*Media Konservasi, 28 (3) 262-272*

RESEARCH ARTICLE

MEDIA
KONSERVASI
SCIENTIFIC JOURNAL IN CONSERVATION OF NATURAL RESOURCES AND ENVIRONMENT

# Ecology of Hornbill Food Trees at Bukit Barisan Selatan National Park

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**Article Info:**
Received 26 June 2023,
Accepted 15 October 2023

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## Abstract

Hornbills play an important role in maintaining tree gene flow among fragmented populations in forests. But hornbill populations in Asia have been declining, mainly due to loss of forest cover and poaching. The presence of hornbills in a forest is highly dependent on environmental factors such as the condition of food trees in their habitat. The purpose of this study was to determine the spatial distribution, dispersion patterns, density, importance value index, and diversity of hornbill food trees at Sukaraja Atas Resort (SA) and Balik Bukit Resort (BB) of Bukit Barisan Selatan National Park (BBSNP). We investigated a total of 10 transects (50 survey plots) for both SA and BB by collecting data on all types of hornbill food trees with a minimum diameter of 10 cm at breast height (DBH). We recorded 64 hornbill food tree species with a total of 98 individuals, which have a clumped and uniform dispersion pattern. This study showed that Lauraceae dominated in both resorts with the highest relative density and importance value index. The results of the diversity index show that 9 transects have moderate diversity whereas 1 transect has low diversity; there was no significant difference between SA and BB. It can be concluded that the existing food trees in SA and BB may support the hornbill populations.

Keyword: composition, distribution, diversity, food tree, hornbill

## 1. Introduction

Hornbills (Bucerotidae) are important seed dispersers that have been referred to as the ‘farmers of the forest’. Their ability to disperse seeds efficiently has been well recorded and is crucial in maintaining forest regeneration [1]. Hornbills are also known to travel long distances and disperse seeds far away from the parent plants, thereby playing an important role in maintaining gene flow of trees among fragmented populations in forests as well as reducing seedling mortality due to competition under the parent trees [1–3].

Hornbills feed on fruits from a variety of tree species. According to [4,5], hornbill food trees consist of species from 21 families, namely Anacardiaceae, Apocinaceae, Annonaceae, Burseraceae, Combretaceae, Clusiaceae, Cucurbitaceae, Connaraceae, Ebenaceae, Elaeocarpaceae, Euphorbiaceae, Lauraceae, Magnoliaceae, Malvaceae, Meliaceae, Moraceae, Myristicaceae, Rubiaceae, Salicaceae, Sapotaceae, and Symplocaceae. However, their diets may vary at the turn of the year and change of seasons due to changes in the diversity and abundance of food trees in their habitat.

Since the 1990s, hornbill populations in Asia have been declining mainly due to forest cover loss and hunting [1,6]. The occurrence of hornbills in a forest highly depends on environmental factors such as the distribution and forest size, habitat structure, and abundance of food trees [7–10]. It has been reflected on previous studies where isolation of food tree patches due to forest cover loss or fragmentation prevents food tracking behavior of avian frugivores which negatively affects their populations as well as the population of food trees through reduced seed dispersal [11].

Bukit Barisan Selatan National Park (BBSNP) is the third largest protected area in Sumatra and consists of various types of ecosystems, ranging from marine ecosystems to lowland and mountain rainforests. The high environmental heterogeneity gave rise to the high biodiversity in BBSNP and it is home to 8 hornbill species with population conditions tending to decline due to hunting pressure and habitat changes that damage the area [12]. One indication of population decline can be seen from changes in protection status in IUCN (The International Union for Conservation of Nature). There is one species with Critically Endangered (*Rhinoplax vigil*), one is Endangered (*Berenicornis comatus*), four are Vulnerable (*Buceros bicornis, Buceros rhinoceros, Anthracoceros malayanus,* and *Rhyticeros undulatus*), one is Near Threatened (*Anorrhinus galeritus*), and one is Least Concern (*Anthracoceros albirostris*) [13]. All hornbill species in Indonesia are protected by the Regulation of the Ministry of Environment and Forestry of the Republic of Indonesia Number P.106/MENLHK/SETJEN/KUM.1/12/2018.

Some of the strategies to conserve hornbills in BBSNP are to protect their habitat and ensure the availability of food trees as stated by Utoyo et al. [14] and Anggraini et al. [7]. Hornbill conditions will change according to environmental conditions which can be influenced by factors such as the availability of hollow trees as nest sites, food availability, and negative interactions with human activities in the area. To do this, it is required to know the ecology of hornbill food trees. So far, hornbill food trees have been well documented in Way Canguk Research Station (WCRS) in BBSNP but none have been documented in Sukaraja Atas and Bukit Balik Resort yet [12]. Therefore, it is necessary to conduct this research to add and fill the information gap related to hornbill food trees. This study aims to determine the spatial distribution, dispersion pattern, density, importance value index, and diversity of hornbill food trees in BBSNP.

