Ecological Questions 36(2025)1 http://dx.doi.org/10.12775/EQ.2025.006

Population structure and spatial patterns of trees in successional stages of tropical forest in Gia Lai, Vietnam

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Received: 21 August 2024 / Accepted: 27 September 2024

Abstract. Regeneration will determine the success of forest restoration and affect the sustainability of future forest ecosystems. Research has been conducted to evaluate the characteristics of the regeneration storey and their spatial distribution on the ground. The study has established 10 plots (100 m x 100 m) for secondary forests, 10 plots for old-growth forests. Sub-plots (2 m x 2 m) were set up systemically to investigate the regeneration. The results showed that 148 species in secondary forest and 130 species in old-growth forest were found. The number of families in the secondary forest was lower than in the old-growth forest by 3 families. The Simpson index of both forest states was high (0.9769 and 0.9799 respectively). Canonical correspondence analysis exposed that species composition of both species and families between the two types of stages was significant dissimilar. There were clear groups of species and families appeared together with similar frequency in plots proved by hierarchical classification. In both stages, the height frequency distribution was inverse-J shape forms. And these distributions were different in studied types. The good regeneration in two studies states of forests were 67.9% and 55.7%. Regeneration quality was significant associated with height and light classes. The number of regenerating trees generated in each 1-hectare plot of the secondary forest was almost twice that of the old-growth forest. In the secondary forest, most plots illustrated that the spatial pattern was random at all scales. Contrary, in the old-growth forest, the patterns were much more complicated.

Keywords: Kon Ka Kinh, old-growth, regeneration biodiversity, secondary, multivariate analysis.

1. Introduction

One of the vital elements that determine the success of forest restoration is regeneration (González-Rivas et al., 2009; Mudappa & Raman, 2010). Therefore, regeneration is also a core factor to cope with deforestation and degradation, a serious global problem, especially in Vietnam (Blanc et al., 2000; FSIV, 2009; Hung, 2018; Löf et al., 2019). Natural regeneration is an inexpensive and effective way of forest restoration (Löf et al., 2019). Importantly, regeneration determines the quantity, quality, and composition of tall trees in future forest successions (Elliott et al., 2008; Pare et al., 2009). However, one difficulty for successful regeneration-based forest restoration is the shortage of regeneration material (Cernansky, 2018; Löf et al., 2019). This provides challenges for selecting species and planting sites for different forest restoration purposes (Löf et al., 2019). The literature on regeneration population change and spatial patterns is limited and effects of human activity on regeneration composition and spatial distribution are scarce (Pare et al., 2009). However, these understandings are important bases for forest restoration and management strategies (P. X. Hoan & Ngu, 2003; Pare et al., 2009).

Regeneration species biodiversity is an important element of forest ecosystems (Rennolls & Laumonier, 2000), but it is in severe degradation (Quyen, 1998; Sukara, 2014). Illegal logging, hunting, firewood collection and non-timber forest product harvesting are factors that reduce regenerative biodiversity, especially in Vietnam (P. X. Hoan & Ngu, 2003; Van Thinh et al., 2015). In addition, many factors affect the quality and quantity of regeneration such as seed source, slope, aspect and soil moisture (Pare et al., 2009; Vieira & Scariot, 2006), or competition for water, light, nutrients and space (González-Rivas et al., 2009; Pare et al., 2009). Therefore, regeneration biodiversity varies greatly from site to site. Species present, their relative abundance, and species composition are the main constituents used to assess forest biodiversity (Rana & Gairola, 2009; Van Thinh et al., 2015). Increasing regeneration success will reduce the risk of loss of species in forests (Strassburg et al., 2016). Furthermore, the diversity of tropical forests, including regeneration, is a source to provide food, health, energy and mitigate negative effects of climate change (Sukara, 2014). Understanding diversity is vital for effective forest management, as well as appreciating the history, function and future of forest ecosystems (Spies, 1998; Van Thinh et al., 2015).

Vietnam has about 12,000 species of plants and is ranked 16th in terms of biodiversity in the world (Quyen, 1998). However, in Vietnam, a small number of studies on biodiversity and spatial distribution of the regeneration storey have been conducted, mainly in the North (Dung, 2000; Hai, 2009; Huu, 2013) and in the Central Highlands (Hung, 2016; Nhung, 2012) for different forest objects such as: evergreen broadleaved forests with *Castanopsis piriformis* in Dak Nong (Thang et al., 2015), moist subtropical evergreen closed forests in Bidoup-Nui Ba national park, Lam dong province (Quang & Minh, 2011), secondary forests in Phi Lieng protection area, Lam Dong province (Nhung, 2012), mixed evergreen broad and needle leaf forest type in Bidoup - Nui Ba national park, Lam Dong province (Binh, 2014). Studies are principally based on establishing 5 sub-plots in each main plot: 4 sub-plots in the four corners and 1 sup-plot in the center (Dien et al., 2010; Dung, 2000). There are no studies that have established multiple sup-plots in a systematic form to assess regeneration biodiversity. In particular, in Kon Ka Kinh national park, Gia Lai, there are no studies on their regeneration and spatial distributions. Therefore, this study will contribute to fill scientific information gaps in regeneration diversity and spatial distribution patterns in Central Highland, Vietnam. The specific objectives of the study are to: i) analyze regeneration characteristics and compare them in two different stages of secondary and old-growth forests in terms of biodiversity, height distribution, quality and relationships with height and light classes; ii) examine and compare the spatial distribution characteristics of the regeneration stratum under the two studied forest types in Kon Ka Kinh national park, Gia Lai province. Findings of this study will be very meaningful for the management and restoration of poor natural forests in the study area in the future.

2. Materials and methods

2.1. Study area description

Kon Ka Kinh National Park was established in 1986 with 41,780 ha in Gia Lai province, Central Highlands of Vietnam. It was selected to conduct this study. The park spreads from 14°09' to 14°30' North latitude and from 108°16' to 108°28' East longitude (Fig. 1). The terrain here has an elevation above sea level of 600 - 1700 m. The study area is influenced by tropical monsoon climate. It has two seasons, a rainy season (May to November) and a dry season (December to April next year). Annually, the park receives an average rainfall of 2000-2500 mm (Bui et al., 2023). The study area has a relatively low average temperature, ranging from 21 °C to 25 °C. The average humidity of the air here is 80%. The entire area of the park is covered with feralit soil. There is not much variation in soil type between different areas of the park. The forests here are evergreen broadleaf forests (Thien et al., 2024). Kon Ka Kinh national park has over 1,754 plant species, of which 22 are listed in the Red Book of Vietnam and the world. (Nguyen Van Hoan, 2013; N. V. Hoan, 2014; Trai et al., 2000).

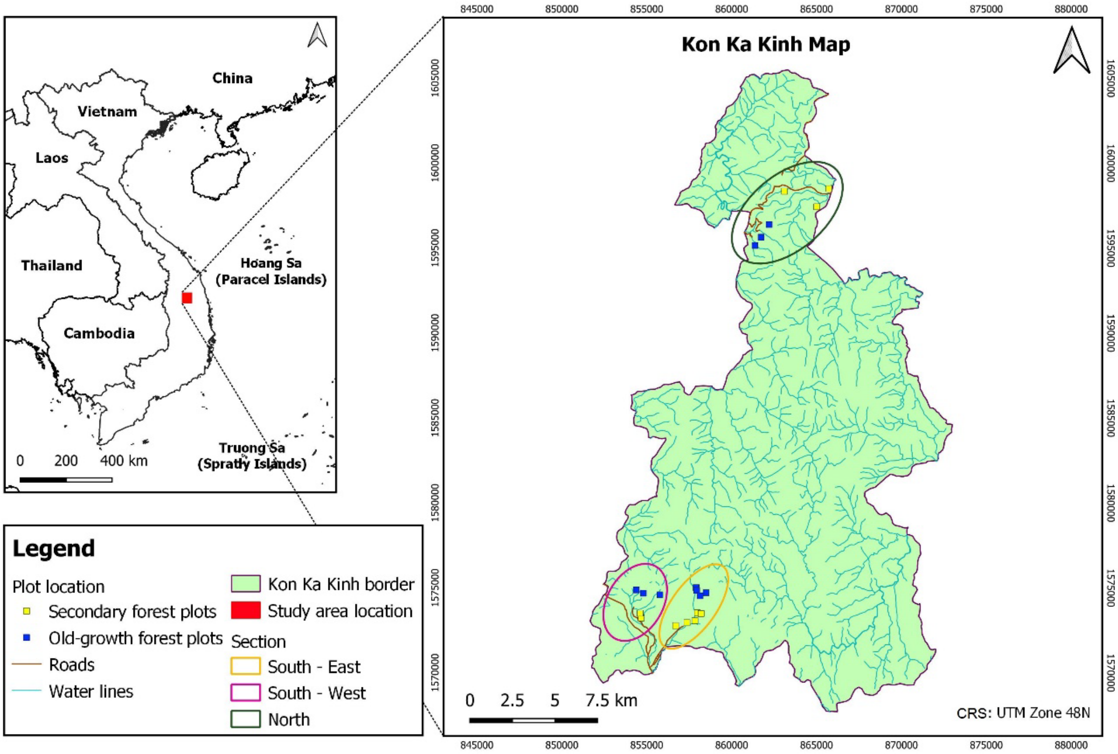


Figure 1. Study area. Maps of Vietnam (left) and Kon Ka Kinh national park (right)

2.2. Sampling design

The research established 20 main plots of 1 ha (100 m x 100 m): 10 plots for the secondary forest and 10 plots for the old-growth forest (Bui et al., 2023). The plot locations were selected based on stratified random sampling method (Shiver & Borders, 1996). In the first step, the Loeschau classification system in Vietnam was used to categorize forest resources into forest stages (P. X. Hoan & Ngu, 2003). The results of forest classification have been verified with the existing forest resource maps of the park. In the second step, we randomly selected the location of plots for each forest stage (Fig. 1). This selection must ensure that the plots had similar factors such as: similar elevation, similar aspect, same soil type and so on.

