Changes in biodiversity and abundance of Lepidoptera individuals in different successional stages in a cloud forest in Costa Rica.

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RESERVA CLOUDBRIDGE NATURE RESERVE

Contents

Abstract

Costa Rica is well known for its high level of biodiversity, this is also apparent within the butterfly communities. Butterflies are an important indicator species, when a specific species is living in a characteristic habitat it can tell something about a plant growing in the ecosystem. The plant can in its turn tell something about the soil or other growth circumstances. Due to this role as a indicator species and the fact that butterflies are easily spotted they become an interesting family to research. The goal of this research was to find out which forestry management practices should be applied to increase the abundance and diversity of these animals. The hypotheses were: old growth has the highest diversity, followed by the natural regrowth and at the end the planted regrowth. So, the assumption for the best way to increase the diversity would be by letting degraded land regrow on its own without human intervention. At the end the old growth came out last, but this is due to the fact that most butterflies live in the canopy there (see discussion). Secondly the natural regrowth had the highest diversity. This results in the fact that when looking at butterflies in the understorey the best way to increase their diversity is with natural regrowth.

Introduction

Costa Rica is known for its high level of biodiversity; it consists of about 0,03% of earth's total area but houses 5% of the total amount of species on earth. This comes down to a beautiful half a million species! (DeVries, 1987). The theory of this high biodiversity is that Costa Rica is the bridge between North and South America. Another reason for the high level of biodiversity are the changes in: elevation, precipitation, light intensity, and temperature. These changes in parameters are explained by both oceans on the side of Costa Rica and the mountain range dividing the country (King, 2024). The continental landmass can be divided into six ecosystems: Pacific slope, Pacific lowland deciduous forest (sea level-600m), Pacific lowland evergreen forest (sea level-800m), Pacific mid-elevation (700m-1600m), high-elevation Pacific and Atlantic (1600m-above 3000m) and Atlantic slope. Each of these different Fauna regions are defined by the different animals living there. This does not mean that animals only live in a specific region, but it is more likely that a certain species can be found within the fauna region (DeVries, 1987). The cloud forest of Costa Rica contains a high level of endemism, including for butterflies. The change in elevation creates a lot of ecosystems, and sometimes these niches induce the creation of new species (Authors: Dr. Emily J. Hartman & Dr. Rajiv S. Patel, 2023). This creates an ecosystem with a high biodiversity but a low abundance of individuals. This high level of biodiversity is also represented by the high amount of different lepidoptera species. This order consists of moths and butterflies. Costa Rica contains about 1500 different species of butterflies and 12 000 different species of moths. It contains 90% of Central American species and ~5% of earth's total species. (Yarlenis L Mercado-Gómez, 2023).