## 2. Research Methodology

This research was conducted from August 5th to September 16th 2022, at Sukaraja Atas Resort (SA) and Balik Bukit Resort (BB), of Bukit Barisan Selatan National Park (BBSNP) (Figure 1) which has various types of ecosystems, namely marine ecosystems and terrestrial ecosystems which include coastal forests, lowland rainforests, mountain rainforests, low mountain rainforests, high mountain rainforests, mangrove ecosystems, swamp ecosystems, and estuarine ecosystems. This causes high biodiversity of plants in BBSNP by having 514 tree species that can be of the hornbill habitat [15].

BBSNP area has six species of endangered mammals, including *Elephas maximus*, *Dicerorhinus sumatrensis*, *Tapirus indicus*, *Panthera tigris*, *Helarctos malayanus*, *Cuon alpinus*. BBNSP is also home to 123 herpetofauna, 53 species of fish, 221 insects, and 450 species of birds [15].

The object of observation in this study are all types of hornbill food trees with a minimum diameter of 10 cm at breast height (DBH). The tools used to collect data were digital cameras, The Global Navigation Satellite System (GNSS) receiver is a Garmin GPSMAP 64s SEA, stationary, tally sheet, phi bands, rulers, sample bags, machete, and the Global Biodiversity Information Facility (GBIF) website to check food trees taxonomy.

Five transects were laid out in each resort using a purposive sampling method to anticipate dangerous terrains by discussing directly with the patrol team and assistants at SA and BB, i.e., SA-A, SA-B, SA-C, SA-D, SA-E, BB-A, BB-B, BB-C, BB-D, BB-E, with the distance between transects > 200 m (Figure 1). Within each transect, 5 observation plots of size 20 x 20 m were laid out with a 300 – 500 m distance between each plot (following the topographic conditions on the transect), bringing the total to 50 observation plots (Figure 2). Transects SA-C and SA-D are partially included in the Pemerihan Resort area in consideration of existing trails and the same topography as SA.

