The influence of native forest patches on the insect pollinator community within an oil palm plantation landscape

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Abstract

Background: Oil palm plantations have replaced large areas of forests in Southeast Asia, causing significant loss of biodiversity. To reduce their negative impacts, some companies follow guidelines for certifications from organizations, such as the Roundtable of Sustainable Palm Oil (RSPO). One measure to reduce impact is to leave intact patches of high conservation value (HCV) forest within the plantation landscape. Few studies have addressed the effect of such forest patches on the pollinator communities in these landscapes. The aim of this study is to document the effect of two such forest patches on insect pollinators within a plantation landscape.

Method: The focal plantation was situated in a drained, previously peat-swamp lowland dipterocarp forest in West Kalimantan, Borneo, Indonesia. Sampling of insects was done by blue, white and yellow pan traps, conducted along transects spanning from the edge of two forest patches and 400 m into the plantation. Pan traps were also placed in the middle of the plantation, more than 1500 m from any forest. Manual visitation observations were performed in parallel on *Ageratum conyzoides*, an abundant and frequently flowering naturalized plant. All insects trapped in pans were sorted to morphospecies, whith bees, beetles, butterflies, moths and syrphid flies defined as pollinators.

Results: A total of 3256 insects were collected in the pan traps – this included 606 potential pollinators distributed among 191 identified morphospecies. The total number of pollinators caught in pan traps increased with distance from forest. There was a detected difference in insect species composition between the areas near the forest compared to those in the middle of the plantation. However, this was not the case when the group of pollinators were analysed separately. Bees showed a trend for increase in size with increasing distance from forest, though based on a small sample size (n=32).

Discussion: The higher number of pollinators found in the middle of the plantation compared to near the forest area was unexpected. The absence of evidence for difference in species composition of the pollinator community between the two areas was equally unexpected, and contradict with results found in similar studies focusing on single pollinator groups.

An increase in the size of pollinators with increasing distance from forest would only be expected if the abundance and diversity of pollinators were higher near the forest areas compared to in the middle of the plantation.

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1 Introduction

1.1 Tropical rain forests

Tropical rain forests, as defined by Malhi et al. (2004), are forests in the tropics with a mean temperature of > 25.4 °C and annual average rainfall > 2180 mm. Several of these forests are classified as biological hotspots (Mittermeier et al., 1998; Mittermeier et al., 2011; Myers et al., 2000), hosting as much as 75% of the Earth's plant and animal species (Donald, 2004). At the same time tropical forests are threatened ecosystems due to fires, conversion and other human-induced habitat degradation (Díaz et al., 2020). These forests serve important local and global ecosystem services (Ghazoul et al., 2010). They act as sources and sinks for key greenhouse gases (Weiss et al., 2002) and as contributors to clean air (Lelieveld et al., 2008). They maintain cycles regulating the global climate, with atmospheric circulation, water transpiration and cloud formation (Devaraju et al., 2015; Gedney et al., 2000; Lawrence et al., 2015; Line et al., 2005) which again could affect recruitment of rain (Sheil & Murdiyarso, 2009). In all, the tropical rain forests provide a number of key ecosystem functions and biodiversity that directly or indirectly maintain ecosystem services, and are thus highly beneficial for humans. One of the most apparent of these services is animal pollination.

1.2 Pollination

For angiosperms, pollen grains contain the male gametes, and pollination is the process of transferring pollen grains from the stamen (male part) of a flower to the stigma (female part) of another flower. For non-selfing angiosperms, this can be done abiotically by the aid of wind or water, or biotically by animals (Willmer, 2011). Without efficient pollination, outcrossing plants can experience inbreeding depression resulting in reduced seed set and/or quality. With total absence of pollinators, seed production might cease (Willmer, 2011). This is a two-way interaction since plants in turn are necessary for the insect pollinators, serving as food source, brood sites or contributors to favourable microclimatic conditions (Willmer, 2011). In fact, the long-term coevolution of plants and pollinators has been instrumental for evolution of diversity in both groups. As dependent as the pollinators are of their plants and vice versa, humans are also depending on this mutualistic relationship. Of the 124 most important crops grown for human consumption, 70% have been estimated to rely on pollinators (Klein et al., 2007). Pascual et al. (2017) estimated the yearly global economic value of pollination to 250 - 500 billion USD, and a number of studies have provided evidence for the important role of pollination for local food access and local income (Bartomeus et al., 2014; Crittenden, 2011; Potts, Ngo, et al., 2016; Priess et al., 2007; Ricketts et al., 2004; Sawe et al., 2020; Veddeler et al., 2008; Willmer, 2011). Since different species of pollinators are able to pollinate different species of plants, maintaining the diversity of pollinators is of upmost importance (Potts, Imperatriz-Fonseca, et al., 2016).

1.2.1 Pollination in the tropics

In tropical rain forests, wind pollination is inefficient due to little wind below the canopy, frequently heavy rains washing out pollen, and high pollen competition due to the high species diversity and long distance between flowering individuals (Dick et al., 2008; Regal, 1982; Regal et al., 1977). As a consequence, as many as 98-99% of all woody tropical species are thought to be pollinated by animals (Bawa, 1990). A striking example is that even some of the grasses, being exclusively wind pollinated in most other habitats, depend on animal pollination in the tropics (Soderstrom et al., 1971). Pollination in the tropics is carried out by animals ranging from tiny thrips to “flying foxes”, i.e. large bats (Willmer, 2011), but in this case, as with so many other processes in nature, it is “the little things that run the world” (Wilson, 1987). Tropical plants are most commonly pollinated by insects (Renner et al., 1993), and among the insects, bees are the dominant group (Momose et al., 1998; Willmer, 2011). Regrettably, habitat loss and fragmentation have over the recent decades caused a significant decline in insect pollinator populations worldwide (Hallmann et al., 2017; Lister et al., 2018; Sánchez-Bayo et al., 2019; Veddeler et al., 2008).

1.3 Loss and fragmentation of tropical rain forests

Conversion of forests to agriculture lands and intensification of agriculture have been listed as the highest present-day threats to global biodiversity (Díaz et al., 2020; Donald, 2004; Green et al., 2005; Tilman et al., 2001). Tropical rain forests are degraded, fragmented or lost to the benefit of timber production, pasture-lands and agriculture on all continents (Meijaard et al., 2005). Southeast Asia is no exception, and with its extraordinarily high level of endemism (Myers et al., 2000), the anthropogenic influence is severe (Sodhi et al., 2004). In West

Kalimantan, Indonesia, on the island of Borneo, where this study was conducted, 63% of protected lowland forest cover was degraded between 1985 and 2001 (Sodhi et al., 2004).

1.3.1 The role of oil palm plantations in tropical rain forests loss

Among the most commonly planted crops in the tropics today is oil palm *Elaeis guineensis* (Fitzherbert et al., 2008). For Southeast Asia, Vijay et al. (2016) have estimated that 45% of the forests were lost to oil palm plantations between 1989 and 2013. More than 50% of oil palm plantations in Indonesia and Malaysia were forests in 1990 (Koh et al., 2008), and logging, beef production, and soybean- and oil palm plantations were responsible for 40% of the loss of tropical rainforest in seven countries in South America and Southeast Asia between 2000 and 2011 (Henders et al., 2015). These findings are disputed, as it has been stated that most of the plantations in Malaysia and Indonesia are planted upon previous croplands (Koh & Wilcove, 2008). In a recent study by Gaveau et al. (2019), it was shown that between 2001 and 2017, 6.20 million ha of old growth forest were converted to oil palm plantations on Borneo. The global demand for food is expected to double by 2050 (Tilman et al., 2002). The demand for vegetable oils are anticipated to surge accordingly, especially in the case of palm oil (Carter et al., 2007; Corley, 2009), as it is not only traded as a food product, but is also used in other products with a predicted increase in demand, such as biofuel (Sheil, Casson, et al., 2009).

Oil palm plantations have received a lot of negative media attention in Europe and the US, although the picture is multifaceted (Meijaard et al., 2005). The establishment of these plantations has generated an important source of income, improving the lives of local people (Meijaard et al., 2019). Oil palm grows best in tropical conditions, and plantations can be established in areas unsuitable to most other crops (Auxtero et al., 1991). They produce more oil per hectare than any other oil crop (Wahid et al., 2004), and the oil can be used in a wide array of products from cooking oil and cosmetics to biofuel (Sheil, Casson, et al., 2009).

Suggestions on how to make the business less of a threat to biodiversity have been presented to companies by scientific communities. They include implementations such as leaving patches and corridors of forest and natural streams intact within plantation areas (Fitzherbert et al., 2008). Several larger companies have recognized the situation, and have expressed intentions to move towards a more environmentally friendly practice (Edwards et al., 2010; Sheil, Casson, et al., 2009). This has lead to the establishment of the Roundtable on

Sustainable Palm Oil (RSPO, 2020) with a certification program. How the agricultural lands are operated and run will have extensive implications on natural systems and biodiversity. Implementations such as leaving patches of high conservation value (HCV) forest within oil palm plantations could help ensure maintenance of biodiversity, not only for the sake of diversity itself, but also to secure valuable ecosystem services, such as pollination (Foster et al., 2011).

1.4 Objectives and hypotheses

Due to the advantages of maintaining pollinator diversity (Potts, Imperatriz-Fonseca, et al., 2016) and the already established practice of leaving HCV forest patches within RSPO certified plantations, the effects of such patches to the local pollinator community merit investigation. The impact of HCV forest patches has been studied for birds (Edwards et al., 2010). Other studies have investigated the impact of conversion from forest to oil palm plantation and value of forest fragments on moth (Alonso-Rodríguez et al., 2017) and butterfly diversity (Lucey et al., 2012), with both studies finding a negative impact from conversion from forests to plantation on both species richness and diversity. Ashraf et al. (2018) and Ghazali et al. (2016) compared local arthropod diversity between polyculture and monoculture plantations, reporting a negative impact on species richness and diversity. Benedick et al. (2006) investigated the general impact of forest fragmentations on butterfly species diversity, finding a positive effect of small remnant forest patches. Still, to the best of my knowledge, no studies have investigated the impact of HCV areas within oil palm plantations on entire insect pollinator communities. The principal goal of the present study is to investigate whether the insect pollinator (pollinator from here on) community at the edge of HCV forest patches differ from that within the plantation landscape. The main objectives are:

Objective I: Assess whether the abundance of pollinators varies with increasing distance from the selected forest patches.

H1: The number of pollinators decreases with increasing distance to the forest

Objective II: Assess whether the size of pollinators changes with increasing distance from the forest.

H2: The size of pollinators increases with increasing distance from forest.

Objective III: Assess whether the pollinator species composition and diversity changes between areas near the forest and in the middle of the plantation landscape.

H3: The pollinator species composition differs between areas near the forest and in the middle of the plantation landscape, and the diversity is higher in the forest area.

As a reference for future studies, investigations on which colours attract which pollinators by analysing the catch in pan traps of different colours were included.

Objective IV: Assess the preference of insect pollinators for different pan trap colours.

H4: There is a preference for particular pan trap colour for the different pollinator groups.

2 Methods

2.1 Study area

The study was conducted from June to November 2017, in a plantation run by the Indonesian company PT Kayung Agro Lestari that is part of PT Austindo Nusantara Jaya Agri (ANJ)[1]. The plantation is situated in the Ketapang province, West Kalimantan, Indonesia (Figure 1).

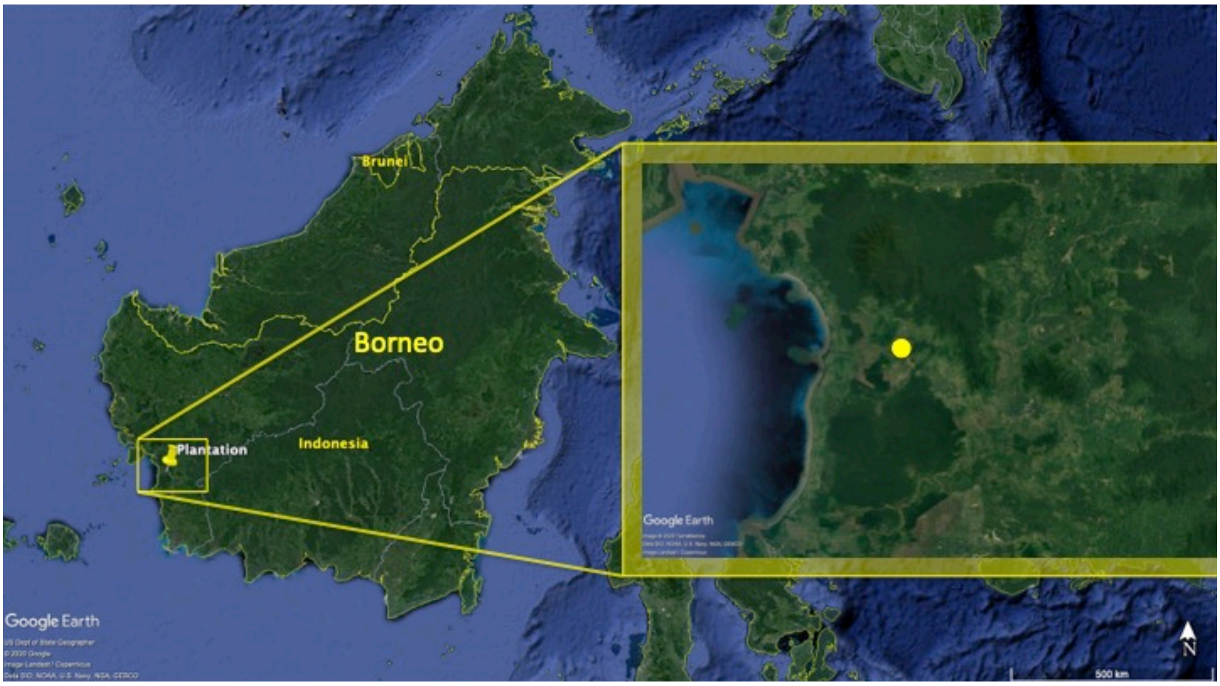

Figure 1: Overview of the island, Borneo, the province, West Kalimantan, and the location of the plantation (yellow dot, 1°25′27.11′′S, 110°10′41.08E).

