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Rehabilitation of loading bays after selective logging at the Pra-Anum forest reserve, Ghana

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https://creativecommons.org/licenses/ by/4.0/ **Abstract:** The exploitation of timber has had a profound impact on tropical forest areas and their structures. This study assessed the effect of selective logging on natural regeneration and soil characteristics in post-loading bay sites at the Pra-Anum forest reserve in Ghana, West Africa. The results showed no difference in the number of species enumerated in the loading bays and the undisturbed area. More trees were observed in the RAT and RNT plots than in the undisturbed area. Relative to the RAT plot, species on the RNT and the undisturbed area were less diverse and less evenly distributed. Mean tree height, diameter, and basal area were higher in the RAT and RNT plots than in the undisturbed plots. Soil bulk density was lower in the RAT and undisturbed plot than in the RAT plot and increased with increased depth. Soil organic matter was 44% and 27% more in the undisturbed and RAT plots, respectively, than in the RNT plot and accounted for 84.75%, 83.97% and 45.33% of variations in soil bulk density, pH, and CEC. The study provides insight into the need to rehabilitate highly disturbed areas in forests, particularly the addition of topsoil on loading bays, skid trails, roads, and gaps after logging to improve the productivity of the forest soils.

Keywords: forest management; loading bay; logging; rehabilitation; soil productivity; tree regeneration

1. Introduction

Timber exploitation (both legal and illegal) has significantly impacted forest areas and structures in the tropics, including Ghana [1]. This applies to forest reserves, which were purposely established to promote environmental stability and serve as the basis for sustainable timber production [2,3]. A greater proportion of closed forest cover in Ghana is found in the forest reserves because almost all the forests in the unprotected areas (off-reserve) have been lost through different human activities, including logging [4,5]. Yet logging is a major source of revenue generation in Ghana and most West African countries. Despite its economic importance, logging is one of the main causes of deforestation in the sub-region [6]. As a result, selective logging, a more sustainable, low-impact alternative to clear-cut logging, has been proposed in Ghana and other tropical countries [7]. More than half of Ghana's 214 forest reserves, which contain 1.8 million hectares of forest, are believed to have undergone selective logging [3,8]. Typically, decades after logging, the results are still visible [9].

The level of disturbance caused by logging is generally related to the number of trees harvested and the type of equipment used in logging. In selective logging, the disturbance has been considered to produce minimal damage to the forest structure,

composition, and dynamics [10]. It is generally expected to positively influence natural regeneration [11]. Nonetheless, different studies have reported significant changes in forest structure, species composition, genetic diversity, and nutrient cycling as well [12–14]. The impacts of logging on plant diversity are well-studied in West Africa, and the results vary significantly as a result of differences in sites, harvest intensity, as well as logging practices [15,16]. Besides the effect of logging on vegetation, activities of logging machines such as skidders and loading trucks also disturb forest soils through compaction and erosion, which in turn hinder natural regeneration [17].

The demand for forest products continues at a higher rate, the pressure to exploit forests, particularly natural forests, has not stopped, and there are several factors indicating that forests will continue to degrade [18]. More effort, therefore, will have to be made to rehabilitate and sustainably manage degraded natural forests and establish productive plantations to meet the predicted increase in demand for forest products [19]. Rehabilitation of declining forests and lands is a pressing issue that necessitates ecosystem enrichment and long-term use of degraded areas on regional and global scales. The accurate assessment of site conditions established during harvesting is critical for successful regeneration and reforestation [20,21].

One of the most important tasks in forest management is to adhere to forest operation ecology and to create and implement techniques and technologies that may efficiently use resources while minimizing damage and overall impacts on the forest environment's structure and function. While research on the regeneration of tree species on skid trails and loading bays has been done [22–24] and on the effect of logging on the forest soil, not much has been done on the growth and diversity of plant species as well as soil characteristics in post-loading bay sites. [12] studied both the tree diversity and soil characteristics of logging disturbances, however, the study neither explored the damage in loading bays nor the growth of trees. Further, little is known about how to manage loading bays after logging. Management of loading bay sites after logging is key because the ecological components including trees, animals, and soil physical, chemical, and biological properties in these areas suffer the most due to the intense activities that are carried out, together with the pressure exerted on the soil by heavy machinery that is kept in these areas. Knowledge of whether to add topsoil or not to the loading bay sites will help forest managers sustainably manage loading bay sites after logging. Hence, this study aimed to assess the effect of selective logging on natural regeneration and soil characteristics in post-loading bay sites at the Pra-Anum forest reserve in Ghana, West Africa. The study's specific objectives were to; 1) identify the floristic composition of regeneration among post-loading bay sites with topsoil added, post-loading bay sites with no topsoil added and an undisturbed site; 2) assess the growth of trees in these sites; and 3) evaluate some soil characteristics among the three sites. These objectives were based on the hypotheses that; 1) H_o: Species diversity will be the same among post-loading bay sites with top soil added, post-loading bay sites with no top soil added and an undisturbed site; 2) H_0 : Growth of trees will not be affected by these different sites; and 3) H_0 : There will be no variations in soil properties within these sites.

2. Methods

2.1. Experimental area and study design

The study was conducted in the Pra-Anum Forest Reserve, which is part of the Southeast subtype of the Moist Semi-deciduous Forest and is situated at latitude 615' N and longitude 112' W in Ghana's high forest zone (**Figure 1**). The forest covers a total area of 12,332 hectares and is generally a gentle slope, with an average elevation of around 140 m above sea level.



Figure 1. The map of compartment 4 of the Pra-Anum forest reserve [25].