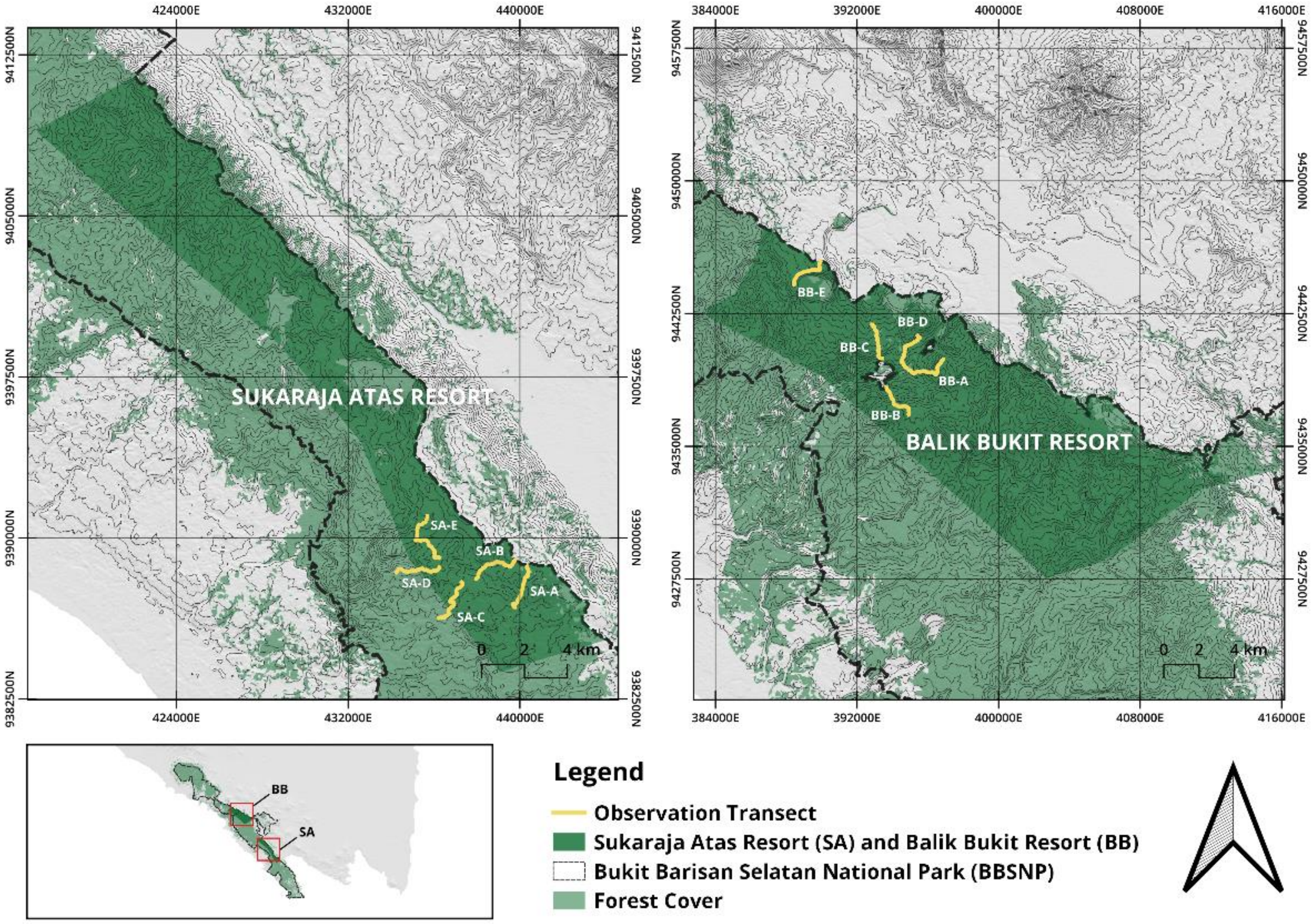

**Figure 1.** Map of study sites in Sukaraja Atas Resort (SA) and Balik Bukit Resort (BB) in BBSNP. Length of each transect (SA-A = 7977 m, SA-B = 8880 m, SA-C = 8022 m, SA-D = 8562 m, SA-E = 9921 m, BB-A = 8700 m, BB-B = 8016 m, BB-C = 7908 m, BB-D = 8403 m, BB-E = 7374 m)

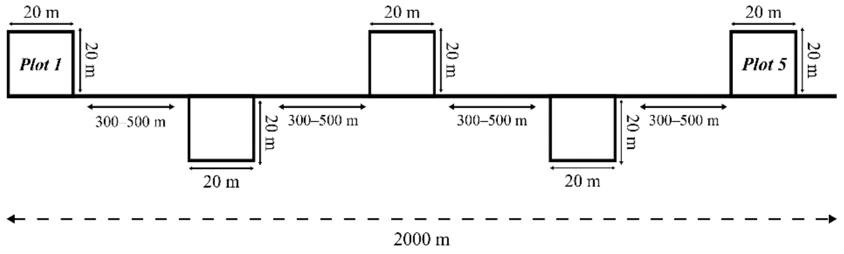

**Figure 2.** Transect and plot design used for data collection

Data collected included the species name of each tree, tree DBH, plot name, plot coordinates, plot precision on GPS, and plot elevation. Sorting of tree data included in the hornbill food tree species follows Fitriansyah et al and Hadiprakarsa and Kinnaird [4,5] research data. All raw data from the observation tally sheets in this study were entered and compiled in Microsoft Excel. Then, data cleaning, data visualization, and all statistical analyzes were carried out in RStudio 2022.12.0+353R.

### 2.1. Spatial Distribution Analysis

The coordinates of food trees were mapped using ArcGIS 10.8 (Esri, California, USA) and QGIS 3.26.3 (QGIS Development Team, Boston, USA) to show their distribution. The number of food trees per plot were counted at each plot and assigned to a category number of individual food trees in each plot. Plots with higher number of trees are represented with a darker shade in the distribution map (Figure 4 and Figure 5).

### 2.2. Dispersion Pattern Analysis

Vegan package [16] is used to calculate the standardized Morisita dispersal index to determine the distribution pattern of each hornbill food tree, the formula is as follows,

Morisita dispersion index (Id)

$$I_d = n\left[\frac{\sum x^2 - \sum x}{(\sum x)^2 - \sum x}\right] \quad (1)$$

where N defined as number of sampling plots, x defined as total of each type of organism per sampling plot, and $\sum x$ defined as total number of each type of organism. If $I_d$ = 1 it indicates a random dispersion, $I_d$ > 1 it indicates a clustered dispersion, and when $I_d$ < 1 it indicates a uniform dispersion [17].

The shape of the standardized dispersion pattern is obtained by calculating $M_u$ dan $M_c$.

Uniform index ($M_u$)

$$M_u = \frac{x^2_{0.975} - n + \sum x_i}{(\sum x_i) - 1} \quad (2)$$

Cluster index ($M_c$)

$$M_c = \frac{x^2_{0.025} - n + \sum x_i}{(\sum x_i) - 1} \quad (3)$$

Where $x^2_{0.975}$ as the value from the table with df (n-1) which has a confidence interval of 97.5%, $x^2_{0.025}$ as the value from the table with df (n-1) which has a confidence interval of 2.5%, $\sum x_i$ defined as number of organisms in the quadrat i (i = 1,...n), and notation $n$ defined as the sum of the quadrat.