The plantation, and its immediate surrounding area, is dominated by flat lowland peat swamp forest, with a rise of topographic complexity represented by an increase in frequency of smaller hills from south to north. The landscape is heterogenic and generally influenced by anthropogenic disturbance. There are two nearly intact forest patches in close proximity to the plantation. One to the north, the national park of Guanung Palung (ca. 90,000 ha), and a peat swamp forest, Sungai Putri, with about 54,000 ha to the south (Meijaard et al., 2016).

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[1] https://anj-group.com/en/home

2.1.1 Plantation

The plantation, consisting of 16,620 ha, was established in 2004. Prior to plating of oil palm, the area was a matrix of fragmented forest of partially logged natural forest and frequently burned grassland areas (Meijaard et al., 2016). Elevation at the sampled plots in the plantation varied between 6 and 33 m.a.s.l, with a mean of 18.3 m.a.s.l ± 0.143 SE. Today, the plantation is well established, with most areas planted in 2011 and 2012. It is planted on a mixture of drained peat and sandy soils (Meijaard et al., 2016). Dirt roads intersect the grid layout of planted rectangles, 1.5 by 0.20 km, often with irrigation canals dug on both sides of the road. Understory vegetation is managed by cutting and by spraying herbicides in small areas in a rotational manner (*pers. obs.*). No cutting or spraying took place in proximity to the focus areas during the study. Ferns, grasses, shrubs and herbs constituted the understory vegetation in successional stages between management cycles of cutting and spraying. The plantation is certified after the criteria of (RSPO). Amongst the criteria listed to satisfy certification is the protection of (HCV) areas. Of the plantation's total 16,620 ha, about 3,800 ha (~20%) is set aside to this purpose. The HCV areas are distributed over 16 forest patches, ranging in size from 20 to 2,300 ha (Appendix A). Two of these forest patches were selected for this study (Figure 2).

A selection of photos from the plantation can be found in Appendix B.

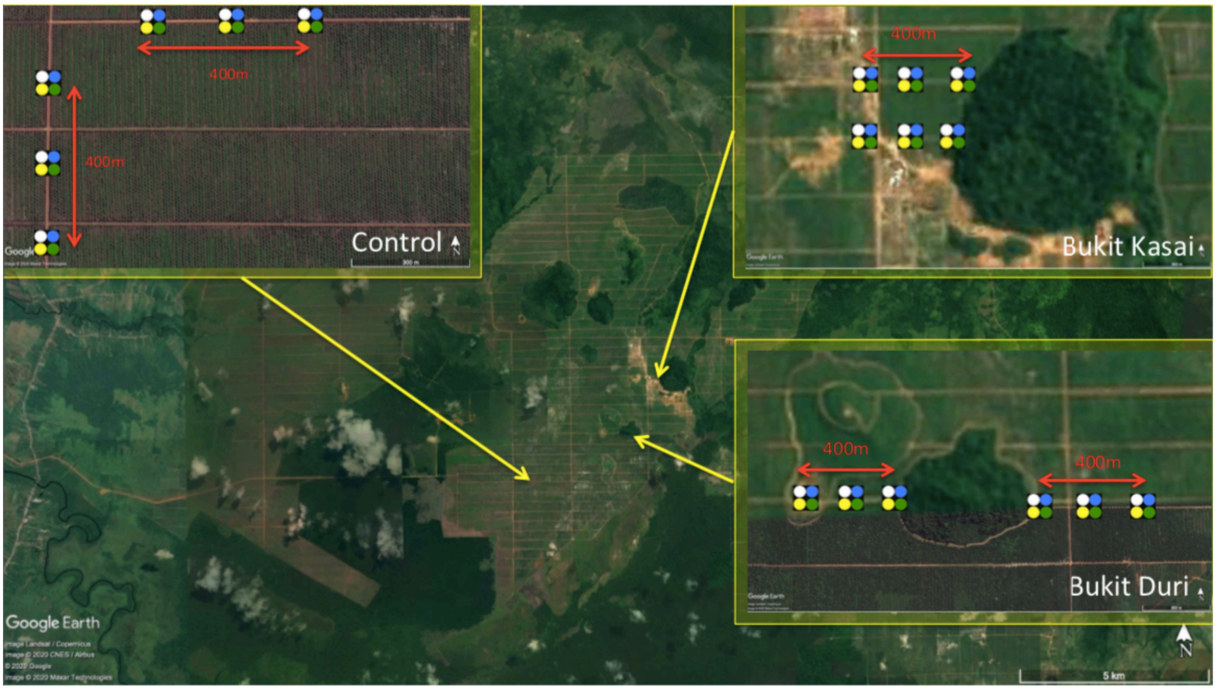

Figure 2: Overview of the plantation and the study setup. One of the patches (57 ha), named "Bukit Kasai", was partly connected to forest remnants outside the plantation, while the other (21 ha), named "Bukit Duri", was completely isolated.

2.2 Study design and data collection

In order to assess the local pollinator community, two ways of sampling were implemented. One included passive sampling with pan traps, and the other consisted in active manual observations of flower visitors to a common weed, *Ageratum conyzoides*. All sampling was done in the plantation, at ground level, resulting in little variation in environmental conditions. The data collection was carried out between July 25th and October 14th. The original plan was to dedicate most of the time during this period to data collection, but several unforeseen practical issues made this challenging (Appendix C).

All sampling was done along established roads functioning as clearings in the plantation landscape (Figure B.2, Appendix B). This was done because sampling for insects in open areas is known to be most efficient, ever since the time of the pioneers (Wallace, 1869). Two transects were established in connection with each of the two forest patches (Figure 2). Each of the transects had three individual plots (each plot consisting of one set of traps), with 200 m between each plot. Starting from the forest edge, each transect spanned 400 m into the plantation (Figure 2). All sampling from these four transects are referred to as sampling in "forest area". In addition, two control lines were established as far from the nearest forest patch as feasible, while at the same time being within reasonable travel-distance. The control-area plots were set up along these two lines after the same procedure as the forest transects, with 200 m between each plot, and three plots alongside the same dirt road (Figure 2). The control plot nearest to any forest patch was 1.5 km away from the forest. For simplicity, each of these six plots was registered with a distance of 1,500 m from the forest. Observations made, and insects trapped within these plots, are referred to as sampling in "plantation area".

2.2.1 Pan trap setup

Pan traps were selected as the main sampling method because of their efficiency (Campbell et al., 2007; Nielsen et al., 2011) and low sampling bias (Westphal et al., 2008). Soup bowls of 400 ml (pans from here on) were painted with the same paint as used in Westphal et al. (2008) and Nielsen et al. (2011). The pans were placed in an aluminium mount, which could be freely adjusted by height on a wooden-pole. The mount had room for four pans. Different colours were used to sample as wide a variety of insects as possible (Campbell & Hanula, 2007), since different insect species are attracted to different colours. The colours used as flower imitations were yellow, blue and white, and the fourth pan was coloured green as control (Figure 3). A plastic see-through roof was mounted on top of each pole to shelter the pans from overflowing during rains (Figure 4).

Figure 3:Pan trap setup, after sampling for 2 days. Photo: K.H.

Figure 4: Pan trap setup in surroundings typical for the plantation. The palms were on average 9 years old, with 3 to 4 m tall trunks. Patches of undergrowth with a varying species composition, degree of vegetation cover and level of maintenance. Photo: K. H.

All pan trap sampling was done between July 25th and October 14th 2017. The pans were deployed at dawn, between 5:00 and 7:00 am. For each sampling repetition, traps were left out for approximately 48 hours. Sampling time varied however, from 33 to 61 hours (mean = 47.5 ± 0.0886 SE) because of practical issues.

All pans were placed at the same height as, or just above, the surrounding understory vegetation. Water was filled leaving 1.5 cm from the surface to the brim. One drop of washing detergent was added to break the surface tension. Upon collecting, all insects > 1 mm were placed in a container with 70% ethanol except for representatives of the order Lepidoptera, as their scales would come off and pollute the samples by getting stuck to other collected individuals. Hence, representatives of order Lepidoptera were only counted as butterfly or moth and present or absent. No morphospecies identification (ID) was given, and no length was measured.

All collected insects were included in a pinned morphospecies reference library, where the first unique morphospecies found was selected as type specimens. Doubleton, triplet etc. individuals were discarded after being noted as present. The reference library was sorted after pre-determined groups, with bees, beetles, butterflies, moths and syrphid flies defined as pollinators. In addition, morphospecies was registered for wasps, flies and all remaining unidentified taxa as “others”. Morphospecies was not sorted into lower taxonomical levels due to limited knowledge of tropical insects. Individual morphospecies were given codes, ranging from “A1” to ”A290”[2]. The reference library was to be brought to the Natural History Museum of Oslo, but the Indonesian government did not grant permits for transportation of biological material. All insects in the reference library were photographed from at least six angles. The length of at least two individuals of each morphospecies was measured and their mean was set as morphospecies length.

2.2.2 Manual flower visitation observation setup

Ageratum conyzoides, which was selected for manual visitation observation, was found in abundance and frequently flowering throughout the plantation (Figure 5). It belongs to the Asteraceae family, which according to (Willmer, 2011) is recommended for visitation

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[2] Only 198 morphospecies were included in the analysis, as I was actively collecting collecting by net and pan traps in parallel to the study. Caught individuals were added to the reference library even though they would not be included in the present study.

observations when mapping bee diversity and abundance. “Magnet species” have also been recommended for visitation studies (Minckley et al., 1999), and among the most commonly found plant species in the understory vegetation community, *A conyzoides* appeared to be the most attractive. Personal observations showed that it was popular amongst a wide range of pollinators. The main criterion for the selection of species for observations was, however, that it should be common all over the plantation, ensuring that it could be found in proximity to all plots used for the pan trap sampling.

Figure 5: *Ageratum conyzoides*, with flower heads in full bloom, and a representative patch of flowers, as used in the manual visitation observation part. Photo: K. H.

Manual visitation observations were done between September 4th and October 13th 2017, and always between 06:00 a.m. and 12:00 p.m. Patches of observed flowers were never more than 15 m away from the pan trap plots.

Sampling with pan traps was never run simultaneously as manual visitation observations in the same area, to make sure that no potential flower visitors were trapped in the nearby pans. Observations were done for 10 min at each plot along the two forest transects next to "Bukit Kasai", and in the plantation area. All plots were observed for between 7 and 11 individual observation periods (repetitions), resulting in a total of 47 repetitions in the "Bukit Duri" forest area, and 46 repetitions in the "plantation area".

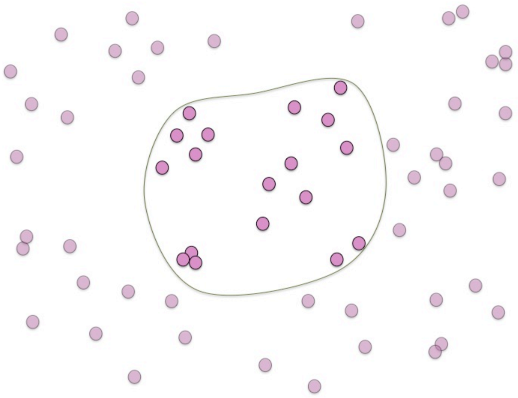

Figure 6: Representation of a flower patch with individuals defined for observation.

Within each patch of flowers, a selection of flowers for observation was defined by a string of dark-green parachute-cord, tied as a circle with a radius of 30 cm to cover the most viable individuals within the given patch (Figure 6). All flower heads within this circle were included in the observations. The average number of flower heads included varied between 10 and 20.

All patches of flowers were under shade from a nearby palm tree during the time of observations. All potential pollination events, including casual visits, were noted as "visitation". The observer was always distanced 2 m from the outer edge of the circle, making sure not to cast a shadow on the observed patch. Visits were only recorded for the insect groups defined as pollinators in the pan trap part (bees, syrphid flies, beetles, butterflies and moths). When a visitor landed on multiple flower heads within the visitation area during one observation session, each visit to a new flower head was noted as a separate visit.

2.3 Environmental conditions

2.3.1 Vegetation cover

In order to separate between potential local influence of flower abundance, the flowering understory vegetation in proximity to all plots were recorded. The percentage of this variable covering the ground within a five-meter radius of each plot was recorded. This was recorded separately for each plot during pan trap sampling, and for each patch of flowers during the manual visitation observations. For pan trap sampling, blooming flowers covered between 1% and 80% of the ground with a mean of 23.3% ± 0.42 SE. For manual observations, blooming flowers covered between 1% and 50% with a mean of 15.7% ± 0.842 SE.