After that, transect walk inventory and systematic sampling method were applied in main plots. Each plot was divided into 5 strips and 25 subplots (2m x 2m) were established. Spacing between transects and distance between 4 m^2 subplots were also 20 m. The 4 m^2 subplot and quadrats arrangement were presented in Figure 2.

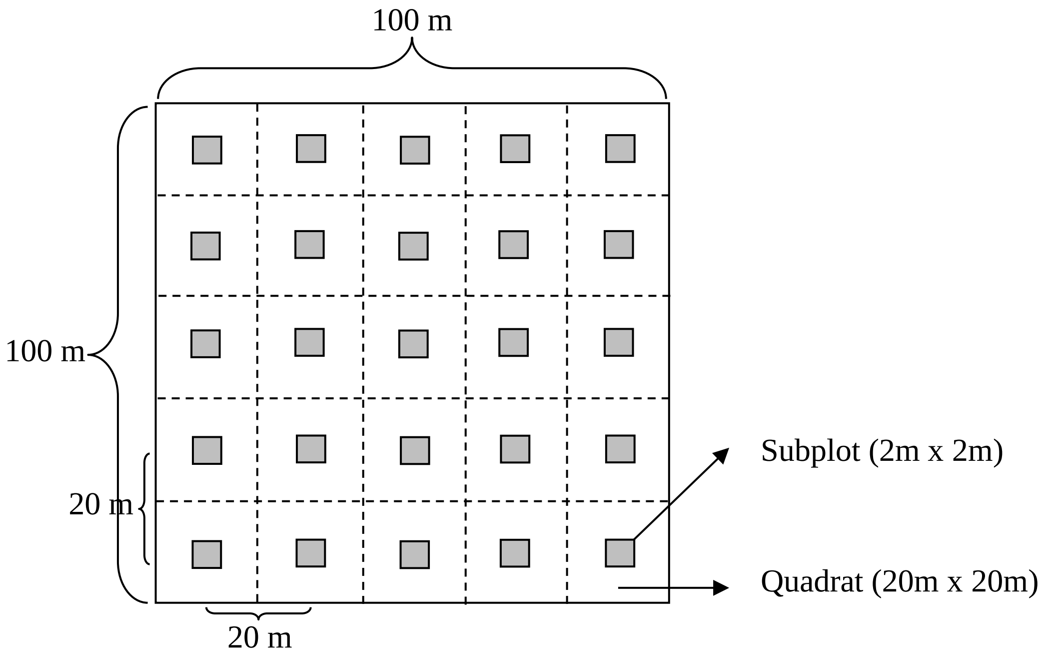


Figure 2. Subplot arrangement for investigating regeneration

2.3. Data collection

For regenerating plants, in each 4 m^2 subplot, information about species name, quality and height was recorded. Expert botanists identified each tree by comparing their morphological features. Initially, Vietnamese names were selected through consultations with reference materials and species identification specialists. The scientific names were later verified using web resources from the Kew Royal Botanic Gardens (Van Khoa et al., 2024). Quality had 3 levels: Good, Medium and Bad. Good regenerating trees were characterized by a straight trunk, healthy growth, a well-formed crown, no signs of disease, and an intact top. In contrast, bad trees had crooked trunks, signs of disease, missing tops, poorly developed crowns, and weak growth. Medium trees exhibited traits that fell between those of good and bad trees (Manh Hung, 2023). Total height was measured using a tape for regenerating trees less than 1 m and using a measurement pole for plants higher than 1 m. Number of light hours in each subplot were also documented using a Horizotoscope, adjusted to the sun movement in Vietnam.

2.4. Statistical analysis

2.4.1. Biodiversity index and comparison

Simpson's index

It is the ability to encounter two plants of the same species in the forest. (McCune et al., 2002). The following formula was used for calculating the index (Magurran, 2004):

$$S = 1 - \sum_{i=1}^{a} \frac{p_i}{p}\left(\frac{p_i - 1}{p - 1}\right) \tag{1}$$

In which, S is Simpson's index a is the number of species; p_i and p are the number of plants of species i and the total number of trees surveyed in the plot, respectively. Simpson's index increase, meaning the diversity rises.

Shannon – Wiener's index

The logarithm of a ratio of the number of trees of species i (p_i) and the total number of trees in the main plot (p) was used to calculate this index. Bigger value of the index, better biodiversity (McCune et al., 2002).

$$SW = -\sum_{i=1}^{a}\left(\frac{p_i}{p}\right)\ln\left(\frac{p_i}{p}\right) \tag{2}$$

Shannon evenness index

This is an indicator used to assess the equality of the number of individuals among species. This index takes values in the range 0-1. Closer values to 1 reflect that the species have similar numbers of individuals, closer values to 0 reflect a huge difference in the number of individuals between species (Alatalo, 1981; McCune et al., 2002).

$$S = \frac{SW}{\ln(R)} \tag{3}$$

In the above formula, S is Shannon evenness index; SW is Shannon – Wiener's index and R is the number of species.

Comparison using linear mixed-effects model

The study used linear-mixed effect models (LMM) to compare biodiversity indices between the two forest stages. Three sections were selected based on the natural and social conditions of the park: South-East, South-West and North (see Figure 1). They are used to check for possible autocorrelation between plots. The average index value was calculated in each plot, taking the plot as the unit for analysis. The plots were randomly sampled in each section within a Loeschau type. LMM has also been shown to be a suitable statistical tool for clustered data (Mathworks, 2016).

The model for the index variable was:

$$Index = (\beta_0) + (\beta_1)Type + (\beta_2)Section + \varepsilon_{i,j} \tag{4}$$

where:

β_0 = the intercept,

β_1 = a parameter estimated for fixed effect (Type),

$$\text{Type} = \begin{cases} 0, & \text{treatment} = \text{old growth} \\ 1, & \text{treatment} = \text{secondary growth} \end{cases}$$

β_2 = a parameter for the random effect (Section),

$$\text{Section} = \begin{cases} 0, & \text{area} = \text{South} - \text{East} \\ 1, & \text{area} = \text{South} - \text{West} \\ 2, & \text{area} = \text{North} \end{cases}$$

ε_{ij} = error.

The nlme R-package was used to check and adjust autocorrelation and normal distribution of the residuals in this analysis (Bates et al., 2015).

2.4.2. Group difference and classification

Canonical correspondence analysis and hierarchical classification

Canonical correspondence analysis (CCA) is a multivariate analysis. CCA is the most popular tool for analyzing community ecology data (McCune et al., 2002). It can analyze metrics across community groups. Given the input matrix was the list of species (or families) and plots. For comparison between communities, the second used matrix was the studied forest states and plots. CCA was based on the chi-square measure distance over totals by species (or families) and by plots. CCA was used to compare the differences in species composition (or families) and the number of individuals present in plots between the two forest states (McCune et al., 2002; Oksanen, 2011; Valenzuela, 2017).

Hierarchical classification (HC) is a method for grouping objects. It is also a useful tool for analyzing multivariate ecological data. This analysis also uses matrices between plots and tree species. The used linkage method was the group average (McCune et al., 2002; Oksanen, 2011). HC grouped tree species (or families) with similar frequencies in plots into a group. They are species, families tended to appear together in plots with different degrees of presence.

Chi-square test and permutational multivariate analysis of variance

Chi-square test is often used to test the independence between two categorical variables. They are based on the squared difference between actual values and expected values over expected values (Thien et al., 2024; Zar, 2010). Chi-square was used to test the independence between regeneration quality levels of the two forest states. At the same time, it was also used to check the independence between the quality levels and height classes and light hour classes.

Regeneration height requency distributions were generated and compared between two forest states by using permutational multivariate analysis of variance (Permanova). Permanova was suitable for comparing frequency distributions, because it did not require any assumption (Anderson, 2011). The study used simulation times of 999 (Oksanen et al., 2013).

2.4.3. Random field and spatial point patterns analysis

Random field method

Random field method was used to transform random field data to point data (Wagner et al., 2016). Based on the number of regeneration trees measured in the subplots to generate random regeneration points in quadrats. The regeneration points were uniformly random as in a Poisson process (Wagner et al., 2016). Next, the study used point data generated in order to analyze the spatial distribution characteristics of regeneration.

