

Vegetation Composition Drives The Hornbill Abundance in Tujuh Bukit Area, PT Bumi Suksesindo

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Abstract

Hornbills, keystone frugivores and bioindicators, reflect forest health. Their abundance depends on specific vegetation, like large cavity-bearing trees for nesting and diverse fruit-producing trees for foraging. In the southern Banyuwangi forests adjacent to mining areas, these characteristics may undergo changes due to operational activities that influence stand structure and the diversity of fruit-bearing trees, potentially affecting overall habitat suitability. A systematic investigation into vegetation composition and hornbill distribution is essential to establish baseline population data and inform targeted conservation strategies. We conducted hornbill and vegetation surveys in the areas adjacent to the mining site in the south of Banyuwangi Regency, East Java, Indonesia. Hornbill survey were conducted using a combination of line transect and point count methods. Vegetation analysis was conducted using plot-based sampling with 20 m x 20 m. All analyses were conducted in R with all visualisation made using package ggplot2. We found that despite of the patchy distribution, the abundance of three hornbill species, *Anthracoceros albirostris*, *Buceros rhinoceros*, and *Rhyticeros undulatus*, is similar across sites. Meanwhile, tree basal area, abundance, and composition differed across ecosystem types. Combining hornbill and tree data, we found that hornbill abundance is associated with tree composition and diversity, not overall plant abundance. To sum up, vegetation composition is a key determinant of hornbill abundance in tropical forests adjacent to mining sites. Therefore, conserving hornbills species requires preservation of the associated tree species providing food resources and nesting habitats.

Keywords: Hornbills, Vegetation, Mining sites

INTRODUCTION

Hornbills, belonging to the Bucerotidae family, are a distinctive group of frugivorous birds that primarily inhabit the forest canopy. Their ecological role is pivotal in maintaining the dynamics of tropical forest ecosystems, as they serve as key agents for seed dispersal, transporting seeds over considerable distances, and contributing to forest regeneration (Datta & Kemp 2024; Pradhan et al., 2024). Furthermore, their specific habitat requirements and

sensitivity to environmental changes make them exceptional bioindicators; the presence of a healthy and diverse hornbill population often signifies a well-preserved and functioning habitat. Therefore, studying them provides valuable insights into the overall health and integrity of the forest they inhabit (Sarkar & Talukda, 2023).

The presence and abundance of hornbills within a forest are not random but are closely correlated with specific vegetation characteristics. A critical factor is the availability of large-diameter, mature trees, which provide the essential cavities that hornbill species require for nesting and raising their young (Kaur et al., 2020; Rahmansyah et al., 2024). Equally important is the abundance and diversity of fruit-producing trees, which constitute their primary food source and determine the carrying capacity of the habitat (Pradhan et al., 2024). Therefore, the structural composition and floristic diversity of a forest directly dictate its suitability for supporting viable hornbill populations.

In the specific context of a forest landscape adjacent to mining activities in South Banyuwangi, these critical vegetation features are under imminent threat. Mining operations can lead to alterations in the forest's stand structure, such as the reduction of large trees for timber or the fragmentation of continuous canopy (Siqueira-Gay et al., 2020; Kumi et al., 2021). Simultaneously, the composition of vegetation may undergo changes, potentially reducing the diversity and abundance of the fruit trees that hornbills depend on. These cumulative alterations in the vegetation have a direct and significant potential to degrade the habitat's suitability, thereby endangering the local hornbill populations (Hata et al., 2015).

Given the potential threats, it is important to conduct a focused study on the relationship between hornbills and their habitat in this mining-adjacent landscape. A systematic investigation into the composition and abundance of hornbill species present will establish a baseline of their population status. By concurrently analyzing the structure and composition of the vegetation, we can identify the specific environmental factors that are driving hornbill distribution and abundance. The findings from this study are fundamental for understanding current habitat conditions and will provide the scientific basis needed to formulate effective strategies for biodiversity management and conservation in this pressured landscape.

METHOD

Study sites

Hornbill and vegetation surveys were conducted in dry season in the areas adjacent to the mining site in the south of Banyuwangi Regency, East Java, Indonesia. We used 8 independent sites/transects situated across two ecosystem types, secondary forests and industrial forests (Figure 1).

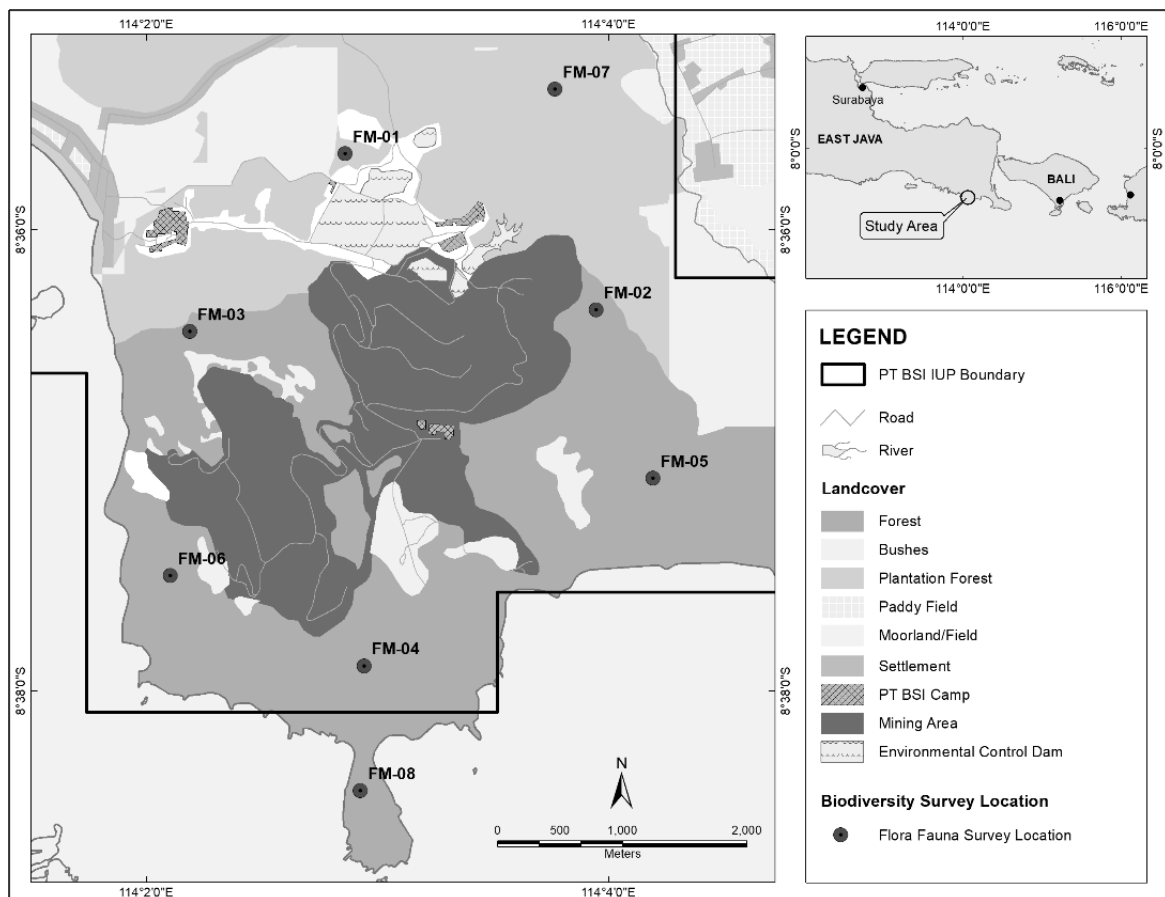


Figure 1. Map of Study Location

Table 1. Description of each study locations

Transects	Descriptions
FM 1	Plantation forest dominated by teak (<i>Tectona grandis</i>) with moderate density, situated adjacent to an access road
FM 2	Lowland secondary forest adjacent to the Mine Access Road (MAR)
FM 3	Lowland secondary forest adjacent to the MAR and located near mining stockpile/unloading activities
FM 4	Lowland secondary forest adjacent to the mine ring road
FM 5	Lowland secondary forest located near exploration drilling activities
FM 6	Lowland secondary forest located near exploration drilling activities and in proximity to the coastal area
FM 7	Plantation forest dominated by teak (<i>Tectona grandis</i>) with low density
FM 8	Lowland secondary forest located along the access road to Candrian Bay, representing the outermost zone of the concession area