2.3.2 Temperature and light intensity

All pan trap-poles were equipped with a Hobo light and temperature-measuring device (HOBO UA-002-64 pendant® Temperature/ Light 64K Data logger), logging every 30 min. In addition, the same device was set up in a representative area of the plantation (1°27′02.08”S 110°13´24.15”E), attached to the stem of an oil palm, in the shade of its leaves, 2 m above the ground. These devices were sampling light and temperature data for the entire duration of the study.

Light intensity for all plots, as measured by these devices under the clear plastic roof of the pan trap-setup, had an average of 27,398 lux, equivalent to direct sunlight. Day and night temperatures for all plots, as recorded by abovementioned devices, varied between 22°C and 34°C with a mean of 25°C. Temperature varied little between the sample plots and the reference measurement-plot in the plantation. Minimum, mean, and maximum temperatures were calculated at six representative times of day and night (Table 1), providing the general temperature conditions in the studied areas of the plantation over the duration of the study.

Table 1: Average daytime and nighttime maximum and minimum temperatures at three representative times.

Time	**Minimum daytime temperatures**	**Mean daytime temperatures**	**Maximum daytime temperatures**
08:00	22°C	25°C	28°C
12:00	23°C	30°C	34°C
18:00	23°C	27°C	33°C
Time	**Minimum nighttime temperatures**	**Mean nighttime temperatures**	**Maximum nighttime temperatures**
00:00	22°C	24°C	27°C
04:00	22°C	23°C	27°C
06:00	22°C	23°C	26°C

2.4 Statistical analyses

All statistical analyses were done by R version 3.6.3 for Mac OS X (R Core Team, 2020).

2.4.1 Abundance of pollinators, distance from forest and pan colour

To assess how the pollinator abundance and flower visit frequency varied with different factors, a GLMM (generalized linear mixed model) approach was applied with Poisson or negative binomial distributed errors, depending on the error distribution in the data. Based on each of the datasets (pan trap data and manual visitation observation data), models were made for each of the pollinator groups, as well as for all the pollinators grouped together. For the insect groups that followed the Poisson distribution, the glmer function from the lme4 package (Bates et al., 2015) was used to generate the models. For the insect groups that were over-dispersed (the variance was higher than the mean), it was assumed that the data followed a negative binomial distribution, and the glmer.nb function from the lme4 package (Bates et al., 2015) was applied.

The response variables used were "number of individual insects per pan" and "number of flower visits per 10 min of observation". Random variables included were a unique ID for each individual trap and repetition/unique ID for each observation and which date the pan traps were placed out/the observation was carried out (Table 2). In the models based on the pan trap data, the number of hours the pan had been sampling was used as an offset variable. No offset variable was included in the models based on the manual visitation observation data, as there was not registered an accurate number of observed flowers for each observation period. The average number of flower heads observed within each observation varied between 10 and 20.

Table 2: Random effects included in the models.

	Random variable ID	**Random variable date**
For models based on pan trap data	ID of unique trap	Date when trap was set out
For models based on manual observation data	ID of unique 10-min observation	Date when observation was done

To identify the model best explaining the variation in the focal response variables, a backward selection approach was applied. Initially a full model was made, including all the fixed effects listed in Table 3 Variables were then removed one by one, starting out with the one with the highest p-value reported. The final, best model contained only variables with a p-value < 0.05. See Appendix D for how the model selection was carried out for the different models.

Table 3: Fixed effects included in the full models, initiating the model selection procedure.

	Fixed effect	**Why it was included**
For models based on pan trap data	Distance from forest (number of meters from forest) / area type (forest area or plantation area)	To see whether the number of insects decreased with the distance from forest (Objective I)
	Pan colour (blue, yellow, white or green)	To see if there was any preference in pan colour (Secondary Objective I)
	Flower coverage (% of green understory vegetation in flower)	Areas with higher flower coverage might attract more pollinators.
	Interaction between flower coverage and distance from forest / area type	Flower coverage might be more important for pollinators within the plantation than near the forest.
For models based on manual observation data	Distance from forest (number of meters from forest) / area type (forest area or plantation area)	To see whether the number of flower visits decreased with distance from forest (Objective I)
	Flower coverage (% of green understory vegetation in flower)	Areas with higher flower coverage might get more flower visits.
	Time of day (linear)	There might be higher pollination activity at certain times of the day.

2.4.2 Insect length and distance from forest

To assess whether the length of the insects caught with pan traps varied with distance from forest, an attempt at making linear regression models for the different pollinator groups (length as response and distance from forest as explanatory variable) was made. However, the assumption for normal distributed residuals was not met for any of the models, nor after applying different transformations to the data. Therefore, the non-parametric Mann-Whitney U test was used to compare the insect lengths between the forest area and the plantation area. To do this, the wilcox.test function was applied.

The approach was carried out for each of the groups “all pollinators”, “beetles” and “syrphid flies”. It was not carried out for butterflies and moths, as their length was not measured. The reason for not carrying out the analysis for bees, was that the distribution of bee lengths in the plantation area did not have the same shape as that in the forest area, and this assumption has to be met in order to use Mann-Whitney U test (Whitlock et al., 2009).

2.4.3 Species composition

To assess whether the species composition differed between the forest area and the plantation area, a beta diversity approach was applied. Based on the frequency of each morphospecies captured in each of the individual pan traps (number of insects per hour the pan had been out), a Bray-Curtis dissimilarity matrix was made, using the bray.part function from the betapart package (Baselga et al., 2018). This matrix was then used as an argument in the betadisper function from the vegan package (Oksanen et al., 2019), to assess the beta diversity between the forest area and the plantation area. I used analysis of variance (ANOVA) to see if there was a significant difference in beta diversity between the two areas. For this I used the anova function. One analysis was made for all captured insects, and one for only pollinators, although butterflies and moths were not included, since the morphospecies was not registered for these groups.

3 Results

3.1 Presentation of raw data

3.1.1 Raw data from pan trap sampling

Sampling with pan traps resulted in 3256 caught insect individuals. Only 606 of these belonged to insect groups defined as pollinators (Figure 7). Flies were by far the most numerous insect group, and syrphid flies were the pollinator group with most trapped individuals (Figure 7). Only 32 trapped individuals belonged to the insect group considered to contain the most efficient pollinators, the bees (Figure 7).

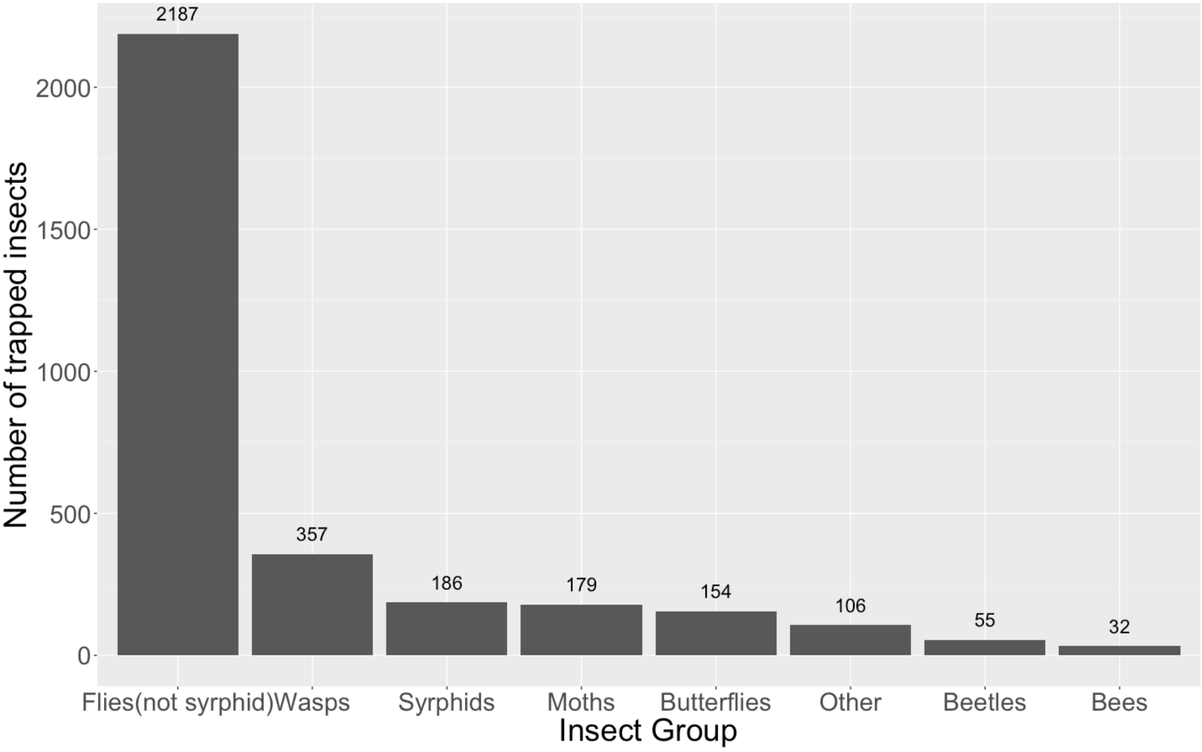

Figure 7: The total number of all trapped insects for each of the insect groups. Syrphids, moths, butterflies, "others", beetles and bees are the groups defined as pollinators.

Among the different taxa, 198 morphospecies were identified (Table 4). See Appendix E for the exact number of individuals caught of each morphospecies in the different area types, and also some pictures of some of the morphospecies.

Table 4: The number of morphospecies trapped divided amongst registered taxa. Groups defined as pollinators are beetles, bees, syrphid flies, butterflies and moths.

Taxon	**Number of morphospecies**
Wasps	63
Beetles	31
Others	27
Bees	26
Flies (not syrphid)	26
Syrphid flies	25
Butterflies and moths	*Not identified to morphospcies*
Total	**198**

The six plots next to the forest patch "Bukit Duri" were each sampled six times/repetitions (285 hours of sampling) and the six plots next to the forest patch "Bukit Kasai" were each sampled three times/repetitions (144 hours of sampling). The six control plots were each sampled four times/repetitions (190 hours of sampling). Added together, the plots from both areas were sampled for 619 hours, or 25.8 days. The number of trapped insects per hour and per repetition was higher in the plantation area compared to the two forest areas (Table 5).

Table 5: The number of trapped individual insects and trap-frequency among the three sampled areas. One repetition equals one round of sampling with pan traps for ~48 hours.

Area	**Number of insects**	**Number of insects per repetition**	**Number of insects per hour of sampling**
Bukit Duri, six repetitions	1283	213.8	4.5
Bukit Kasai, three repetitions	531	177.0	3.7
Plantation, four repetitions	1442	360.5	7.6

For all pollinator groups, except bees, the highest number of individuals were trapped in the control plots 1,500 m away from the forest, whereas there was less difference in numbers along the transects (0, 200 and 400 m) in the forest area (Figure 8). Most pollinator groups showed clear preferences for certain colours of the pan traps. Syrphid flies for white, bees for blue, beetles and butterflies for yellow (Figure 9).

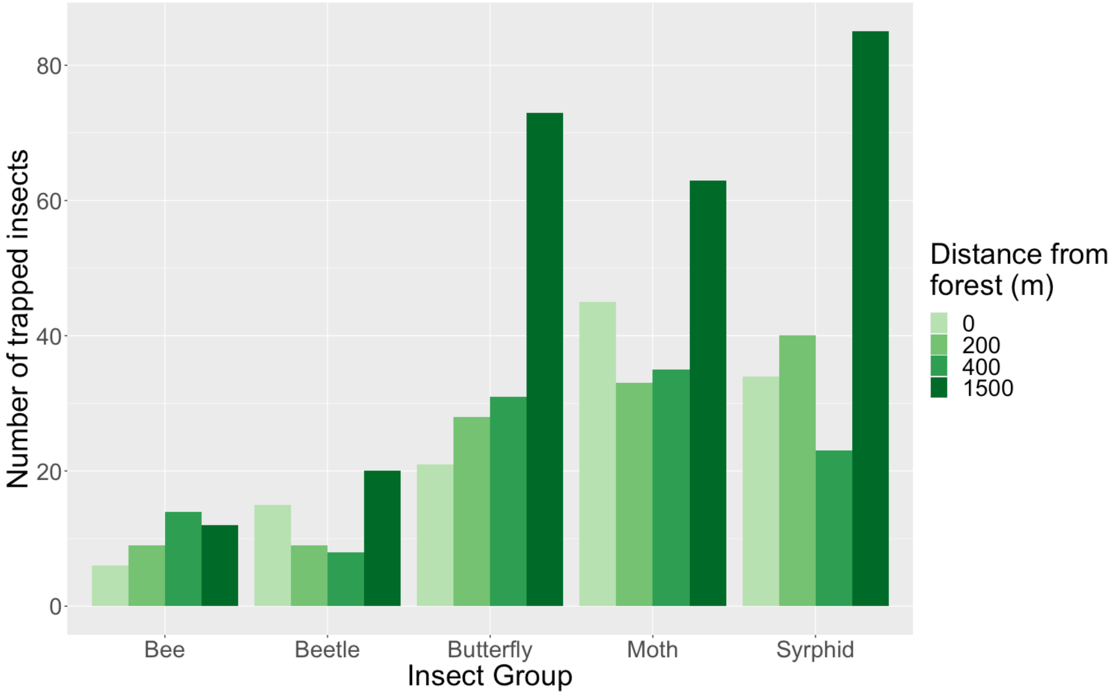

Figure 8: The absolute number of insect groups trapped at different distances from forest. Plots 0, 200 and 400 m from forest were all sampled for 143 hours. Plots more than 1,500 m from forest were sampled for 190 hours.