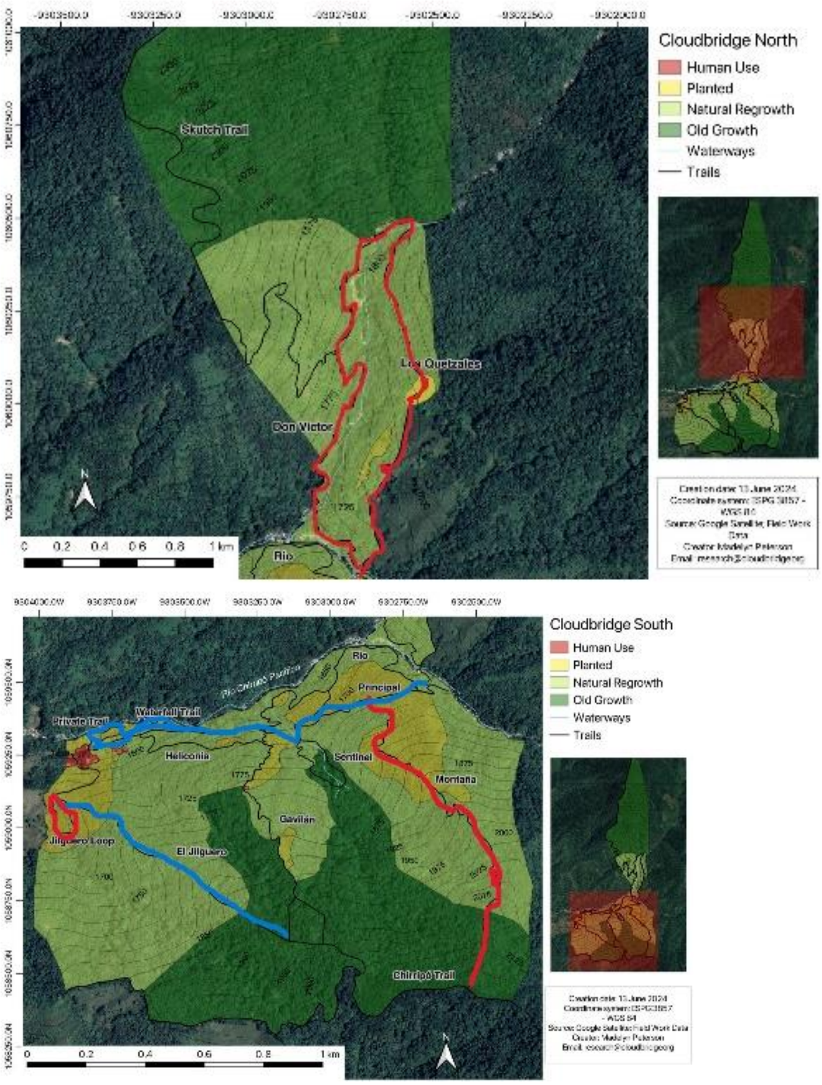
Butterflies are important pollinators, diet for predators and indicators of the overall health of an ecosystem. For this reason, it is important to research these animals. Another important reason why researching butterflies is beneficial is due to the fact that they are compared to other animals very visual, they are easy to catch without damaging them with a net and very abundant within the cloud forest. The main goal of this research is finding out how well it is going with the butterfly population within the different forest types. With the results of this research different forestry management practices can be applied to increase the abundance and diversity of butterflies. The expected results of this research would be that the old growth contains the highest diversity, followed by the natural regrowth and lastly the planted regrowth So it was assumed that to let the forest grow back without human intervention, would be the best forest management practices.

Materials and Methods

Study area

The research was conducted within Cloudbridge Nature Reserve close to the city San Isidro. Cloudbridge Nature Reserve is a located within the Talamanca Mountain range that stretches from 1550 to 2600m high and it is bordered by Chirripó National Park. Since 2002, 255 hectares (630 acres) of cattle pasture or cultivated land with a further 28 hectares (70 acres) of primary forest have been purchased by the reserve. Some of the pastured land is left alone so the forest can regrow into a secondary forest. And in the past, some of the old pastured land has been planted (Reserve, 2024) (King, 2024). The research area is situated within a cloud forest on Cloudbridge, which are heavily influenced by the elevation and precipitation. Cloud forests are located all over the world and are situated on slopes of mountains. The forest is distinguished by the warm and moist air coming up the mountain and condensing due to the colder temperature. Most of the moisture in the forest comes from the moisture stored within the clouds. The moisture condenses on the leaves or needles of trees, then evaporates, and eventually forms a drop of water which falls to the ground. This process is called fog drip. Cloud forests are characterized by the abundance of epiphytes, mosses, and ferns (Reserve, 2024).

To answer the main question the surveys were conducted on different trails, preferably with a gradient from planted to old growth forest. The trails where this research was conducted on are: El Jilguero, Montaña, Don victor/Los quetzales, Principal and Private/Waterfall.



Map of the survey trails.

Study community

The cloud forests of Costa Rica are well-known for their high level of endemism; this is the same for butterflies. The change in elevation creates a lot of ecosystems, and sometimes these niches induce the creation of new species. This creates an ecosystem with a high biodiversity but a low abundance of individuals. This high level of biodiversity is also represented by the high amount of different lepidoptera species(King, 2024). For this research we will only look at butterflies, the superfamily Papilionoidea. Butterflies have an important relation with their hostplants. The first stage of their life is the egg stage; after hatching they go into the larval stage. The larval stage is the caterpillar, the main activity of a caterpillar is feeding and growing. Their first meal is usually their eggshell, afterwards they will feed on plants. Some species are generalist and other species are specialist. The specialist feed on specific hostplants, some species do this to absorb the toxic components of the plant. A good example is the Heliconiinae subfamily. This subfamily exclusively lays its egg on hostplants of the Passifloraceae, a toxic vine. The caterpillar feeds on the vines and in process it absorbs the toxins and utilizes them in their later life stages (DEVRIES1, 2000). The butterflies of this subfamily usually show bright red colours to warn predators of their toxicity. Due to the relationship with their hostplants butterflies can be seen as good indicator species; if a specific species of butterfly is present then the hostplant should be present (DeVries, 1987).