The 134-ha compartment that made up the experimental block is Compartment 4 in the Research Working Circle (RWC), which is a section of forest reserves designated for research. Swiss Lumber Company harvested the timber in the compartment. In July and August of 2000, trees were harvested via chainsaw felling and log extraction with rubber-tired skidders. After the logging, permanent sampling plots were marked and tagged on logging gaps and undisturbed areas of the forest.

Two rehabilitation techniques used on the loading bays, Regeneration Added Topsoil (RAT) and Regeneration No Topsoil (RNT), as well as intact sites (unlogged areas (UL)), were re-identified in 2019, approximately 18 years after the logging. A complete Randomized Design was used to create the plots. To create a nested sample plot design, the 10 m \times 10 m (100 m²) plot was divided into two sub-plots, each measuring 5 m \times 5 m (25 m²). The sub-plots were then further divided into sub-sub-plots (SSP), each measuring 1 m \times 1 m (1 m²). A total of 27 plots, thus, 9 plots for each method were used for this study.

2.2. Soil sampling

Soil samples were taken at random from 0–15 and 15–30 cm depths from each plot. Five (5) soil samples were taken in each plot at both depths and combined into a composite sample representing each plot. Soils were collected diagonally from three sampling points (the middle and two corners) in the plots for bulk density and nutrient determination. A total of 54 soil samples, each for chemical analyses and bulk density determination (27 for each depth), were taken for the study. Soil samples were packed in airtight zip-lock bags, clearly labeled with the name of the plot and date/time of sampling, and transported to the laboratory for various analyses to be carried out.

2.3. Data collection

2.3.1. Plant species

Following plot re-establishment (August 2018), emerging post-logging plant species were counted on the loading bays and undisturbed areas to examine the composition of advanced regeneration of tree species. In each of the 27 sample plots, all tree size classes, including those in the undergrowth (less than 2.0 cm dbh), saplings (2.0–10.0 cm dbh), and trees (>10.0 cm dbh) were recognized, measured, and recorded. Species names were updated using The Plant List [26], and enumerated trees were identified using known taxonomic keys [27]. Trees and saplings were tagged to avoid double enumeration. All measurements were recorded on a standardized data sheet. An experienced botanist was engaged to identify plant species, and data on dbh and total tree height were also collected.

2.3.2. Conservation status

Forest vegetation recovery was rated according to Hawthorne's [28] Star Rating Conservation Status, which is divided into Black, Gold, Blue, Scarlet, Red, Pink, and Green Star species.

2.3.3. Functional groups classification

Functional grouping categorization was chosen based on the finding that varied levels of disturbance (such as logging intensities) affect light availability, which affects regeneration and growth in the groups [29]. The plant species in the two separate rehabilitation loading bays and unlogged areas were determined based on their group composition as pioneer (P), non-pioneer light demanders (N.P.L.D.), and shade-bearers (SB) using [28] classification.

2.3.4. Laboratory analyses

Laboratory analyses were carried out in the Soil Science Laboratory of the Department of Crop and Soil Sciences, KNUST. Soil samples were air-dried, crushed, and sieved through a 2 mm mesh sieve. Core samples were dried in an oven at 105 °C for 24 h for bulk density determination. In a 1:1 soil: water suspension, the pH of the soils was determined using a pH meter (PHS–3E 510). The conductivity meter was

used to determine the electrical conductivity, as described by Black [30]. The Walkley and Black wet oxidation method was used to estimate soil organic carbon (SOC), while the Kjeldahl method was used to determine total nitrogen (N). Soil organic matter (SOM) content was determined by multiplying the SOC by 1.724; OM = % SOC × 1.724 (1.724 is the Van Bemellean factor). The amount of phosphorus that was readily accessible was determined using the Bray 1 method [31]. Exchangeable hydrogen and aluminium were extracted with 1.0 M KCl and titrated with HCL and 0.1 M NaOH, while exchangeable bases (Ca²⁺, Mg²⁺, K⁺, and Na⁺) were extracted using ammonium acetate (1.0 M NH₄OAc) at pH 7 [30]. The sum of the exchangeable bases was used to calculate the cation exchange capacity (CEC).

2.4. Statistical analyses

2.4.1. Species abundance and composition

The field data were entered into Microsoft Excel and screened for data entry errors. Data from the entire plot laid to sample all life forms were pooled for each site before the analysis. A priori test for normality of data distribution was carried out, using the Shapiro-Wilk test. This was to determine the appropriate statistical test for the subject data (i.e., parametric or nonparametric data analysis approach) [32]. The Kruskal-Wallis test (a rank-based nonparametric test approach) was used to test whether overall species abundance differed significantly between the three plots since the data set was not normally distributed. Using Dunn's post hoc multiple comparison tests [33], the variations in species abundance and richness between each of the three plots were then determined. The Levene test was used to test the homogeneity of species variance across sample plots [34].

2.4.2. Species diversity determination

Species diversity was extrapolated using Hill's [35] diversity numbers. This can be calculated mathematically by the equation below;

$$qD_a = \left(\sum_{j=1}^{N} w_j \sum_{i=1}^{s} p_i^q\right)^{\frac{1}{(1-q)}}$$
(1)

where:

 ${}^{q}D_{\alpha}$ represents alpha diversity concerning the first three non-decimal hill numbers i.e., q = 0 equals species richness, q = 1 equals the exponential of Shannon index and q = 2 equals the reciprocal of Simpson's index. N denotes the number of samples; S is the number of categories within each sample, i and j are the categories and sample indices respectively, pi/j is the proportional abundance of the *i*-th species in the *j*-th sample, and wj is the proportional abundance of the *j*-th sample relative to the entire dataset.