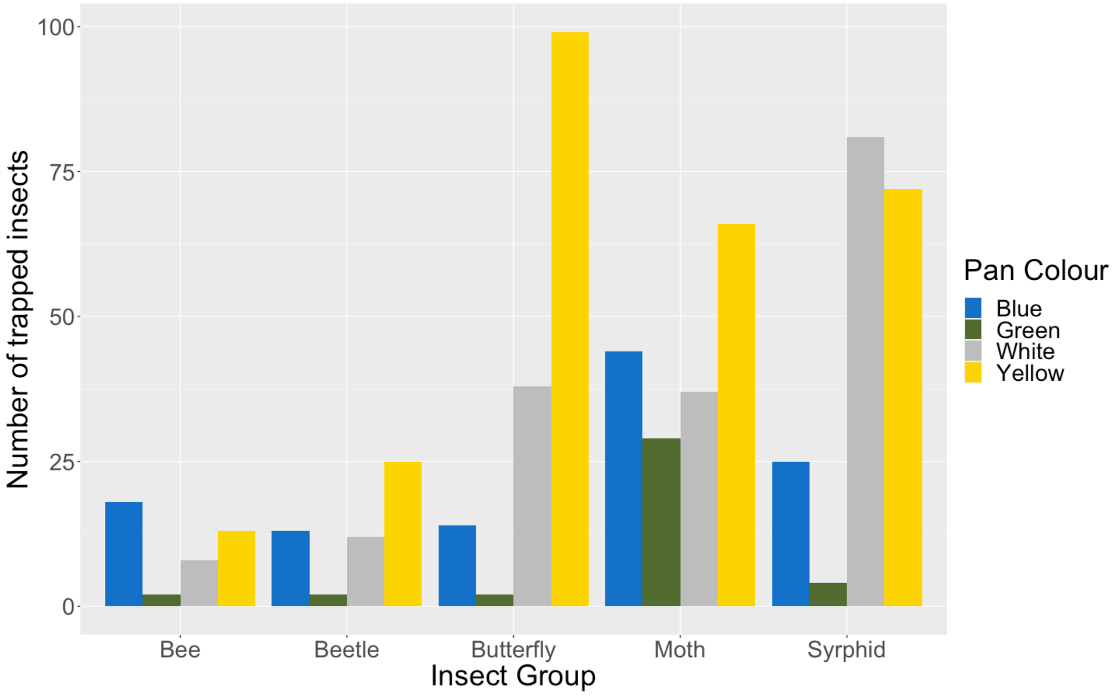

Figure 9: The absolute number of pollinators trapped in the different coloured pans. The different coloured pans had been sampling for an equal amount of time.

The length of the insects varied between 1 and 17 mm, with a mean of 6.4 mm ± 0.052 SE. Syrphid flies had the highest median of all pollinator groups (11 mm), and other flies had the lowest (4 mm) (Figure 10). When comparing the length distribution of insect groups between the forest area and the plantation area, bees was the only group indicating some difference in size between the two areas (Figure 11).

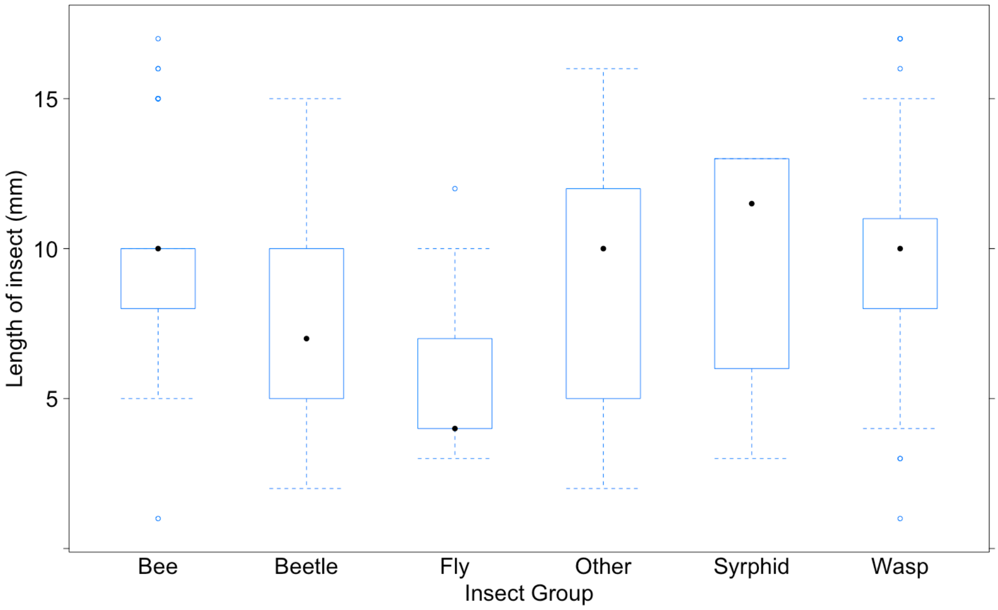

Figure 10: Representation of the measured length for all trapped insects in the different pollinator groups.

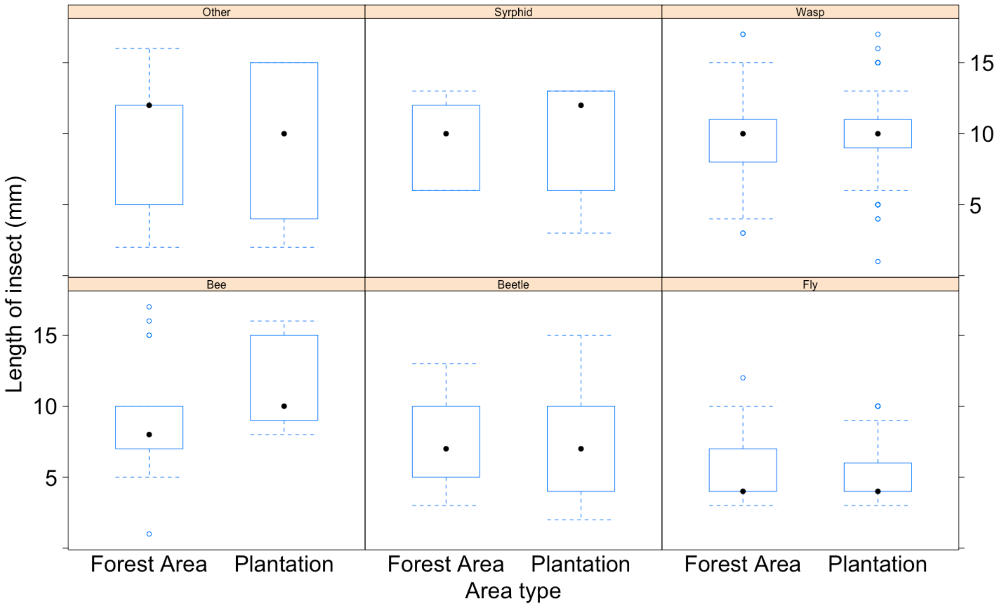

Figure 11: Comparison of trapped insect’s length between the two areas ”Forest area” and ”Plantation”.

3.1.2 Raw data from manual visitation observations

The manual observations resulted in 306 observed flower visits, over half of them carried out by bees, while butterflies and syrphid flies accounted for the vast majority of the remaining visits (Figure 12). When carrying out manual observations, visits were recorded. Table 6 lists the minimum number of observed individuals during these observations. These numbers are reported in order to have some comparable numbers to the pan trap sampling, where individuals were caught and no visits were registered.

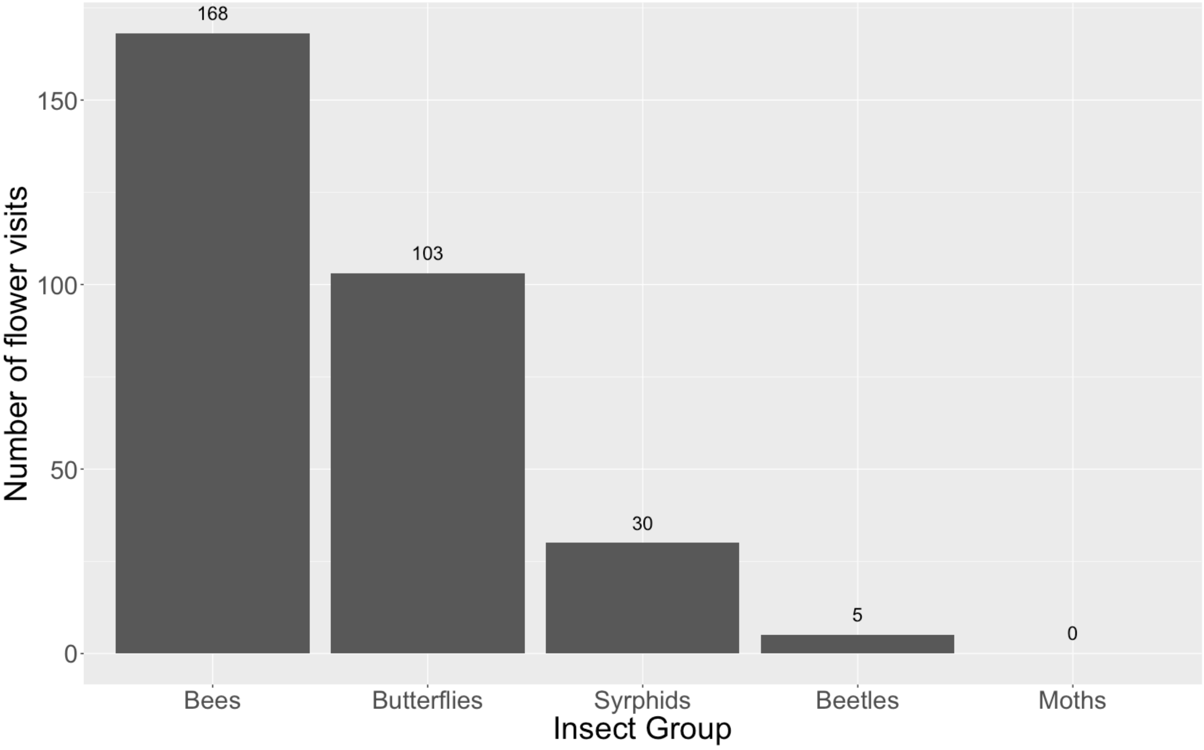

Figure 12: The number of visits from the separate pollinator groups in the manual observation part.

Table 6: The minimum number of observed visitors during the manual observation sampling. These numbers were found by counting the number of observation periods where at least one visit by the focal insect group was registered.

Insect Group	**Minimum number of observed visitors**
Bees	37
Butterflies	31
Syrphid flies	20
Beetles	5 (actual number)
Moths	0 (actual number)

In total, 93 10-min observations were carried out, summing up to 15.5 hours of observation. Forty-seven repetitions were done in the two transects stretching from the forest patch "Bukit Duri", and 46 repetitions were done in the six plots in the control plantation area. The highest visitation frequency was observed closest to the forest border (0 m), but when considering the visitation frequency across the whole transect (0, 200 and 400 m), it was somewhat lower than the visitation frequency of the plantation area (Table 7).

Table 7: Number of observed visits and visit frequency within the two observation areas. 0 m had 15 repetitions, and 200 and 400 had 16 repetitions each.

Area	**Distance from forest**	**Number of visits**		**Number of visits per 10-min observation period**	
Bukit Duri 47 repetitions	0	102	Total: 217	6.8	Total: 4.6
	200	81		5.1	
	400	34		2.1	
Plantation 46 repetitions	1500	257		5.6	

The highest number of flower visits was registered for bees, followed by butterflies. Both groups had highest number of visits at distances furthest from the forest (1500 m) (Figure 13).

