BRANCH MANAGERS: HOW ECUADORIAN BIRDS RESPOND TO REFORESTATION

AN HONORS THESIS

SUBMITTED ON THE 25 DAY OF APRIL, 2026

TO THE DEPARTMENT OF ECOLOGY AND EVOLUTIONARY BIOLOGY

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS

OF THE HONORS PROGRAM

OF NEWCOMB-TULANE COLLEGE

TULANE UNIVERSITY

FOR THE DEGREE OF

BACHELOR OF SCIENCES

WITH HONORS IN ECOLOGY AND EVOLUTIONARY BIOLOGY

BY

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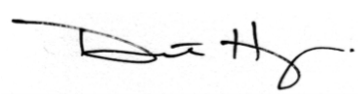

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Abstract

Continued deforestation of the Chocóan rainforest in Northwestern Ecuador has created stress for both humans and wild animals alike. This study explores the avian response to an ongoing applied nucleation experiment within the Fundación para la Conservación de los Andes Tropicales (FCAT) reserve, using bird community compositions as a metric to determine the treatments' success. The questions asked are: do the species richness values of each treatment change over time or as an aggregate, are the community compositions of each treatment significantly different, do the treatments attract different proportions of birds from different feeding guilds, and do the treatments attract different proportions of birds from different vertical niches over time or as an aggregate. The results of statistical analysis of point count data over the past 4 years is that of early succession. The community compositions of the reforestation plots do not undergo broad-scale changes, but some birds of different feeding guilds and vertical niches are present in higher concentrations in certain treatment types depending on tree diversity differences. For feeding guilds, Nectarivores see consistently higher proportions in High diversity plots, and Insectivores see consistently higher proportions in Low diversity plots. For vertical niches, Canopy bird abundance proportions are significantly higher in Low diversity plots, Open bird proportions are declining significantly over time, Understory bird proportions are increasing significantly over time, and High diversity plots support significantly more understory specialists. Overall, high diversity tree mixes seem to be fostering more complex bird communities, but continued monitoring is needed.

Introduction

The Chocó Biogeographical Region is a biodiversity hotspot, characterized by high rates of endemism and deforestation alike (Myers, 2000). High levels of human-induced habitat loss threaten the unique biodiversity of the region's Ecuadorian rainforests (Karubian et. al 2025). Particularly, in the Chocó, past governmental incentives in the 1960's to gain land titles though deforestation encouraged local farmers to convert more forest to pasture, even if it wasn't planned for immediate use. Now, deforestation is perpetuated due to economic necessity and how land is distributed across generations (Perlin 2022). Deforestation has destroyed about 60 percent of Ecuadorian land formerly inhabited by endemic species (Fagua and Ramsey 2019). If the habitats of keystone species disappear, so will the roles they provide. Once critical functions like seed dispersal and predator-prey balance are lost, the whole ecosystem risks a total collapse (Terborgh et. al. 2001).

To best protect these species, conservation groups like the Fundación para la Conservación de los Andes Tropicales (FCAT), an Ecuadorian NGO, have been working within Ecuador's Mache-Chindul ecological reserve to prevent further forest loss and restore deforested land to rainforest. The method FCAT is using is known as applied nucleation, which is planting tree islands across deforested land to attract local wildlife to help disperse seeds and naturally. Applied nucleation is a more effective method of reforestation because it mimics the patchy distribution of species natural succession (Holl et. al. 2020)

Specifically, FCAT is modeling their efforts after an applied nucleation study in Costa Rica that saw significantly higher biodiversity, woody plant recruitment, and seed dispersal when compared to both natural regeneration and mixed-tree plantations after fifteen years (Holl et. al. 2020). This study examines how the spacing of the tree islands, the diversity of the trees in the islands, and how the connective frugivore network resulting from the islands affects the regrowth of the plots (Holl et. al, 2020). Ensuring that these reforestation methods are effective is critical not only for the health of the forest, but also the people that live in the area. The Chocóan rainforest provides necessary ecosystem services to the community within it, such as providing water, timber, air purification, and land to sustain crops for their livelihoods, but the balance between using resources and replenishing them is an ongoing struggle (Eguiguren et. al. 2020). Furthermore, rainforests provide critical carbon stocks that mitigate the effects of climate change (Pan et al. 2011).

One way to assess forest health and the efficacy of restoration techniques is to regularly survey the avian community response to habitat changes. Birds are bioindicators (Anderle et. al., 2024; Van Bael 2013); their presence or absence in a place can provide insights into the biological health of an area due to species' survival needs. Many species of birds, like the *Ramphastos* toucans, are seed dispersers, meaning they play an active role in the reforestation of forests (Birds of the World 2026). In the rainforest specifically, birds account for most of the seed dispersal (Howe & Smallwood 1982). Additionally, nearly sixty percent of birds in tropical regions like the Chocó are especially sensitive to human-induced change, having played a major role in their declines (Sherry 2021; Rosenberg et al. 2019). As such, measuring bird diversity is a meaningful way to monitor the efficacy of reforestation efforts.

This project aims to analyze any changes in avian communities to applied nucleation treatments in the Ecuadorian Chocó, specifically testing whether treatment differences within tree spacing or tree diversity influence bird species diversity, community composition, guild makeup, and vertical niche makeup: all metrics which capture both quantitative and functional dimensions of avian community response, which can be used to determine the efficacy of the current reforestation efforts and FCAT's future endeavors. Four hypotheses were developed to guide the analysis.

The first hypothesis tests whether tree diversity or tree spacing within the islands influences the raw species richness of birds within the plots. Based on a habitat heterogeneity theory (Tews et al. 2004)., I predict that plots with lower spacing and more tree diversity will support a greater number of species of birds as the plots will provide a greater number of niches to be filled. However, lower diversity and higher spaced plots support for the intermediate disturbance hypothesis, predicting both early and late successional species can coexist within the same area without competitive exclusion (Connell 1978; Van Bael 2013).

The second hypothesis aims to test whether community composition differs between the individual plots beyond raw diversity metrics. Following the same ecological justification as the first hypothesis, I predict that differences in the tree islands' spacing and species diversity will produce significantly different bird communities between treatments, considering birds are very sensitive to even minute changes within a habitat due to their long history of evolutionary specialization (Sherry 2021). The distinct resource environments and structural conditions created by each treatment should selectively attract different species assemblages, producing communities that differ not just in how many species are present, but which species are present and in what proportions (Tews et al. 2004; Van Bael 2013).