Replicated point pattern analysis

Replicated point pattern analysis was used in the study to analyse spatial patterns of gaps on the ground, because it is excellent for small investigated plots with repetitions (Ramón et al., 2016). Spatstat R-package was used for this analysis (Baddeley & Turner, 2014). For testing for randomness, the pair correlation function were applied (Hung, 2016).

The pair correlation function g(r) is shown to be the most effective technique to characterize observable spatial patterns (Illian et al., 2008). The spatial correlations between pairs of regenerations were analysed using this functions (Wiegand & Moloney, 2014). The function was a ratio between Poisson and real probabilities of two regenerations with a distance r (Baddeley, 2008). Illian et al. (2008) also illustrated the g(r) can be calculated using the following formula:

$$g(r) = \frac{K^{'}(r)}{2\pi r} \qquad for \;\; r \geq 0 \qquad (5)$$

Based on calculated results can be used to conclude the type of spatial distribution. The distribution will be random if g(r) is 1. The distribution will be clustered when g(r) is greater than 1 and regular when g(r) is less than 1 (Illian et al., 2008).

All computations were performed using R software version 3.3.2 (package: ape, nlme, spatstat, vegan (R, 2023) and SPSS software version 26 (Carver & Nash, 2011).

3. Results

3.1. Population structure of regeneration

3.1.1. Regeneration characteristics

With one hectare subplot area, the study has measured regenerating plants 2283 in secondary forests and 1378 regenerating stems in old-growth forests. They used to compute biodiversity indices. The index, height and light mean values of the two forest states were summarized in Table 1.

Table 1. Biodiversity indices, regeneration height and light.

Forest type	Richness	Simpson	Shannon	Jevenness	Height (m)	Light (h/year)
Secondary forest	148	0.9769	4.29	0.861	1.43 ± 1.21	645.70 ± 235.51
Old-growth forest	130	0.9799	4.30	0.884	1.61 ± 1.17	265.47 ± 84.94

An interesting result was that although the number of species in old-growth forests was less than secondary forests, the biodiversity indicators showed that old-growth forests have higher levels of biodiversity. The number of species in old-growth forest (130 species) was significantly lower than in the secondary forest (148 species) (Linear mixed model, $p = 0.0024$). In contrast, the old-growth forest had the Simpson, Shannon and Jevenness indices slightly higher than that of the secondary forest. However, these differences were not significant (Linear mixed model, all p values > 0.05).

The average height of regenerating trees and the number of hours of light were statistically different between the two forest states (Linear mixed model, all p values < 0.01). The average height of the old-growth forest was 0.18 m higher than that of the secondary forest. Opposite, the light hour of the old-growth forest (265.47±84.94) was significantly lower than that of the secondary forest (645.70 ± 235.51) (Linear mixed model, $p < 0.0001$).

Table 2. Dominant families obtained in Kon Ka Kinh.

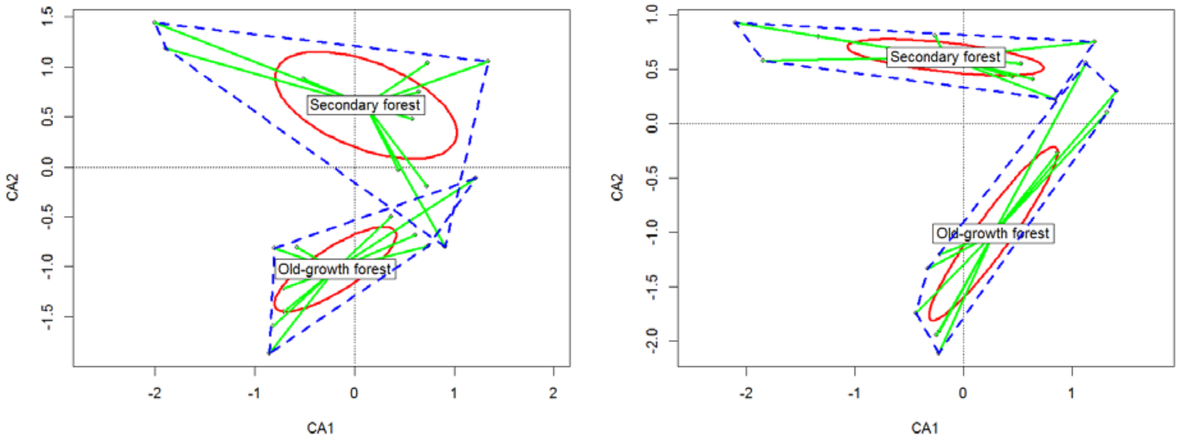
	Secondary forest			Old-growth forest		
No.	Family	Number of species	Percent	Family	Number of species	Percent
1	Lauraceae	16	10.81	Euphorbiaceae	16	12.31
2	Fagaceae	14	9.46	Lauraceae	14	10.77
3	Euphorbiaceae	13	8.78	Moraceae	9	6.92
4	Rubiaceae	10	6.76	Fagaceae	8	6.15
5	Meliaceae	9	6.08	Guttiferae	8	6.15
6	Sapindaceae	8	5.41	Myrtaceae	8	6.15
7	Guttiferae	7	4.73	Elaeocarpaceae	7	5.38
8	Elaeocarpaceae	6	4.05	Meliaceae	7	5.38
9	Myrtaceae	6	4.05	Rubiaceae	5	3.85
10	Ebenaceae	5	3.38	Sapindaceae	4	3.08
11	Moraceae	5	3.38	Anacardiaceae	3	2.31

12	Sterculiaceae	5	3.38	Annonaceae	3	2.31
	Others (27)	44	29.73	Others (30)	38	29.23

Table 2 showed the dominant families in the forest types. Overall, there was not much difference between the studied forest types. Although the number of species in the secondary forest was higher than in the old-growth forest, the number of families was lower by 3 families. For the secondary forest, ten species with the highest average height were *Syzygium zeylanicum* (4.70 m), *Randia fasciculata* (4.70 m), *Litsea baviensis* (3.30 m), *Disoxylum binateriferum* (3.00 m), *Aquilaria crassna* (3.00 m), *Amesio dendron* (2.80 m), *Croton chevalieri* (2.42 m), *Vitex leptopotrys* (2.39 m), *Canarium lyi* (2.39 m), *Acmena acuminatissimum* (2.17 m). The list of 10 species with the lowest average height in this state were: *Castanopsis longipetiolata* (0.42 m), *Trevesia burkii* (0.40 m), *Pterospermum megalocarpum* (0.38 m), *Cratoxylon formosum* (0.37 m), *Alstonia angustifolia* (0.36 m), *Pterspermum diversifolium* (0.30 m), *Acer heptaphlebium* (0.20 m), *Hopea helferi* (0.18 m), *Aporosa planchoniana* (0.17 m), *Garcinia oligantha* (0.03 m). The list of 10 species with the highest and lowest average height of the old-growth forest was very different. The ten tallest species were *Oroxylon indicum* (5.10 m), *Ficus variegata* (3.70 m), *Litsea cubeba* (3.60 m), *Mallotus philipensis* (3.21 m), *Nephelium lappaceum* (2.87 m), *Aglaia anamensis* (2.56 m), *Lindra annamensis* (2.52 m), *Elaeocarpus grandiflorus* (2.51 m), *Dillenia pentagyna* (2.45 m), *Michelia constricta* (2.45 m). And the list of 10 species with the lowest height were: *Litsea olongata* (0.84 m), *Cratoxylum cochinchinensis* (0.83 m), *Pterospermum diversifolium* (0.71 m), *Semecarpus annamensis* (0.65 m), *Stranvaeria nussia* (0.64 m), *Lagerstroemia ovalifolia* (0.62 m), *Brownlowia tabularis* (0.58 m), *Calophyllum rugosum* (0.55 m), *Greenia corymbosa* (0.32 m), *Ixora eugenoides* (0.18 m).