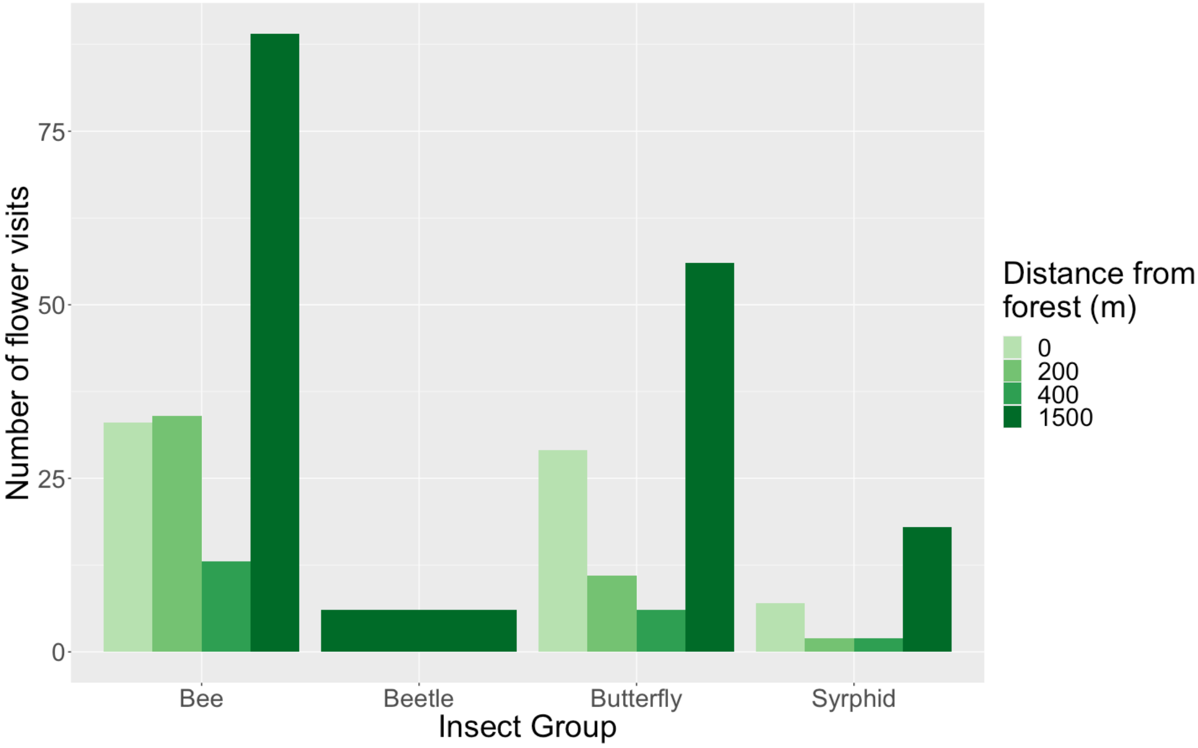

Figure 13: The absolute number of observed flower visits for the separate pollinator groups. Note that the number of observations differed between the different distances: 15 repetitions were done for plots 0 m from forest, 16 repetitions for plots 200 and 400 m from forest and 46 repetitions for plots 1500 m from forest (plantation). The same coloured representation of beetles is due to that all visits by beetles were observed in the plantation area.

3.2 Abundance of pollinators related to distance from forest and pan colour

The best models for all pollinators as one group, and for the separate pollinator groups, are presented in Table 8.

Butterflies and pollinators (as one group) were the only groups where distance from forest had a linear effect on abundance. Syrphid flies had a significant difference in abundance between forest area and plantation area. For all of the abovementioned groups, the abundance was higher in the plantation than near the forest.

All pollinator groups showed a significant preference for pan colour, although it varied which group preferred which colour. All pollinators as a group preferred yellow or white pans over blue pans. Bees preferred blue or yellow pans over white and green. Both syrphid flies and butterflies preferred the yellow and white pans over the blue pans. The beetles preferred yellow over blue pans, but there was no difference in preference between yellow and white or blue and white. The green pans were the least (or partly least) preferred colour for all the groups.

Table 8: The best models (found by backwards p-value selection) for the different pollinator groups, explaining the number of trapped individuals per trap per hour.

				95% confidence limits		
	Fixed effect	**Estimate**	**SE**	**Lower**	**Upper**	**P value**
All pollinators	Intercept	-3.72	0.149	-4.01	-3.43	<0.001
	Distance from forest	0.000252	0.000121	1.48×10^{-5}	0.000489	0.0371
	Pan colour (green)	-1.03	0.206	-1.43	-0.626	<0.001
	Pan colour (white)	0.445	0.151	0.149	0.741	0.00312
	Pan colour (yellow)	0.919	0.143	0.639	1.199	<0.001
Bees	Intercept	-6.07	0.425	-6.90	-5.24	<0.001
	Pan colour (green)	-2.62	1.03	-4.67	-0.611	0.0108
	Pan colour (white)	-1.25	0.567	-2.36	-0.135	0.0279
	Pan colour (yellow)	-0.0741	0.385	-0.829	0.681	0.847
Syrphid flies	Intercept	-5.83	0.337	-6.49	-5.17	<0.001
	Area type (plantation)	0.642	0.310	-1.25	-0.0346	0.0382
	Pan colour (green)	-1.85	0.567	-2.96	-0.734	0.00113
	Pan colour (white)	1.03	0.287	0.468	1.59	<0.001
	Pan colour (yellow)	0.886	0.291	0.315	1.46	0.00234
	Flower coverage	0.0120	0.00530	0.109	0.130	0.0239
Butterflies	Intercept	-6.26	0.379	-6.98	-5.53	<0.001
	Distance from forest	0.000633	0.000262	0.000120	0.00115	0.0155
	Pan colour (green)	-1.87	0.762	-3.36	-0.376	0.0142
	Pan colour (white)	1.11	0.326	0.466	1.75	<0.001
	Pan colour (yellow)	2.02	0.303	1.43	2.62	<0.001
Beetles	Intercept	-6.00	0.342	-6.67	-5.33	<0.001
	Pan colour (green)	-1.79	0.764	-3.29	-0.29	0.0190
	Pan colour (white)	0.285	0.382	-0.464	1.03	0.446
	Pan colour (yellow)	0.734	0.351	0.0456	1.42	0.0366
Moths	*No fixed effects were significant*					

3.3 Flower visit frequency and distance from forest

The best models for all pollinators as one group, and for the separate pollinator groups, are presented in Table 9. For all groups, the time of day had a significant effect on the observed flower visit frequency, where the abundance was highest at 12:00. For all pollinators (as one group), bees and butterflies, this was the only significant effect. Visit abundance by syrphid flies was significantly higher in the plantation area than in the forest area, and decreased with flower coverage.

Table 9: The best models (found by backwards p-value selection) for the different pollinator groups, explaining the number of flower visits per 10-min observation.

				95% confidence limits		
	Fixed effect	**Estimate**	**SE**	**Lower**	**Upper**	**P value**
All pollinators	Intercept	-5.39	1.47	-8.26	-2.51	<0.001
	Time of day	14.3	3.50	7.44	21.2	<0.001
Bees	Intercept	-8.14	2.03	-12.1	-4.17	<0.001
	Time of day	17.9	4.67	8.77	27.1	<0.001
Syrphid flies	Intercept	-3.63	0.00215	-3.63	-3.62	<0.001
	Area type (plantation)	0.572	0.00215	0.568	0.576	<0.001
	Flower coverage	-0.0109	0.00214	-0.0151	-0.00671	<0.001
	Time of day	3.55	0.00215	3.546	3.555	<0.001
Butterflies	Intercept	-5.31	1.92	-9.06	-1.55	0.00564
	Time of day	9.93	4.66	0.804	19.1	0.0329
Beetles	*Only 5 visits observed, not enough data to produce a model.*					
Moths	*No visits by moths were observed.*					

3.4 Insect length and distance to forest

The non-parametric Mann-Whitney U test showed that there was no significant difference in the length of any insect groups between the forest and plantation areas (Table 10).

Table 10: The results of Mann-Whitney U tests, comparing the insect lengths between forest area and plantation area. The analyses were based on the lengths of 73 beetles (52 in forest area and 21 in plantation) and 180 syrphid flies (97 in forest area and 83 in plantation area).

Insect group	**W statistic**	**P value**
Beetles	502.5	0.583
Syrphid flies	3663.5	0.275
All pollinators	7719	0.0964

3.5 Species composition and diversity in plantation and forest area

There seemed to be somewhat of a difference in species composition between the forest area and the plantation area when all insects were included in the beta dispersion analysis, as the dispersions of the different area types are slightly separated (Figure 14). This was, however, not the case when only pollinators were included, as the dispersions of the different area types are highly overlapping (Figure 15).

The beta diversity was significantly lower in the plantation area than in the forest area when all the insect groups were included in the analysis (Figure 14, Table 11), but when only pollinators were included there was not a significant difference in beta diversity between the two area types (Table 11).

Table 11: Analysis of variance, comparing the beta diversity between the forest area and the plantation area.

	F statistic	**P value**
All insects	8.84	0.00396
Pollinators only	1.23	0.271

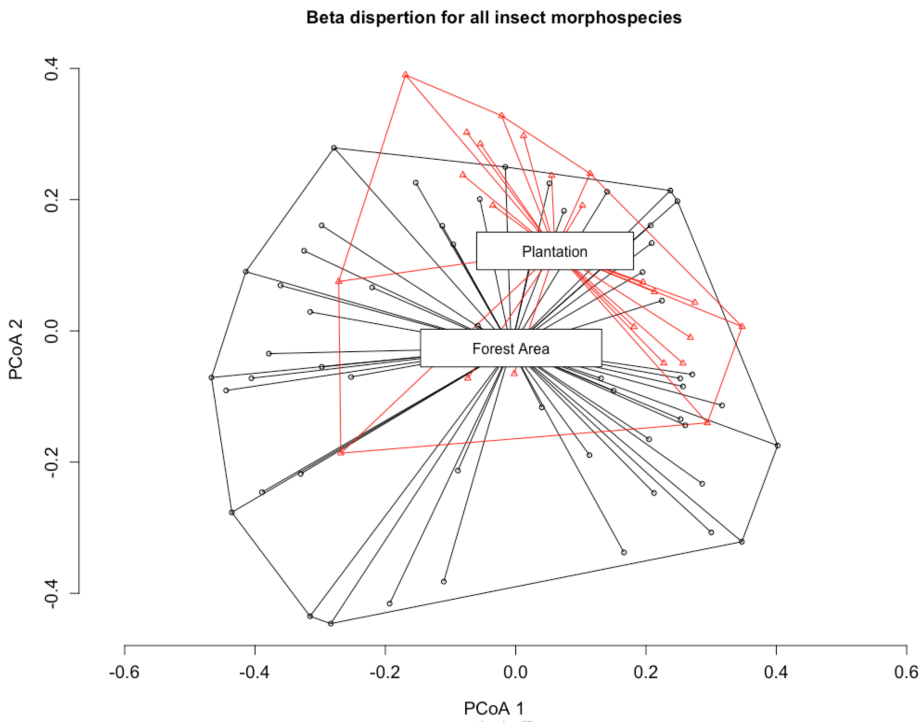

Figure 14: Betadisper plot of all insects (198 different morphospecies). Each dot in the plot represents a trap (78 traps in total), and its placement is dependent of the abundances of the different morphospecies in the trap. Red triangles are traps that were placed in the plantation area (24 traps), and black circles are traps that were placed in the forest area (54 traps).

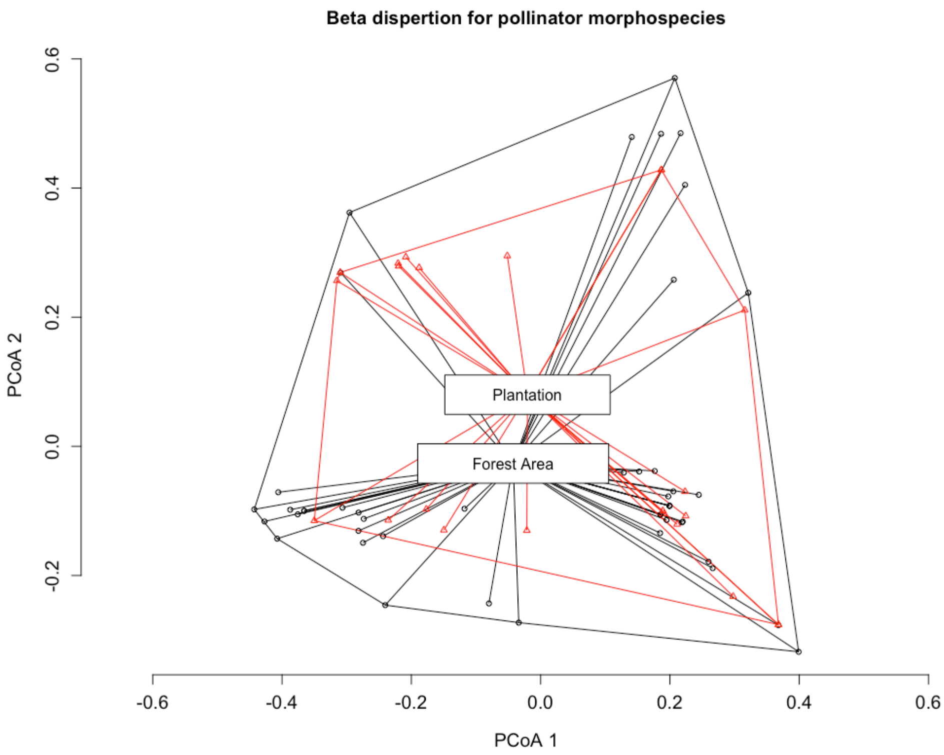

Figure 15: Betadisper plot for pollinators (82 different morphospecies). Each dot in the plot represents a trap (70 traps in total), and its placement is dependent of the abundances of the different morphospecies in the trap. Red triangles are traps that were placed in the plantation area (47 traps), and black circles are traps that were placed in the forest area (23 traps).

4 Discussion

4.1 Pollinator abundance, flower visit frequency and distance from forest

In contradiction to hypothesis H1, lower numbers of all pollinator groups combined were trapped in the forest area compared to deeper within the plantation area. The same result was found for syrphid flies and butterflies when analysed separately, and there was also a higher frequency of syrphid fly flower visits in the plantation area compared to the forest area. Curiously, the flower visit frequency of all pollinators combined declined from 0 to 400 m, but then increased again in the plantation area (> 1500 m) (Table 7).