The third hypothesis examines how the feeding guild composition responds to changes in the tree island diversity and spacing. Plant diversity is known to directly correlate with bird diversity (Whelan et al. 2015), so I predict that plots with higher tree diversity and less spacing will attract more frugivores due to the more complex floral landscape, which will overall support reforestation efforts and seed dispersal (Howe & Smallwood 1982). Conversely, I expect plots with with lower diversity and higher spacing to attract more insectivorous birds. These plots retain more early successional habitat characteristics, which have been demonstrated to support more arthropod diversity in dry forest (Díaz-Álvarez et al. 2023). This is also consistent with the intermediate disturbance hypothesis, as open habitats maintain greater heterogeneity at ground and shrub level, potentially making invertebrate prey more abundant (Connell 1978).

The fourth and final hypothesis explores how vertical niche composition responds to changes in tree island diversity and spacing. Based on habitat heterogeneity theory (Tews et al. 2004), I predict plots with less tree spacing and more tree diversity will be able to support a greater proportion of understory and canopy specialist birds, as the densely planted diverse tree community will support a greater variety of vertical niches. In contrast, the higher spaced, less diverse plots will lack canopy cover like an early successional area, attracting more shrub and open habitat birds (Díaz-Álvarez et al. 2023).

Methods

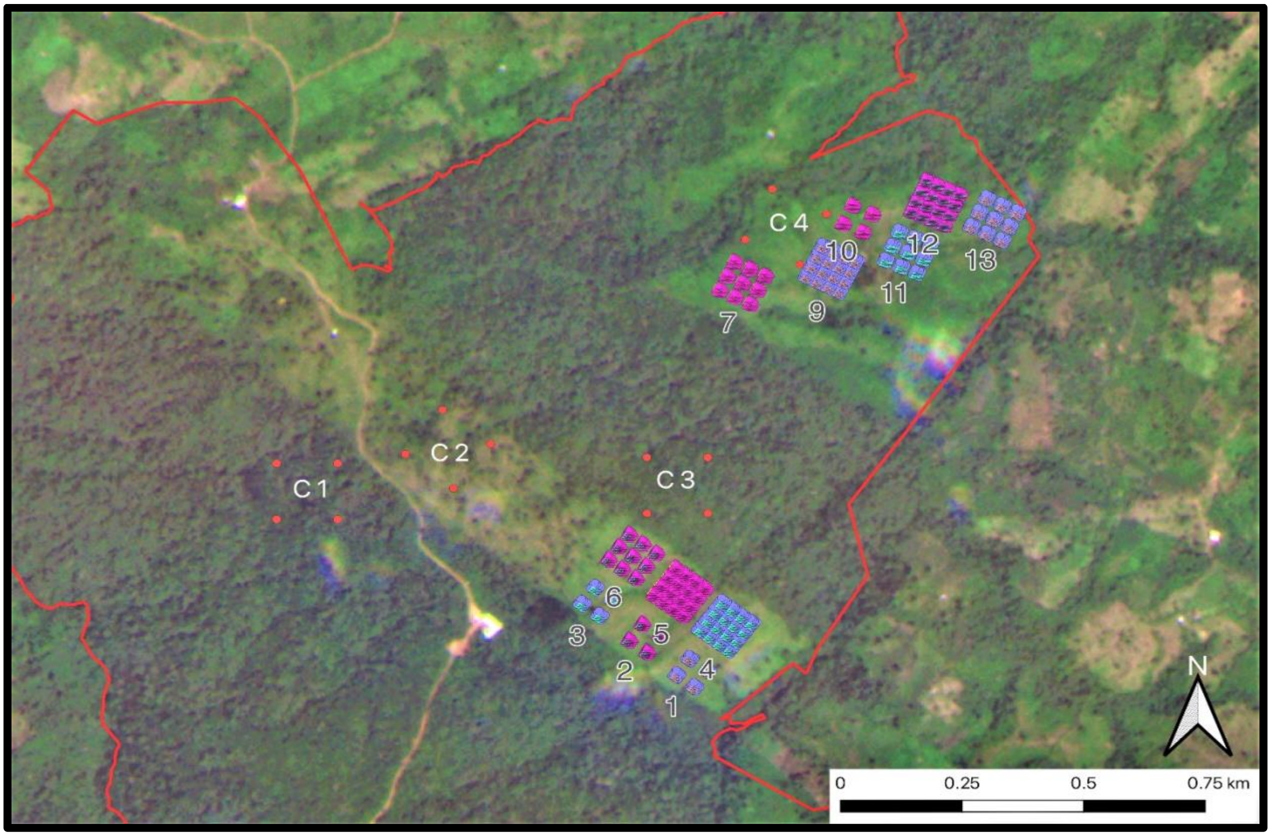


Figure 1: The location of the restoration plots for the applied nucleation experiment within FCAT's reserve, labeled by number. The red line represents the border of FCAT's reserve. Control plots are labeled with a C; C1 is a 15–20-year-old secondary forest. C2 is a 6-month-old abandoned cattle pasture with a high density of remnant trees. C3 is an old-growth forest. C4, also referred to as plot 8, is a randomly assigned treatment plot where no action was taken except removing cattle. Each square within each plot represents a tree nucleus. Refer to Table 1 to see the specific treatments for each plot.

Located in the FCAT reserve in Esmeraldas Province, Northwest Ecuador (Fig. 1). The restoration project is comprised of 12 125x125m plots, divided evenly among two tracts of land. Each of the twelve plots are being reforested though the process of applied nucleation, which involves planting islands of trees, 25 each, to catalyze the restoration process (Fig. 2). Three management variables are being tested in the FCAT study: the diversity of the trees planted, the connectivity of the trees planted (a relative measure of how many species is attracted to the fruit of the trees), and the spacing of the tree islands from one another (Table 1). However, since these are still early successional plots and many of the hardwood trees planted in high diversity plots have not matured enough to grow fruit, only tree diversity and spacing will be considered as variables in this study, creating a 3x2 factorial design with two replicates each.