There is a total of six families of butterflies within the reserve, each family is divided into subfamilies of which there are a total of 21. Each subfamily is divided into tribes and each tribe is divided into species. Because of the high number of species for this research only the families and subfamilies will be considered, this is due to the large number of species found on the reserve (Reserve, 2024). The most seen family of butterflies within the study area is the Ithomiinae family (glasswings).

Methods

The catching of butterflies was done in the different forest types (planted regrowth, natural regrowth, and old growth.). The sampling was done from the 27th of September to the 10th of December. The sampling was done during the rainy season. The netting was done 4 times per trail; this means that each forest type was surveyed for at least 20 times. The method of netting was done by starting the survey at 8 AM, then walking down the trail at a slow pace. The pace of the survey was about 20 minutes per forest type (University, 2024) (Spooner, 2016 updated 2018). If a species of butterfly was identifiable through sight, it would be noted down without being caught.

The catching was done using butterfly nets. When an individual was caught the butterfly was put in a jar, photographs were taken and the butterfly was released. This needed to be done within ten seconds to ensure the wellbeing of the butterfly. Through the use of this method no butterflies were hurt or killed, the downside of this method is that it is harder to identify a butterfly using pictures and videos. This view of non-killing is not shared with every researcher in the field. The euthanising of an individual of a new species can be beneficial for research purposes. But the killing of species that have already been researched thoroughly is not necessary (Spooner, 2016 updated 2018).

Every butterfly whose family was identifiable through observation was noted. The individuals who weren't identified through observation were caught and identified through the use of different literature sources.

Data analysis

The data was gathered and analysed on a Microsoft Excel sheet. To prove the significant difference between the different trails and different forest types a Kruskal-Wallis test was implemented, the non-parametric equivalent to the Anova-test. This test was chosen because of the fact that the data is not normally distributed which means that the data does not meet the assumptions of the Anova-test. The results of the KW-test are expressed in a H-value, the chi^2 distribution table was used to find the P-value. When the H value is higher than the critical value found on the chi^2 distribution then the null-hypothesis cannot be rejected. The null hypothesis was that the samples medians are equal, while the alternative hypothesis was that there is difference of medians within the samples (Bynum, x).

$$H=\left[\frac{12}{n(n+1)}\sum_{j=1}^{c}\frac{T_j^2}{n_j}\right]-3(n+1)$$

The formula for the Kruskal-wallis test

To test the difference in diversity two different diversity indexes where implemented. The the Shanon-Wiener index and the Simpson reciprocal index (Gownaris, diversity indices, 2008).

$$H' = \sum_{i=1}^{S} (p_i)(\ln p_i)$$

The formula for the Shanon-Wiener index

$$D = \sum_{i=1}^{S} \frac{n_i(n_i-1)}{N(N-1)}$$

Tthe formula for the Simpson's reciprocal index

The evenness of the different forest types and trails was tested with the Simpson's evenness index. This is a test where E=1 is the maximum evenness and the evenness is calculated through dividing the outcome of the results of the Simpson's reciprocal index with the maximum amount of species. If the outcome of E is a low number the evenness is very low, while if the outcome of E is high it means that the amount of species in the sample is quite even (Sohier, 2004).

E=D/S

The formula for the Simpson's evenness index

Materials

- Butterfly net
- Glass jar
- Notebook
- Pencil

- Camera (phone)
- Timer (phone)
- Laptop

Results

A total of 106 individuals were caught over a period of three months. The Ithomiinae had the highest amount of individuals caught (53 individuals; 50%), followed by Pieridae (15 individuals; 14,1%), Heliconiinae (11 individuals; 10,4%), Papilinodae (6 individuals; 5,7%), Dismorphia (5 individuals; 4,7%), Mesosemia (5 individuals; 4,7%), Nymphalinae (4 individuals; 3,8%), Drucina (2 individuals; 1,9%), Hesperiidae (2 individuals; 1,9%),Diaethria (1 individual; 0,9%) and Morphinae (1 individual; 0,9%)(see appendix 1 for total amount of sampled individuals).

The most species were found within the planted regrowth sections of the forest (57 individuals; 53,8%), followed by natural regrowth (48 individuals; 45,3%) and lastly the old growth sections (1 individual; 0,9%). All sub-families were found within the planted regrowth and the natural regrowth, due to the low amount of data found in the old growth only one family was found (Papilinodae).