Based on the results of $M_u$ or $M_c$, the standardized Morisita dispersion index ($I_p$) is calculated based on one of the four equations. If $I_d \geq M_c > 1$ then use the equation 1 $0.5 + 0.5\left(\frac{I_d - M_c}{n - M_c}\right)$, $M_c > I_d \geq 1$ use the equation $0.5\left(\frac{I_d - 1}{M_u - 1}\right)$, but $1 > I_d > M_u$ use the equation $-0.5\left(\frac{I_d - 1}{M_u}\right)$, and when $1 > M_u > I_d$ use the equation $-0.5 + 0.5\left(\frac{I_d - M_u}{M_u}\right)$.

The value of the standardized Morisita dispersion index ($I_p$) is in the interval [-1, 1] and with confidence limits of -0.5 and 0.5. If $I_p$ = 0 it indicates a random dispersion, $I_p$ > 0 it indicates a clustered dispersion, and $I_p$ < 0 it indicates a uniform dispersion [18].

### 2.3. Density and Importance Value Index Analysis

BiodiversityR package [19] is used to analyze the density and importance value index of food trees, with the following equations [20].

Density of food tree (D)

$$D = \frac{\sum \text{individuals of a family}}{\text{plot area}} \quad (4)$$

Relative density of food tree (RD)

$$RD = \frac{\text{Density of each family}}{\text{Density of all family}} \times 100\% \quad (5)$$

Importance value index (IVI)

$$IVI = RD + RF + RD' \quad (6)$$

Where RD as relative density, RF as relative frequency, and RD' as relative dominance.

### 2.4. Diversity Index Analysis

Vegan package [16] is used to analyze the Shannon-Wiener diversity index (H') [21], with the following equations:

$$H' = -\sum \frac{ni}{N} \log \frac{ni}{N} \quad (7)$$

where ni defined as number of individuals in one species and N as total number of individuals of all species found. The diversity index value is defined as low if H' < 1, moderate if 1 < H' < 3, and high when H' > 3.

## 3. Result and Discussion

### 3.1. Hornbill Food Tree Distribution

A total of 10 food tree families were found in SA, i.e., Lauraceae (1 *Litsea robusta*, 2 *Litsea umbellata*, four *Litsea* sp., and 6 unknown Lauraceae), Annonaceae (1 *Polyalthia macropoda*, 3 *Polyalthia* sp., and 2 unknown Annonaceae), Myristicaceae (1 *Myristica* sp. and 1 unknown Myristicaceae), Elaeocarpaceae (3 *Elaeocarpus glaber* and 5 *Elaeocarpus* sp.), Moraceae (1 *Ficus caulocarpa*), Burseraceae (1 *Canarium denticulatum*, 3 *Canarium* sp., 3 *Dacryodes rostrata*, and 3 *Dacryodes* sp.), Meliaceae (2 *Dysoxylum* sp.), Malvaceae (4 *Sterculia* sp.), Ebenaceae (2 *Diospyros* sp.), and 2 unknown Rubiaceae. Meanwhile, 9 food tree families were found in BB, i.e., Lauraceae (1 *Actinodaphne borneensis*, 1 *Alseodaphne* sp., 2 *Litsea robusta*, 4 *Litsea umbellata*, and 8 *Litsea* sp.), Magnoliaceae (1 *Magnolia* sp.), Myristicaceae (4 *Horsfieldia sucosa* and 4 *Horsfieldia* sp.), Elaeocarpaceae (1 *Elaeocarpus glaber* and 2 *Elaeocarpus* sp.), 1 unknown Euphorbiaceae, Moraceae (1 *Ficus obscura*, 1 *Ficus* sp. 1, and 1 *Ficus* sp. 2), Burseraceae (8 *Canarium* sp. and 2 *Dacryodes* sp.), Meliaceae (1 *Dysoxylum* sp.), and Ebenaceae (5 *Diospyros* sp.) (Figure 3). The distribution of hornbill food trees in SA is showed in Figure 4, and the distribution in BB is showed in Figure 5.