Hill diversity number was used because it has a high tendency to give much priority to both rare and dominant species and also takes into consideration the relative abundance of species. This was done using PAST software version 3.22. Kruskal-Walli's test was used to test the significant difference within samples with a 95%

confidential level.

2.4.3. Species richness determination

Species richness was determined by the construction of graphs using individual rarefaction curves in PAST software version 3.22. This curve normally plots the number of individual species on the *x*-axis, which denotes the richness of species, and the species abundance on the *y*-axis. The Wilcoxon one-sample matched-pair test was used to test the significant differences within samples with a 95% confidence level.

2.4.4. Species evenness determination

Species evenness was calculated as:

$$E = H'/\ln S \tag{2}$$

where E is the equitability index, H' is the Shannon diversity index, and S is the total diversity plot species richness [36].

2.4.5. Species similarity determination

Species composition in terms of abundance within all sites was compared using the Bray-Curtis similarity index computed as follows;

$$BCij = (2Cij/Si + Sj) \tag{3}$$

(5)

where *BCij* is the Bray-Curtis index, *i* and *j* are the two sites, *Si* is the total number of species counted on site *i*, *Sj* is the total number of species counted on *site j*, and *Cij* is the sum of only the lesser counts for each species found in the sites.

2.4.6. Species pioneer index (Pi) determination

The species pioneer index (Pi) was calculated using the formula below;

 $Pi = ((Number of Pioneer \times Pioneer) + (NPLD \times Number of NPLD weight)/Total (4)$ number of individual species sampled) × 100

where:

Pioneer weight = 2, NPLD weight = 1, Pioneers—Number of Pioneer species, NPLD—Number of NPLD species [37].

2.4.7. Species genetic heat index (GHI) determination

The Genetic Heat Index (GHI) of species was calculated using the formula below;

 $GHI = ((BK \times BK \text{ weight}) + (GD \times GD \text{ weight}) + (BU \times BU \text{ weight}) + (RD \times RD \text{ weight}) + GN \times GN \text{ weight})/BK + GD + BU + RD + GN) \times 100$

where:

BK, GD, BU, and GN represent Black, Blue, Gold, and Green star species, respectively; RD represents red, scarlet, and pink star species. BK weight = 27, GD weight = 9, BU weight = 3, RD weight = 1 and GN weight = 0 [37].

Using Statistix 8.0 software, the growth and soil data were subjected to analysis of variance (ANOVA). At a 5% probability level, mean separations were done using the Tukey HSD method. The relationships between bulk density, pH, EC, OM, and CEC were determined using regression and correlation analysis. The significance of the relationships was determined at a 5% level of probability.

3. Results

3.1. Floristic composition of regenerated species

A total of 231 individuals from 38 different species in 20 families and 6 life forms were recorded across the sampled plots used for the study (**Table 1**). The highest number of individuals (104) from 21 different species in 14 groups and 5 lifeforms were found at loading bay sites that had no topsoil added (RNT). This was followed closely by the undisturbed (control) plots with 84 individuals from 19 different species in 14 families and 2 lifeforms, while the loading bay with topsoil added (RAT) had the least number of individuals (43) from 17 different species in 12 families and 4 life forms. *Neuropeltis prevosteoides* (7), *Culcasia scandens* (7), and *Hymenostegia afzelii* (5) were the three most dominant species in RAT plots. On the RNT plots, *Diospyros canaliculata* (27), *Griffonia simplicifolia* (18), and *Celtis milbreadii* (13) were dominant. The dominant species within the control (UL) plots were *Culcasia scandens* (17), *Chlamydocarya macrocarpa* (16), and *Griffonia simplicifolia* (10). The significance test showed no significant differences in the number of species among all treatment plots (H = 1.193, P = 0.502, Kruskal-Wallis Test).

Table 1. Summary distribution of species within treatment plots.

| Treatment plots | Number of individuals | Taxa | Mean species occurrence (±SD) | Family | Lifeform |
|-----------------|-----------------------|------|-------------------------------|--------|----------|
| RAT | 43 | 17 | 1.13 ± 0.3 | 12 | 4 |
| RNT | 104 | 21 | 2.74 ± 0.9 | 14 | 5 |
| Control (UL) | 84 | 19 | 2.21 ± 0.7 | 14 | 2 |
| Total | 231 | 38 | | 20 | 6 |

3.2. Species similarity in different disturbance regimes

High correspondence analysis (HCA), according to a test for species composition similarity, linked blocks of similar species assemblage. The degree of species resemblance between each of the three treatment plots is represented by the Euclidean distance. The level of dissimilarity increases as the Euclidean distance from zero increases. The observations in **Figure 2** show that species observed on RNT plots were more similar to species on the control (UL) plots than species on the RAT plot compared to those on the control (UL) plots. However, the farther the Euclidean distance from zero, the higher the level of dissimilarity, and since the Bray-Curtis values recorded were closer to 0 than 1, the treatment plots are said to have dissimilar species among them.



Figure 2. Similarity of plant species composition among the three sampling sites.