3.1.2. Floristic differences between stages

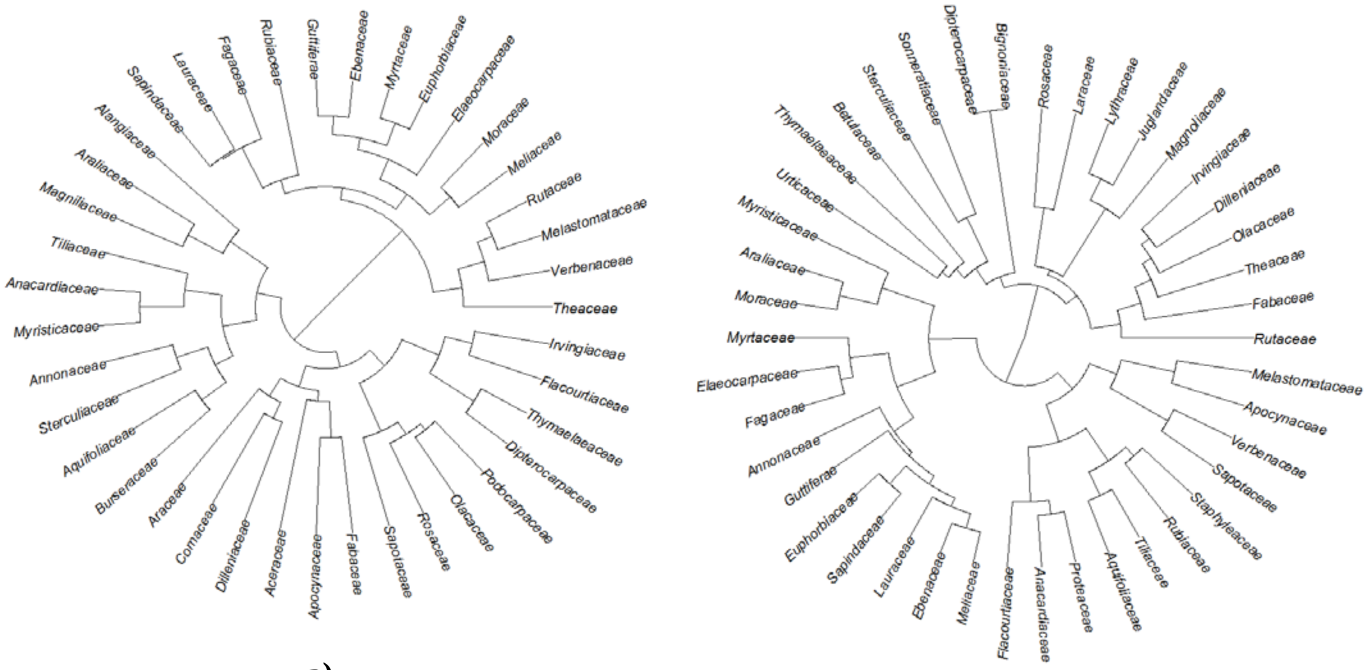
Correspondence analysis was used to explore the differences in the number and frequency of species and family occurrences between the two forest states (Fig. 3).



a) **b)**

Figure 3. Biodiversity comparison between forest stages. Dots were plots and the red line was 95% estimation. a) for families and b) for species.

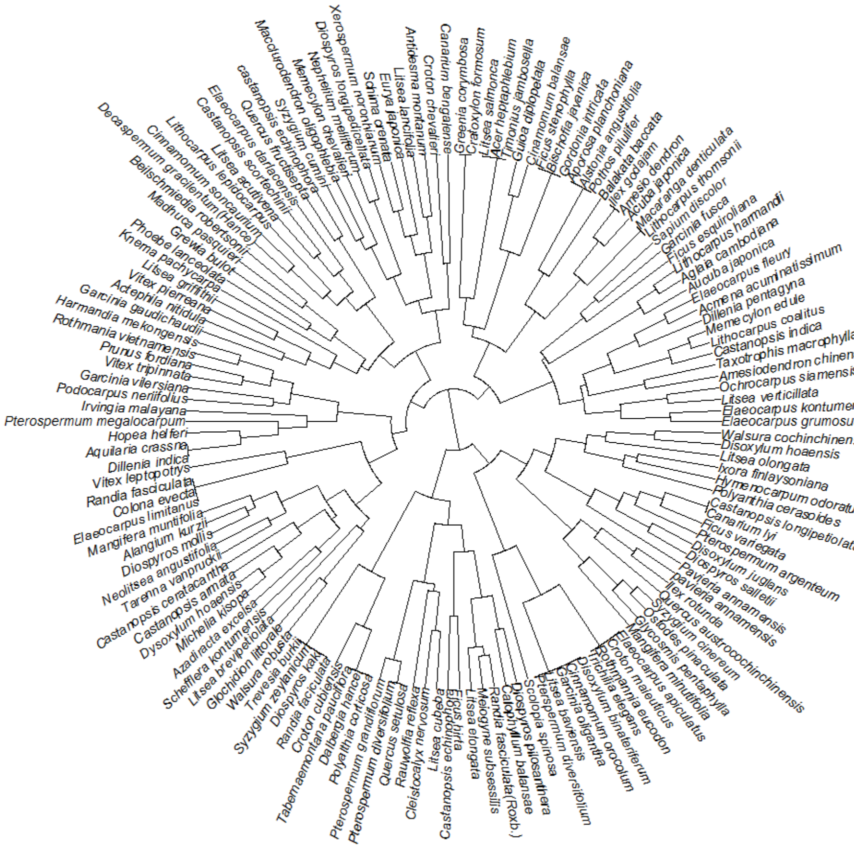
The results showed that the composition of both species and families between the two types of states was really different (Goodness of fit, p value = 0.001 and 0.002, respectively). However, family differences were lower than the species difference.



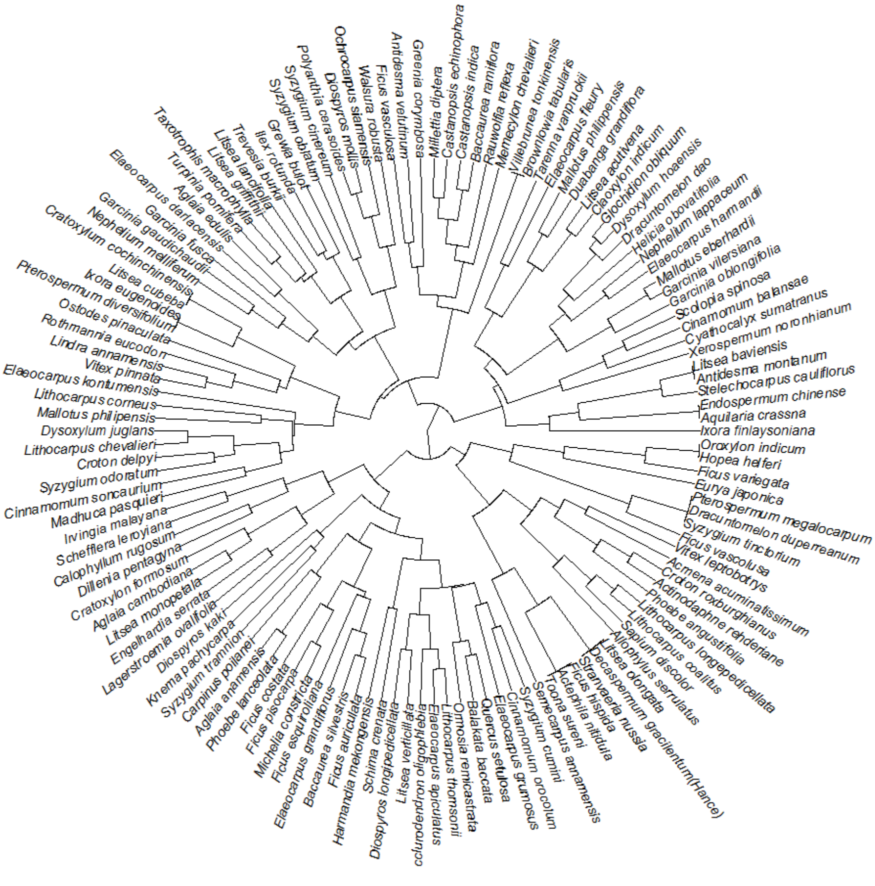
a)

b)

Figure 4. Family group classification in forest stages, a) for the secondary forest and b) for the old-growth forest.