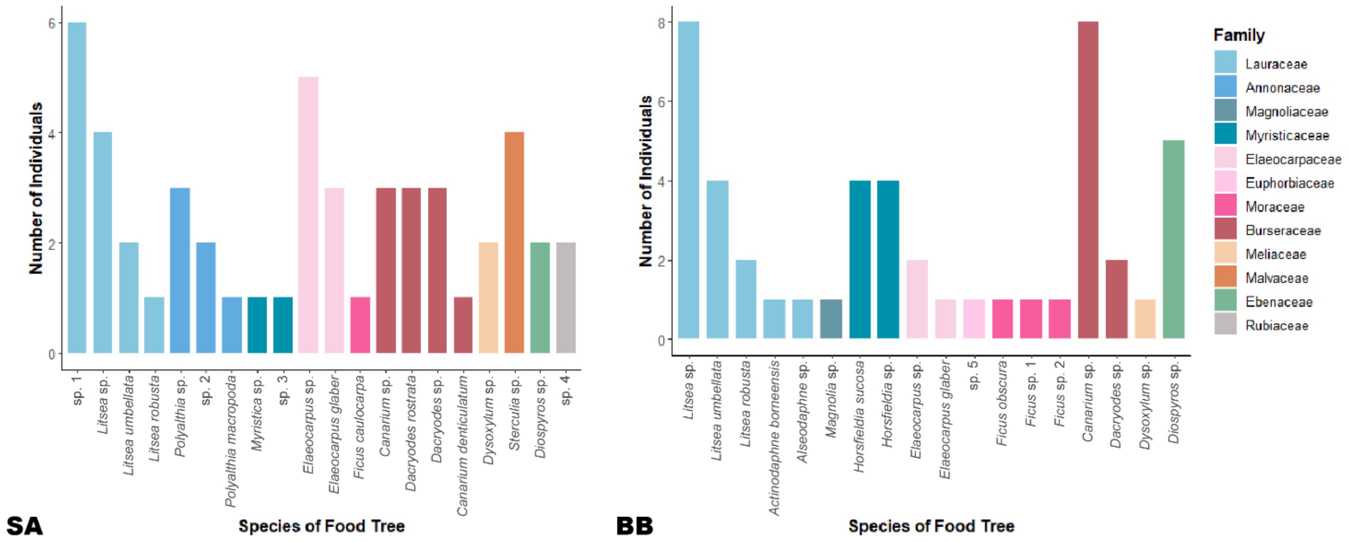

**Figure 3.** Composition of hornbill food trees in SA and BB. On sp. 1 belongs to Lauraceae, sp. 2 belongs to Annonaceae, sp. 3 belongs to Myristicaceae, sp. 4 belongs to Rubiaceae, and sp. 5 belongs to Euphorbiaceae

### 3.2. Hornbill Food Tree Dispersion Pattern

The results of the dispersion pattern analysis in the detected food tree families in SA show that 4 families have a clustered dispersion pattern, i.e., Annonaceae, Burseraceae, Lauraceae, and Malvaceae, while the other 4 families have a uniform dispersion pattern, i.e., Elaeocarpaceae, Meliaceae, Myristicaceae, and Rubiaceae (Table 1). Ebenaceae and Moraceae could not be analyzed due to a lack of detection during field data collection.

While analysis of the dispersion pattern of hornbill food tree families in BB shows 4 families with a clustered dispersion pattern, i.e., Burseraceae, Ebenaceae, Elaeocarpaceae, and Myristicaceae, on the contrary 2 families have a uniform dispersion pattern, i.e., Lauraceae and Moraceae (Table 2). Euphorbiaceae, Magnoliaceae, and Meliaceae could not be analyzed due to a lack of detection during data collection.