The results of the Kruskal-Wallis test (KW-test) concerning the trails; the H-value of the trails was 6,56 (H=6,56) with a degrees of freedom of 4 (df=4), this meant that the P-value was 0,16 (P=0,16). The H-value of the forest types was 10,96 (H=10,96) with a degrees of freedom of 2 (df=2), this resulted in a P-value of 0,00416 (P=0,00416) (see table 1 and table 2 appendix).

Both the diversity of the forest types and trails were calculated with the Simpson's reciprocal index. The highest diversity within the forest types was found within the Natural regrowth with a value of 4,65 (D=4,65), followed by planted regrowth with a value of 2,58 (D=2,58) and the lowest diversity was found within the old growth with a value of 0 (D=0) (see discussion). The results for diversity concerning the trails are as follows; the highest diversity was found at Don victor with a D value of 5,2 (D=5,2), followed by El Jilguero with a D value of 2,51 (D=2,51), Principal with a D value of 0,62 (D=6,2), La montaña with a D value of 0,53 (D=0,53) and lastly Private/Waterfall with a D value of 0,25 (D=0,25), (see table 3 and table 4 appendix).

The results of the evenness test of the forest types are as follows; Natural regrowth with a E value of 0,39 (E=0,39), Planted regrowth with a E value of 0,21 (E=0,21) and Old growth a E value of 0 (E=0) (see discussion). The results of the trails are as follows; Don victor with a E value of 0,44 (E=0,44); El Jilguero with a E value of 0,21 (E=0,21); Principal with a E value of 0,052 (E=0,052); La Montaña with a E value of 0,044 (E=0,044) and Private/Waterfall with a E value of 0,021 (E=0,021), (see table 5 appendix).

A Venn-diagram was created to visualize the overlap in families concerning trails (see appendix).

Discussion

The results from the data analysis showed that there is a significant difference between the forest types (P=0,00416). This is true concerning the understorey of the forest types. Due to the shortcomings within the methodology no butterflies were sampled within the canopy. This is an explanation why there are so little samples from the old growth. When walking through the old growth most observed individuals were found in the higher canopy, this made it impossible to catch or identify with sight.

When looking at the results it shows that the highest biodiversity was found within the natural regrowth forest type. This shows that this would be the best forestry practice if the goal is increasing biodiversity and abundance of butterflies. A reason for this high biodiversity comes from the fact that there are a lot of different species of plants similar to the old growth. But the reason why the natural regrowth is the best for butterflies consist of the higher amounts of canopy gaps. Butterflies have been caught and observed mostly in open areas or forest edges with lots of flowering vegetation. When looking at the evenness concerning the forest types the natural regrowth also has the highest results. (Carreira1, 2019)

Concerning the different trails there is no significant difference (P=0,16). There is a difference in biodiversity which can be attributed to the size of the trail, elevation, and side of the mountain. A good example would be Jilguero and Don Victor, because of the location of Don Victor the sun shines earlier on this trail so the butterflies come out earlier. If sampling started later in the day, then Jilguero would be more abundant than Don victor. This shows that the sunlight influences a lot of the behaviour of butterflies. The results of the evenness test show that Don Victor has the highest evenness of all the trails.

To test the difference in diversity two different diversity indexes were implemented. (Gownaris, diversity indices, 2008) (Bynum, x) (Sohier, 2004) The two indexes who were used are the Shanon-Wiener index and the Simpson reciprocal index. The results of the Simpson's index were more realistic because of the fact that the Simpson's index focuses more on the more abundant species and filters out exceptions. A good example would be Principal: the results of the Shanon-wiener index showed a higher biodiversity then the Simpson's index, but this is due to some exceptions. The Simpson's index filtered out these exceptions and showed a more realistic view on the trail's biodiversity. (Dr. Lisa M. Thompson & Dr. Michael R. Jensen, 2023)

To have valuable data the research should be continued over a longer period of time. But if the reserve would like to do continuous monitoring of butterflies, a method should be developed so that the different layers within the forest types could be sampled. This could be done through the use of waterproof butterfly traps.

One of the interesting observations was the feeding behaviour of the Ithomiinae family. Individuals of the family Ithomiinae were observed feeding on diseased or deceased oak trees. Some trees had oozing black spots from a unknown disease ravaging the oak population on the reserve. A lot of butterfly species are well known for their feeding on clay, salt deposits or even tears of other animals. (Dr. Sarah H. Langston & Dr. Kevin M. Torres, 2024) And the Ithomiinae family is no exception with this behavior, but the feeding on diseased trees is not yet observed. Due to time limitation no further research was conducted about this subject. It will be beneficial for the reserve if research was conducted about this observation in the future.