Hornbill survey

Hornbill observations were conducted using a combination of line transect and point count methods (Persulessy & Putuhena, 2020). A transect with 1,000 meters was established, along which six point count stations were systematically placed at 200 meters intervals. Each point count had a fixed radius of 30 meters, and observations were conducted for 45 minutes per points. Surveys were carried out during peak activity periods, namely in the morning (06:00–10:30 WIB) and in the afternoon (15:00–17:00 WIB).

Vegetation survey

Vegetation analysis was conducted using plot-based sampling established along a 1,000 meters transect line. Plot sizes were determined according to vegetation strata, namely 20 m × 20 m for trees, 10 m × 10 m for poles, 5 m × 5 m for saplings, and 1 m × 1 m for seedling and ground cover vegetation. A total of 5–10 plots were established along each transect. Sampling units were arranged using a systematic sampling approach with a random starting point, followed by the systematic placement of subsequent plots along the transect.

Data Analysis

All analyses were conducted in R with all visualisation made using package ggplot2. Data cleaning was using dplyr package. All generalized linear model (GLM) analyses used glm function. All Non-metric Multidimensional Scaling (NMDS) tests were based on Bray–Curtis dissimilarity using the metaMDS function in the vegan package. All permutational multivariate analysis of variance (PERMANOVA) tests were based on Bray–Curtis dissimilarity in the vegan package.

For the hornbill abundance data, the differences in hornbill abundance among species were assessed using GLM with a Poisson error distribution and log link function. Species identity was included as a categorical predictor and abundance was treated as the response variable. In addition, model-estimated marginal means (EMMs) for hornbill abundance was derived from the Poisson GLM using the emmeans function of emmeans package.

For the tree abundance data, we conducted separate analysis for the abundance per species and abundance per family using GLM with a Poisson error distribution and log link function. Tree abundance was calculated as the total number of individuals per species. Ecosystem type and species identity were included as explanatory variables. Moreover, differences in tree community composition between ecosystem types were tested using PERMANOVA. For the tree basal area data, we conducted separate analysis for the tree basal area per species and per family. Differences in tree basal area, either abundance per species or per family, between ecosystem types were analyzed using GLM with a Gaussian error distribution. Tree basal area was calculated as the mean basal area of all individuals per species. Ecosystem type and species identity were included as explanatory variables. Basal area dominance was calculated as the proportion of total basal area contributed by each species within each transect. Data were analyzed using a beta regression mixed-effects model implemented in glmmTMB with a logit link function.

Differences in plant community composition among ecosystems were visualized using NMDS. Community differences between ecosystems were tested using PERMANOVA. Species

list focuses on the top 10 most dominant tree species while the rest are categorized into “others” category. Basal area dominance of tree species was analyzed using GLM with a Gaussian error distribution and identity link function. The response variable was the percentage dominance of the basal area. Predictor variables included transect identity and tree species to evaluate spatial variation and species-level differences in dominance across the study area.

For the association between vegetation community composition and hornbill abundance, NMDS was used. Hornbill abundance variables were fitted to the ordination using the `envfit` function to examine their association with variation in vegetation composition. Moreover, the relationship between hornbill abundance and plant abundance as well as plant diversity was examined using Spearman's rank correlation coefficient, a non-parametric test that assesses the strength and direction of monotonic relationships between two variables.

Plant diversity was quantified using three commonly used indices: species richness, Shannon diversity, and Simpson diversity. The analysis tested whether hornbill abundance was associated with plant abundance or with plant diversity across sampling units. In addition to the correlation test, the relationship between hornbill abundance and plant abundance was examined using simple linear regression, where hornbill abundance was treated as the response variable and plant abundance as the explanatory variable. Similarly, separate linear regression models were fitted to evaluate the relationship between hornbill abundance and each diversity metric.

RESULT

Hornbill abundance across sites

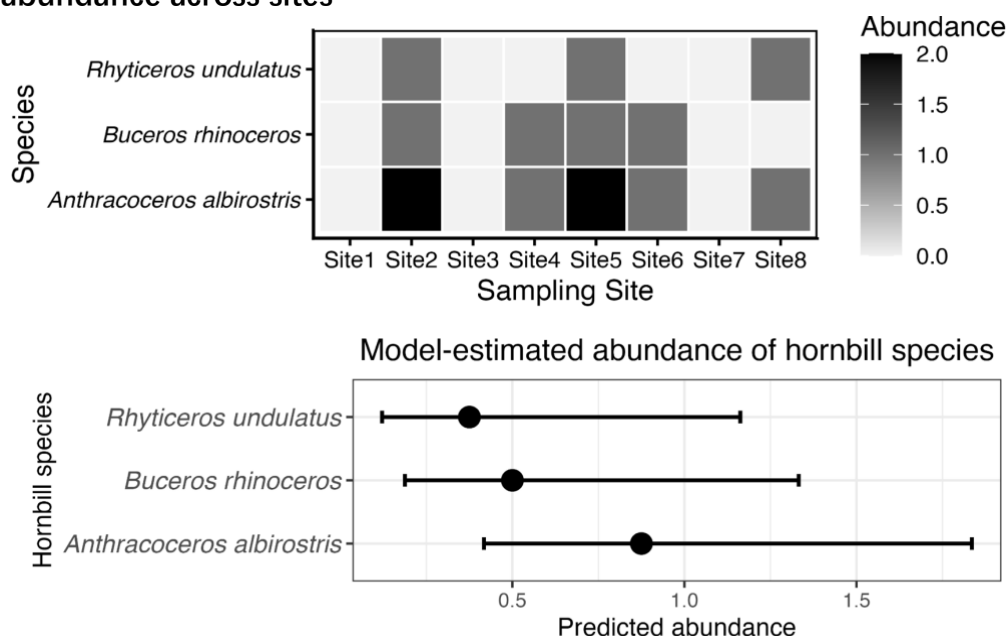


Figure 2. Absolute Abundance (upper) and Model-estimated Abundance (lower) of Three Hornbill Species at The Different Sampling Sites

In the study sites, three hornbill species were observed: *Anthracoseros albirostris*, *Buceros rhinoceros*, and *Rhyticeros undulatus*. When analysing the species composition across

all locations, one particular species exhibited a clear numerical dominance which is *Anthracoseros albirostris*. However, hornbill abundance statistically did not differ significantly among species (Poisson GLM, Figure 1 upper). Relative to *Anthracoseros albirostris*, the abundance of *Buceros rhinoceros* ($\beta = -0.56 \pm 0.63$ SE, $z = -0.89$, $p = 0.37$) and *Rhyticeros undulatus* ($\beta = -0.85 \pm 0.69$ SE, $z = -1.23$, $p = 0.22$) was lower but not statistically significant.