3.3. Species distribution among the families

A total of 20 different families were recorded across the study site, namely, Adiantaceae, Apocynaceae, Araceae, Caesalpiniaceae, Caesalpiniaceae, Celastraceae, Chrysobalanaceae, Commelinaceae, Convolvulaceae, Ebenaceae, Malvaceae, Meliaceae, Icacinaceae, loganiaceae, Mimosaceae, Moraceae, Olacaceae, Papilionaceae, Rubiaceae and Sapindaceae (Figure 3). The family with the highest number of individual plant species was Ebenaceae (23) and was predominant in the RNT plots. This was followed closely by Araceae and Caesalpiniaceae, 18 individual species each in the control (UL) and RNT plots, respectively. However, the most dominant family across the study sites was *Caesalpiniaceae* (14%), followed by *Araceae* (13%) and *Convolvulaceae* (12%).



Figure 3. Distribution of families of individual species in the study site.

3.4. Species distribution among the life forms

Six (6) different lifeforms were observed across the treatment plots: climbers, ferns, herbs, lianas, shrubs, and trees (**Figure 4**). Four (4) of the lifeforms (climbers, lianas, shrubs, and trees) were present on the RAT plots, five (5) were on the RNT plots (climbers, ferns, herbs, lianas and trees) and only two (2) were present on the

control (UL) plots, climbers and trees. Climbers were the dominant lifeforms (61.5%) across the plots, followed by trees (32.5%), ferns (2.6%), lianas (2.2%), shrubs (0.9%) and herbs (0.4%). Among the treatment plots, the control (UL) had the highest number of climbers (72 species), while the RAT plots had the least (23 species). Trees were dominant in the RNT plots (46 species), followed by the RAT plots (17 species) and less dominant in the control (UL) plots (12 species).



Figure 4. Distribution of lifeforms of individual species in the study site.

3.5. Functional groups of species

Shade-bearers (45%) and non-pioneer light-demanders (43%) were the two species that were most prevalent across the treatment plots, while pioneer species were the least (13%). Pioneers were higher in RAT and RNT plots than in the control (UL) plots, however, there was a significantly higher number of NPLD in the control (UL) plots than in the RAT plots (**Figure 5**). Given this, the RNT plots had the highest pioneer index (30), followed by the control (UL) plots (22), and the RAT plots had the least (20).



Figure 5. Functional group of species within the treatment plots.

3.6. Conservation status of species within the treatment plots

Figure 6 presents the various plant species' star ratings for their conservation

status. Green star species were the dominant species across the treatment plots at 82%, followed by Blue star species (12%). The remaining species were Pink and Scarlet stars, 2% each, and Gold, Red, and Black stars making up 1% each of the plant species. The genetic heat index (GHI) for the star-rated species was highest in RAT plots (116) followed by the control (UL) plots (92) and the RNT plots had the least (36).



Figure 6. Star ratings for the plant species sampled from the treatment plots.

3.7. Species diversity

The species diversity curve was plotted using Hill diversity numbers (**Figure 7**). The shallower curve implies a higher diversity, whereas the steeper curve denotes a less diverse site. Relatively, species on the RAT plots were the most diverse with a hill number of 2.785, followed by control (UL) plots, 2.496, while the RNT plots had the least diversity of species (2.383). However, no significant differences in species diversity were observed among the treatment plots (H = 0.09, P = 0.96, Kruskal-Wallis Test).



Figure 7. Species diversity within treatment plots.

3.8. Species richness

Species rarefaction curve was used to extrapolate the species richness (Figure 8).

A Wilcoxon one-sample pairwise test showed no significant difference in species richness among treatment plots. (W = 1.5, P = 1.0, Wilcoxon Test). Nonetheless, RNT plots comparatively had the highest species richness (21 individual species). This was followed by the control (UL) plots, with 19 species, while the RAT plots had the least richness with 17 species.



Figure 8. Species richness within treatment plots.

3.9. Species evenness

Figure 9 presents the species evenness with the treatment plots. Species on the RAT plots were the most evenly distributed with a Pielou's equitability index of 0.904 J, followed by species on the control (UL) plots (0.837 J) and RNT plots had the least distribution of species (0.816 J).



Figure 9. Species evenness within the treatment plots.

3.10. Regeneration of plant species

Mean height, diameter, basal area of plant species

Tree height, diameter, and basal area were measured, and the means of the results are presented in **Table 2**. Averagely, plants were significantly (p < 0.05) taller in RAT (8.91 m) and RNT (10.64 m) plots than the control (UL) plot (5.69 m). Similarly, the mean diameter of the plant species was larger in the RAT and RNT plots, 7.49 and 8.58 cm, respectively, compared to that of the control (UL) plot (2.35 cm). The mean basal area of the plant species was largest on the RNT plots (113.27 m²) followed by the RAT plots (68.81 m²), and least on the control (UL) plots (5.21 m²).

| Treatment plot | Height (m) | DBH (cm) | Basal area (m ²) |
|----------------|-----------------------|-----------------------|------------------------------|
| Control (UL) | 5.69 ± 3.6^{b} | 2.35 ± 1.8^{b} | $5.21 \pm 4.2^{\circ}$ |
| RAT | $8.91\pm5.2^{\rm a}$ | 7.49 ± 5.6^{a} | 68.81 ± 20.3^b |
| RNT | $10.64\pm7.3^{\rm a}$ | $8.58\pm 6.6^{\rm a}$ | $113.27\pm41.2^{\rm a}$ |

Table 2. Mean (\pm SD) tree height, DBH, and basal area, and of plant species on the treatment plots.

Means with different letter superscripts in a column are significantly different (p < 0.05).