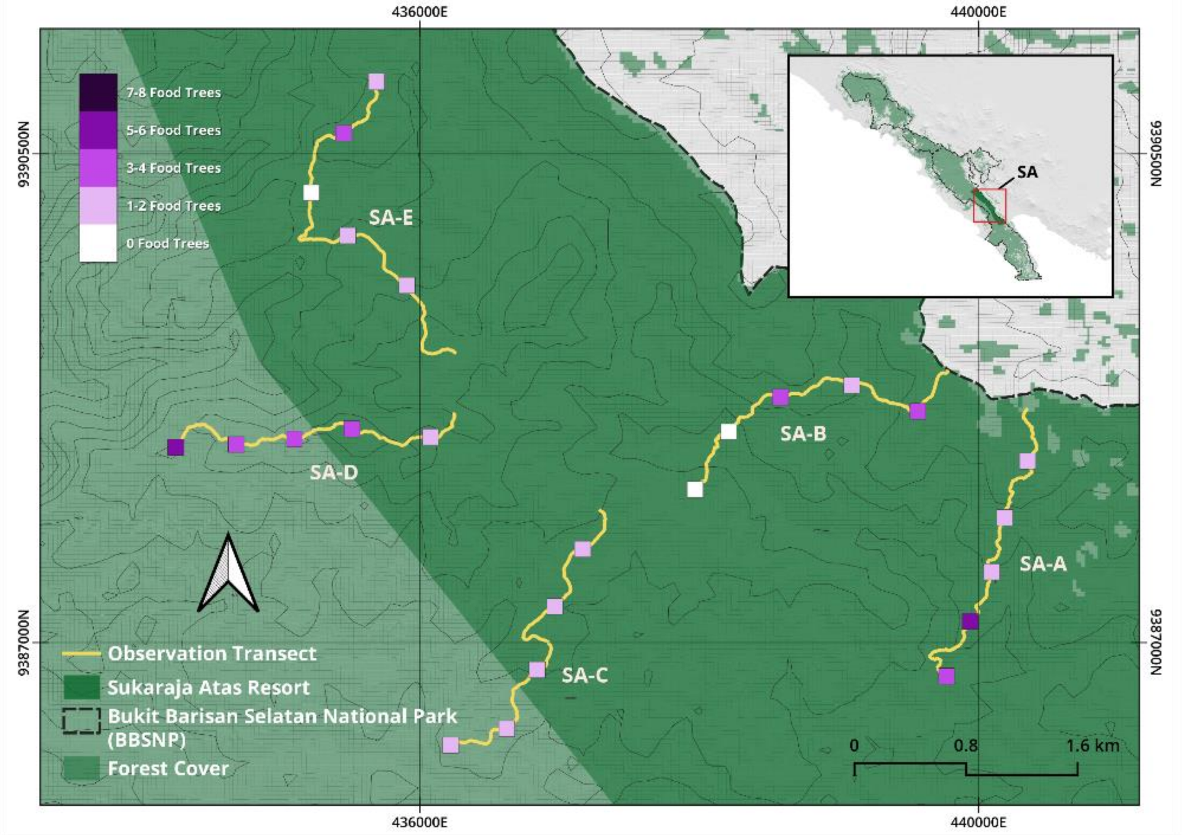

**Figure 4.** Number of hornbill food trees per plot in SA

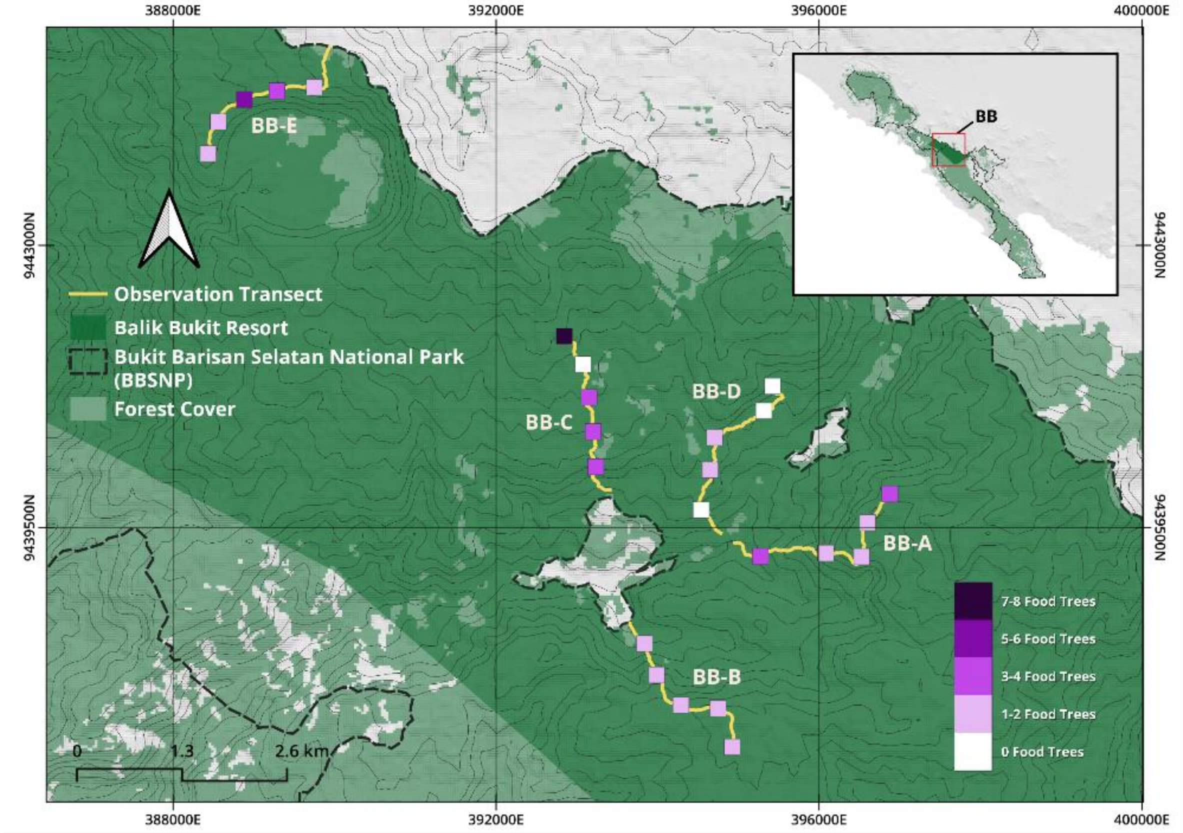

**Figure 5.** Number of hornbill food trees per plot in BB

**Table 1**. Dispersion pattern of hornbill food trees in SA

| Family | $I_p$ | Dispersion pattern |
|---|---|---|
| Annonaceae | 0.38 | Clustered |
| Burseraceae | 0.03 | Clustered |
| Elaeocarpaceae | -0.03 | Uniform |
| Lauraceae | 0.11 | Clustered |
| Malvaceae | 0.31 | Clustered |
| Meliaceae | -0.04 | Uniform |
| Myristicaceae | -0.04 | Uniform |
| Rubiaceae | -0.04 | Uniform |

Description: $I_p$ = Standardized Morisita dispersion index

**Table 2**. Dispersion pattern of hornbill food trees in BB

| Family | $I_p$ | Dispersion pattern |
|---|---|---|
| Burseraceae | 0.50 | Clustered |
| Ebenaceae | 0.56 | Clustered |
| Elaeocarpaceae | 0.47 | Clustered |
| Lauraceae | -0.10 | Uniform |
| Moraceae | -0.08 | Uniform |
| Myristicaceae | 0.38 | Clustered |

Description: $I_p$ = Standardized Morisita dispersion index

### 3.3. Density and Importance Value Index of Food Trees

The density, relative density, and importance value of hornbill food trees can be seen in Table 3. The relative density value of families in SA showed the highest value in Lauraceae (26%) and the lowest in the Moraceae (2%). In comparison, the relative density value of families in BB showed the highest value in the Lauraceae (33.33%) and the lowest in the Euphorbiaceae, Magnoliaceae, and Meliaceae (2.08%). The importance value index of families in SA showed the highest value in Lauraceae (80.05%) and the lowest in the Moraceae (4.56%), while the importance value index of families in BB showed the highest value in the Lauraceae (118.23%) and the lowest in the Meliaceae (5.35%).