Similarly, model-estimated mean abundance differed slightly among hornbill species but confidence intervals overlapped widely. The predicted abundance of *Anthracoseros albirostris* was 0.88 individuals per sampling unit (95% CI: 0.42–1.84), compared with 0.50 (95% CI: 0.19–1.33) for *Buceros rhinoceros* and 0.38 (95% CI: 0.12–1.16) for *Rhyticeros undulatus* (Figure 1 lower). These results indicate no significant differences in abundance among species.

Tree basal area, abundance, and composition across ecosystem types

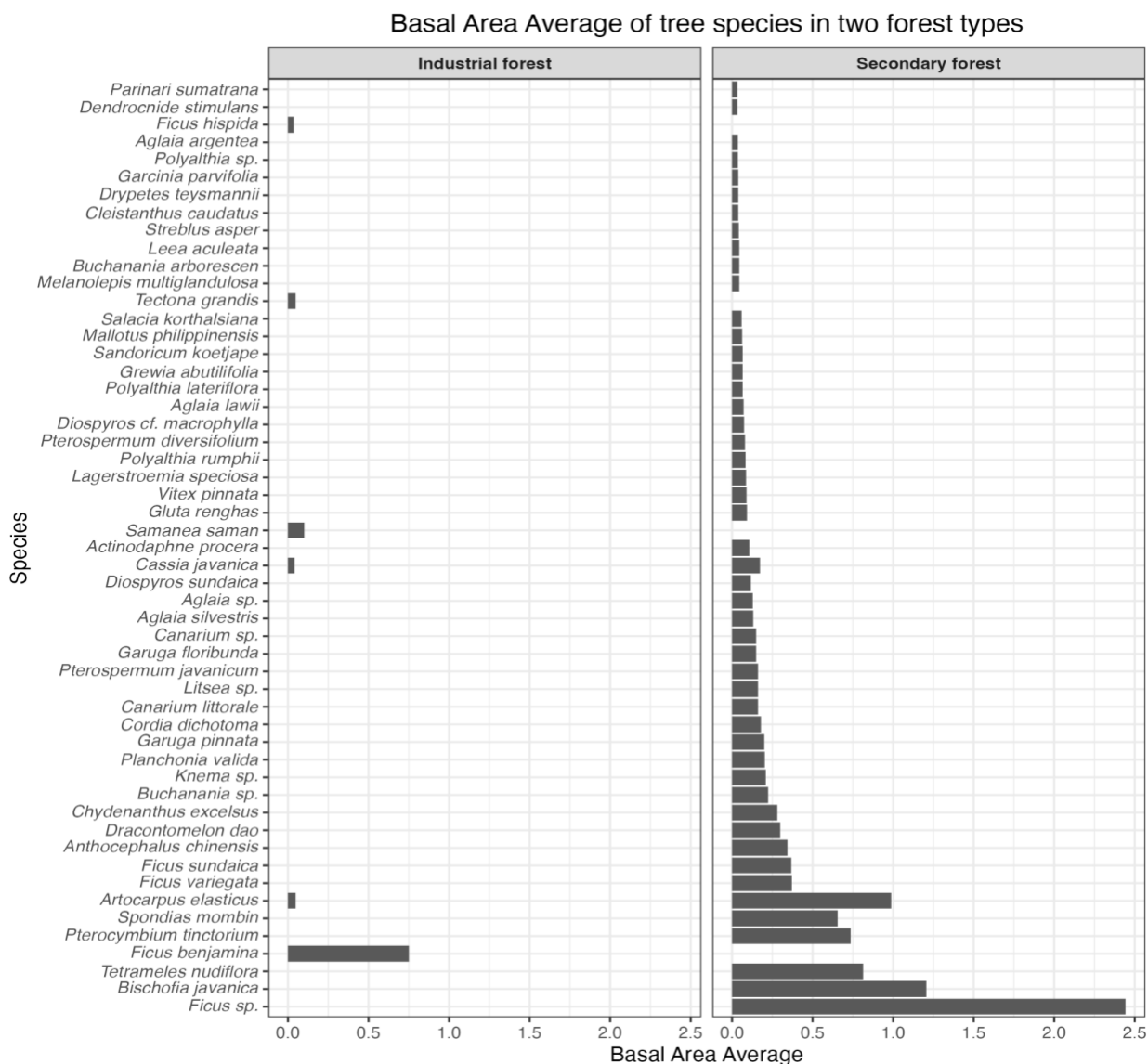


Figure 3. Basal Area of Tree Species between Secondary and Industrial Forests

There were 49 tree species found in the secondary forest while there are only 6 tree species in industrial forests (Figure 3). As the stark difference is obvious, the analysis also shows that ecosystem type significantly influenced basal area ($F_{1,1144} = 8.84$, $p = 0.003$), with trees in secondary forest exhibiting higher mean basal area than those in the industrial ecosystem. Species identity also had a strong effect on basal area ($F_{76,1068} = 17.62$, $p < 0.001$), indicating substantial variation in tree size among species. Several species exhibited particularly large basal areas relative to the reference species, including *Ficus* sp., *Artocarpus elasticus*, *Tetrameles nudiflora*, *Spondias mombin*, *Pterocymbium tinctorium*, and *Ficus benjamina*. These species therefore contributed disproportionately to forest structural dominance. In addition, estimated marginal means (effect size) indicated that basal area per species was substantially higher in secondary forest (0.162 ± 0.015 SE; 95% CI: 0.133–0.191) than in industrial forest (0.016 ± 0.049 SE; 95% CI: –0.080–0.111), averaged across species.