3.11. Soil characteristics of the treatment plots

Except for bulk density, all soil properties measured generally decreased with increasing depth across the treatment plots. Soil bulk density at the 0–15 cm depth was significantly (p < 0.05) highest on the RNT plots (1.69 g cm⁻³) followed by the RAT plots (1.53 g cm⁻³), and least on the control (UL) plots (1.05 g cm⁻³) (**Figure 10**). A similar trend was observed at the 15–30 cm depth. Soil pH was similar between the control (UL) and RAT plots, 6.12 and 6.05, respectively, but significantly higher (p < 0.05) pH was recorded on the RNT plot (5.7) at the 0–15 cm depth (**Figure 11**). However, there were no significant differences in pH among the treatment plots at 15–30 cm depth. Electrical conductivity (EC) of soil was not significantly different between the control (UL) and the RAT plots at both depths (**Figure 12**). However, EC recorded in soils of the control (UL) plots, 300 and 138 us cm⁻¹ at the 0–15 and 15–30 cm depths, respectively, was significantly (p < 0.05) higher than values recorded in the RNT plots, 213 and 59 us cm⁻¹. EC was similar between the RAT and RNT at the 0–15 cm depth, but different at the 15–30 cm depth.



Figure 10. Soil bulk density at two different depths within the treatment plots.



Figure 11. Soil pH at two different depths within the treatment plots.



Figure 12. Electrical conductivity of soils at two different depths within the treatment plots.

Soil organic carbon (SOC) and organic matter (SOM) were not different (p > 0.05) between the control (UL) and RAT plots at both depths (Table 3). SOC and OM were 44% and 48% more in the control (UL) plot at the 0-15 and 15-30 cm depths, respectively than in the RNT plot. Also, at the 15–30 cm depth, the RAT plot had higher SOC and OM contents, 1.60% and 2.75% respectively, than the RNT plot, 1.17 and 2.02%. Soils in the control (UL) plots had higher nitrogen (N) content (0.52%) at the 0–15 cm depth compared to the RAT and RNT plots. At 15–30 cm depth, N was similar between the control (UL) and RAT plots, 0.17% each, but higher than the RNT plot (0.12%). The control (UL) and RNT plots significantly (p < 0.05) had higher available phosphorus (P) content (2.85 and 2.26 mg kg⁻¹) at the 0–15 cm depth than the RAT plot (1.08 mg kg⁻¹). At the 15–30 cm depth, P content was in increasing order of 0.5 < 1.67 < 2.85 mg kg⁻¹ in the RAT, RNT, and control (UL) plots respectively. Exchangeable potassium (K^+), calcium (Ca^{2+}), and magnesium (Mg^{2+}) were similar (p > 0.05) among the soils in all the treatment plots at the 0–15 cm depth, however, at the 15–30 cm depth, the control (UL) had higher K⁺ and Mg²⁺ than the RNT plot. Cation exchange capacity (CEC) at the 0–15 cm depth was significantly (p < 0.05) higher in the control (UL) plot (10.15 cmol₍₊₎ kg⁻¹) than the RAT and RNT plots, 7.68 and 7.56 $\text{cmol}_{(+)}$ kg⁻¹ respectively. A similar trend was observed at the 15–30 cm depth.

No significant (p > 0.05) differences in exchangeable sodium (Na⁺), hydrogen (H⁺), and aluminium (Al⁺) were observed among the treatment plots at both depths (**Table 3**).

| Treatment | Depth (cm) | Organic carbon | Organic matter | Total nitrogen | Ava phosphorus | Exch. K ⁺ | Exch. Ca ²⁺ | Exch. Mg ²⁺ | Exch. Na ⁺ | CEC | Exch. H ⁺ | Exch. Al ³⁺ |
|-----------|------------|----------------------|-------------------------|------------------------|---|-------------------------|------------------------|------------------------|--------------------------|--------------------------|-------------------------|------------------------|
| | | (%) | | (mg kg ⁻¹) | (cmol ₍₊₎ kg ⁻¹) | | | | | | | |
| Control | 0–15 | 2.65 ± 0.2^{a} | 4.57 ± 0.4^{a} | 0.52 ± 0.1^{a} | $2.85\pm0.4^{\rm a}$ | 0.68 ± 0.2^{a} | $7.27 \pm 1.0^{\rm a}$ | 2.20 ± 0.3^{ab} | 0.002 ± 0.0^{a} | 10.15 ± 1.3^{a} | 0.61 ± 0.2^{a} | 0.45 ± 0.2^{a} |
| RAT | | 2.34 ± 0.3^{a} | $4.04\pm0.5^{\rm a}$ | 0.22 ± 0.1^{b} | 1.08 ± 0.2^{b} | 0.41 ± 0.2^{ab} | 5.67 ± 0.5^{ab} | 1.60 ± 0.2^{ab} | 0.002 ± 0.0^{a} | $7.68 \pm 1.1^{\rm b}$ | $0.61\pm0.2^{\text{a}}$ | 0.35 ± 0.1^{a} |
| RNT | | 1.84 ± 0.1^{b} | 3.17 ± 0.3^{b} | 0.18 ± 0.0^{b} | $2.26\pm0.3^{\rm a}$ | 0.56 ± 0.1^{ab} | 5.00 ± 0.3^{ab} | 2.00 ± 0.1^{ab} | $0.002\pm0.0^{\text{a}}$ | 7.56 ± 0.8^{b} | 0.61 ± 0.1^{a} | $0.67\pm0.2^{\rm a}$ |
| Control | 15–30 | 1.73 ± 0.0^{b} | $2.98\pm0.3^{\text{b}}$ | 0.17 ± 0.0^{b} | $2.85\pm0.3^{\rm a}$ | $0.62\pm0.2^{\text{a}}$ | 6.00 ± 0.6^{ab} | 3.53 ± 0.2^{a} | 0.01 ± 0.0^{a} | $10.16\pm1.3^{\text{a}}$ | 0.56 ± 0.1^{a} | 0.45 ± 0.1^{a} |
| RAT | | 1.60 ± 0.1^{b} | $2.75\pm0.2^{\text{b}}$ | 0.17 ± 0.0^{b} | $0.50\pm0.0^{\rm c}$ | 0.47 ± 0.1^{ab} | 5.07 ± 0.7^{ab} | 1.80 ± 0.1^{ab} | 0.01 ± 0.0^{a} | 7.36 ± 0.7^{b} | 0.61 ± 0.2^{a} | 0.61 ± 0.2^{a} |
| RNT | | $1.17\pm0.0^{\rm c}$ | $2.02\pm0.2^{\rm c}$ | $0.12\pm0.2^{\rm c}$ | $1.67\pm0.2^{\rm b}$ | 0.28 ± 0.0^{b} | 3.60 ± 0.3^{b} | 1.20 ± 0.1^{b} | 0.01 ± 0.0^{a} | $5.10\pm0.4^{\rm c}$ | $1.28\pm0.4^{\rm a}$ | 0.78 ± 0.2^{a} |