### 3.4. Diversity of food trees

Species diversity analysis (Shannon-Wiener) of food trees in SA showed that all observation transects had moderate species diversity, while species diversity in BB showed that 4 observation transects had moderate species diversity and 1 transect (BB-D) had low species diversity (Table 4).

Based on the *t*-test of diversity index analysis for both resorts ($H'$ SA = 1.763 and $H'$ BB = 1.508) with 95% Confidence Interval (-0.480, 0.991), there was no significant difference between SA and BB (*t*-test = 0.841, degrees of freedom = 6.225, *p* = 0.431).

**Table 3**. Density value and importance value index of food trees

| Family | $D_x$ | $D_y$ | $RD_x$ | $RD_y$ | $IVI_x$ | $IVI_y$ |
|---|---|---|---|---|---|---|
| Annonaceae | 0.0006 | - | 12 | - | 27.30 | - |
| Burseraceae | 0.001 | 0.001 | 20 | 20.83 | 73.79 | 61.02 |
| Ebenaceae | 0.0002 | 0.0005 | 4 | 10.42 | 8.20 | 20.71 |
| Elaeocarpaceae | 0.0008 | 0.0003 | 16 | 6.25 | 53.39 | 16.32 |
| Euphorbiaceae | - | 0.0001 | - | 2.08 | - | 6.38 |

| Family | $D_x$ | $D_y$ | $RD_x$ | $RD_y$ | $IVI_x$ | $IVI_y$ |
|---|---|---|---|---|---|---|
| Lauraceae | 0.0013 | 0.0016 | 26 | 33.33 | 80.05 | 118.23 |
| Magnoliaceae | - | 0.0001 | - | 2.08 | - | 6.57 |
| Malvaceae | 0.0004 | - | 8 | - | 22.14 | - |
| Meliaceae | 0.0002 | 0.0001 | 4 | 2.08 | 10.27 | 5.35 |
| Moraceae | 0.0001 | 0.0003 | 2 | 6.25 | 4.56 | 14.58 |
| Myristicaceae | 0.0002 | 0.0008 | 4 | 16.67 | 10.28 | 50.83 |
| Rubiaceae | 0.0002 | - | 4 | - | 10.02 | - |

Description: $D_x$ = Density of SA, $D_y$ = Density of BB, $RD_x$ = Relative density of SA (%), $RD_y$ = Relative density of BB (%), $IVI_x$ = Importance value index of SA (%), and $IVI_y$ = Importance value index of BB (%)