Plot	Diversity	Connectivity	Spacing (m)
01	Low	Low	30
02	High	High	30
03	Low	High	30
04	Low	High	10
05	High	Low	10
06	High	High	20
07	High	Low	20
08	control plot with no islands planted		
09	Low	Low	10
10	High	Low	30
11	Low	High	20
12	High	High	10
13	Low	Low	20

Table 1: Description of the variables for each restoration plot. "Low" and "high" within each category are relative measures of the variable, refer to Figure 2a for the visual representation of nucleus spacing, and Figure 2b for the exact tree compositions of each variable.

Small teams of 2-5 observers conducted point counts at a location as close to the center as possible, recording all birds both seen and heard (Siegel et al., 2001; Fontúrbel et al., 2020; Cambria et al., 2012; Petit et al., 1995), and been utilized in reforestation projects in Hawaii (Pejchar et al. 2018). Since 2018, FCATeros, local Ecuadorians with extensive knowledge of the avifauna of the rainforests, Gregory Paladines and Gloria Loor have been collecting data beginning in November 2022 under the supervision of Juan Freile, an expert Ecuadorian ornithologist and author of *The Birds of Ecuador* field guide. All point counts were conducted on eight days between 5-18 June 2025. Point counts for parcels 1-6 were conducted from hours 7:00-11:00 and point counts for parcels 7-12 were conducted from hours 15:00-17:00, if weather was deemed not severe enough for birds to retreat. Sampling periods were 10 minutes, except for July 2026, where it was 15. Alternatively, if a bird was heard within an estimated 50 meters for a prolonged period, it was also recorded. All observers served as spotters, and we communicated to ensure no individual birds were counted more than once. The date, starting time, and ending time were also recorded at the beginning of each period. Using the GPS of a mobile device, I recorded the coordinates of each point in degrees, minutes, and seconds.

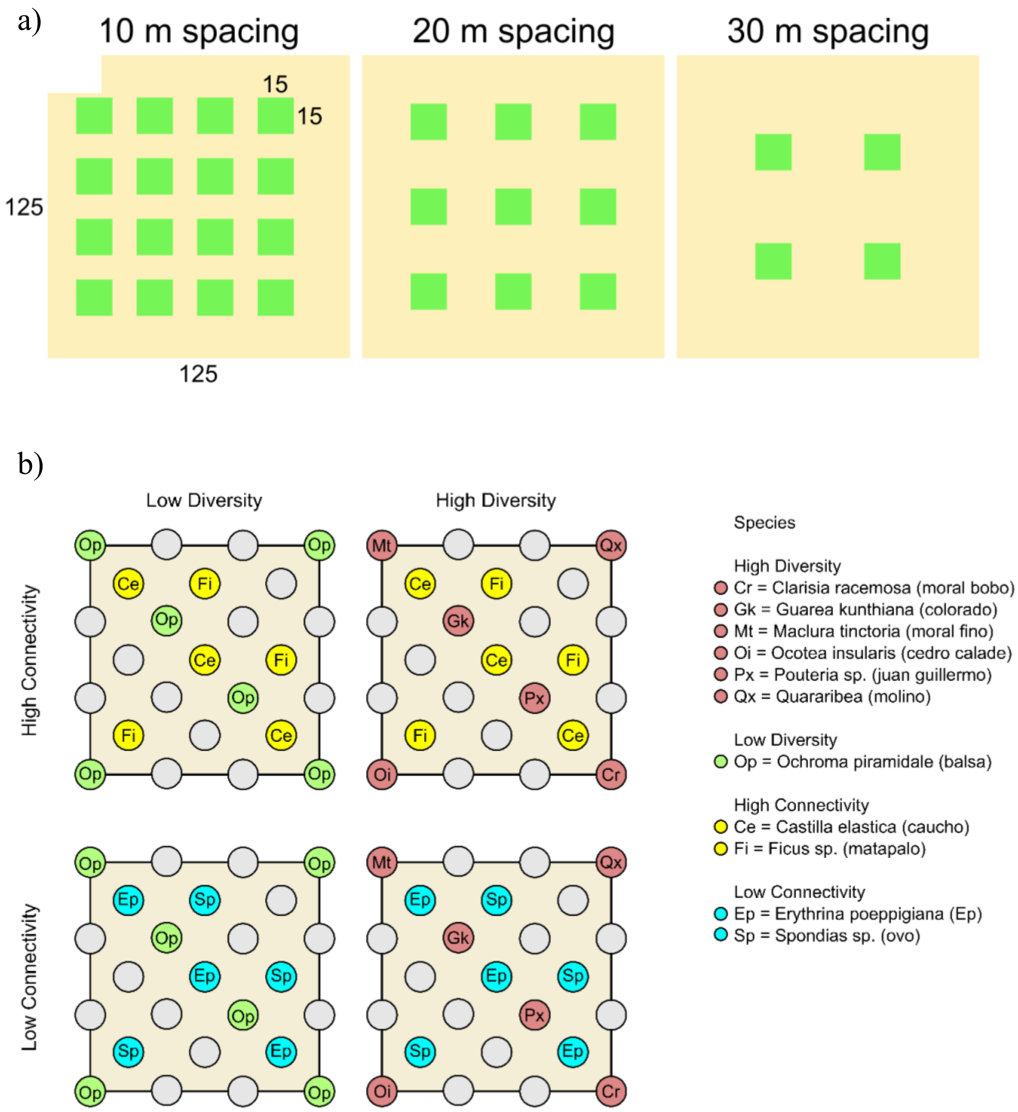


Figure 2: a) A visual representation of the tree nuclei spaced within a 12x12 meter plot. Each green box approximates one nucleus. **b)** A matrix of the tree makeup of each tree nucleus, with the defining species of each variable described in the right-side legend. High diversity nuclei are composed of a mix of native hardwoods. Low diversity nuclei contain only *Ochroma piramidale* balsa. High connectivity is defined by the presence of fruiting trees that are readily eaten by a wide variety of organisms. Low connectivity is defined by the presence of fruiting trees readily eaten only by a few organisms.