Pterospermum megalocarpum
Irvingia malayana
Podocarpus neriifolius
Garcinia vilersiana
Vitex tripinnata
Prunus fordiana
Rothmania vietnamensis
Harmandia mekongensis
Garcinia gaudichaudii
Actephila nitidula
Vitex pierreana
Litsea griffithii
Knema pachycarpa
Phoebe lanceolata
Grewia bulot
Madhuca pasquieri
Beilschmiedia robertsonii
Decaspermum gracilentum(Hance)
Cinnamomum soncaurium
Lithocarpus lepidocarpus
Litsea acutivena
Castanopsis scortechinii
Elaeocarpus darlacensis
Quercus fructisepta
castanopsis echinophora
Syzygium cumini
Macclurodendron oligophlebia
Memecylon chevalieri
Nephelium melliferum
Diospyros longipedicellata
Xerospermum noronhianum
Schima crenata
Eurya japonica
Litsea lancifolia
Antidesma montanum
Croton chevalieri
Canarium bengalense
Greenia corymbosa
Cratoxylon formosum
Litsea salmonica
Acer heptaphlebium
Timonius jambosella
Guioa diplopetala
Cinamomum balansae
Ficus stenophylla
Bischofia javanica
Gordonia intricata
Aporosa planchoniana
Alstonia angustifolia
Pothos pilulifer
Balakata baccata
Ilex godajam
Amesio dendron
Acuba japonica
Macaranga denticulata
Lithocarpus thomsonii
Sapium discolor
Garcinia fusca
Ficus esquiroliana
Lithocarpus harmandii
Aglaia cambodiana
Aucuba japonica
Elaeocarpus fleury
Acmena acuminatissimum
Dillenia pentagyna
Memecylon edule
Lithocarpus coalitus
Castanopsis indica
Taxotrophis macrophylla
Amesiodendron chinense
Ochrocarpus siamensis
Litsea verticillata
Elaeocarpus kontumensis
Elaeocarpus grumosus
Walsura cochinchinensis
Disoxylum hoaensis
Litsea olongata
Ixora finlaysoniana
Hymenocarpum odoratum
Polyanthia cerasoides
Castanopsis longipetiolata
Canarium lyi
Ficus variegata
Pterospermum argenteum
Disoxylum juglans
Diospyros salletii
Pavieria annamensis
pavieria annamensis
Ilex rotunda
Quercus austrocochinchinensis
Syzygium cinereum
Ostodes pinaculata
Glycosmis pentaphylla
Mangifera minutifolia
Elaeocarpus apiculatus
Croton maieuticus
Rothmannia eucodon
Trichilia elegans
Disoxylum binateriferum
Cinnamomum orocolum
Garcinia oligantha
Litsea baviensis
Pterspermum diversifolium
Scolopia spinosa
Diospyros pilosanthera
Calophyllum balansae
Randia fasciculata(Roxb.)
Meiogyne subsessilis
Litsea elongata
Ficus hirta
Castanopsis echinophora
Litsea cubeba
Cleistocalyx nervosum
Rauwolfia reflexa
Quercus setulosa
Pterospermum diversifolium
Pterospermum grandiflorum
Polyalthia corticosa
Dalbergia hancei
Tabernaemontana pauciflora
Croton cubiensis
Randia faciculata
Diospyros kaki
Syzygium zeylanicum
Trevesia burkii
Walsura robusta
Glochidion littorale
Litsea brevipetiolata
Schefflera kontumensis
Azadiracta excelsa
Michelia kisopa
Dysoxylum hoaensis
Castanopsis armata
Castanopsis ceratacantha
Tarenna vanpruckii
Neolitsea angustifolia
Diospyros mollis
Alangium kurzii
Mangifera muntifolia
Elaeocarpus limitanus
Colona evecta
Randia fasciculata
Vitex leptopotrys
Dillenia indica
Aquilaria crassna
Hopea helferi

a)


Elaeocarpus kontumensis
Vitex pinnata
Lindra annamensis
Rothmannia eucodon
Ostodes pinaculata
Pterospermum diversifolium
Ixora eugenoides
Litsea cubeba
Cratoxylum cochinchinensis
Nephelium melliferum
Garcinia gaudichaudii
Garcinia fusca
Elaeocarpus darlacensis
Aglaia edulis
Turpinia pomifera
Taxotrophis macrophylla
Litsea griffithii
Litsea lancifolia
Trevesia burkii
Ilex rotunda
Grewia bulot
Syzygium oblatum
Syzygium cinereum
Polyanthia cerasoides
Diospyros mollis
Ochrocarpus siamensis
Walsura robusta
Ficus vasculosa
Antidesma velutinum
Greenia corymbosa
Millettia diptera
Castanopsis echinophora
Castanopsis indica
Baccaurea ramiflora
Rauwolfia reflexa
Memecylon chevalieri
Villebrunea tonkinensis
Brownlowia tabularis
Tarenna vanpruckii
Elaeocarpus fleury
Mallotus philippensis
Duabanga grandiflora
Litsea acutivena
Claoxylon indicum
Glochidion obliquum
Dysoxylum hoaensis
Dracuntomelon dao
Helicia obovatifolia
Nephelium lappaceum
Elaeocarpus harmandii
Mallotus eberhardii
Garcinia vilersiana
Garcinia oblongifolia
Scolopia spinosa
Cinamomum balansae
Cyathocalyx sumatranus
Xerospermum noronhianum
Litsea baviensis
Antidesma montanum
Stelechocarpus cauliflorus
Endospermum chinense
Aquilaria crassna
Ixora finlaysoniana
Oroxylon indicum
Hopea helferi
Ficus variegata
Eurya japonica
Pterospermum megalocarpum
Dracuntomelon duperreanum
Syzygium tinctorium
Ficus vascolusa
Vitex leptobotrys
Acmena acuminatissimum
Croton roxburghianus
Actinodaphne rehderiane
Phoebe angustifolia
Lithocarpus longepedicellata
Lithocarpus coalitus
Sapium discolor
Allophylus serrulatus
Litsea olongata
Decaspermum gracilentum(Hance)
Stranvaeria nussia
Ficus hispida
Actephila nitidula
Toona sureni
Semecarpus annamensis
Syzygium cumini
Cinnamomum orocolum
Elaeocarpus grumosus
Quercus setulosa
Balakata baccata
Ormosia remicastrata
Lithocarpus thomsonii
Elaeocarpus apiculatus
cclurodendron oligophlebia
Litsea verticillata
Diospyros longipedicellata
Schima crenata
Harmandia mekongensis
Ficus auriculata
Baccaurea silvestris
Elaeocarpus grandiflorus
Ficus esquiroliana
Michelia constricta
Ficus pisocarpa
Ficus costata
Phoebe lanceolata
Aglaia anamensis
Carpinus poilanei
Syzygium tramnion
Knema pachycarpa
Diospyros kaki
Lagerstroemia ovalifolia
Engelhardia serrata
Litsea monopetala
Aglaia cambodiana
Cratoxylon formosum
Dillenia pentagyna
Calophyllum rugosum
Schefflera leroyiana
Irvingia malayana
Madhuca pasquieri
Cinnamomum soncaurium
Syzygium odoratum
Croton delpyi
Lithocarpus chevalieri
Dysoxylum juglans
Mallotus philipensis
Lithocarpus corneus

b)

Figure 5. Species group classification in forest stages a) for the secondary forest and b) for the old-growth forest.

Both forest states had groups of species and families appeared with similar frequency in plots. This clustering was quite clear and showed in Figures 4 and Figure 5. For the families in the secondary forest, the group with high frequency included Lauraceae, Fagaceae and Sapindaceae. The group with medium frequency consisted of Sterculiaceae and Annonaceae. The group with the lowest frequency had Thymaelaeaceae and Dipterocarpaceae. This clustering was very different in old-growth forests. The families with high frequency together were Guttiferae, Lauraceae, Meliaceae and Ebenaceae. Families that occured together with the medium frequency in this state comprised Rubiaceae, Staphyleaceae, Tiliaceae and Aquifoliaceae. Families that arised together with low frequency had Dipterocarpaceae and Bignoniaceae.

For species, species were also classified and differentiated quite clearly in both states. For the secondary forest, *Nephelium melliferum* and *Diospyros longipedicellata* tended to occur together in high number of individuals. And there were many species that appeared together but in very low number of individuals such as *Cinnamomum orocolum*, *Garcinia oligantha*, *Disoxylum binateriferum* and so on. For old-growth forests, these groups were not same as the secondary. Species with high number of stems were *Ochrocarpus siamensis*, *Diospyros mollis* and *Polyanthia cerasoides*. In contrast, the species occurring with the lowest number of individuals were *Decaspermum gracilentum*, *Litsea olongata* and *Stranvaeria nussia*.

3.1.3. Height class distribution

Both forest states had a descending frequency distribution, meaning the number of stems in classes decreased as the height size increased (Fig. 6).

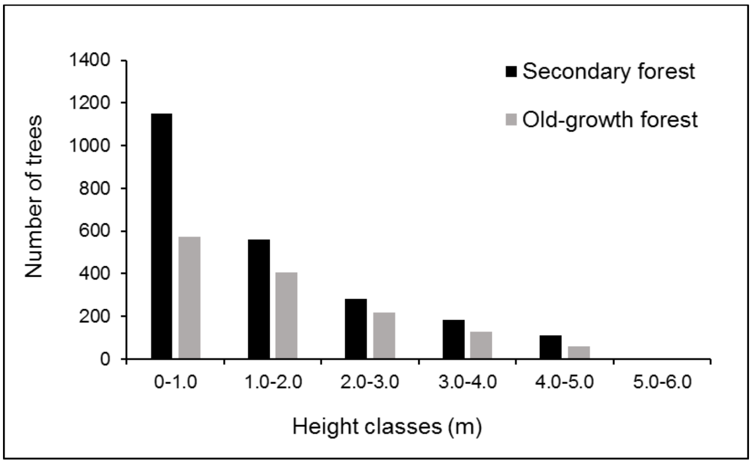


Figure 6. Height frequency distributions.

However, the rate of reduction in number of trees with height size was greater in the secondary forest. In the first class, the number of regenerating trees in the secondary forest was twice of that in the old-growth forest. However, in the next groups, this difference gradually decreased. Pair comparison results using Mann and Whitney test showed that the number of regenerating trees in classes 0-1.0 m, 1.0-2.0 m and 4.0-5.0 m was significantly different between the two forest stages ($p = 0.000$, $p = 0.001$ and $p = 0.000$, respectively). For the remaining three groups (2.0-3.0 m, 3.0-4.0 m and 5.0-6.0 m), the number of stems in each group was not statistically different between forest states (All p values > 0.05).

Simultaneously the study used all values of number of stems in all classes and repeat 10 times (10 plots) for Permutational muiltivariate analysis of variance to compare height frequency distributions between two forest states. The results indicated that the frequency distribution was statistically different between secondary and old-growth forests (Permanova, $p = 0.001$). Even section element was added to the command, there was no difference in results.