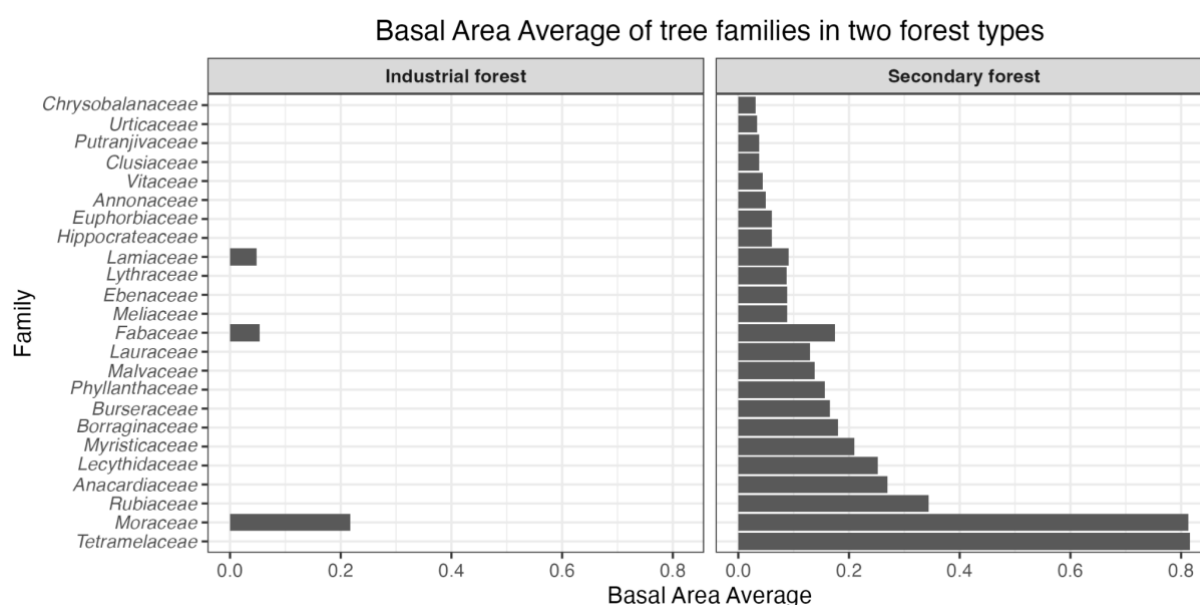


Figure 4. Basal Area of Tree Families between Secondary and Industrial Forests

Similar to the basal area per species data, where secondary forests have a higher species richness, there were 24 tree families found in the secondary forest while there are only 3 tree families in industrial forests (Figure 4). Corresponding to that, the basal area of trees differed significantly between ecosystem types and among taxonomic families. The generalized linear model with Gaussian error distribution showed that ecosystem type had a significant effect on basal area (GLM: $F = 4.36$, $p = 0.037$), with tree families in secondary forest exhibiting higher basal area than those in the industrial forest ($\beta = 0.087 \pm 0.036$ SE). Tree family also significantly influenced basal area ($F = 2.61$, $p < 0.001$), indicating substantial variation in basal area among families. Several families showed significant differences relative to the reference family (Lamiaceae). Basal area was significantly lower in families such as Annonaceae ($\beta = -0.167$, $p = 0.0019$), Ebenaceae ($\beta = -0.138$, $p = 0.027$), Euphorbiaceae ($\beta = -0.164$, $p < 0.001$), Phyllanthaceae ($\beta = -0.168$, $p < 0.001$), and Putranjivaceae ($\beta = -0.176$, $p = 0.0014$). In contrast, Tetramelaceae exhibited significantly higher basal area relative to the

reference family, Lamiaceae ($\beta = 0.637$, $p = 0.017$). Overall, the model explained a portion of the variation in basal area, reducing the deviance from 82.75 to 77.55, suggesting that both ecosystem type and taxonomic family contribute to differences in tree basal area across the study sites. Moreover, estimated marginal means (effect size) indicated that trees in secondary forests had a higher adjusted mean basal area (0.107 ± 0.025 SE) than those in industrial forests (0.019 ± 0.041 SE), averaged across families, with 95% confidence intervals of 0.057–0.157 and –0.060–0.099, respectively.

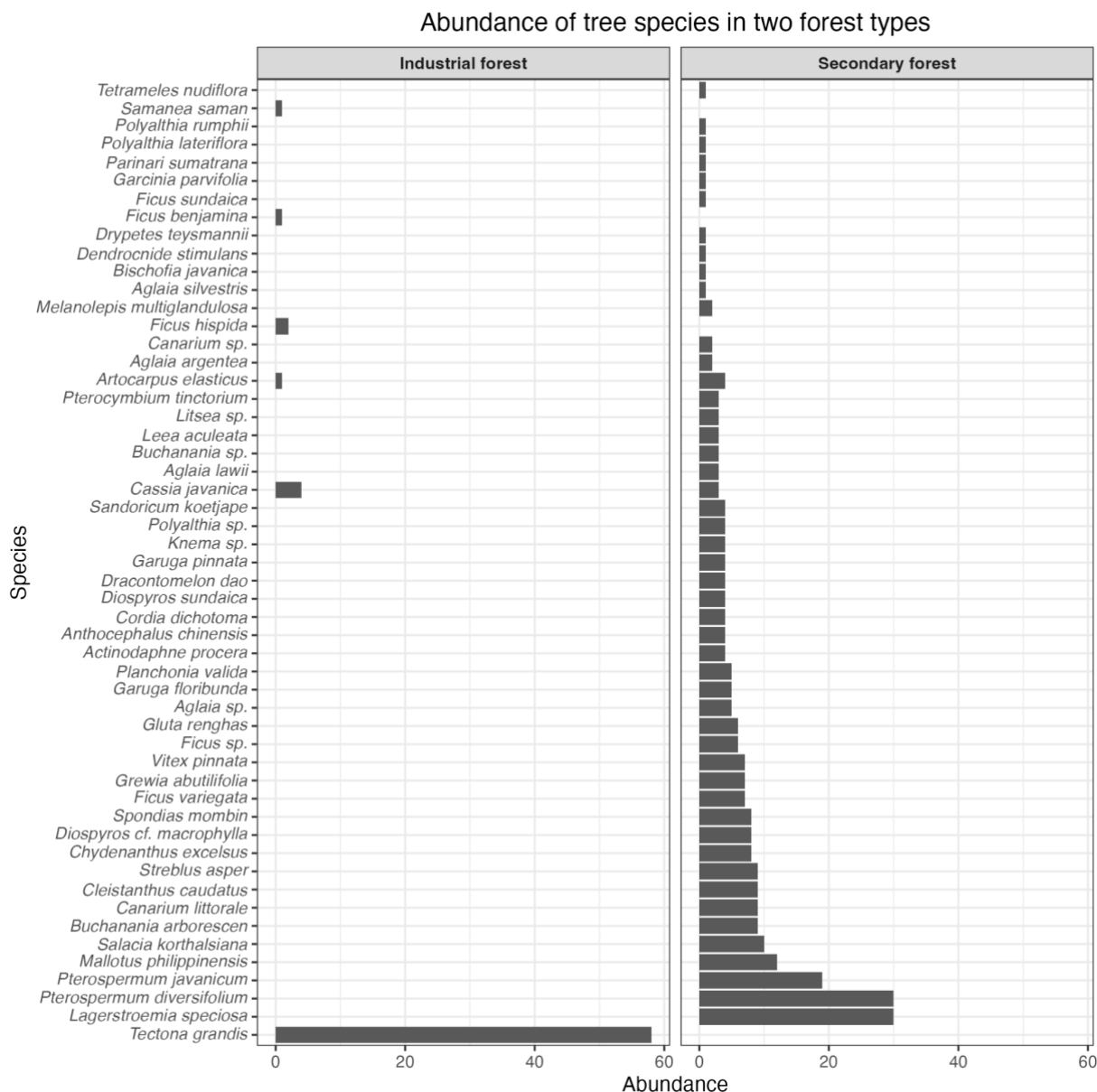


Figure 5. Abundance of Tree Species Between Secondary and Industrial Forests

Tree species abundance varied strongly among species (GLM, $\chi^2 = 2406.65$, $p < 0.001$). Ecosystem type had a marginal effect on abundance ($\chi^2 = 3.22$, $p = 0.073$), with higher predicted abundance in secondary forest compared with the reference ecosystem. Several species showed particularly high abundances, including *Tectona grandis*, *Cleistanthus caudatus*, and *Streblus spinosus* (Figure 5). In addition, tree community composition differed

significantly between ecosystem types (PERMANOVA, $F_{1,6} = 4.72$, $R^2 = 0.44$, $p = 0.041$), indicating distinct species assemblages between the two ecosystems.