Elevation is an important aspect of butterflies distribution area. Some species only live in the lowlands and some species prefer higher elevation. One of the limitations was the fact that not all trails are on the same elevation. This difference in elevation also creates a difference in observed families. A good example would be Don victor and Jil guero: Don victor is located on a lower elevation and the different families are more equally distributed. Jilguero is located on a higher elevation and has a high abundance of Ithomiinae but is less diverse when looking at different butterfly families. Ithomiinae is a real higher elevation specialist and for that reason is the most abundant family on Jilguero.

The research was conducted by a student who did not have any experience with researching butterflies. Over the period the sampling was conducted a lot of different volunteers and researchers joined with the sampling effort. This helped the sampling greatly, but it also created a collector's bias. Not everyone is as good with spotting and catching butterflies, this bias does not influence the results greatly but it is something to keep in mind. This bias will always be an influence within the reserve; this is due to the fact that there is a high rotation of researchers. One of the bigger limitations was the researchers lack of knowledge concerning the sampled species. After two months of sampling butterflies this limitation was mostly gone, but at the start of the research it could be seen as an issue.

Conclusion

The results from the research show that there is significant difference between the forest types. The understorey of the natural regrowth is the most biodiverse. When reforesting with the desire of higher biodiversity and abundance of butterflies, the area should be left to grow on its own. The old growth is home to a lot of butterflies but they are mostly higher up in the canopy, this was not taken into consideration for this research due to limitations in the methodology. The biodiversity calculation results for the planted regrowth are higher than the old growth, but this is due to the fact that the butterflies in the planted regrowth stay in the understorey. It could be possible that when doing research in the canopy of the old growth the biodiversity would be higher. When looking at the species evenness natural regrowth is also the highest.

When looking at the trails the results show that there is no significant difference between the trails. The most biodiverse trails were Don victor, this can be explained because the sun shines earlier on Don victor. When looking at species evenness the most even trail is Don victor.

To make have valuable data the monitoring effort should be done continuously, this is hard at Cloudbridge due to the fact of the high rotation of researchers. Even though it is hard to continuously research butterflies it is my recommendation to keep up the effort. Butterflies are an important group of animals, they are a good indicator species, important pollinators, prey for a lot of animals and they are beautiful.

Another recommendation I have would be to look into the feeding behaviour of the glaswings on the diseased trees. The disease is still quite a mystery for the reserve and this might be a connection concerning spreading the disease. A good start would be to research the liquid which oozes out of the black spots on the oaks.

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Appendix

kruskal-wallis-test			H0'= all families are equally distributed									
frequencie of families												
family	total frequency		don victor	rank	El jilguero	rank	la montañ	rank	PR/WF	rank	Principal	rank
diaethria	1		1	10,5								
dismorph	5		5	25								
drucina	2				2	18						
heliconiir	11		6	26	3	22			2	18		
hesperida	2				2	18						
heteropte	1		1	10,5								
ithomiina	54		17	30	20	31	8	27,5	1	10,5	8	27,5
mesosem	5		3	22					2	18		
morphina	1										1	10,5
nymphali	4		1	10,5	1	10,5	1	10,5			1	10,5
papilinod	7		4	24	1	10,5	2	18				
pieridae	15		11	29	3	22			1	10,5		
total '=	108											
0		rank sum'=		187,5		132		56		57		48,5
		mean rank sum'=		20,83333		18,85714		18,66667		14,25		16,16667
		expected value H0'=	6,5									
		df'=	4									
		N=	31									
		(12/(N(N+1))'=	0,0120968									
		sum(T^2/n)	8478,2429									
		=-3*(N+1)	-96									
		h-value'=	6,5593894									
		p value'=	0,16109	not significant								

Table 1: Kruskal-wallis test trails

A	B	C	D	E	F	G	H	I
kruskal-wallis test								
frequency of families on the different forest types								
families	totals		PG	rank	NG	rank	OG	rank
diaethria	1		1	8				
dismorphia	5		2	13	3	17		
drucina	2		1	8	1	8		
heliconiinae	11		5	20	6	21,5		
hesperidae	2		2	13				
heteropterinae	1				1	8		
ithomiinae	54		38	25	20	7		
mesosemia	5		2	13	3	17		
morphinae	1		1	8				
nymphalinae	4		1	8	3	17		
papilinodea	7		3	17	3	17	1	8
pieridae	15		6	21,5	9	23		
total '=	108							
rank' sum=				154,5		135,5		8
mean rank sum=				14,04545		15,05556		8
expected value H0'=				6,5				
df'=				2				
			N'=	25				
			(12/N(N+1))'=	0,018462				
			sum (T^2/n)	4818,851				
			=-3*(N+1)	-78				
			H'=	10,96339				
			p'=	0,00416	significant			