Table 3. Soil chemical properties at two different depths within the treatment plots.

Means with different letter superscripts in a column are significantly different (p < 0.05).

3.12. Relationships between soil properties

Regression and correlation analyses were done to establish relationships between some soil properties. A significant and very strong negative relationship was observed between soil organic matter (SOM) and bulk density (BD) (r = -0.92) with OM accounting for 84.75% ($R^2 = 0.8475$) of variations in BD across the treatment plots (**Figure 13A**). SOM significantly positively correlated with soil pH (r = 0.91) and was responsible for 83.97% of changes in soil pH ($R^2 = 0.8397$) within the treatment plots (**Figure 13B**). **Figure 13E** revealed that there was a very strong positive relationship between SOM and EC (r = 0.97) and variations in EC across the treatment plots were 94.19% dependent on SOM ($R^2 = 0.9419$). SOM again accounted for 45.33% variations in CEC across the treatment plots (**Figure 13C**), and a strong positive relationship (r = 0.67) was observed between the two properties. There was also a strong positive relationship between CEC and pH across the treatment plots, as the former accounted for 56.29% of variations in the latter (**Figure 13D**).



Figure 13. Relationship between soil properties. (A) relationship between SOM and soil bulk density; (B) relationship between SOM and soil pH; (C) relationship between SOM and soil CEC; (D) relationship between soil CEC and soil pH; (E) relationship between SOM and soil EC; *= significant at a 5% level of probability (p < 0.05).

4. Discussion

4.1. Species composition, abundance, and distribution

The results of this study revealed no significant differences (H = 1.193, P =0.502, Kruskal-Wallis Test) in the number of individual species enumerated among the loading bay with topsoil added (RAT), loading bays with no topsoil added (RNT) and the undisturbed site (control). However, other studies have reported a higher number of species in logged areas (skid trails, felling gaps) than in undisturbed forest areas [12,22,25,38]. The fact that there was no significant difference between the number of species recorded on the undisturbed plot and loading bay with topsoil added (RAT) is an indication that top soils can be added to highly disturbed areas such as loading bays, skid trails, and gaps in forest ecosystems after logging as a rehabilitation strategy. Also, the same number of species recorded between the unlogged areas and loading bay with no topsoil added (RNT) could mean that 18 years after logging is not exhaustive enough as depicted by the shape of the species accumulation curves (Figure 8), which indicates that none of them had reached the point of plateau. The differences in the dominant species composition observed in this study among the rehabilitation strategies can be due to differences in each species' unique pattern of regeneration as a result of disturbance from logging. This finding supports the commonly held belief that forest regrowth following logging typically takes years and results in significant variations in the species composition, diversity, and structure from the original vegetation [39–41]. The test of similarity and dissimilarity (Figure

2) showed that species composition was dissimilar, as the Bray-Curtis values were closer to 0 than 1. [22] observed Musanga cercropoides, Ceiba pentandra, and Albizia zygia as the dominant species on the study site seven years after logging and predicted changes in species composition with time. The prediction was evident in the present study as these species did not show up or were insignificant, and the changes could account for the higher dissimilarity of species composition. The RNT plot was the most disturbed site among the study sites since the RAT plot was at least rehabilitated with topsoil to improve the soil. The findings, however, support the theory that the disturbed site emulates the pre-existing site because it has an identical species composition to the undisturbed area. The three most dominant families across the study sites were Caesalpiniaceae (14%), Araceae (13%), and Convolvulaceae (12%). The dominance of these families was inevitable, as 61.5% of the lifeforms across the study sites were climbers (Figure 4). The higher number of tree species enumerated in the RNT (46) and RAT (17) plots than the undisturbed plot (12) indicates that the loading bays are recovering from the impact of logging. There is a conception that climbers prefer gaps and open canopies [42], which was manifested in this study as more climbers were recorded in the loading bays compared to the other lifeforms.