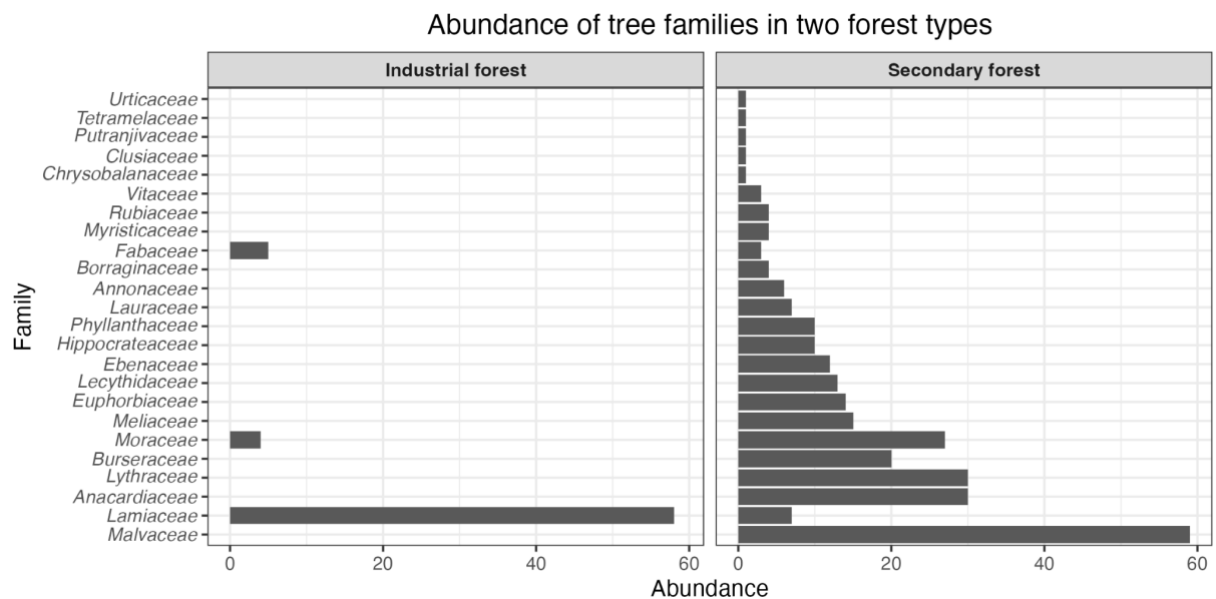


Figure 6. Abundance of Tree Families between Secondary and Industrial Forests

Plant family had a strong effect on abundance ($\chi^2 = 1610.23$, $df = 27$, $p < 0.001$), indicating substantial differences in abundance among families. In contrast, ecosystem type did not significantly influence tree abundance ($\chi^2 = 0.19$, $df = 1$, $p = 0.667$). Several families showed significantly higher abundances relative to the reference family, including Phyllanthaceae ($\beta = 1.77$, $SE = 0.16$, $p < 0.001$), Moraceae ($\beta = 0.71$, $SE = 0.17$, $p < 0.001$), Lamiaceae ($\beta = 0.77$, $SE = 0.17$, $p < 0.001$), and Malvaceae ($\beta = 0.37$, $SE = 0.18$, $p = 0.036$). Conversely, families such as Fabaceae, Rubiaceae, Rutaceae, Lauraceae, and Myristicaceae exhibited significantly lower abundances relative to the reference category (Figure 5).

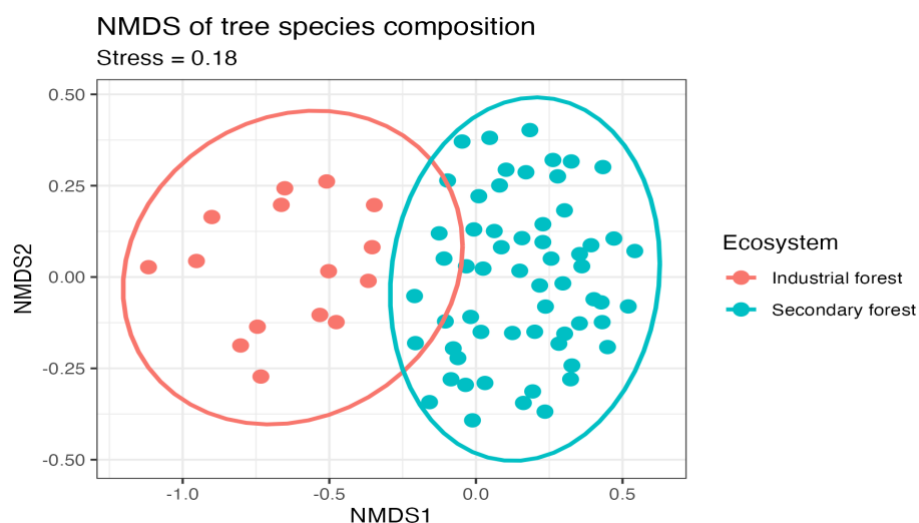


Figure 7. NMDS of Tree Species Composition

(The Ellipse Groupings for Each Ecosystem Typology is Based on A 95% Confidence Interval)

The NMDS ordination based on Bray–Curtis dissimilarity revealed variation in plant community composition among plots (stress = 0.12). Plots from secondary forest tended to cluster separately from those in industrial forest, indicating differences in species composition between ecosystems (Figure 7). Plant community composition differed significantly between ecosystems based on Permutational Multivariate Analysis of Variance (PERMANOVA) using Bray–Curtis dissimilarity. The analysis showed that ecosystem type explained 14.4% of the variation in species composition among plots ($R^2 = 0.144$), and this effect was statistically significant ($F_{1,73} = 12.28$, $p = 0.001$). The remaining 85.6% of the variation in plant community composition was attributed to within-ecosystem variability and other unmeasured factors.