To supplement our limited data collection period, point-count data from 2021 onwards conducted within the plots were also used in analyses. In data processing to avoid pseudoreplication, only the maximum count per species per plot within each continuous sampling effort was retained for analysis. Sampling efforts conducted within three days of one another were grouped into a single sampling effort, resulting in 17 sampling efforts across the study period. I also assigned each species of bird a primary feeding guild, a secondary feeding guild, and a habitat niche based on the species accounts found within the Cornell Lab's Birds of the World online resource. The guilds chosen were Carnivore, Frugivore, Granivore, Nectarivore, and Generalist. I chose primary and secondary guilds based on which food type appeared first in the species account. For niche, I categorized all birds into Ground, Shrub, Understory, Canopy, and Open.

Data analysis was conducted using R in RStudio. Prior to all parametric tests, normality was verified using the Shapiro-Wilk test, with Kruskal-Wallis substituted for ANOVA where assumptions were violated. To measure if spacing or tree diversity alone influence bird diversity, I measured raw alpha diversity, Shannon's diversity index, and Simpson's diversity index at both a single-aggregate and sampling effort level, with an aggregate being all data points for a treatment across the five years of data collection. I used a t-test for diversity and a One-Way ANOVA for spacing on each metric. I also utilized Liner Mixed Models (LMMs) to explore any temporal effects on species diversity within each treatment type. To explore community composition similarity between the individual plots, I used an NMDS to visualize the area and a Mantel test on the matrices themselves, supplemented by IndVal results to determine if any birds were significant indicators in any specific plots. To determine if guild composition differed by tree diversity, I used a two-sample proportion test on raw abundance, abundance proportion and species richness proportion per guild. For spacing, I used a one-way ANOVA and Kruskal-Wallis where appropriate on the same metrics. I applied Bonferroni and FDR correction applied to all test results, used direction tables to confirm if there was consistency across the tests, and run a Fisher's exact test on the matrix. I also ran another two-way ANOVA on the abundance proportion ~ Group × PGuild to test overall treatment effectiveness across all guilds and a one-way ANOVA per guild to test whether specific treatments differ across each guild, supported by IndVals. The same group of ANOVAS and direction tables were run to test if plots with higher tree diversity and lower spacing will support a greater proportion of vertical niche specialists relative to open habitat generalists. This was run in conjunction with temporal LMMs and a singleton analysis to examine change in vertical niche proportions over time, as well as flagging species that only appeared once across the five years of data.

Results

Spacing does not significantly affect bird species diversity by any metric when considered statically or temporally. This is supported by the LMMs, confirming that birds are neither accumulating nor disappearing in terms of raw diversity numbers across each unique treatment. Similarly, tree diversity does not significantly affect bird species diversity by any metric when considered as an aggregate or temporally. Total bird abundance did not differ significantly between treatments or over time. Thus, neither prediction was supported.

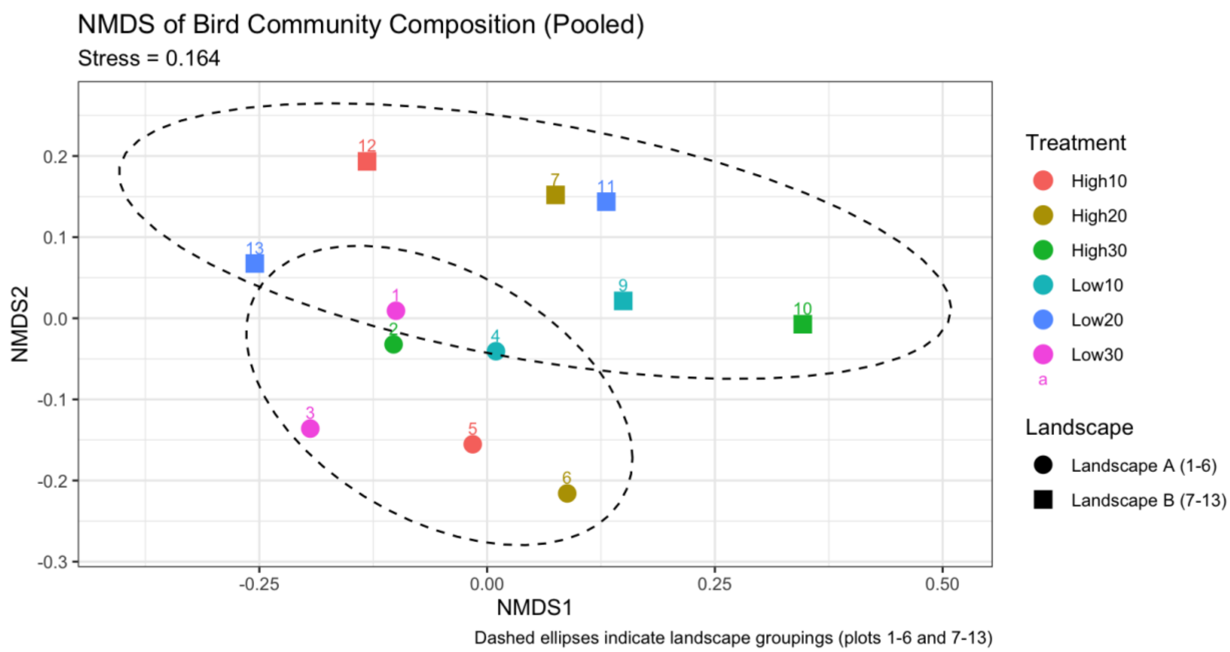


Figure 3: NMDS visualization of the plot community compositions. Plots with the same tree diversity (High or Low) and tree diversity (the number, in meters) are the same color. Plots that are spatially close to each other have the same symbol and are circled by the dashed ellipse.

NMDS results visually reveals no clear clustering of the plots by community composition (Fig. 3). This is supported by IndVal results, demonstrating that no species define the communities of any treatment types. The Mantel test also returned non-significant, further supporting this conclusion.