Across the study sites, shade bearers were the most dominant species; however, pioneer species were dominant in the RAT and RNT plots compared to the undisturbed plot (**Figure 5**). These observations correspond to the results of previous studies on the same site. The first study by [22] on seedling census showed pioneers as the dominant species guild. However, [38] observed non-pioneers as the dominant species three years following the first study. The shift in dominance from more light-

demanding pioneers to the shade-loving species could be due to the intrinsic responses of the guilds to changes in the microclimate of the sites with time. The authors hypothesize that initial logging operations' high levels of light may have encouraged the regeneration of pioneers, while later, lower levels of irradiance and temperature may have favored non-pioneers, particularly shade bearers. The larger number of pioneers and NPLDs in RAT and RNT plots compared to undisturbed plots can be attributed to logging disturbance creating canopy gaps and increasing the incidence of sunlight on the forest floors [43,44]. Lower pioneer index values (20-30) throughout the plots in this study are an indication that the plots are progressing toward achieving primary status since a higher pioneer index denotes a forest's secondary character [45]. Studies have revealed that green star species are dominant in most forest ecosystems in Ghana [3,46]. Hawthorne and Gyakari [45] further revealed that the species are of no particular conservation concern in Ghana. The dominance of green star species in this study was expected. Comparatively, GHI was higher in the RAT plot (116) and could be categorized as having moderate conservation value ($100 \ge GHI \le 150$) than the undisturbed plot (92) and RNT plot (36) within categories low (50 < GHI < 100) and very low (<50), respectively [37]. The higher GHI observed in the RAT plot suggests the potential for rehabilitation of disturbed areas in the forest ecosystem to encourage the growth of species of high conservation status. The GHI values obtained in this study were lower compared with values documented of 301 in the Ankasa Conservation Area and 269 in Neung North Forest Reserve [37,47]. This result is not surprising because reports show that even under pristine conditions, the moist semideciduous forest zone, including the current study area, tends to have low to moderate GHI values compared to the wet evergreen forests and southern dry forests [37,47].

The use of Hill numbers to measure diversity within the plots showed that the RAT plot (Hill number = 2.785) was more diverse, followed by the control (UL) plots (Hill number = 2.496), and the RNT plots had the least diversity of species (Hill number = 2.383). Shannon Weiner's diversity index, Simpson's diversity index, and species relative abundance are all taken into account in diversity calculations using Hill numbers. Therefore, a more diversified site also has the most evenly distributed species. This was evident from the study, as the RAT plot with a higher diversity of species also had the most even distribution of species compared to the RNT and the control. The result contradicts the observation made by [48], where higher diversity was recorded in an unlogged part than in the disturbed part of the forest in Asankrangwa in the Western region of Ghana. Nonetheless, there is no significant difference in both diversity (H = 0.09, P = 0.96, Kruskal-Wallis Test) and richness (W = 1.5, P = 1.00, Wilcoxon Test) within all treatment plots, implying that topsoil addition has minimal impacts on species diversity and richness.

4.2. Regeneration of plant species

Tree height, diameter, mean basal area, and volume were measured to examine the regeneration capacity of the forest in loading bays following logging. The results revealed that growth was generally profuse in the disturbed plots compared to the undisturbed plots. Average tree height, basal area, and volume significantly increased in the RAT and RNT plots over the undisturbed plot (**Table 2**). This was a result of relatively higher numbers of trees recorded on these disturbed plots than the undisturbed plot (**Figure 4**) as trees have bigger diameters and higher heights compared to other lifeforms in the forest ecosystem. According to [49], in most forests, the number of trees decreased with increased diameter, but the results of this study did not follow such an assumption as the RNT and RAT plot recorded a higher number of plant species than the control (UL) (**Table 1**) and also recorded an averagely bigger tree diameter than the control (UL). The observations in this study conform to the results of other studies where the growth of plants was higher in disturbed sites than in undisturbed sites. For example, [50] reported higher basal area following disturbances compared to undisturbed sites. Contrarily, other researchers have reported higher basal area in intact areas relative to disturbed sites: [51] in Kibale National Park, Uganda; [52] in Little Andaman Island, India, and [40] Asenanyo Forest Reserve, Ghana. These were evidence of the impact of logging on the regeneration of forests. Higher basal areas in the undisturbed areas were attributable to the absence of disturbances, which mostly remove large trees or cause significant damage to undergrowth [52].

4.3. Soil characteristics of the study sites

Soil is one of the most affected resources during the harvesting of tree crops in forest ecosystems [53]. The maintenance of soil sustainability is highly questioned in commercially managed forests where stands are clear-cut and heavy machinery is used for harvesting and site preparation because the plant cover is disturbed and the risk of soil erosion increases [54,55]. Disturbances may cause degradation of soil properties, which may reduce the productivity of the soil. Soil compaction as well as a decrease in total porosity are unavoidable results of ground skidding operations that can vary in intensity and distribution as a result of the interaction between machine and site factors at the time of harvest [56]. Soil bulk density, a commonly used property to determine the compactness of soil, was significantly higher in the disturbed plots (RNT and RAT plots) at both depths than in the undisturbed plot (Figure 10). This could be due to the impact of heavy machine activities in these sites during the logging period, as many activities are carried out at loading bays that result in compaction of the soil. Topsoil removal and heavy traffic on the soil during the timber extraction may have also contributed to the high bulk density within the loading area. This observation could also be attributed to the higher soil organic matter (SOM) recorded in the undisturbed plot since SOM can improve the structure of the soil. The negative correlation recorded between SOM and soil bulk density (Figure 13A) further supports the importance of SOM in improving soil structure. Other studies have also reported higher compaction in disturbed sites than in undisturbed sites in forests [57–59]. Lower bulk density values recorded in the RAT plot compared to the RNT plot indicate that disturbance sites, such as loading bays, skid trails, and gaps, can be rehabilitated through the addition of topsoil to reduce compaction after logging.