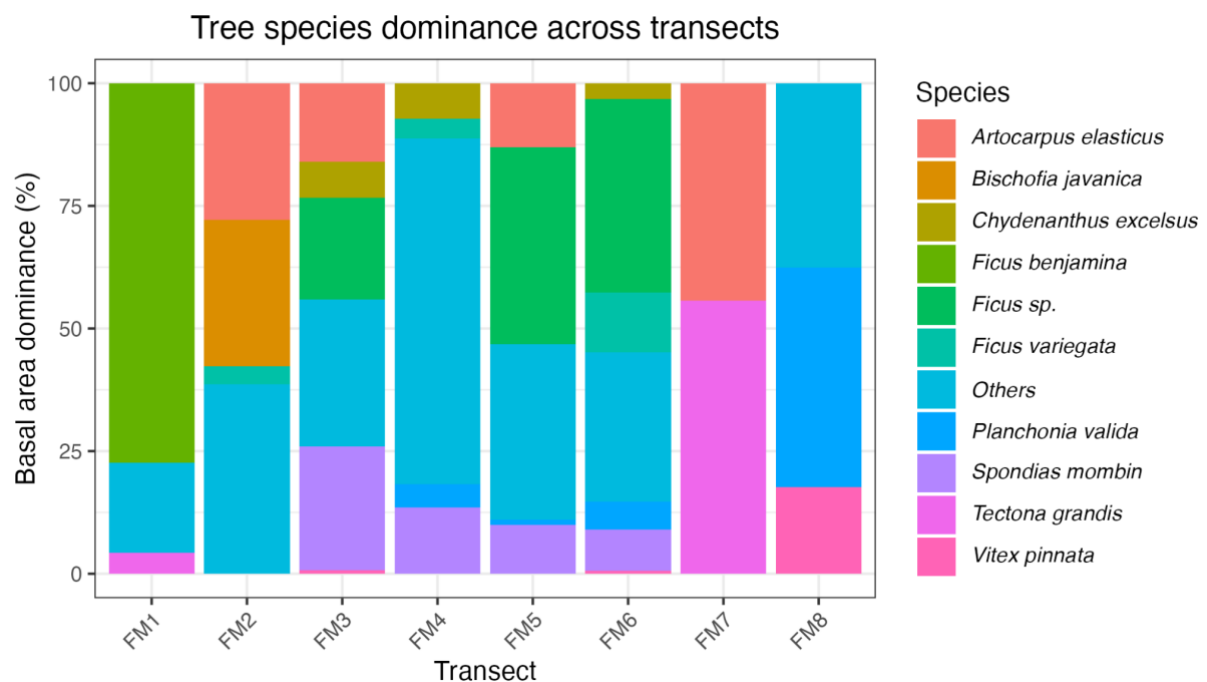


Figure 8. Tree Species Basal Area Dominance across Transects

Basal area dominance varied significantly among transects and tree species (Figure 7). Analysis of deviance indicated that transect identity significantly influenced dominance values ($F = 3.16$, $p = 0.025$), suggesting spatial variation in basal area distribution across sampling transects. Tree species identity had a stronger effect on dominance ($F = 6.09$, $p < 0.001$), indicating that dominance patterns were largely determined by species-specific differences in basal area contribution. In addition, several species showed notable dominance relative to the reference species. In particular, *Ficus benjamina* exhibited significantly higher dominance (Estimate = 79.20, $p < 0.001$). The aggregated category "Others" also showed a significant positive effect on dominance (Estimate = 18.34, $p = 0.036$). In contrast, most other species did not show statistically significant differences from the reference species.

Association between hornbills and tree composition and diversity

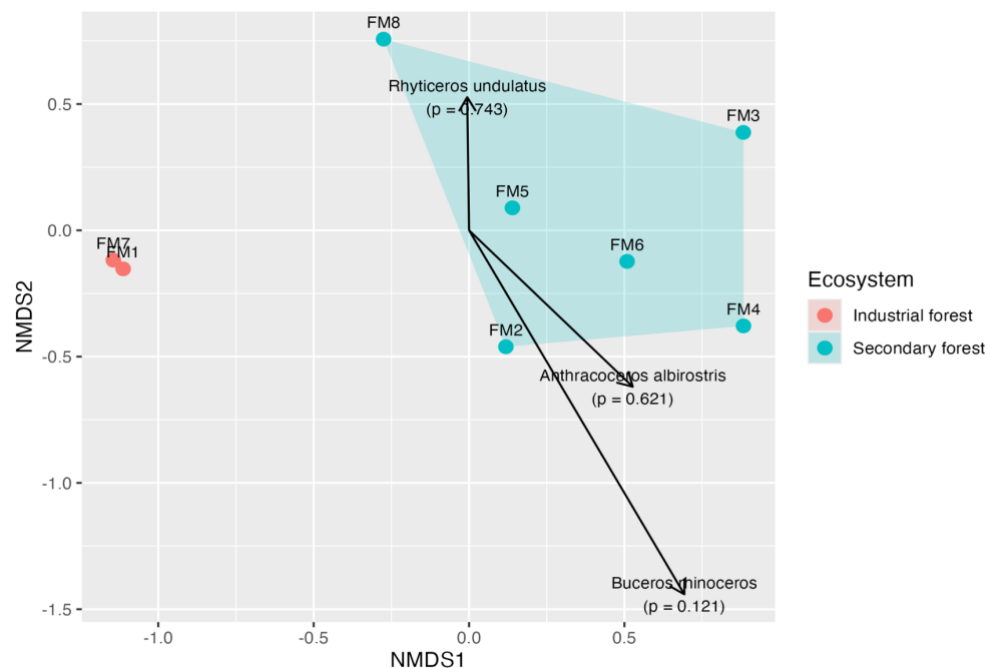


Figure 9. Association Between Hornbill Abundance and Tree Composition

There was no significant correlation and relationship between hornbill abundance and plant abundance (Figure 9). The Spearman rank correlation analysis showed a correlation coefficient close to zero ($\rho = -0.013$), indicating virtually no monotonic relationship between the two variables. The relationship was not statistically significant ($p = 0.976$), suggesting that variation in plant abundance did not correspond with variation in hornbill abundance across the sampled sites. Similarly, the linear regression analysis showed that the effect of plant abundance on hornbill abundance was not significant ($\beta = -0.007 \pm 0.014$ SE, $t = -0.52$, $p = 0.623$). The overall model was also not significant ($F_{1,6} = 0.27$, $p = 0.623$), and explained only a small proportion of the variance in hornbill abundance ($R^2 = 0.043$).

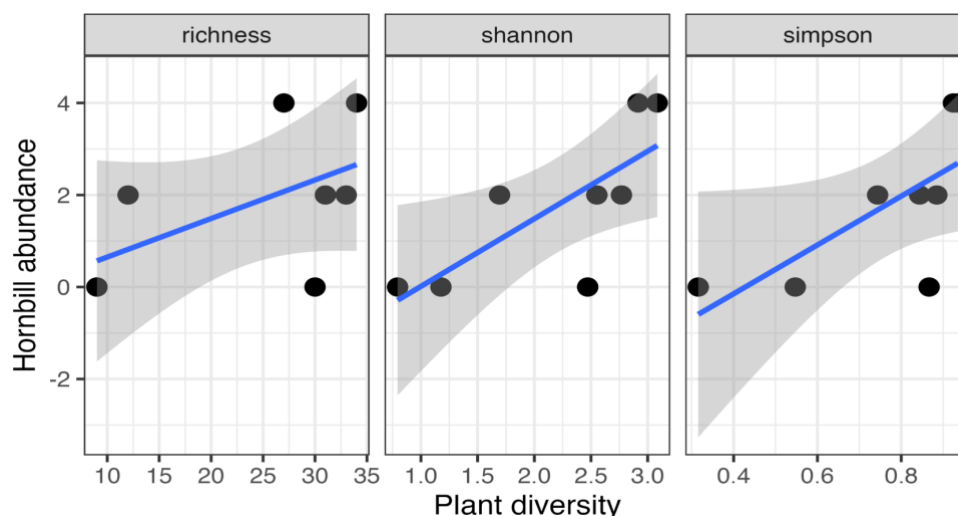


Figure 10. Correlation Between Hornbill Abundance and Tree Diversity.
The Grey Shade Is Based On A 95% Confidence Interval

However, when the analysis focuses on the correlation and relationship between hornbill abundance and plant diversity, we found that hornbill abundance showed a varied association with plant species richness metrics (Figure 9). Hornbill abundance was strongly positively correlated with plant diversity measured using the Shannon index (Spearman's $\rho = 0.87$, $p = 0.005$). A similarly positive relationship was observed with Simpson diversity ($\rho = 0.79$, $p = 0.019$). In contrast, plant species richness alone was not significantly correlated with hornbill abundance ($\rho = 0.61$, $p = 0.11$).