Table 2: Kruskal-wallis test forest types

simpson's index forest types

PG	n	n-1	n(n-1)		N(N-1)'=	3782
diaethria	1	0	0			
dismorphia	2	1	2			
drucina	1	0	0			
heliconiinae	5	4	20			
hesperidae	2	1	2			
heteropterinae			0			
ithomiinae	38	37	1406			
mesosemia	2	1	2			
morphinae	1	0	0			
nymphalinae	1	0	0			
papilinodea	3	2	6			
pieridae	6	5	30			
total	62		1468			
D'=	2,576294					

NG	n	n-1	n(n-1)		N(N-1)'=	2352
diaethria						
dismorphi	3	2	6			
drucina	1	0	0			
heliconiin	6	5	30			
hesperidae		-1	0			
heteropter	1	0	0			
ithomiinae	20	19	380			
mesosemi	3	2	6			
morphinae		-1	0			
nymphalin	3	2	6			
papilinode	3	2	6			
pieridae	9	8	72			
total	49		506			
D'=	4,648221					

OG	n	n-1	n(n-1)		N(N-1)'=
diaethria					
dismorphia					
drucina					
heliconiinae					
hesperidae					
heteropterinae					
ithomiinae					
mesosemia					
morphinae					
nymphalinae					
papilinode	1	0	0		
pieridae					
total	1		0		
D'=0					

Table 3: Simpson’s reciprocal index forest types

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	simpson reciprocal indexes														
2															
3	Don victor	n	n-1	n(n-1)		N(N-1)'=	2352		el jilguero	n	n-1	n(n-1)		N(N-1)'=	992
4															
5	diaethria	1	0	0					diaethria	0	x	x			
6	dismorphia	5	4	20					dismorphia	0	x	x			
7	drucina	0	x	x					drucina	2	1	2			
8	heliconiinae	6	5	30					heliconiinae	3	2	6			
9	hesperidae	0	0	0					hesperidae	2	1	2			
10	heteropterinae	1	0	0					heteropterinae	0	x	x			
11	ithomiinae	17	16	272					ithomiinae	20	19	380			
12	mesosemia	3	2	6					mesosemia	0	x	x			
13	morphinae	0	x	x					morphinae	0	x	x			
14	nymphalinae	1	0	0					nymphalinae	1	0	0			
15	papilinodea	4	3	12					papilinodea	1	0	0			
16	pieridae	11	10	110					pieridae	3	2	6			
17	total	49		450					total	32		396			
18															
19	simpson index'=	5,226667							simpson index'=	2,505051			Chart Area		
20	D'=	5,226667							D'=	2,505051					
21															
22	Principal								La montaña						
23		n	n-1	n(n-1)		N(N-1)'=	90			n	n-1	n(n-1)		N(N-1)'=	110
24	diaethria	x	x	x					diaethria	x	x	x			
25	dismorphia	x	x	x					dismorphia	x	x	x			
26	drucina	x	x	x					drucina	x	x	x			
27	heliconiinae	x	x	x					heliconiinae	x	x	x			
28	hesperidae	x	x	x					hesperidae	x	x	x			
29	heteropterinae	x	x	x					heteropterinae	x	x	x			
30	ithomiinae	8	7	56					ithomiinae	8	7	56			
31	mesosemia	x	x	x					mesosemia	x	x	x			
32	morphinae	1	0	0					morphinae	x	x	x			
33	nymphalinae	1	0	0					nymphalinae	1	0	0			
34	papilinodea	x	x						papilinodea	2	1	2			
35	pieridae	x	x						pieridae	x	x	x			
36	total	10		56					total	11		58			
37															

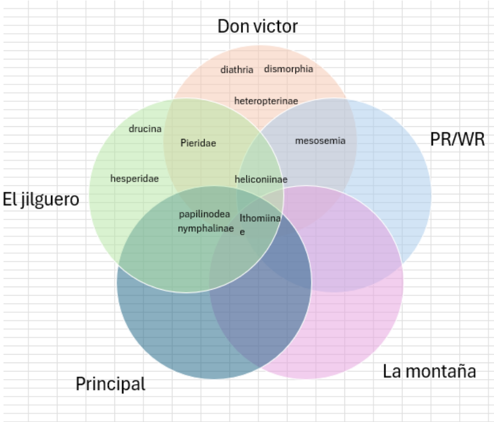
Table 4a: Simpson's reciprocal index forest trails