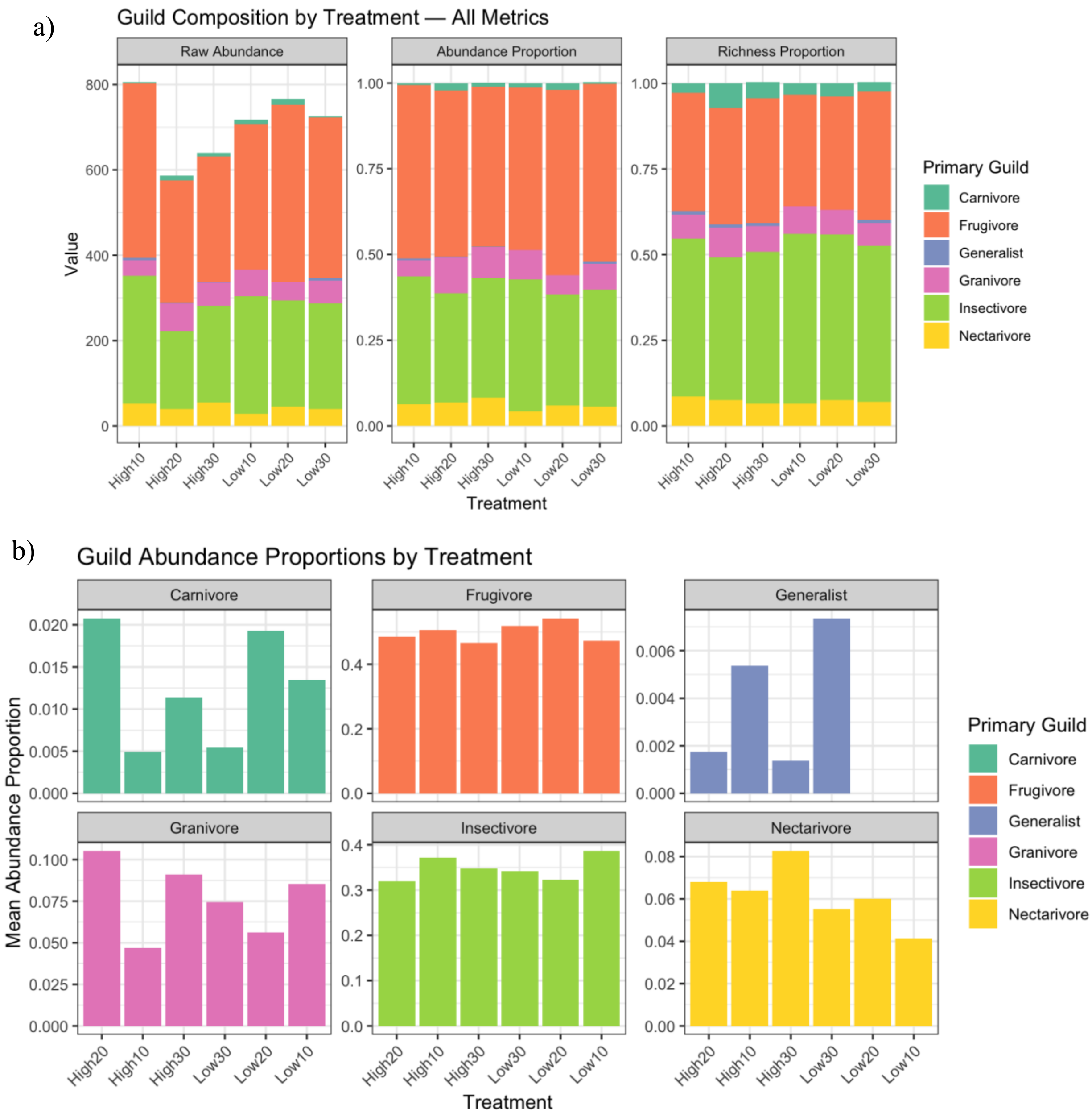
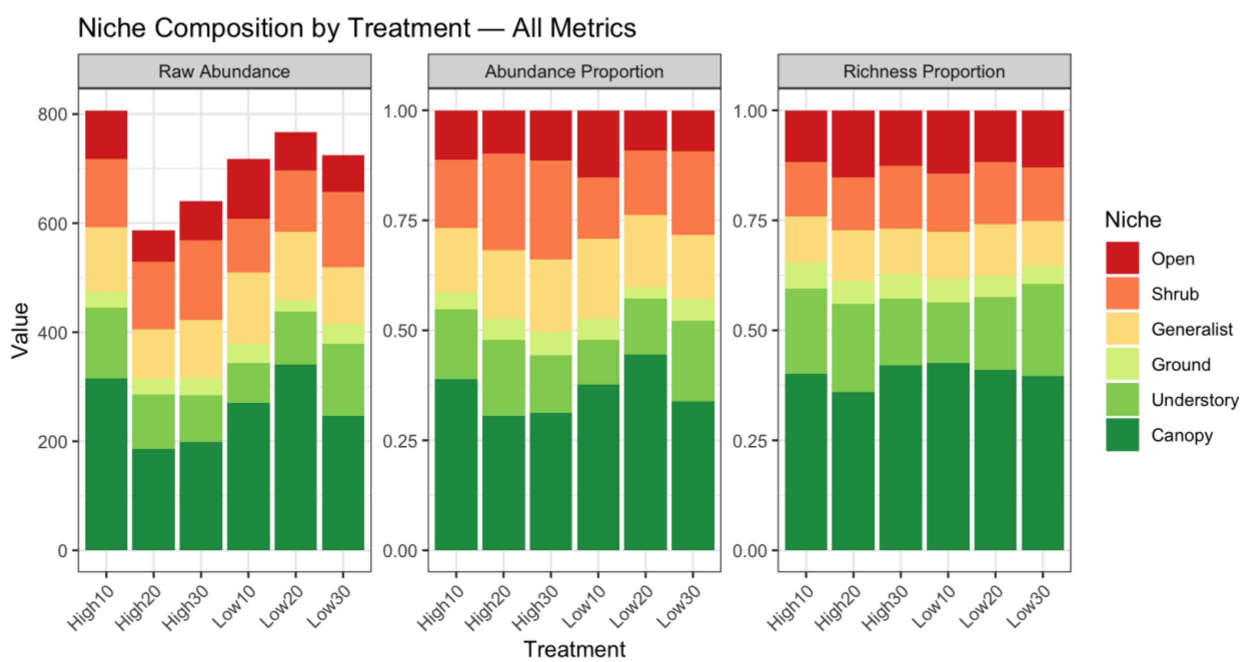


Figure 3: a) Guild composition differences by treatment. Each color represents a primary feeding guild. The leftmost graph shows raw abundance values per guild collected over the 4 years; the center graph represents the same abundances as a proportion; the rightmost graph shows the species richness values per guild as a proportion. **b)** The same abundance proportion graph (centermost), with the bars placed next to each other for visual clarity.