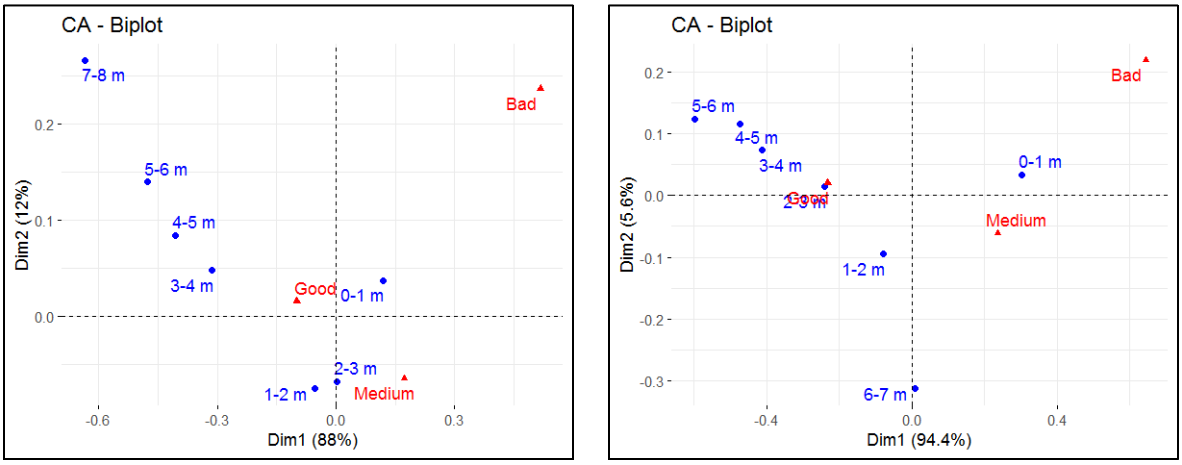
3.1.4. Regeneration quality

Results of the percentage of trees by quality classes were shown in Table 3.

Table 3. Percentages of trees by quality classes.

Type	**Count**	**Quality**			**Total**
		Good	**Medium**	**Bad**	
Secondary forest	Count (trees)	1550	654	79	2283
	% within Type	67.9%	28.6%	3.5%	100.0%
Old-growth forest	Count (trees)	767	531	80	1378
	% within Type	55.7%	38.5%	5.8%	100.0%
Total	Count (trees)	2317	1185	159	3661
	% within Type	63.3%	32.4%	4.3%	100.0%

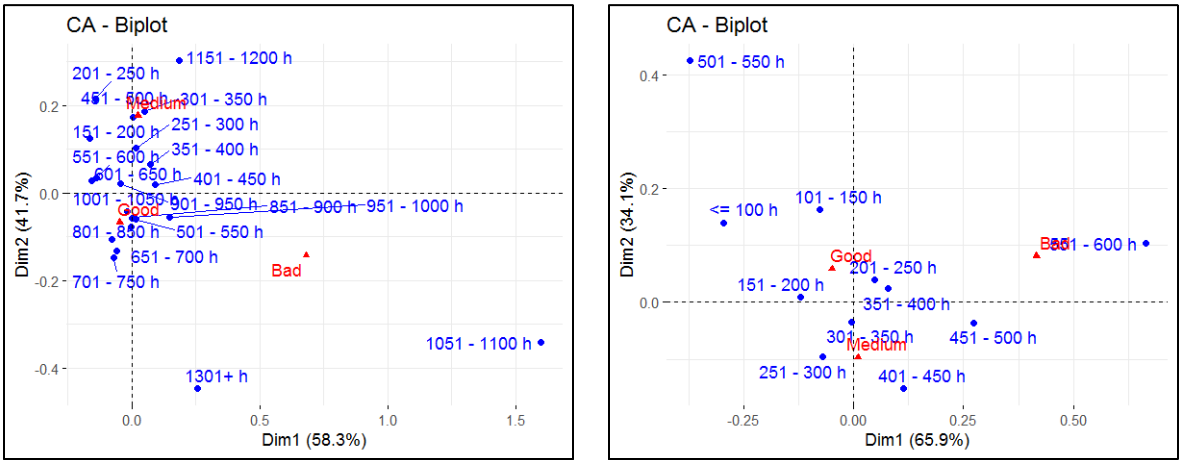
For both forest states, the percentage of good trees was the highest, followed by the percentage of medium and bad trees. Tree quality was dependent of forest states, meaning tree quality was statistically different between the two forest states (Chi-squared test, p-value < 0.0001).



a) **b)**

Figure 7. Correspondence analysis between regeneration quality (red text) and height classes (blue text), a) for the secondary forest and b) for the old-growth forest.

The results of correspondence analysis illustrated that regeneration quality was significantly associated with height classes (Chi square test, p-value = 5.65155e-09 and p-value = 5.458266e-18, respectively). In secondary forests, good quality regenerating trees were often trees with a height of 3-4 m, 4-5 m and 5-6 m. Medium regeneration was often found in height groups such as 1-2 m and 2-3 m. Regenerating trees of bad quality often had a very low height of 0-1 m. Thus, in secondary forests, good trees had the greatest height, followed by medium trees and bad trees. This trend was not obvious in the old-growth forest. The height of good regenerating trees tended to be 1 m lower than in secondary forests. Medium quality trees were 1-2 m and 6-7 m tall. Trees with poor quality were more strongly related to the height class of 1-2 m, compared to secondary forests.



a) **b)**

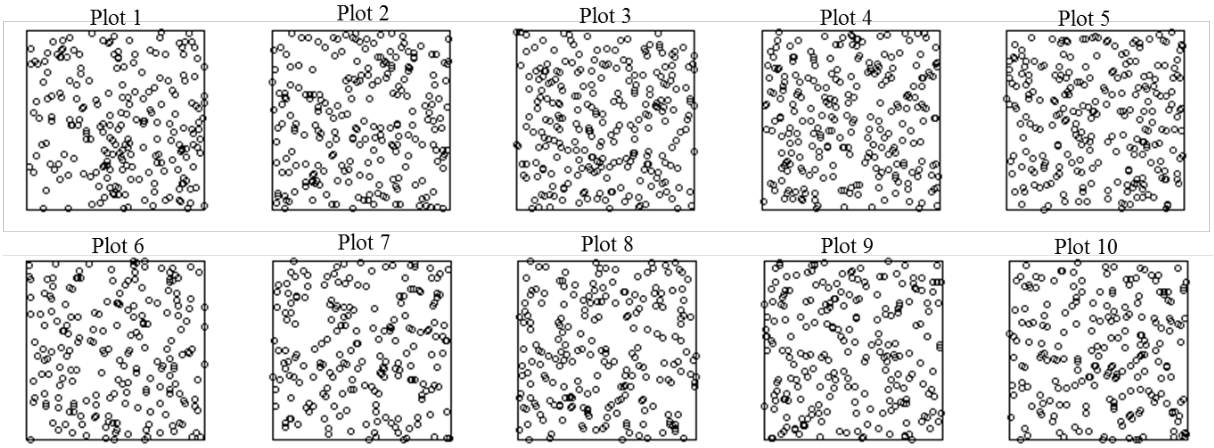
Figure 8. Correspondence analysis between regeneration quality (red text) and light classes (blue text), a) for the secondary forest and b) for the old-growth forest.

For secondary forests, well-regenerated trees often grew in areas with 1001-1050 h/year, 801-850 h/year and 651-750 h/year. Medium regenerating plants were most commonly found in areas with 301-350 and 451-500 h/year. Plants of poor quality usually grew in areas with number of light hour 951-1000 and 1051-1100 h/year. Thus, the bad trees were found in the area with the largest number of light hours, followed by the good and the medium. And the density of regenerating trees was often greater in areas with more hours of light. This association was significant in the secondary forest (Chi square test, p-value = 0.002698863). In old-growth forests, well-regenerating trees often lived in areas with 101-200 h/year. Medium quality trees were often in the area from 301-305 h/year and 401-450 h/year. Bad regeneration plants were found in zones of 551-600 h/year. A trend was that in old-growth forests, trees with bad quality often appeared in areas with a lot of light, then medium and good regenerating trees. However, the association was not statistically significant in the old-growth forest (Chi square test, p-value = 0.2435452).