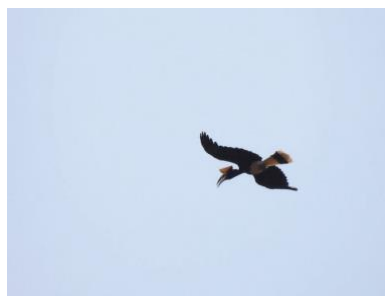
Among the three diversity metrics tested, only Shannon diversity showed a significant positive relationship with hornbill abundance ($\beta = 1.47 \pm 0.53$ SE, $p = 0.032$), explaining 56% of the variation in hornbill abundance ($R^2 = 0.56$). Simpson diversity showed a marginally positive relationship ($p = 0.056$), whereas species richness alone did not significantly predict hornbill abundance ($p = 0.152$).

DISCUSSION

Hornbill abundance is similar across sites



Anthracoceros albirostris



Buceros rhinoceros



Rhyticeros undulatus

Figure 11. Hornbills spotted in the study sites

In the study sites, three hornbill species were observed: *Anthracoceros albirostris*, *Buceros rhinoceros*, and *Rhyticeros undulatus* (Figure 11). *A. albirostris* was recorded in higher numbers than any other hornbill species. In addition, *A. albirostris* is a medium-sized hornbill distributed throughout South and Southeast Asia (Lilik & Dedy, 2020). It inhabits lowland forests, mangroves, riverine forests, and occasionally disturbed habitats and plantations with remaining large trees (Franco & Minggu, 2019). The species is predominantly frugivorous, feeding on figs and other fruits, but also consumes insects, small vertebrates, and carrion opportunistically. As a mobile seed disperser, it plays a crucial ecological role in forest regeneration, particularly for large-seeded plants. It readily utilises forest edges and fragmented landscapes when suitable nesting trees are available (Liang et al., 2024; Yahya et al., 2024). Its prevalence across the sites suggests that it is highly adaptable and capable of thriving in the range of habitats surveyed. This species' generalist diet and ability to nest in a variety of substrates likely contribute to its status as the most abundant.

However, based on the GLM and effect size analysis, despite *A. albirostris* tended to have a higher abundance, these analyses indicate that there were no significant differences in abundance among species. The similar types of diets and habitat types might affect the similar

abundance among species. Similar to *A. albirostris*, *B. rhinoceros* is a canopy-dwelling hornbill native to the lowland and hill forests of Southeast Asia. It relies heavily on primary and mature secondary forests with large emergent trees for nesting. Its diet consists mainly of fruit (especially figs), supplemented by insects, reptiles, and small birds (Borode, 2024). This species functions as a keystone seed disperser, capable of transporting large seeds over extended distances, thereby contributing significantly to tropical forest dynamics and plant recruitment (Naniwadekar et al., 2019).

Similarly, *R. undulatus* is a hornbill found in evergreen and semi-evergreen forests across South and Southeast Asia. It frequently travels in flocks and undertakes seasonal movements in response to fruit availability (Ramel, 2025). The species primarily feeds on fruit, particularly figs and other canopy fruits, but also consumes small animals such as insects and reptiles (Lamperti et al., 2014). Due to its extensive daily movement distances and flocking behaviour, it is considered an important long-distance seed disperser, facilitating the connection of forest patches across the landscape (Naniwadekar et al., 2015).

It is essential to clarify that the survey did not document the complete absence of all hornbill species across the entire study area. Rather, no hornbill of any species was observed at three specific locations: site 1, site 3, and site 7. The conditions or resources at these particular sites appear to be unsuitable for supporting any hornbill populations. This patchy distribution underscores that hornbills exhibit selective habitat preferences and are not uniformly distributed across the landscape. Previous research, Hamzah et al., (2024) showed that the distribution of hornbills was dominated by clumped related to availability of primary resources, such as fig trees as nesting sites and mayflies as food resources. The availability of primary resources is a priority for hornbills to reproduce and survive in their habitat. In stark contrast to the absence of hornbills at these sites, two locations emerged as significant hotspots for hornbill activity and abundance. Site 2 and site 5 recorded the highest numbers of hornbills, indicating that they provide optimal foraging or nesting conditions. The density of birds observed at these sites was considerably greater than at any of the other surveyed locations. These sites likely feature key resources such as abundant fruiting trees or suitable large cavities for nesting.

Tree basal area, abundance, and composition across ecosystem types

Basal area

Forest structure differs between primary and secondary forests. Secondary forests exhibit a higher basal area, indicating larger trunk diameters and more mature tree growth. This suggests fundamental structural differences in the storage of woody biomass. Secondary forests have been shown to contain twice as many tree species as plantation plots of the same age, as well as a higher basal area. They are capable of natural regeneration and are prior to plantations forests in terms of species diversity (Nichol & Abbas, 2021).

Tree size distribution varies among species, with a few dominant species accounting for the majority of structural biomass. These dominant species are typically large, emergent trees belonging to genera such as *Ficus* and *Tetrameles*. Their physical dimensions influence basal area and forest architecture. Native *Ficus* have an important role in the forest landscape in maintaining the frugivorous fauna community due to production of abundant amounts of fruit

each year and providing places for vertebrates to roost for shelter and nesting (Raji & Downs, 2022). Ficus trees are key species whose presence can influence other species, including hornbills. The ficus species preferred by hornbills are typically characterized by its ripe, purplish-red fruit, high water content, and large size (Pratama et al., 2021).

From a family level taxonomic standpoint, Ficus species within the Moraceae family dominate basal area in both forest types. The Moraceae family is followed by the Tetramelaceae family, indicating a consistent biomass contribution hierarchy. Trees from the Moraceae family play a pivotal ecological role in both ecosystems, particularly in secondary forests, where their substantial girth contributes significantly to basal area. The presence of ficus trees in forests demonstrates a consistent biomass contribution to the environment, animals, and humans. Ficus trees can serve as environmental indicators and solutions for plant restoration (Qayim & Chikmawati, 2022). Ficus species support forest balance, which can impact the biosphere by providing food and shelter. *Ficus racemosa* has a single root system as stores water and maintains slope balance. This tree also provides extensive green roofs, maximizing carbon dioxide absorption (Sharmila & Jalindarnath, 2025). The consistent observation of larger tree basal areas in secondary forests, despite variations among tree families, suggests that these forests support greater woody biomass per unit area. This implies distinct habitat structures and carbon storage capacities compared to industrial forests, underscoring their unique ecological values.

Abundance

In general, the trend of the tree basal areas across ecosystem types is similar to those of tree abundance. Tree assemblages differ markedly between the two ecosystem types, with secondary forests exhibiting significantly higher tree species and family diversity. This pattern is consistent with successional theory, which posits that secondary forests, regenerating after disturbance, often pass through an initial phase of high species richness as they recover (Nichol & Abbas, 2021). The increased diversity in these areas likely results from a combination of factors, including a wider array of niche opportunities from past land use, and the stochastic recruitment of a variety of pioneer and early-successional species from the surrounding landscape (Gee et al., 2025).

The species composition of the tree communities in the two forest types is, in general, non-overlapping, indicating a fundamental shift in community structure. This floristic dissimilarity suggests that each ecosystem supports a distinct species assemblage, with little species interchange between them. Such compositional turnover, or beta diversity, implies that the two forests represent discrete community types, each potentially governed by a unique set of environmental filters or successional trajectories that prevent the widespread establishment of species from the other ecosystem. Despite the largely different composition, In both forest types, trees of the genus *Ficus* (Moraceae) hold a disproportionately large ecological importance, as evidenced by their dominance in total basal area. This metric indicates that while *Ficus* species may not be the most numerous individuals, they contribute the most to the overall above-ground woody biomass and physical structure of the forest. As a keystone genus, the prevalence of *Ficus* in terms of basal area underscores its critical role in providing resources,

such as fruits for frugivores, and in structuring the physical habitat across both disturbed and mature forest landscapes. Based on research by Raji & Downs (2022) it is stated that *Ficus* species as producers of abundant fruit throughout the year are also recorded as being able to facilitate other trees for the development of seedlings of other species even in disturbed conditions.