Proportions tests (n=12) on raw abundance, abundance proportions, and species richness proportion suggest tree diversity significantly affects abundance proportions of frugivores ($p < 0.001$, Bonferroni), nectarivore ($p < 0.001$) and insectivores ($p = 0.003$). Nectarivores consistently higher in High diversity plots across all three metrics, supported by direction tables

(Fig. 3). Frugivores diverge between metrics; high diversity has more species, but low diversity has more individuals (Fig. 3). Spacing was non-significant across all guilds and all three metrics. Fisher's exact test was non-significant, meaning the number of species per guild does not differ between treatments. This test was run to determine whether guild differences were driven by species richness or abundance, in combination with the prior IndVal results. Two-way ANOVA done on treatment groups significant (n=12, p = 0.037), therefore treatments differ significantly in overall functional abundance proportions. Group x PGuild interaction was non-significant, indicating treatment effect is general rather than guild specific. One-way ANOVA (n=12) on abundance proportion per guild non-significant for all guilds after p-value corrections. Non-significance confirms the difference is distributed across guilds rather than concentrated in one. Upon ranking treatments, High30 was the most effective for nectarivores, Low10 most effective for insectivores, and Low20 most effective for frugivores.



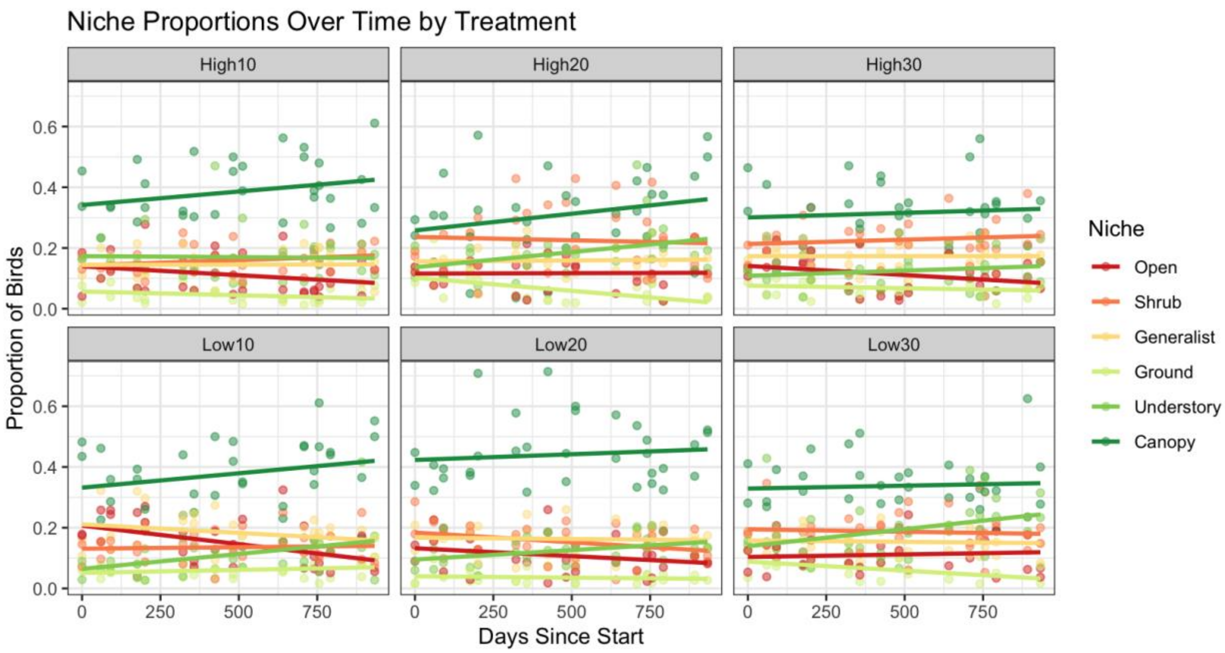


Figure 4: a) Vertical niche composition differences by treatment. Each color represents a vertical niche. The leftmost graph shows raw abundance values per niche collected over the 4 years; the center graph represents the same abundances as a proportion; the rightmost graph shows the species richness values per niche as a proportion. The very first day, day 0, was November 15, 2022. **b)** The shift in vertical niche proportions over time per treatment type. Each color represents a different vertical niche, with each point being the proportion of a sampling effort. A line of best fit is drawn through each vertical niche.

Proportions tests (n=12) on raw niche abundance, abundance proportions, and species richness reveal spacing has no influence on the niche proportions of each treatment type. Canopy abundance proportion significantly higher in Low diversity plots ($p < 0.001$, Bonferroni), consistent across all three metrics (Fig. 4). Shrub abundance proportion only significantly higher in High diversity plots ($p = 0.007$) Generalist abundance proportion significantly higher in Low diversity plots ($p = 0.003$), consistent across all three metrics. Open abundance proportion marginally significant ($p = 0.044$ Bonferroni, $p = 0.011$ FDR); Low diversity higher in abundance only. Understory and Ground were non-significant in proportion tests. LMMs reveal Open bird proportions are declining significantly over time ($p = 0.0004$), Understory bird proportions increasing significantly over time ($p = 0.017$), High diversity plots support significantly more understory specialists ($p = 0.028$), and 30m spacing + high diversity combination partially undermines positive diversity effect on understory birds ($p = 0.041$). Shrub birds bear no significant temporal or treatment effects. 30m spacing plots are declining in ground birds over time (p = 0.015), 20m + high diversity interaction (p = 0.040) also was significant. Canopy birds bear no significant temporal or treatment effects.

Notable species include open habitat indicators like the Smooth-Billed Ani (*Crotophaga ani,* r = -0.603) and the Tropical Kingbird (*Tyrannus melancholicus,* r = -0.414) which are declining consistently over time. The Plumbeous Kite (*Ictinia plumbea)* is increasing over time (r = +0.805). The High10 treatment attracted the most singleton interior forest specialists (n=8 of n=20 total singletons) including the Bicolored Antbird (*Gymnopithys bicolor),* Ornate Hawk-Eagle (*Spizaetus ornatus)* and Rufous Motmot (*Baryphthengus martii)*. The Swallow Tanager (*Tersina viridis)* is completely absent from High diversity plots. *Myiothlypis* warblers were completely absent from Low diversity plots. Yellow-Throated Toucan (*Ramphastos ambiguus)* numbers were higher in High diversity, while Chocó Toucans (*Ramphastos brevis)* were higher in Low diversity.