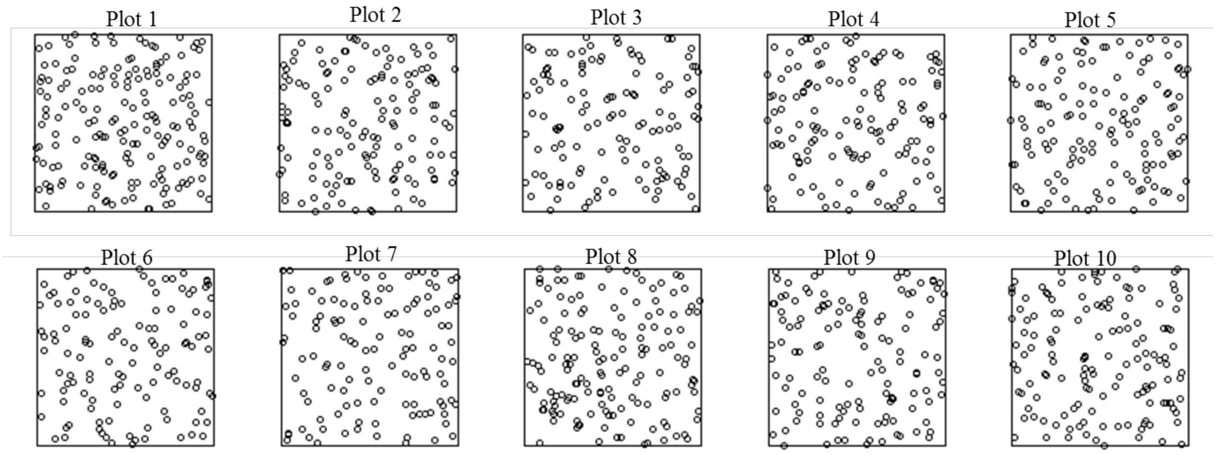
3.2. Spatial patterns of regeneration

3.2.1. Spatial distribution of regeneration

Positions of regenerating plants generated for quadrats based on the number of regeneration in subplots was shown in Figure 9.



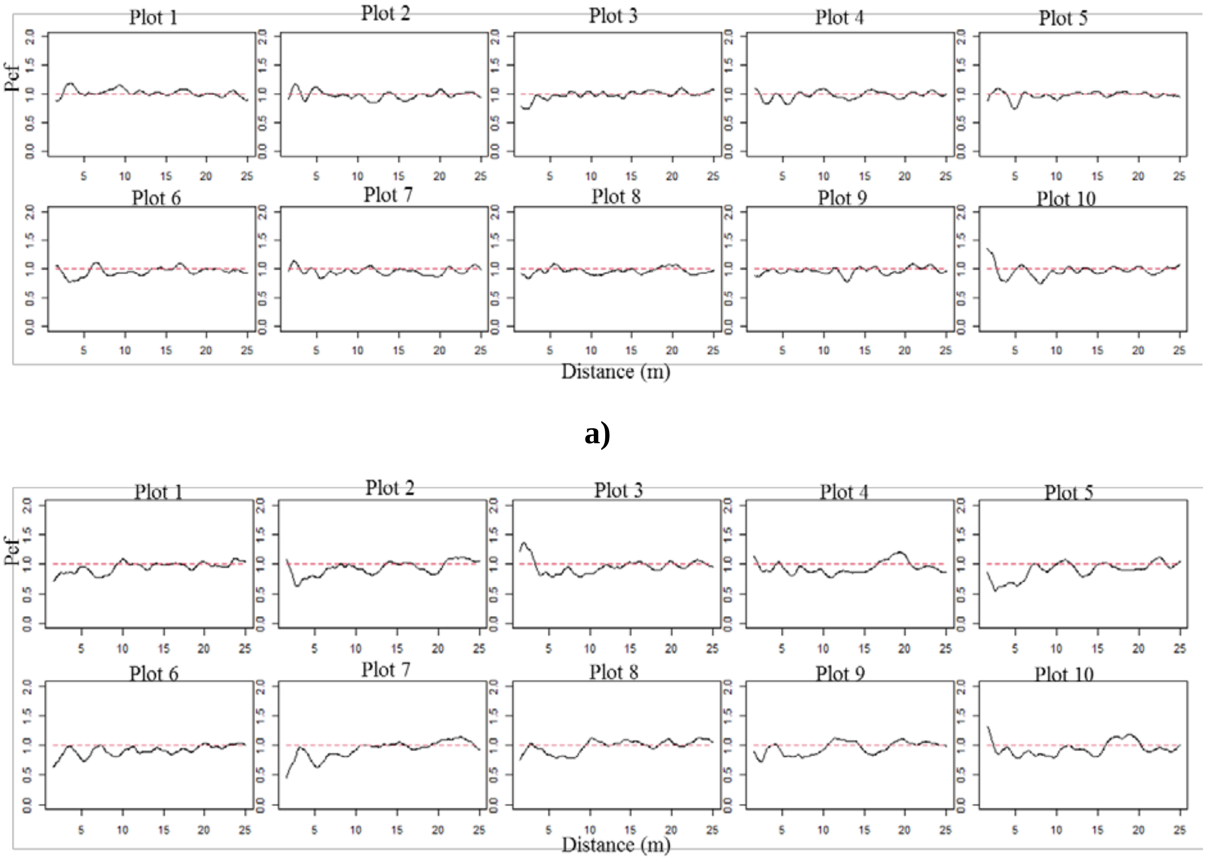
a)



b)

Figure 9. Generated regeneration positions. a) for the secondary forest, b) for the old-growth forest.

The number of regenerating trees generated in each 1-hectare plot of the secondary forest was almost twice that of the old-growth forest. The density of regenerating stems between the two forest states was statistically different (Point process model, P value = 2.115568e-29).

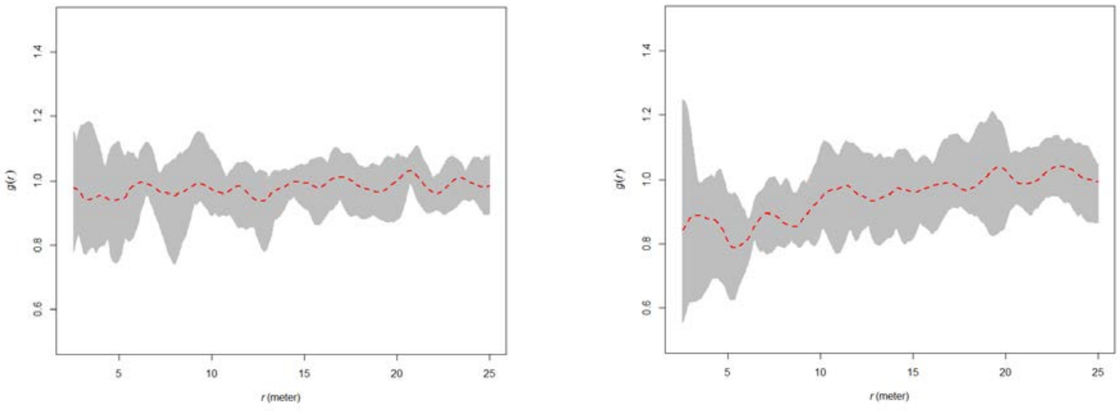


a)

b)

Figure 10. Pair correlation function results. a) for the secondary forest and b) for the old-growth forest. Red dashed line is a reference line, curvy black line is the pcf line over distances.

In the secondary forest, almost all plots indicated that the spatial pattern was random at all scales. Contrary, in the old-growth forest, the all most of patterns in plots were regular at the scale of 0-12 m, and then the spatial pattern was random, sometimes clustering. Figure 11 indicated that the variation of pcf functions (the gray area) in the secondary forest was smaller and narrower than the old-growth forest. Therefore, spatial patterns of regeneration in the old-growth forest was more statistically complicated than that in the secondary forest (Studentized permutation test, T = 423.22, p-value = 0.001).



a) **b)**

Figure 11. Variation of pcf results (the gray area). a) for the secondary forest and b) for the old-growth forest. Red dashed line is a random line.

4. Discussion

4.1. Regeneration biodiversity and frequency distribution

The regeneration density is 2283 seedlings/ha in the secondary forest, much higher than that of the old-growth forest (1378 seedlings/ha). Girma and Mosandl (2012) and Chapman and Chapman (1997) found the higher regeneration density in Ethiopia and Uganda than this study's results. However, the regeneration concentration is greater than the density that Woo et al. (2011) found in Vietnam. The regeneration density is very comparable to the conclusions of Binh (2014) in Da Lat province with similar forest stages (1928-2205/ha).

In general, after selective cutting, the seeding density is substantially higher. This conclusion is supported by the research of Dien et al. (2010) and Khang (2014) in Vietnam, as well as Chapman and Chapman (1997) in Uganda and Gardinnge et al. (1998) in Indonesia. The forest structure can be reasons for this phenomenon. After logging single trees selection, an intermediate disturbance will be generated. Both near and far distance mother trees can provide seeds for germination in the secondary forest (Connell, 1978). Hung (2016) indicated that the secondary forest had greater overstorey tree densities, which may be the origin of higher regeneration densities in this stage. Another explanation is that a thinner canopy and more gaps existed in the secondary forest (Hung, 2016). This will increase the amount of light reaching the ground, promoting germination, particularly for pioneers (Barnes et al., 1998; Mabberley, 1992). Additional cause may be the short distance from old-growth forest, where many mother trees are living, causing outstanding seed supply for the secondary forest.