According to McNabb et al. [60], the best soil for the growth of tropical trees must have a pH range between 6.0 and 7.0. Soil pH values recorded in the RAT and undisturbed plots at the 0–15 cm depth were within this range, while the rest were below. However, pH values recorded across the plots indicated that the soils were slightly acidic. Soils from the RNT plots were more acidic than the undisturbed plot probably because of higher SOM and CEC obtained in the undisturbed plot than the

RNT plot (**Table 3**). The relationships between these properties and pH were positive (**Figure 13B,D**), indicating that the higher the SOM and CEC in the soil, the lower the acidity. Kinjanjui et al. [41] also reported higher pH in undisturbed forest soil than in disturbed soils in the Mau Forest complex, Kenya. However, reports from other studies prove otherwise where there was an increase in pH, Ca, and Mg in an eastern Amazon Forest after 16 years of logging in areas such as forest roads and loading bays with reducing conditions which may result from Fe reduction, freeing exchange sites that can retain these cations [61]. Variations in EC across the plots and between the depths can also be attributed to the variations in SOM content recorded in the study. A positive relationship observed between SOM and EC (**Figure 13C**) further explains the significance of SOM to EC of the soil. The results of this study also show that pH and EC were similar between the RAT and undisturbed plots, signifying the importance of topsoil addition as a rehabilitation strategy in managing disturbed areas after logging.

Tropical forest soils are generally known to be poor in nutrients, and much of the nutrients are held in the aboveground vegetation. Apart from soil organic carbon (SOC) and total nitrogen (N), which were high and adequate, respectively, the amounts obtained for all other nutrients were generally low across all the plots. SOC, SOM, and N were higher in the undisturbed plots compared to the RNT plot at both depths (Table 3). This is a result of the removal of the topsoil, where most SOC and SOM are stored within the soil profile from the loading bay after logging. A study on the impact of selective logging on SOC by [62] also reported a lower SOC pool in the first 30 cm of disturbed forest area compared to the amount recorded in the undisturbed forest. Losses of carbon from forest soils after selective logging activities were observed by [63] until a new equilibrium was established between 10 and 18 years after logging, and the forest soil stopped losing SOC. On the other hand, reductions in SOM, N, and P with increasing forest disturbances were observed at the Mau Forest complex, Kenya, by [41], but similar concentrations of K, Ca, Mg, and Na were observed in disturbed and undisturbed forests, as observed in this study (Table 3). Loss of organic matter through the removal of topsoil, accelerated oxidation, higher daytime temperatures, and reduced daytime humidity through open canopies probably accounted for the low soil nutrient levels in the RNT plot [41,64]. However, [65] observed that SOC can react differently to different levels of disturbances, which probably explains the similarly high amount of SOC recorded between the RAT plot (2.65%) and the undisturbed plot (2.34%), as the addition of topsoil altered the level of disturbance compared to the RNT plot. A measure of the ability of soil to hold positively charged ions is termed cation exchange capacity (CEC). Several negative charges on the soil colloids, resulting from increased SOM content in the soil, enhance CEC and promote nutrient retention in the topsoil [66]. Hence, the higher SOM content of the undisturbed plot (10.15 and 10.16 $\text{cmol}_{(+)}$ kg-1) explains its higher CEC compared to that of the RAT (7.68 and 7.36 cmol₍₊₎ kg-1) and RNT (7.56 and 5.10 $cmol_{(+)}$ kg-1) plots at 0-15 and 15-30 cm depths, respectively. This was further confirmed by the regression and correlation analyses, where a strong positive relationship was recorded between SOM and CEC, with SOM accounting for 45.33% of the variations in CEC (Figure 13C).

5. Conclusions

The result of the study showed no difference in the number of species enumerated in the loading bays and the undisturbed area 18 years after logging. The higher number of trees observed in the loading bay with topsoil added (RAT) and the loading bay with no topsoil added (RNT) compared to the undisturbed area indicates that the loading bays are recovering from the impact of logging. The higher number of pioneers and NPLDs in RAT and RNT plots compared to undisturbed plots can be attributed to the openings of canopy gaps. The higher GHI observed in the RAT plot suggests the potential for rehabilitation of disturbed areas in the forest ecosystem to encourage the growth of species of high conservation status. However, species diversity and richness were the same across the plots which implies that topsoil addition had minimal impact on species diversity and richness.

Mean tree height, diameter, basal area, and volume increased in the RAT and RNT plots over the undisturbed plot due to the relatively higher numbers of trees recorded on these disturbed plots than the undisturbed plot which suggests that the growth of tree species was profuse in the disturbed plots compared to the undisturbed plot.

Topsoil removal and heavy traffic from logging machinery resulted in the higher soil bulk density in the RNT plot. The lower soil bulk density recorded in the RAT plot compared to the RNT plot indicates that disturbance sites, such as loading bays, skid trails, and gaps can be rehabilitated through the addition of topsoil to reduce compaction after logging. Further, the similar soil pH and EC recorded between the RAT and undisturbed plots signifies the importance of topsoil addition as a rehabilitation strategy in managing disturbed areas in forests after logging. The similar high amount of SOM recorded between the RAT and the undisturbed plots further confirms the importance of adding topsoil to disturbed areas after forest logging to improve the fertility of the forest soil.

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Abbreviations

BDH = Diameter at breast height CEC = Cation exchange capacity EC = Electrical conductivity GHI = Genetic heat index HCA = High correspondence analysis KNUST = Kwame Nkrumah University of Science and Technology N = Nitrogen NPLDs = Non-pioneer light demanders P = Phosphorus RAT = Regeneration added topsoil RNT = Regeneration no topsoil RWC = Research Working Circle SOC = Soil organic carbon SOM = Soil organic matter UL = Unlogged area

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