Discussion

Over the five years of data collected, evidence suggests that FCAT's applied nucleation is successfully initiating succession in the Chocóan lowlands, regardless of the differences in diversity and spacing of the tree nuclei (Holl et. al, 2020). This is supported by the trend of the proportion of open habitat birds declining and understory birds increasing across all plots over time (Van Bael 2013). There is no significant difference in total abundance or species richness, since abundance and species richness measures remained static as time progressed. This is consistent with Holl (2020), which demonstrates that bird species richness and abundances between applied nucleation and plantation treatments stay numerically stable, but do differ significantly from the reference forest.

What is changing with time, however, is how those birds are functionally distributed. The proportional representation of feeding guilds and vertical niche categories shifts significantly between treatments and over time. In other words, we're seeing groups of the same birds, in different numbers, flock to different plots. Each treatment is creating a different environment that attracts different numbers of individuals of the same functional group, rather than filtering out which guild species colonize (Tews et. al, 2004). The main driver of these changes is tree diversity, consistent with Whelan (2015) and the habitat heterogeneity theory (Tews et al. 2004); in all tests, tree spacing had no effect on the proportional representation of feeding guilds and vertical niche categories, consistent with proportion test results ($p < 0.001$ to $p < 0.05$) and two-way ANOVA findings ($p = 0.037$).

The developing vegetation structure of each plot is reflected especially well in the vertical niche proportion analysis. Namely, the trend the proportion of open habitat birds declining and understory birds increasing across all plots over time. Additionally, certain species are beginning to signal that forest conditions are emerging (Terborgh 2001). Particularly, the High10 treatment is attracting the most singleton interior forest specialists including the Bicolored Antbird (*Gymnopithys bicolo)r*, Ornate Hawk-Eagle (*Spizaetus ornatus)* and Rufous Motmot (*Baryphthengus martii).* It's important to note that the 30m spacing and high diversity combination partially undermines the positive diversity effect on understory birds, which warrants further investigation. Furthermore, these 30m plots also have more canopy birds, likely attributed to the fact that they are comprised primarily of balsa, which develops canopy structure more rapidly than the native hardwoods (J. Karubian, pers. comm.).

These analyses were not without their limitations. I would highly recommend FCAT to create more replicates of these plots, if possible, to provide more statistical power to the analyses, since the sample size is n=12 with groups of two, which will reduce to only one replicate when the hardwood trees begin to bear fruit and yield connectivity differences. Additionally, point counts done in a control plot of primary forest would open the door for more complex and robust analyses. This would be particularly helpful in determining true community composition differences because attempts for a robust analysis for community composition resulted in pseudoreplication or severely underpowered tests. It is also worth noting the temporal limitations of the current point count system, as plots 1-6 are only monitored in the morning and 7-13 in the afternoon, and only on non-heavily rainy days. It's possible that the visible bird community changes across these plots as weather, temperature, and time shift.

Point-count data is not infallible, and a large reason why open habitat birds may be perceived as declining over time and understory birds are increasing is simply because they become harder and easier to spot, respectively (Fontúrbel 2020). Additionally, in the NMDS (Fig. 3), plots that were grouped together geographically had more similar community compositions, suggesting that larger landscape effects may be at play (Van Bael 2013). This is supported also by exploratory spatial autocorrelation tests run in ArcGIS Pro using a subset of the data collected, which revealed no significant global clustering but identified individual plots as abundance outliers, consistent with the landscape effects observed in the NMDS. Along with the plots influencing each other, edge effects may be at play (Laurance et al. 2002; Sherry 2021). Since the reforestation plots are surrounded by primary forest the communities of each plot may reflect the species in the primary forest, not true recruitment. To help alleviate this, greater distances between plots is recommended, but may not be possible due to land availability. I also recommend supplementing the point count data with other types of resources, like acoustic monitoring or mist netting, which is known to collect a high amount of understory specialists that may go unnoticed in early successional vegetation (Fontúrbel 2020).

Furthermore, this study calls into question the degree to which birds actually view a habitat. A 125x125m plot is only a tiny fraction of the true home ranges of many birds, like *Ramphastos* toucans, that have home ranges that span hundreds of hectares (Birds of the World 2026). The degree to which a given species will utilize the resource environment of a given plot varies: any of the species spotted may simply have been a transient indivudual rather than a habitat resident (Siegel et al. 2001). As such the fine-scale nature of this analysis may only be applicable to certain focal species, like the understory specialist singletons detected within this analysis.

Most of the hypotheses were not supported, but the strongest, most ecologically important finding of this study was the partial support of hypotheses 3 and 4. The same species, in the same numbers, distribute themselves in different concentrations across the treatment types based on tree diversity. These proportions could be interpreted as a success at replicating the Holl (2020) study in Costa Rica, indicating that applied nucleation is successful at initiating habitat restoration. continued monitoring of these reforestation plots is essential, as these analyses reveal that the communities within these plots undergo flux as succession continues. More temporal data will help reveal the true efficacy and differences between the treatments, especially as connectivity becomes a factor. Increased effort should be put into monitoring the High10 plots, as they show the most promise for creating the most diverse reforested ecosystem.

Acknowledgements

This research was supported by Tulane University, the Tulane Center for Engaged Learning and Teaching (CELT), and Tulane's Newcomb-Tulane College Undergraduate Research funding program. Fieldwork was conducted in partnership with the Fundación para la

Conservación de los Andes Tropicales (FCAT), whose resources and infrastructure made this study possible.

Dr. Jordan Karubian's guidance made the study design possible. Data collection in the field would not have been achievable without the mentorship of Gloria Loor and Gregory Paladines, whose deep knowledge of Ecuadorian avifauna and the FCAT reserve was invaluable, and by Juan Freile, expert ornithologist and co-author of The Birds of Ecuador, who lent his expertise directly in the field and via his book. Fellow student Benjamin Kenny provided essential support during data collection.

I am deeply grateful to my academic advisors: Dr. Donata Henry, who served as both thesis advisor and CELT mentor for my senior year and general mentor through my entire undergraduate career, and Dr. Alex Gunderson, whose expertise on statistical analyses shaped this work considerably. Dr. Keena Kareem provided invaluable assistance with GIS analyses. I would additionally like to thank Dr. Leighton J. Reid, whose statistical insights during our correspondence meaningfully informed the analytical framework of this study.