0	PR/WR						
1		n	n-1	n(n-1)		N(N-1)'=	20
2	diaethria	x	x	x			
3	dismorphia	x	x	x			
4	drucina	x	x	x			
5	heliconiinae	2	1	2			
6	hesperidae	x	x	x			
7	heteropterinae	x	x	x			
8	ithomiinae	1	0	0			
9	mesosemia	2	1	2			
0	morphinae	x	x	x			
1	nymphalinae	x	x	x			
2	papilinodea	x	x	x			
3	pieridae	x	x	x			
4	total	5		4			
5							
6	D'=	0,25					
7							
8							
9							

Table 4b: Simpson's reciprocal index forest trails

Species evenness							
E= D'/D'max							
D'max=	12						
Don victor=			Principal			PR/WR	
D'=	5,23		D'=	0,622		D'=	0,25
E=	0,435833		E=	0,051833		E=	0,020833
El jilguero=			La montaña				
D'=	2,51		D'=	0,527			
E=	0,209167		E=	0,043917			
PG=			NG=			OG=	
D'=	2,576294		D'=	4,648221		D'=	0
E=	0,214691		E=	0,387352		E=	0

Table 5: Simpson's evenness test



diathria	Don victor
dismorphia	Don victor
heliconiinae	EJ/DV/PRWR
drucina	EL Jilguero
hesperidae	EL Jilguero
Heteropterinae	Don victor
ithomiinae	everywhere
mesosemia	DV/PRWR
nymphalinae	DV/EJ/LM/PRIN
Papilinodea	DV/EJ/LM/PRIN
Pieridae	DV/EJ

Venn-diagram overlap different trails

date	trail	forest type	net	spotted	familie	genus
27-sep	Don victor	NG	x		Papilionidae	Parides
27-sep	Don victor	NG	x		Pieridae	x
27-sep	Don victor	NG	x		Mesosemia	Mesosemia
27-sep	Don victor	NG	x		Pieridae	(leodonta)
27-sep	Don victor	NG	x		Heliconiinae	x
27-sep	Don victor	NG	x		Nymphalinae	x
27-sep	Don victor	NG	x		Pieridae	Leptophobia
27-sep	Don victor	NG	x		Mesosemia	Mesosemia
27-sep	Don victor	NG	x		Heliconiinae	x
27-sep	Don victor	NG	x		Ithomiinae	Greta
27-sep	Don victor	NG	x		Mesosemia	Mesosemia
27-sep	Don victor	NG	x		Heliconiinae	Actinote
27-sep	Don victor	NG	x		Heliconiinae	Actinote
30-sep	El Jilguero	NG	x		Ithomiinae	Greta
30-sep	El Jilguero	NG	x		Nymphalinae	x
9-okt	El Jilguero	PG	x		Hesperiidae	x
11-okt	El Jilguero	PG	x		Heliconiinae	heliconius
11-okt	El Jilguero	PG	x		Heliconiinae	x
11-okt	El Jilguero	PG		x	Ithomiinae	x
11-okt	El Jilguero	PG		x	Ithomiinae	x
11-okt	El Jilguero	PG		x	Ithomiinae	x
13-okt	PR/WF	PG		x	Ithomiinae	x
13-okt	PR/WF	PG	x		Heliconiinae	heliconius
13-okt	PR/WF	PG	x		Heliconiinae	heliconius
15-okt	El Jilguero	PG	x		Hesperiidae	x
17-okt	Principal	PG		x	Ithomiinae	x
17-okt	Principal	PG	x		Ithomiinae	x
19-okt	PR/WF	PG		x	Mesosemia	x
19-okt	PR/WF	PG		x	Pieridae	x
20-okt	PR/WF	PG		x	Mesosemia	x
22-okt	Principal	PG		x	Nymphalinae	Marpesia
23-okt	Principal	PG		x	Morphinae	Morpho
27-okt	Principal	PG		x	Ithomiinae	x
27-okt	Principal	PG		x	Ithomiinae	x
28-okt	Principal	PG	x		Ithomiinae	x
28-okt	Principal	PG	x		Ithomiinae	x
28-okt	Principal	PG	x		Ithomiinae	x
28-okt	Principal	PG	x		Ithomiinae	x
28-okt	La montaña	PG	x		Ithomiinae	x
28-okt	La montaña	NG		x	Nymphalinae	Marpesia
29-okt	El Jilguero	PG	x		Ithomiinae	x
29-okt	El Jilguero	PG	x		Ithomiinae	x
29-okt	El Jilguero	PG	x		Drucina	leonata