It is possible that the higher number of pollinators trapped further away from the forest patches reflects a more generalist species composition, and that individuals found near the forest patches included more specialized pollinators, better adapted to pollinating the remaining flora within the forest patches. The forest patches had little observed flowering, both in understory and canopy during the study period. If a higher number of species flowering within the forest patches occur at later point in time, the forest patches would attract more pollinators, and the observed distribution would differ.

4.2 Pollinator size and distance from forest

Hypothesis H2, stating that size of pollinators would increase with increasing distance from forest, was not confirmed for any of the analysed pollinator groups. There was a slight trend for increase in size with increasing distance from forest for the bees, as the only pollinator group (Figure 11), but this was not confirmed by statistical analysis. The lack of difference in size was perhaps not as surprising as it would have been if hypothesis H1 and H3 (see next section) would have had stronger support. If the majority of the pollinator community in the plantation landscape operates with the forest patches as a base, and from there forages for pollen and nectar in the understory of the plantation, one could expect to detect the larger pollinators to be capable of foraging at longer distances from their nests as shown in Greenleaf et al. (2007).

4.3 Variation in species composition

There was not found any strong support for hypothesis H3, that the species composition of pollinators would differ between the areas near the forest and in the middle of the plantation, and that the diversity would be higher in the forest area, as the produced beta dispersion plot indicates an overlap in the pollinator species composition between the two areas (Figure 15).

Interestingly, when analysing all trapped insects (including non-pollinator groups), the species composition differed somewhat between the forest area and the plantation area. Additionally, the diversity was higher in the forest patches compared to that of in the middle of the plantation, but only when the non-pollinator groups were included (Table 11).

Better taxonomic resolution, and deeper knowledge of the local pollinator community would be required to fully address hypothesis H3. Due to insufficient knowledge on taxonomic and dietary affinities among the enormous diversity of tropical insect families, a somewhat coarse generalization of trapped morphosepecies as pollinators and non-pollinators, respectively, was adopted during this study as a suboptimal solution.

Trapped insects were sorted after well-recognized pollinator groups (bees, beetles, syrphid flies, butterflies and moths), not taking into account whether the morphospecies were generalist or specialist pollinators, indigenous or exotic, nor any measure on their effectiveness as pollinators on local plants. The fact that a certain morphospecies was trapped in the pans, or belonging to a well-known pollinator-rich group, does not itself make it an effective pollinator of the local flora. On the other hand, within some groups treated as non-pollinator groups in the present study, such as wasps and flies, some families or species could potentially be viable and even highly specialized pollinators. This leaves the possibility that if a higher definition in the taxonomical categorisation of morphospecies to pollinators and non-pollinators had been applied, a stronger support for hypothesis H3 could have been found.

When comparing the absolute number of morphospecies trapped in the two areas (> 1,500 m from forest and < 400 m from the forest), there was a distinct difference in numbers between areas for some morphospecies (Appendix E). This could suggest preference for a certain habitat, at least for the morphospecies with highest representation (Appendix E). This was primarily the case for groups counted as non-pollinators in this study, such as flies and wasps, in accordance to the results of the beta diversity analysis (Figure 14-15, Table 11). This comparison did not, however, take into account the variation in sampling time between the two areas, and is therefore more of a strong indication than a certain result. Since butterflies and moths were not categorized to morphospecies, similar comparisons could not be made for these groups.

4.4 Pollinator preference for pan colours

I found that there was a strong variation in the number of insects caught in the pan traps of different colours, which varied among the taxonomical groups, giving support to hypothesis H4. Other studies have also found that different coloured pan traps catch different pollinators (Campbell & Hanula, 2007; Gollan et al., 2011; Laubertie et al., 2006; Vrdoljak et al., 2012), and further that same coloured pan traps catch different insect groups when trapping in different habitats (Saunders et al., 2013). The results found in the present study are relevant as a future reference for other studies in oil palm plantations using coloured pan traps. Most bees were trapped in blue and yellow pans, in accordance with the results found by Moreira et al. (2016). Most beetles were trapped in yellow pans. No previous studies were found that assessed the preference for pan trap colour in beetle communities. Syrphid flies had a preference for white and yellow traps. This is in accordance with the results found by Laubertie et al. (2006), where yellow was the most popular colour (the study did not take white traps into account). A curious observation was that the number of syrphid flies showed a positive correlation with percentage of understory vegetation in flower for the pan trap part, whilst the opposite was found for the manual visitation part. This could stem from a lower likelihood of getting the syrphids within the observed patch with more flowers to choose from over a 10 min observation period, whilst with the pan traps 48 hours sampling time, curious individuals could eventually get trapped. Butterflies had a preference for yellow and white pans. Interestingly, Vrdoljak and Samways (2012) concluded that pan traps were not efficient for butterfly surveys, as they only found three individuals of the same species with over 10,000 trap hours in South-Africa. This low catch-rate, compared to the 154 butterflies (unknown number of species) trapped over 1,548 trap-hours in the present study highlights the difference in trapping in different habitats. Moths did not show any distinct preference for pan trap colour.

4.5 The influence of forest patches

Oil palm plantations offer spatial complexity with room for epiphytes, flowering understory vegetation, in addition to being relatively stable, as they are not ploughed and sowed again for up to 20 years. Hence, they are able to support more biodiversity than that of comparable tropical crops, such as soy bean or rice (Foster et al., 2011). The understory in the focal study area is managed with rotational cutting and spraying, but at a pace allowing for most of the herbaceous understory vegetation to flower. Herbicides could obviously be affecting both plant ant pollinator community on a longer timescale (Setyawan et al., 2019), but falls beyond the scope of my study. Some degree of spatial complexity is present in the plantation landscape of this study (Figure 4). Since most of the palm trees are over 9 years old, they could offer substrate to epiphytes. The ground between the palms is for the most part covered by grasses, ferns, herbs, herbaceous shrubs and bushes, dead palm leaves and empty fruit bunches, offering nesting and roosting sites in addition to pollen and nectar sources, at least for some insect genera. The higher number of pollinators found in the plantation compared to the forest area could indicate that for the species found there, the plantation harbours enough suitable nest sites and food resources. With oil palms being able to produce for up to 20 years, spatial complexity within the plantation landscape could be expected to increase over the years, possibly increasing the potential for species diversity.

Still, it is obvious that oil palm plantations never will be able to sustain the same biodiversity as natural forests (Fitzherbert et al., 2008; Foster et al., 2011). It has been found that oil palm plantations negatively affect local arthropod diversity, both for moths in the Neotropics (Alonso-Rodríguez et al., 2017), orchard bees in Costa Rica (Livingston et al., 2013), diversity of butterflies (Lucey & Hill, 2012), ground dwelling ants (Brühl et al., 2010), and dung beetles in Malaysian Borneo (Gray et al., 2014), whilst polyculture plantations have been shown to host a higher diversity of arthropod orders compared to monoculture ones (Ashraf et al., 2018; Ghazali et al., 2016).

Microclimatic conditions are more diverse in an intact forest, and oil palm plantations have been shown to have an average temperature at least two degrees hotter than nearby forests (Lucey & Hill, 2012). They experience more abrupt temperature fluctuations, in addition to higher and lower both maximum and minimum temperatures, which certainly will affect the entomofauna composition. Undisturbed forest patches in Southeast Asia were found to harbor a greater diversity of bees when compared to disturbed forest patches (Liow et al., 2001), however, the disturbed sites harboured a higher number of solitary bees, making the total species richness higher. This seemed not to be the case in the focal study area, as the beta diversity analysis comparing trapped pollinators between the two areas did not show any significant difference.

Although Ghazoul (2005) highlights in his review several studies showing that tropical bees are surprisingly resistant to habitat fragmentation, they also mention how oceanic island pollinators are more prone to extinctions due to small population sizes. This is relatable to forest patches in monoculture areas, such as for butterflies in the study by Benedick et al. (2006), and the isolated forest patch "Bukit Duri" in the present study, for all taxa not able to bridge monoculture gaps between areas of natural vegetation, larger than a given size. The effects from fragmentation of landscapes have been shown to range from negative through neutral to positive on general biodiversity (Fahrig, 2003). However, the general, fragmentation of landscapes has been shown to negatively affect pollination services (Haddad et al., 2015). For the very same reasons, the importance of maintaining these fragments is increasing. Forest fragments in monoculture fields have been found to improve pollination for a number of crops, such as coffee (Priess et al., 2007; Ricketts et al., 2004; Veddeler et al., 2008) and as mentioned by Ghazoul (2005), for cashew, macadamia and mango. In addition, Kremen et al. (2002) demonstrated the effectiveness of native bee communities in pollination services to a number of crops, as long as the crops were within reasonable distances to natural forest patches. This is relevant for the pollination of remnant plant species within the forest patches themselves, as for the two forest patches in the studied plantation, "Bukit Duri" and "Bukit Kasai". As a higher diversity of pollinators presents a higher likelihood of plant pollinator match (Potts, Imperatriz-Fonseca, et al., 2016), potentially ensuring mutualistic ecosystem services, where plants offer food, nesting sites and favourable microclimatic conditions, and pollinators provide pollination. It cannot be ruled out that there are pollinator species present in the forest patches of this study area that was not detected due to sampling bias. They could be canopy dwelling, not foraging in the understory of the forest nor the plantation and hence not being registered. If so, these pollinators could be ensuring the pollination of remnant plant species within these forest patches.

Pollination is crucial for the prosperity of many tropical tree taxa, and the quality of pollination has been shown to decline for tropical trees in fragmented populations (Cascante et al., 2002; McKey, 1989). The size of remaining forest patches is crucial to remaining diversity and abundance of pollinators within these patches (Benedick et al., 2006; Rosenzweig, 1995; Steffan-Dewenter et al., 2006). In her chapter on fragmentation, Willmer

(2011) highlights a study by Aizen et al. (1994) conducted in the more dry Argentinian subtropics, finding that forest fragments smaller than 5 ha were unable to host populations of wild pollinators. In these forest patches, the wild pollinators were exchanged with an introduced *Apis*, leading to a decline in the productivity of at least 16 tree species. Wilson (1987) highlights that even a small patch of forest, at 10 ha, could be large enough to sustain a community of plant or invertebrate species, and therefore would be well worth protecting. The sizes of the two forest patches “Bukit Duri” and “Bukit Kasai” were 21 and 57 ha, respectively, and should have potential to sustain a high diversity of pollinators. Any given size of forest patch will be a contribution to the diversity of species. This holds true from European farmlands (Duelli et al., 2003; Marshall et al., 2006) to tropical oil palm plantations (Klein, 2009; Liow et al., 2001; Lucey & Hill, 2012; Marshall et al., 2006; Ricketts et al., 2001). The results found in the present study, with higher number of pollinators at increasing distance from forest, could be due to sampling of only the community at ground level. A great deal of the pollinator community in tropical rain forests is normally found in the canopy (Willmer, 2011). Hence, a more open understory could potentially support a higher level of understory pollinator species, but in turn fewer species associated with the forest canopy. Sampling of the canopy community was not implemented in this study, as this would require equipment, time and labour well above the reach of this thesis.

Trees in the forest patches of the plantation were often over 20 m high, and occurrences of flowering in the canopy were observed on several separate occasions, attracting large numbers of pollinators. This could additionally be serving as an unknown factor, where periodic flowering of dipterocarp trees could be attracting long distance flyers (Ashton, 1988), either away from, or into to study area. Such trees could be expected to have a short-term benefit as pollen and nectar source of local pollinators whilst in flower, and a long-term benefit in providing nest sites and favourable microclimatic conditions. It should also be mentioned that potential foraging distance of trapped pollinators could be longer than 1500 m. If so, the forest patches could be hosting a higher number of pollinators than the plantation without the study design being able to detect this difference.

The results from the present study did interestingly enough differ from a similar study done in the same plantation, at the same time (Power, 2018). This study also set out to detect the role of forest patches to the pollinator community, only with a main focus on manual observations on a different study species, *Turnera subultata*. The results presented by Power (2018) were in accordance with hypothesis H1 in the present study, showing a decrease in expected pollinator visitation frequency with increasing distance from forest up to 300 m from forest edge. The same results were obtained for visitation frequency in the manual visitation observation part of the present study, but only up to 400 m. Interestingly, the visitation frequency increased again with observations done in the plantation area.

The finding that visitation frequency increased again at 1500 m from forest could be due to a different species composition, where certain generalist pollinator taxa have benefited from the new landscape as shown by Fahrig (2003). The present study could have failed to detect this potential difference in species composition due to the coarse taxonomical division. In the study by Power (2018), all data retrieved were observational, whereas the present study invested more time in pan trap sampling. The different results obtained could be related to bias in either of the two approaches. Time would not allow for equal sampling time between the manual observation and the pan trap part in the present study.

One interesting find in difference between these two methods, in the present study, is that pan traps caught 32 bees over 619 hours of total sampling time, compared to the 37 observations made of bees in the manual observation part from only 15.5 hours of total sampling time. Considering the total sampling time, the high number of bees observed in the manual visitation part compared to the pan trap part indicate that the traps were not as efficient at trapping bees. It is possible that a longer sampling time in the manual observation part could have corrected for a potential sampling bias in the pan trap part. Bias in the pan trap approach could stem from certain taxonomical pollinator groups being dubious of pans, and others too large to get trapped by pans. Representatives of the bee-genus *Xylocopa* (often 2-3 cm long) were frequently observed as far into the plantation as 1500 m from any forest patch. Only one of these individuals was trapped in pans during this study. At one specific occasion, another individual was observed swimming and later climbing out of the pan. As preparation for the study, a small pilot study was done on the effectiveness of pans, in which it was often observed that several different bee genera were attracted close to, but not into the pans. Shape, colour, scent or another unknown factor was setting them off. Scent has for instance been found to play a role in pan trapping of syrphid flies (Laubertie et al., 2006). The genera able to escape traps when caught or not being trapped at all would hence have a higher likelihood of being counted in a flower visitation study than in a pan trap study. On the other hand, it cannot be ruled out that sampling bias is high in manual visitation observations, as a result of the observer's personal biases. Pan traps have been shown to have the lowest sampling bias of these two approaches (Campbell & Hanula, 2007; Nielsen et al., 2011; Westphal et al., 2008).