The average number of species in the plots of the secondary forest is significantly higher than the old-growth stage. This is equivalent to findings of Richards (1996) and Khang (2014) in Vietnam. Conversely, this discovery contradicts results of Brown and Lugo (1990). This phenomenon can be explained by a number of factors. Single tree selection harvest have been occurred from 1960-1990 in the park, making secondary forests (KKK, 2013). This logging made an intermediate disturbance as mentioned above, so seeds from near and far mother trees can reach to canopy opening areas and grow there. This may cause higher richness (Connell, 1978). Additional explanation may be strict protection from local people activities after selection logging. Therefore, the regenerating trees after growing in the secondary forest will be protected and well developed, leading to a higher number of species in this stage (KKK, 2013).

In opposition to number of species, other biodiversity indicators were lower in the secondary forest. The first reason is more equal number of individuals between species in the old-growth forest, making some bigger indices. The species biodiversity in park is totally supported by findings of previous research carried out in Vietnam such as Blanc et al. (2000), Woo et al. (2011), Khanh (1996), Thang et al. (2015).

The average regeneration height of both stages are approximately equal to the results found by Binh (2014) at Bioup-Nui Ba national park (about 1.39 m). However, this height is lower than findings of Woo et al. (2011) (about 2.1 m). This study results are slightly higher than average results calculated by Dung (2000) in Hoa Binh province. For the secondary forest, results of Dung (2000) run from 1.2 m - 1.35 m, while those of the old-growth forest are 1.34 m -1.43 m. He also concluded that the average height of regeneration is higher in the old-growth forests. This difference may be due to different study locations. Therefore, soil conditions, climate and forest structures are also different in these studies. The number of light hours in old-growth forests is lower than in secondary forests. This finding is also proved in a study of Montgomery and Chazdon (2001) in tropical wet forests, Costa Rica. This may be due to the thicker canopy of old-growth forests (Hung, 2016). Thicker canopy and more branches and leaves may block more light.

In terms of number of species, the most dominant families are similar between the two forest stages such as Fagaceae, Rubiaceae, Euphorbiaceae and so on. The results above are also in agreement with studies of Binh (2014), Khanh (1996), Woo et al. (2011), Dung (2000), Chokchaichamnankit et al. (2008) in Vietnam and the world. Reasons may be that the species of these families are pioneers. Therefore, after anthropological or natural disturbances, these species appear first and develop well. Or these families have genetic structures adapted to montaine forests in Indochina, including Vietnam (Chokchaichamnankit et al., 2008). These families also have a great number of individuals, especially in secondary forests.

Regarding the number of individuals, the species with the largest number of individuals in both states also concentrated on the dominant families analyzed above. However, there are also many species that only have 1 individual in the investigation area, for examples: *Cinnamomum orocolum*, *Garcinia oligantha*, *Disoxylum binateriferum* in the secondary forest and *Decaspermum gracilentum*, *Litsea olongata* and *Stranvaeria nussia* in the old-growth forest. This will cause concern for managers and ecologists, if they want to restore forests with the aim of enhancing biodiversity. And these are also the species to focus on when the park wants to conduct enrichment planting.

Biodiversity and composition of species and families are statistically different between the two forest stages. A changing the species composition from shade-intolerant, fast-growing species with shade-tolerant, slower-growing species may cause this dissimilarity (Chazdon, 2012). The difference also can be a result of natural competition processes, different soil and climate conditions, and especially measures of human and natural influences.

The regeneration height frequency distribution is reverse J-shaped curves in both forest states. This finding supports previous studies (Binh, 2014; Dung, 2000). Meaning, the number of trees in the first height class is biggest, then decrease in the next classes. This could indicate that the forests are healthy, sustainable and have a good supply of regeneration (Endris et al., 2017; P. X. Hoan & Ngu, 2003; Jew et al., 2016; Maua et al., 2020). One difference between the two types is that the mortality rate in secondary forests is very large in the first 2 groups (nearly 50%) and then gradually decreases. In the old-growth forest, mortality is relatively uniform across all height levels. This difference between the two forest states is significant. The difference in the amount of light reaching the ground, the composition and the structure of overstorey trees can be the cause of this difference (P. X. Hoan & Ngu, 2003).

4.2. Regeneration quality

The number of regenerating trees with good quality was highest, then gradually decreased in the medium and bad quality groups. The quality of regeneration in the secondary forest is significantly different from the old-growth forest. This trend was also found in other studies (Binh, 2014; Dung, 2000; Thang et al., 2015). This is a good sign for natural regeneration-based forest restoration in the study area.

There are many factors affecting the quality of regeneration (McWilliams et al., 2015). The results indicated that the relationship between the quality of regeneration and the height size classes and the number of lighting hours is significant. These relationships were rarely analyzed in previous studies. In secondary forests, when tending regeneration and vegetation clearance, care should be taken with trees with a height from 3 m to 6 m. And need pay attention in areas with average lighting hours from about 650 to 1000 h/year. For old-growth forests, attention should be paid to trees with a height of 2 - 5 m and areas with low lighting hours (100-200 h/year). Because these areas are where good regeneration often appears. Corresponden analysis also illustrated that regeneration species in old-growth forests often are shade-tolerant, and in secondary forests, they are light-demanding (Chazdon, 2012).

One weakness of these results is the classification of regenerating plant quality into Good, Medium and Bad. Although there are clear criteria, the classification still depends on the surveyor's experiences.

4.3. Spatial patterns of regeneration

The random field method showed that most of the regenerative tree distribution is random at all scale, except for 0-12 m distances in old-growth forests. Distribution characteristics of the old-growth forest are more complex and different from the secondary forest significantly. These distribution characteristics are published in the studies of Hai (2009), Nhung (2012) and Huu (2013) in same forest states as our study in Vietnam. However, this conclusion is not the same as the research of Anh (1998), Pare et al. (2009) and Quang and Minh (2011).

A common trend seen in the development of plant communities is that the distribution tends to shift from aggregate to random and regular as the forest changes from young to old (Zhang et al., 2020). This also perform in this study. In old-growth forests, regular patterns become more popular, especially at distance of 0-12 m. This may be due to the relatively uniform density of regeneration in the subplots. Regular distribution may be the result of good environmental conditions including light, nutrient and moisture (González-Rivas et al., 2009) and many seed trees in adjacent forests (Gebrehiwot, 2003) in the old-growth forest.

When studying the spatial distribution characteristics of regenerating trees, there are many difficulties, especially in data collection. For tropical forests, the number of species and the number of individuals is huge, so if researchers want to measure coordinates of all regenerating plants in a plot (eg 1 hectare plot) is extremely challenging and expensive, in many cases it is impossible (Zagidullina & Tikhodeyeva, 2006). Therefore, studies on spatial distribution of regeneration are still limited, especially in evergreen broadleaf tropical forests. To overcome the difficulty, researches will only be conducted on 1 or a few selected species

(Muhamed, 2019; Rodrigues et al., 2016). Or set limits to measure for example height > 50 cm (Fajardo et al., 2006) or diameter > 1 cm (Lan et al., 2012) and so on. Another solution is to analyze spatial patterns using different methods. A classic and popular method, especially in Vietnam, is based on the number of regenerating plants collected in many small fixed plots. Then calculate a ratio between the mean and the variance to conclude the spatial distribution characteristics (Dien et al., 2010; Dung, 2000; Payandeh, 1970; Stein, 1992). However, this method may have limitations for inferring uninvestigated areas. Another method is to use coordinates of the plot centers and the number of regeneration in them for analyses (Rodrigues et al., 2016). In this study, the random field method is used. It has an advantage that it is not necessary to measure the coordinates of all regenerating trees in 1ha and still generate point data for un-plotted areas. This method is suitable for mobile objects and coverage data (Wagner et al., 2016). The subplots are evenly distributed, which is excellent to use this method (Stoyan & Wagner, 2001; Wagner et al., 2016).

5. Conclusion

In conclusion, biodiversity, species composition and spatial distribution characteristics were statistically different between the two studied forest states. The number of regenerating trees in secondary forests was nearly twice of that in old-growth forests. Overall, the biodiversity in the secondary forest was slightly lower. Reverse J-shaped curves was the shape found for the height frequency distribution in both stages. The rate of good regeneration was higher in secondary forests. The quality of regeneration was significantly related to height size and number of lighting hours. The regeneration distribution pattern was random in both types. However, with the distance from 0-12m, the distribution of regeneration was regular in the old-growth forest. The study results showed that regeneration supply was very good in both stages. They were well distributed in different locations on the ground. Therefore, this is a favourable condition for Kon Ka Kinh national park to restore secondary forests based on assisted natural regeneration. The park should also focus on species with very low number of individuals to protect and develop, avoid extinction of these species and enhance biodiversity and sustainability for the forests in the area. Future studies could expand the area of the subplots and conduct annual measurements to more accurately assess the change in regeneration layer characteristics over time.

Acknowledgements

The authors would like to thank the leaders and staff of Kon Ka Kinh National Park for their help and support in data collection and reference materials. We are also grateful to the government of Vietnam, the Rufford Organization and Graduate Academy of TU-Dresden for providing financial support to carry out this study. We also appreciate the technical and analytical support from Institute of Silviculture and Forest Protection, TU-Dresden, Faculty of Forestry, Vietnam National University of Forestry and Nong Lam University to complete the research.

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