**Table 4.** Diversity index value of food trees

| $Transect_x$ | $Transect_y$ | $H'_x$ | $H'_y$ |
|---|---|---|---|
| SA-A | BB-A | 2.138 | 1.465 |
| SA-B | BB-B | 1.550 | 1.332 |
| SA-C | BB-C | 1.550 | 1.936 |
| SA-D | BB-D | 2.101 | 0.637 |
| SA-E | BB-E | 1.475 | 2.168 |

Description: $Transect_x$ = Observation transect of SA, $Transect_y$ = Observation transect of BB, $H'_x$ = Diversity index of SA, and $H'_y$ = Diversity index of BB

### 3.5. Existing Food Trees to Support Hornbill Population

There were differences in the hornbill food tree composition and diversity, which might be due to the variation on land elevation; both SA (514 m elevation) and BB (930 m elevation) can be categorized as high land area. In SA, 10 families of food trees were found, while there were only 9 families of food trees in BB. These results are different from the previous studies in Way Canguk Research Station of BBSNP [22], a lowland area (0–100 m elevation) which detected 21 hornbill food tree families [4,5]. This can occur because there are different sampling efforts, in this study 50 sampling plots were made, while in Fitriansyah *et al*. (2022) research sampling was carried out on 200 plots. However, the food tree dispersion patterns in this study are in line with the results of Fitriansyah et al. [5] and Sumihadi et al. [23], which did not produce a random distribution pattern even though the research was conducted on different altitudes and habitat types.

Dispersion patterns in an organism cannot be separated from the interaction between biotic and abiotic elements, e.g., the characteristics of other associated organisms, availability and preference of food, weather, physical and chemical factors, and the unique reproductive arrangement of each species [24,25]. According to Nurjaman et al. [26], environmental factors such as altitude may affect plant species diversity, where according to Krebs [27], the interaction of various factors, e.g., time, spatial heterogeneity, competition, predation, environmental stability, and productivity of its constituent components results in different structures and species diversity.

According to Firdaus and Aunurohim [28], the condition of hornbills will closely related to the dispersion of food trees that serves as hornbill primary resources. Environmental conditions in an area can be seen through the dispersion pattern analysis since organisms and their environment depend to each other. If there is a disturbance in the organism or its environment, it will surely affect the structure of the community [29]. Based on the results of distribution, dispersion, density, and diversity of hornbill food trees on both resort (BB and SA), it could support the population of hornbill species. In line with Ardiantiono et al. [30], the presence of hornbills is closely related to the availability of food trees. Moreover, the number of hornbill detections is also influenced by the maturity level of the available food fruit. However, this research did not observe the maturity of the hornbill food fruit.

## 4. Conclusion

In this study, 10 families of hornbill food trees were detected in SA and 9 families in BB. The dispersion pattern of hornbill food trees in SA consisted of 4 families with clustered patterns and 4 families with uniform patterns, while in BB there were 4 families with clustered patterns and 2 families with uniform patterns. In both resorts, the dominance of the Lauraceae family (relative density and importance value index) was equally high. Diversity index values in all transects had moderate species diversity (SA-A = 2.138, SA-B = 1.550, SA-C = 1.550, SA-D = 2.101, and SA-E = 1.475) in SA and 4 transects had moderate species diversity (BB-A = 1.465, BB-B = 1.332, BB-C = 1.936, and BB-E = 2.168) and 1 transect had low species diversity (BB-D = 0.637) in BB. This study shows that the existing food trees may support the hornbill populations in both resorts. However, this result is far to conclude the good habitat for sustainable hornbill population. Therefore, further research is needed on sampling hornbill food trees by adding new sampling plots in the hope of enriching existing data, feeding behavior on food tree species, and inventory of the availability of hollow trees that can become hornbill nests.

## Author Contributions

**MRM**: Conceptualization, Methodology, Software, Investigation, Writing - Review & Editing; **NN:** Writing - Review & Editing, Supervision; **TVZ:** Writing - Review & Editing, Supervision; **LS:** Writing - Review & Editing, Supervision; and **LU:** Writing - Review & Editing, Supervision.

## Conflicts of interest

There are no conflicts to declare.

## Acknowledgements

We thank the authorities of Bukit Barisan Selatan National Park (BBSNP) for issuing our permission to access and survey the area (SIMAKSI No. SI. 35/T.7/BIDTEK/KSA/7/2022). This study was supported through 2022/2023 Research Fellowship Program (RFP) by Wildlife Conservation Society-Indonesia Program (WCS-IP). The authors would also like to thank the BBSNP and WCS field staff, i.e., Mr. Janjianto, Mr. Rahman Sudrajat, Mr. Kariyono, Mr. Widianto, Mr. Reli, Mr. Habzyi, Mr. Uncu, Mr. Wahyudin, Mr. Aan, and Mr. Kevin.

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