A combination of the two methods, as done in the present study, but with a more equal amount of time spent on the two, as initially planned, could offer as a solution.

5 Conclusion

The goal for this thesis was to investigate to what extent two high conservation value forest patches within an oil palm plantation affect the amount and species composition of flying insect pollinator groups and to see how pan tap colours attracted different type of pollinators. The number of pollinators caught and observed was higher in the middle of the plantation compared to near the forest areas. There was not detected difference in pollinator species composition between the two areas. There was, as expected, significant preference for different pan colours among bees, butterflies, syrphid flies and beetles. With the applied sampling techniques, taxonomical resolution and statistical analyses, the forest patches in focus did not have any detected influence on the pollinator community within the studied plantation landscape.

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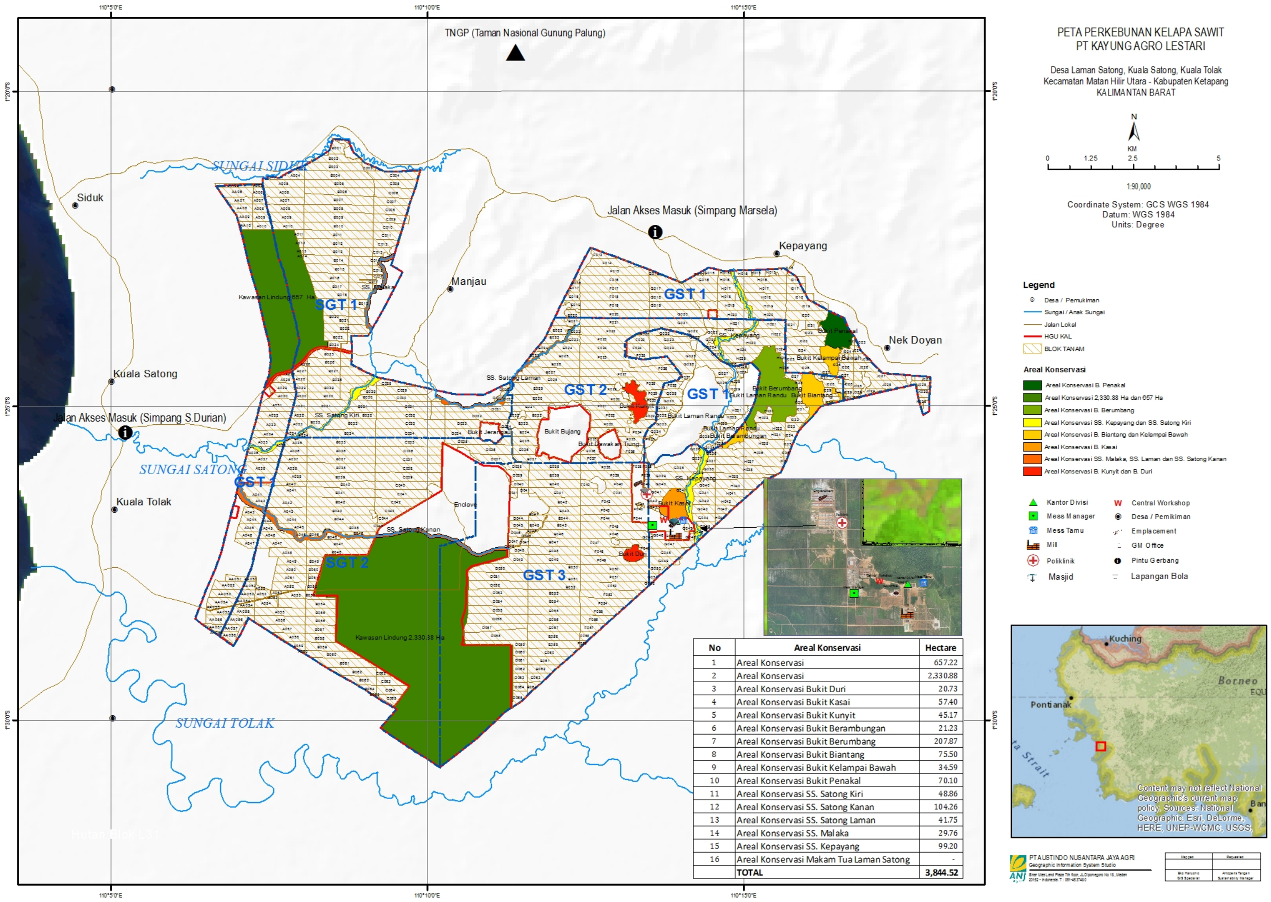
Appendices

Appendix A

This appendix provides a key map of the palm oil plantation PT Kayung Agro Lestari (Figure A.1).



No	Areal Konservasi	Hectare
1	Areal Konservasi	657.22
2	Areal Konservasi	2,330.88
3	Areal Konservasi Bukit Duri	20.73
4	Areal Konservasi Bukit Kasai	57.40
5	Areal Konservasi Bukit Kunyit	45.17
6	Areal Konservasi Bukit Berambungan	21.23
7	Areal Konservasi Bukit Berumbang	207.87
8	Areal Konservasi Bukit Biantang	75.50
9	Areal Konservasi Bukit Kelampai Bawah	34.59
10	Areal Konservasi Bukit Penakal	70.10
11	Areal Konservasi SS. Satong Kiri	48.86
12	Areal Konservasi SS. Satong Kanan	104.26
13	Areal Konservasi SS. Satong Laman	41.75
14	Areal Konservasi SS. Malaka	29.76
15	Areal Konservasi SS. Kepayang	99.20
16	Areal Konservasi Makam Tua Laman Satong	-
	TOTAL	**3,844.52**

Figure A.1: Detailed overview of the plantation, provided by PT Austindo Nusantara Jaya

Appendix B

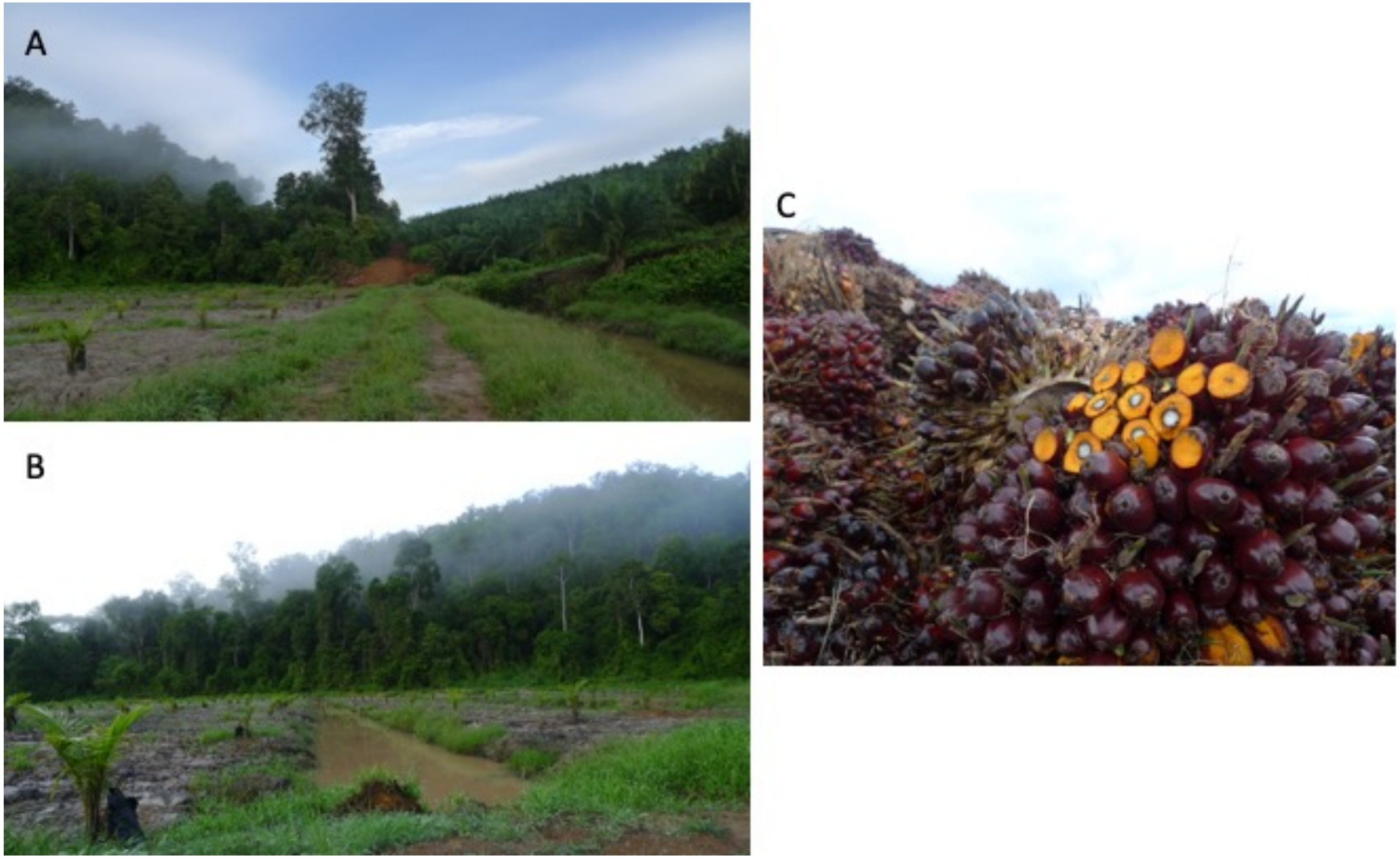


Figure B.1: A) Parts of the forest patch ”Bukit Kasai” in contrast to the fields planted with oil palm trees. B) Parts of the forest patch ”Bukit Kasai”, with a newly established plantation field planted with young oil palm saplings. C) shows oil palm fruit bunches and a cross section of the fruits. Photo: K.H

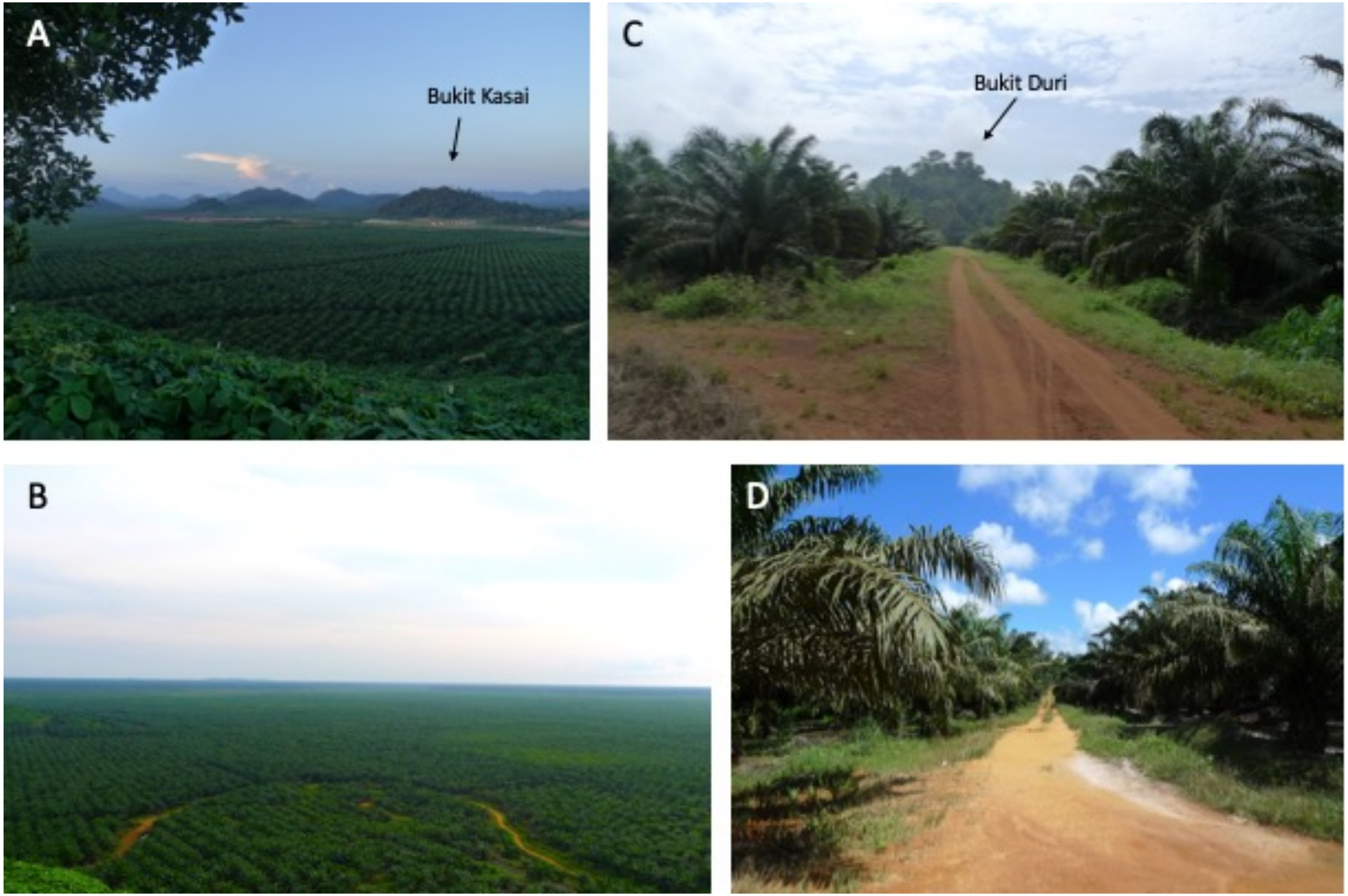


Figure B.2: A) Picture taken from a hilltop in the plantation with the forest patch ”Bukit Kasai” visible in the top right corner. B) Overview of the plantation, looking towards the area where the control plots was established. Picture taken from the same hilltop as picture A. C) Picture from one of the forest transects looking towards the forest patch ”Bukit Duri”. D) Representative photo from the plantation area where the control plots were situated.