29-okt	El Jilguero	NG	x		Ithomiinae	x
29-okt	El Jilguero	NG		x	Drucina	leonata
29-okt	El Jilguero	NG		x	Ithomiinae	x
29-okt	El Jilguero	PG		x	Pieridae	x
10-nov	El jilguero	NG		x	Ithomiinae	x
10-nov	El Jilguero	NG	x		Ithomiinae	x
20-nov	El Jilguero	PG	x		Ithomiinae	x
20-nov	El Jilguero	PG	x		Ithomiinae	x
20-nov	El Jilguero	PG	x		Ithomiinae	x
20-nov	El Jilguero	PG	x		Ithomiinae	x
20-nov	El Jilguero	PG	x		Ithomiinae	x
20-nov	El Jilguero	PG	x		Ithomiinae	x
20-nov	El Jilguero	PG	x		Pieridae	x
20-nov	El Jilguero	PG	x		Pieridae	x
20-nov	El Jilguero	NG	x		Ithomiinae	x
20-nov	El Jilguero	NG	x		Ithomiinae	x
20-nov	El Jilguero	NG	x		Papilionidae	x
22-nov	La montaña	PG		x	Ithomiinae	x
22-nov	La montaña	PG		x	Ithomiinae	x
26-nov	El Jilguero	PG	x		Ithomiinae	x
26-nov	El Jilguero	PG	x		Ithomiinae	x
26-nov	El jilguero	PG		x	Heliconiinae	heliconius
29-nov	Don victor	PG		x	Ithomiinae	x
29-nov	Don victor	PG	x		Ithomiinae	x
29-nov	Don victor	PG		x	Papilionidae	x
29-nov	Don victor	PG		x	Papilionidae	x
29-nov	Don victor	PG	x		Pieridae	x
29-nov	Don victor	PG	x		Pieridae	x
3-dec	La montaña	PG	x		Ithomiinae	x
3-dec	La montaña	PG		x	Papilionidae	x
3-dec	La montaña	OG		x	Papilionidae	x
6-dec	Don victor	PG		x	Ithomiinae	
6-dec	Don victor	PG		x	Ithomiinae	x
6-dec	Don victor	PG		x	Ithomiinae	x
6-dec	Don victor	PG		x	Ithomiinae	x
6-dec	Don victor	NG	x		Pieridae	x
6-dec	Don victor	NG	x		Heliconiinae	x
6-dec	Don victor	NG	x		Dismorphia	crisia
6-dec	Don victor	PG		x	Dismorphia	crisia
6-dec	Don victor	PG		x	Dismorphia	crisia
6-dec	Don victor	PG	x		Diaethria	anna(?)

9-dec	La montaña	PG	x		Ithomiinae	x
9-dec	La montaña	PG		x	Ithomiinae	x
9-dec	La montaña	NG		x	Ithomiinae	x
9-dec	La montaña	NG		x	Ithomiinae	x
10-dec	Don victor	NG	x		Pieridae	x
10-dec	Don victor	NG	x		Pieridae	x
10-dec	Don victor	NG	x		Pieridae	x
10-dec	Don victor	NG		x	Pieridae	x
10-dec	Don victor	NG		x	Pieridae	x
10-dec	Don victor	NG	x		**Heteropterinae**	x
10-dec	Don victor	NG	x		Dismorphia	crisia
10-dec	Don victor	NG		x	Dismorphia	crisia
10-dec	Don victor	NG		x	Heliconiinae	x
10-dec	Don victor	NG	x		Ithomiinae	x
10-dec	Don victor	NG	x		Ithomiinae	x
10-dec	Don victor	NG	x		Ithomiinae	x
10-dec	Don victor	NG	x		Ithomiinae	x
10-dec	Don victor	NG	x		Ithomiinae	x
10-dec	Don victor	NG		x	Ithomiinae	x
10-dec	Don victor	NG		x	Ithomiinae	x
10-dec	Don victor	NG		x	Ithomiinae	x
10-dec	Don victor	NG		x	Ithomiinae	x
10-dec	Don victor	NG		x	Ithomiinae	x
10-dec	Don victor	NG		x	Papilionidae	

Total amount of sampled individuals.