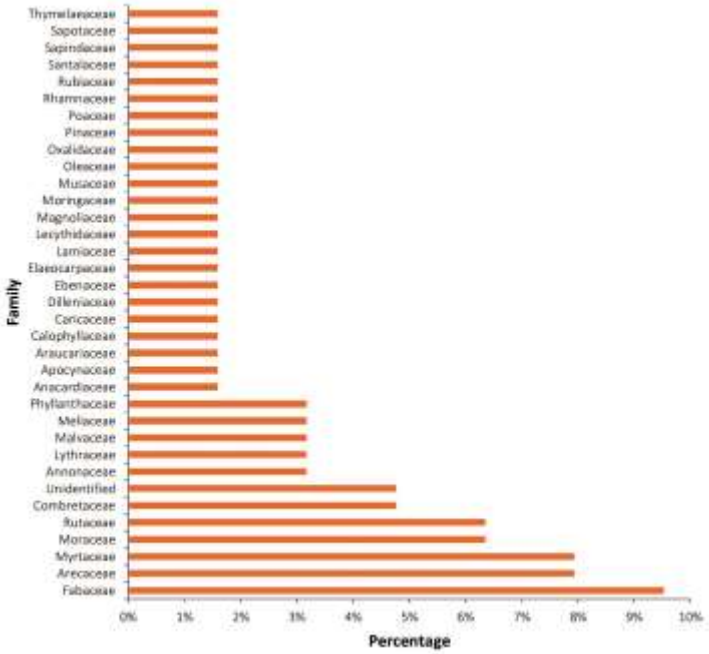

Fig. 10**.** Family wise tree species in the BNM premises.

Plate 2. Some breeding birds in the BNM premises (Photo credit: Author).

Breeding birds in the BNM premises: Among the total recorded species 31.11% birds (Plate 2) used the study area for breeding purposes. Tree holes, bank of the pond, tree canopies and roof top of the main building of the Bangladesh National Museum were the preferred breeding sites in this area (Plate 3).

Interaction of birds with tree species: A total of 63 tree species (556 individuals), under 34 families were recorded to be used by birds for different purposes. Family Fabaceae was dominant (9.52%) (Fig. 10). Most of the trees (59%) were used for roosting followed by feeding (30%) and nesting (11%).

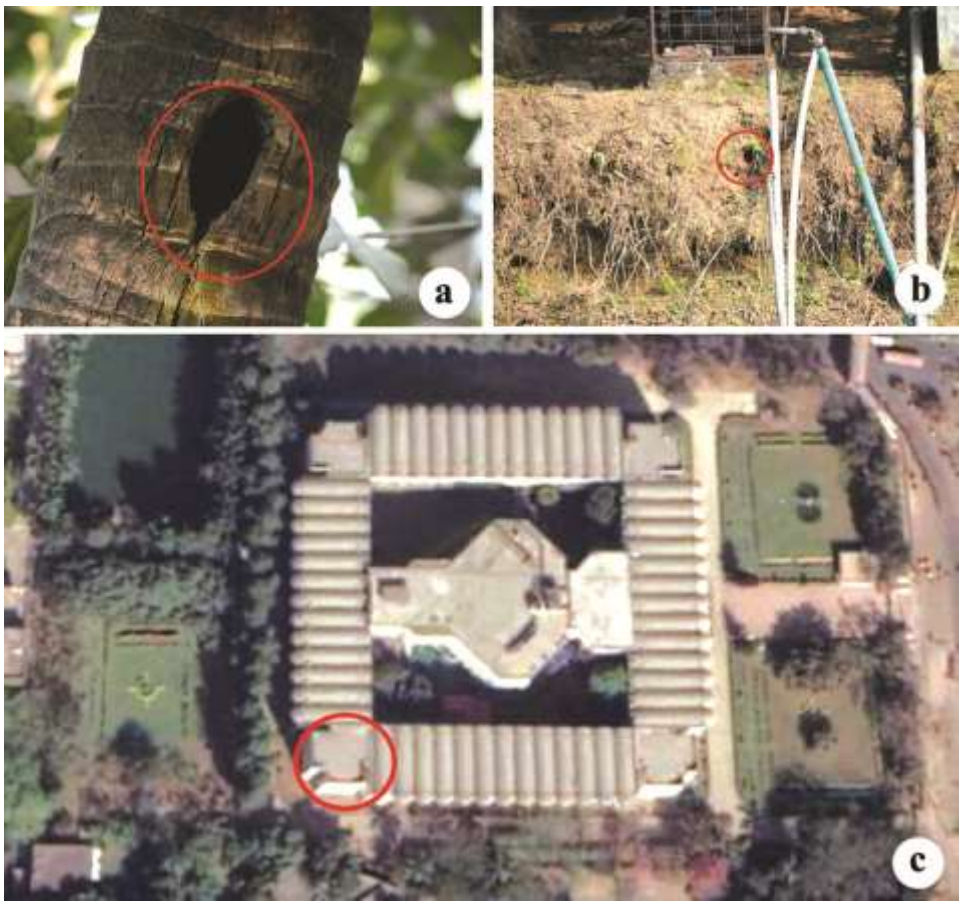

Plate 3. Some preferred bird breeding sites in the BNM premises; (a) tree hole, (b) bank of the pond and (c) roof top of the museum's building (Photo credit: Author).

Conservation values: This study revealed that the diversified habitats of BNM premises i.e.; aquatic habitat (pond), flowering, fruiting, roosting and nesting trees supports different types of bird. Different habitats shelter different species of birds, such as a large pond (0.50 acres) containing fishes and aquatic insects which supports 8 species of piscivorous birds. This habitat occupied by 30% fruit plants which provide food (fruits) for frugivorous birds (6 species).

Conclusions

Bangladesh national museum (BNM) premises are restricted and prohibited to access general people for avoiding excessive crowd, ensuring museum safety and healthy environment of avifaunal species. There is no record of anthropogenic activities in this area. Birds are enjoying this area through nesting, foraging, feeding and resting. Some of the species are living throughout the year in this area without any human disturbance. Even migratory birds are using this area as a stopover while they are flying over a thousand miles from their home country. Thus, BNM ensures a healthy and secure habitat which is rich with different foods and nesting opportunities, provides tremendous ecological benefits along with functional value to birds as well as other animals. BNM plays a great role in conservation of bird species in such an overcrowded unplanned capital city.

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