The vegetation community is overwhelmingly dominated by a select few plant families, namely Phyllanthaceae, Moraceae, Lamiaceae, and Malvaceae. Some of these families are the families of the tree species with the highest tree basal areas. This taxonomic concentration suggests that these families possess adaptive traits that confer a competitive advantage under the prevailing environmental conditions. Their dominance indicates that these families are likely to have a higher competitiveness relative to other less dominant families. For example, Phyllanthaceae, Moraceae, Lamiaceae, or Malvaceae. Based on the previous research, Aulia et al., (2026) shows that families are among the dominant vegetation communities used as food sources and nesting sites for hornbills in their natural habitat. The structures of these families are tall and large, suitable for hornbills to live in the wild as a breeding ground and shelter from predators.

Ecosystem type is the primary driver of community variation, explaining more than half of the compositional differences a strong ecological signal that underscores the distinctness of the two forest types. The distinct communities are a product of the unique ecological and historical contexts that define each ecosystem. In this case, industrial forests are highly influenced by active planting by humans for timber production. Under this controlled situation, the community variation is also suppressed. Meanwhile, the secondary forests are more influenced by natural processes such as natural regeneration, allowing more diverse community composition to thrive.

Variation across transects

Based on the tree dominance variation across transect results, it can be observed that species identity is the primary driver of basal area dominance. In this case, a few species, most notably *Ficus benjamina*, strongly dominate the forest structure, a pattern that is ecologically plausible given the unique biology of the genus. Large *Ficus* trees, including *F. benjamina*, often contribute disproportionately to total basal area in tropical forests due to their expansive crowns and massive stems, which allow them to capture a larger share of resources (Almeida-Cerino et al., 2024). Furthermore, their significance extends beyond mere structure, as they function as keystone resources, producing asynchronous fruit crops that sustain frugivore populations, such as hornbills, during periods of general food scarcity (Sreenath, 2026). The structural dominance of this species thus has cascading effects on both the physical environment and the higher trophic levels within the ecosystem.

Hornbill abundance is associated with tree composition and diversity, not overall plant abundance

This result suggests that overall plant abundance alone does not explain variation in hornbill abundance in the study area. Hornbills may respond more strongly to specific plant

characteristics, such as the availability of fruiting tree species, nesting trees, or particular plant families, rather than total plant abundance. Similarly, the positive but non-significant relationship suggests that more diverse plant communities may provide more resources or habitat heterogeneity for hornbills, potentially supporting higher abundances. However, the lack of statistical significance indicates that plant richness alone may not be sufficient to explain hornbill distribution, and other factors such as fruiting tree availability, nesting tree presence, or forest structure may play a more important role.

Many hornbill species rely on forest trees that provide both food resources and suitable habitat structures. The three species considered here *Anthracosceros albirostris*, *Buceros rhinoceros*, and *Rhyticeros undulatus* are predominantly frugivorous and depend heavily on fruiting trees in tropical forests. Among the recorded tree families, several are known to produce fleshy fruits that constitute important components of hornbill diets. In particular, species within Moraceae, Myristicaceae, and Lauraceae are widely recognized as key food resources for hornbills in Southeast Asian forests (Mukhtadina et al., 2023). Figs (*Ficus* spp.) from Moraceae are especially important because they fruit asynchronously throughout the year and provide a reliable food supply for large frugivores (Walther et al., 2017). Other families such as Annonaceae, Burseraceae, Anacardiaceae, Ebenaceae, Rubiaceae, and Vitaceae also produce fleshy fruits that may be consumed by hornbills, although their importance may vary depending on local fruit availability and forest composition.

In addition to providing food, several tree families contribute important structural habitat for hornbills. Large emergent trees within families such as Meliaceae, Malvaceae, Fabaceae, Tetramelaceae, and Lecythidaceae can develop natural cavities that are essential for hornbill nesting and roosting (Aulia et al., 2026). Hornbills are secondary cavity nesters and depend on large, mature trees with suitable hollows for reproduction, making the presence of these structural tree species an important component of suitable habitat (Pawar et al., 2016). Other families in our observation, including Euphorbiaceae, Phyllanthaceae, and Clusiaceae, may provide additional food resources or perching sites but are generally considered to play a more supplementary role (Fitriansyah et al., 2022; Aulia et al., 2026). Collectively, the presence of diverse fruiting trees and large canopy species is likely to enhance habitat suitability for hornbills by supporting both their dietary requirements and nesting ecology.

In terms of the association between hornbill abundance and plant community diversity, it was found that hornbill abundance was positively associated with plant community diversity, as measured by the Shannon index, but not with plant species richness alone. This suggests that hornbills respond not only to the number of plant species present but also to the evenness and structure of the plant community. Forests with higher Shannon diversity likely contain a more balanced distribution of plant species, which may increase the availability and temporal stability of food resources such as fruits and nesting sites. In addition, hornbills respond more strongly to overall plant community structure and evenness rather than simply the number of plant species present, which is supported by the finding of the previous research Nagendra (2002) stated that the abundance of a species can be calculated by community diversity using the Shannon Index which places more emphasis on the richness and rare species components, while the Simpson Index takes into account the same and dominant components in a habitat.

Despite these patterns, the results should be interpreted with caution due to the limited number of sampling transects, which reduces statistical power and may limit the detection of ecological relationships. Future studies incorporating larger spatial scales and additional ecological variables, such as fruiting phenology, availability of key hornbill food trees, and forest structural attributes, would provide a more comprehensive understanding of the factors influencing hornbill abundance.

CONCLUSION

In conclusion, this study reveals a complex interplay between forest structure, tree community composition, and the distribution of hornbill populations in tropical forest landscapes near active mining sites. The persistent dominance of the genus *Ficus*, particularly *Ficus benjamina*, in terms of basal area across both primary and secondary forests underscores its crucial role as a keystone resource in these disturbance-prone environments. The structural dominance of such species, which provide abundant asynchronous fruit crops and large canopy frameworks, is likely a key factor supporting hornbill populations despite the anthropogenic pressures of nearby mining activities, especially considering the birds' reliance on fleshy fruits and large trees for nesting cavities. However, the patchy distribution of hornbills, marked by complete absence at some sites and high abundance at others, suggests that total tree abundance or simple species richness are not the sole predictors of habitat suitability in these modified landscapes. Instead, the positive association with plant community diversity (Shannon index) and the likely concentration of specific fruiting and nesting families (e.g., Moraceae, Meliaceae) at hotspot sites indicate that hornbills selectively persist in habitat patches that retain sufficient structural complexity and resource availability despite proximity to mining disturbances. This highlights that the ecological value of forests adjacent to mining concessions is not solely determined by the number of trees, but rather by the presence of key structural species and a diverse, resource-rich plant community that can buffer against the impacts of habitat alteration and support essential ecological functions such as seed dispersal. Therefore, conserving hornbills species requires preservation of the associated tree species providing food resources and nesting habitats.

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