I would also like to thank my Honors cohort peers and FCAT cohort for their unwavering support throughout this process, as well as the entire FCAT team whose dedication and love for the conservation of the Ecuadorian Chocó makes work like this possible. I am also grateful to my parents for their unconditional support throughout this journey. Finally, I would like to give my thanks for the birds of the Chocó, whose beautiful songs and plumage gave me the energy to keep hiking through the mountains of Esmeraldas.

Appendix

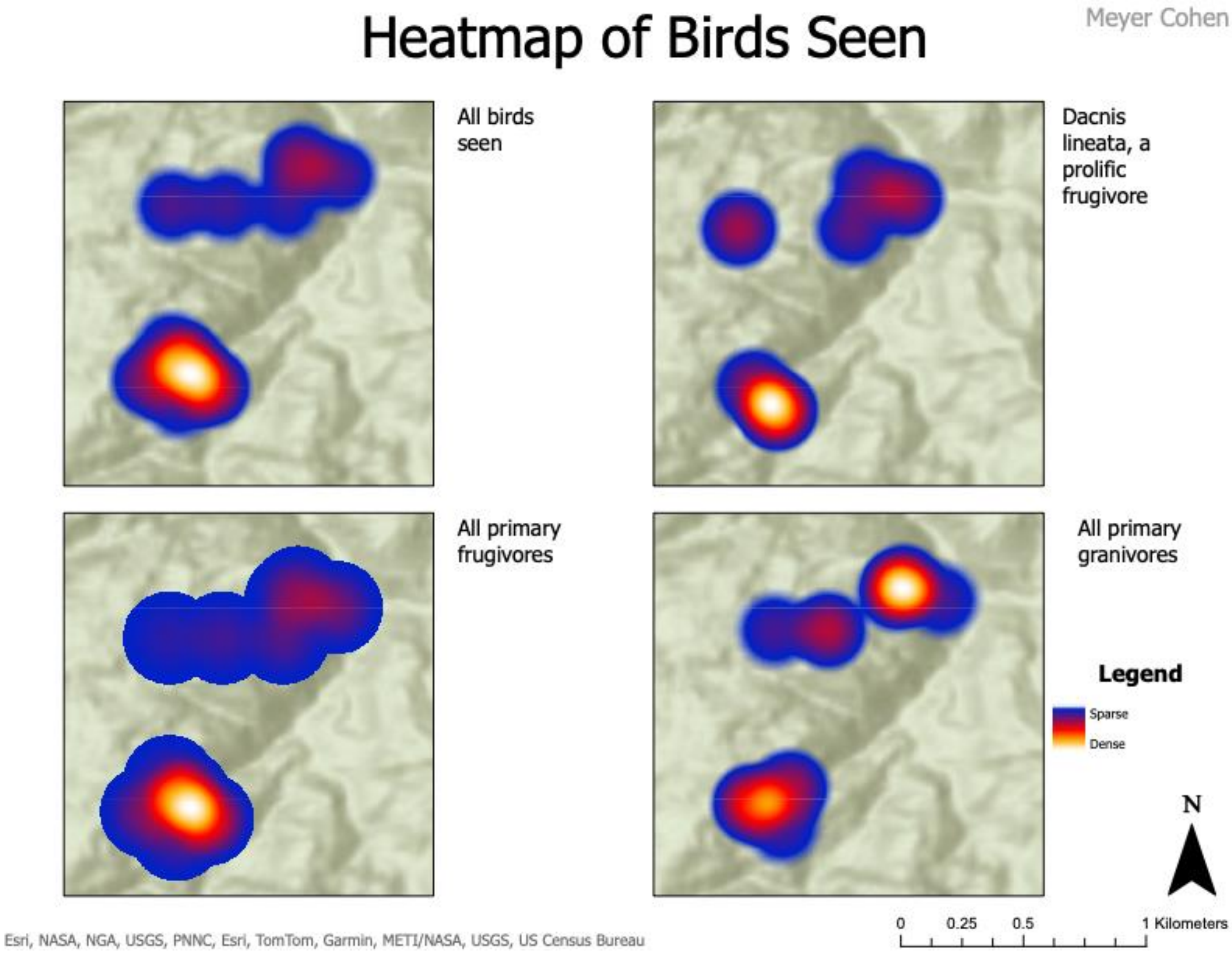


Figure 5: A supporting ArcGIS Pro heatmap of all birds seen in the July 2025 subset of the data. Top Left: All birds seen. Top Right: The Black-Faced Dacnis distribution (*Dacnis lineata)*, among the most common frugivorous birds in this data subset. Bottom Left: all primary frugivores. Bottom Right: all primary granivores.

Species	Treatment	Guild	Niche
Spizaetus ornatus	High20	Carnivore	Canopy
Pachysylvia decurtata	Low20	Insectivore	Canopy
Setophaga pitiayumi	Low20	Insectivore	Canopy
Veniliornis callonotus	High10	Insectivore	Canopy
Geranospiza caerulescens	High30	Carnivore	Generalist

Capito aurovirens	High10	Frugivore	Generalist
Sporophila telasco	High20	Granivore	Ground
Tiaris olivacea	High30	Granivore	Ground
Gymnopithys bicolor	High10	Insectivore	Ground
Falco rufigularis	High10	Carnivore	Open
Gampsonyx swainsonii	Low30	Carnivore	Open
Fluvicola nengeta	Low30	Insectivore	Open
Saltator striatipectus	Low20	Frugivore	Shrub
Myiozetetes granadensis	High10	Insectivore	Shrub
Chaetocercus bombus	Low20	Nectarivore	Shrub
Baryphthengus martii	High10	Frugivore	Understory
Lepidothrix coronata	Low30	Frugivore	Understory
Trogon comptus	High10	Frugivore	Understory
Xenops rutilans	Low20	Insectivore	Understory
Xyphorhynchus lacrymosus	High10	Insectivore	Understory

Table 2: A detailed list of all singleton species, which plot they appeared in, their primary feeding guild, and their vertical niche. It is worth noting there were 8529 individuals in this study, across 192 species.

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