Appendix C

Certain difficulties were faced in doing fieldwork this far away from home. The plantation was in a rural area. There was a two-hour drive to the nearest town "Ketapang". Transportation had to be arranged by the company (ANJ), and preferably be noted two days in advance. Any additional supplies needed to complement the fieldwork (small things that you realize is missing during the process) took a full day to get. In addition, shopping was done in bulk, so a lone missing measure tape did not justify such a trip on its own. This was my first experience with the tropics. Getting to known the plantation and its forest patches before setting up transects and observation plots took some time. Several minor pilot studies were set up, not included in the thesis. Unfavorable weather such as heavy rains and lightning limited sampling on several occasions. Road conditions after heavy rains (unpaved roads turning slippery) could increase these working-halts further. Research permits had to be renewed on two occasions, and required travel by airplane or boat to the nearby town of "Pontianak". This process could for reasons unknown to me take between several days up to two weeks on the one occasion. No data was retrieved for these days. I was dependent on a field assistant for transportation of equipment in the pan trap part of the study. As we did not speak the same languages, misunderstanding was common. Language barriers were an additional factor often complicating matters and leading to delays on other additional matters. The friendly culture experienced in Indonesia also lead to more pleasurable hindrances such as invitations to activities and arrangements that for the sake of common politeness could not be turned down. Amongst there are visits to people's homes, attending church services and weddings.

All this added together cut down on the total number of sampling days. This is mentioned here to give perspective on discrepancy between total duration of the field study period and active sampling days.

Appendix D

This appendix shows how the model selection procedure was carried out for each of the models made for the GLMM analyses.

D.1 Models based on the pan trap data

D.1.1 Pollinators: Bees, syrphid flies, beetles, butterflies and moths combined

```
modPollinators1 <- glmer.nb(Pollinators ~
                   DistFromForest + PanColour + FlowersP +
                   DistFromForest*FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)
```

There was an error. Remove the interaction term.

```
modPollinators1 <- glmer.nb(Pollinators ~
                   DistFromForest + PanColour + FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)
summary(modPollinators1)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Negative Binomial(3.6199)  ( log )
## Formula:
## Pollinators ~ DistFromForest + PanColour + FlowersP + (1 | SamplingID) +
##     (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##   1063.0   1096.6   -522.5   1045.0      299
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.3079 -0.6731 -0.2855  0.5608  3.2761
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.07341  0.2709
##  Date.in    (Intercept) 0.03103  0.1762
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -3.7736080  0.1816160 -20.778  < 2e-16 ***
```

```
## DistFromForest  0.0002651  0.0001287   2.059  0.03946 *
## PanColourG     -1.0294285  0.2061594  -4.993 5.93e-07 ***
## PanColourW      0.4463764  0.1503530   2.969  0.00299 **
## PanColourY      0.9136051  0.1434103   6.371 1.88e-10 ***
## FlowersP        0.0017111  0.0033272   0.514  0.60706
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY
## DistFrmFrst -0.528
## PanColourG  -0.345 -0.002
## PanColourW  -0.476 -0.007  0.421
## PanColourY  -0.456 -0.023  0.441  0.604
## FlowersP    -0.547  0.174  0.000  0.016 -0.064
## convergence code: 0
```

FlowersP (flower cover) has the highest p value. Remove.

```
modPollinators2 <- glmer.nb(Pollinators ~
                   DistFromForest + PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)


summary(modPollinators2)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Negative Binomial(3.583)  ( log )
## Formula: Pollinators ~ DistFromForest + PanColour + (1 | SamplingID) +
##     (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##   1061.3   1091.2   -522.7   1045.3      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.3063 -0.6798 -0.2791  0.5609  3.5311
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.07929  0.2816
##  Date.in    (Intercept) 0.02283  0.1511
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)    -3.7216592  0.1485973 -25.045  < 2e-16 ***
## DistFromForest  0.0002521  0.0001210   2.084  0.03718 *
## PanColourG     -1.0295457  0.2063517  -4.989 6.06e-07 ***
## PanColourW      0.4450329  0.1505895   2.955  0.00312 **
## PanColourY      0.9186119  0.1433935   6.406 1.49e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW
## DistFrmFrst -0.515
## PanColourG  -0.422 -0.001
## PanColourW  -0.573 -0.010  0.421
## PanColourY  -0.603 -0.010  0.442  0.606
```

All fixed effects are now significant. Keep this as the best model.

D.1.2 Bees

```
modBees1 <- glmer(Bees ~
                    DistFromForest + PanColour + FlowersP +
                    DistFromForest*FlowersP +
                    (1 | SamplingID) + (1 | Date.in) +
                    offset(log(Sampling.time)),
                  data = pan_data_compact, family = "poisson")


summary(modBees1)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Bees ~ DistFromForest + PanColour + FlowersP + DistFromForest *
##     FlowersP + (1 | SamplingID) + (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    206.9    240.5    -94.5    188.9      299
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9507 -0.2991 -0.2109 -0.0967  6.4182
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.6029   0.7765
##  Date.in    (Intercept) 0.3208   0.5664
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
```

```
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -5.904e+00  5.914e-01  -9.984   <2e-16 ***
## DistFromForest          -4.298e-04  6.601e-04  -0.651   0.5150
## PanColourG              -2.642e+00  1.108e+00  -2.385   0.0171 *
## PanColourW              -1.249e+00  6.075e-01  -2.055   0.0399 *
## PanColourY              -8.194e-02  4.128e-01  -0.198   0.8427
## FlowersP                 1.980e-03  1.260e-02   0.157   0.8751
## DistFromForest:FlowersP  3.453e-06  2.293e-05   0.151   0.8803
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY FlwrsP
## DistFrmFrst -0.639
## PanColourG  -0.125  0.000
## PanColourW  -0.228 -0.001  0.121
## PanColourY  -0.341  0.033  0.178  0.325
## FlowersP    -0.690  0.550  0.000  0.001  0.019
## DstFrmFr:FP  0.352 -0.664  0.000  0.000 -0.060 -0.608
```

FlowersP (flower coverage) has the highest p value. Remove the interaction DistFromForest*FlowersP

```
modBees2 <- glmer(Bees ~
                   DistFromForest + PanColour + FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBees2)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Bees ~ DistFromForest + PanColour + FlowersP + (1 | SamplingID) +
##      (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    204.9    234.8    -94.5    188.9      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9514 -0.2969 -0.2104 -0.0984  6.4133
## Random effects:
##  Groups     Name        Variance Std.Dev.
```

```
##  SamplingID (Intercept) 0.6221   0.7887
##  Date.in    (Intercept) 0.3099   0.5567
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.9395676  0.5800400 -10.240   <2e-16 ***
## DistFromForest -0.0003683  0.0004831  -0.762   0.4458
## PanColourG     -2.6390470  1.0347660  -2.550   0.0108 *
## PanColourW     -1.2456622  0.5673669  -2.196   0.0281 *
## PanColourY     -0.0764831  0.3851277  -0.199   0.8426
## FlowersP        0.0031569  0.0098000   0.322   0.7474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY
## DistFrmFrst -0.529
## PanColourG  -0.119  0.000
## PanColourW  -0.219 -0.002  0.122
## PanColourY  -0.307 -0.007  0.179  0.327
## FlowersP    -0.574  0.236  0.000  0.000 -0.021
```

FlowersP (flower coverage) has the highest p value. Remove.

```
modBees3 <- glmer(Bees ~
                   DistFromForest + PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBees3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## Bees ~ DistFromForest + PanColour + (1 | SamplingID) + (1 | Date.in) +
##     offset(log(Sampling.time))
##    Data: pan_data_compact
##
##      AIC      BIC   logLik deviance df.resid
##    203.0    229.1    -94.5    189.0      301
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -0.9565 -0.2975 -0.2117 -0.0992  6.5467
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.6164   0.7851
##  Date.in    (Intercept) 0.3307   0.5751
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.8373941  0.4784050 -12.202   <2e-16 ***
## DistFromForest -0.0004029  0.0004743  -0.849   0.3956
## PanColourG     -2.6390478  1.0347549  -2.550   0.0108 *
## PanColourW     -1.2458025  0.5673190  -2.196   0.0281 *
## PanColourY     -0.0741023  0.3850356  -0.192   0.8474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW
## DistFrmFrst -0.499
## PanColourG  -0.144  0.000
## PanColourW  -0.266 -0.003  0.122
## PanColourY  -0.388  0.000  0.179  0.327
```

DistFromForest (distance from forest) has the highest p value. Change with area.type (plantation vs. forest area)

```
modBees4 <- glmer(Bees ~
                   area.type + PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBees4)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Bees ~ area.type + PanColour + (1 | SamplingID) + (1 | Date.in) +
##     offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    202.2    228.3    -94.1    188.2      301
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -0.9584 -0.3091 -0.2117 -0.0917  6.4568
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.5438   0.7374
##  Date.in    (Intercept) 0.3263   0.5713
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -5.81867    0.43717 -13.310   <2e-16 ***
## area.typePlantation -0.80711    0.64114  -1.259   0.2081
## PanColourG          -2.63908    1.03481  -2.550   0.0108 *
## PanColourW          -1.24639    0.56727  -2.197   0.0280 *
## PanColourY          -0.07411    0.38506  -0.192   0.8474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) ar.tyP PnClrG PnClrW
## ar.typPlntt -0.348
## PanColourG  -0.158  0.000
## PanColourW  -0.292  0.000  0.122
## PanColourY  -0.424  0.000  0.179  0.327
```

area.type is not significant. Remove.

```
modBees5 <- glmer(Bees ~
                   PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBees5)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## Bees ~ PanColour + (1 | SamplingID) + (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    201.7    224.1    -94.9    189.7      302
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9606 -0.2946 -0.2189 -0.0992  6.4230
```

```
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.5249   0.7245
##  Date.in    (Intercept) 0.4647   0.6817
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -6.06765    0.42475 -14.285   <2e-16 ***
## PanColourG  -2.63904    1.03475  -2.550   0.0108 *
## PanColourW  -1.24718    0.56725  -2.199   0.0279 *
## PanColourY  -0.07411    0.38503  -0.192   0.8474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##            (Intr) PnClrG PnClrW
## PanColourG -0.162
## PanColourW -0.300  0.122
## PanColourY -0.436  0.179  0.327
```

The only remaining explanatory variable is significant. Keep this as the best model.

D.1.3 Syrphid flies

```
modSyrphid1 <- glmer.nb(Syrphid.Flies ~
                   DistFromForest + PanColour + FlowersP +
                   DistFromForest*FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)
```

There was an error. Remove the interaction term.

```
modSyrphid1 <- glmer.nb(Syrphid.Flies ~
                   DistFromForest + PanColour + FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)
```

Error again. Remove the random factor Date.

```
modSyrphid2 <- glmer.nb(Syrphid.Flies ~
                   DistFromForest + PanColour + FlowersP +
                   (1 | SamplingID) +
```

```
                     offset(log(Sampling.time)),
                   data = pan_data_compact)


summary(modSyrphid2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Negative Binomial(1.2408)  ( log )
## Formula: Syrphid.Flies ~ DistFromForest + PanColour + FlowersP + (1 |
##     SamplingID) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    559.4    589.2   -271.7    543.4      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.8884 -0.5300 -0.2877  0.0981  7.3786
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.6404   0.8003
## Number of obs: 308, groups:  SamplingID, 77
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.8675913  0.3569396 -16.439  < 2e-16 ***
## DistFromForest  0.0004069  0.0002343   1.737 0.082471 .
## PanColourG     -1.8476061  0.5671739  -3.258 0.001124 **
## PanColourW      1.0279254  0.2869989   3.582 0.000341 ***
## PanColourY      0.8842670  0.2910806   3.038 0.002383 **
## FlowersP        0.0115905  0.0053459   2.168 0.030151 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY
## DistFrmFrst -0.512
## PanColourG  -0.262  0.002
## PanColourW  -0.544  0.006  0.337
## PanColourY  -0.468 -0.024  0.337  0.655
## FlowersP    -0.546  0.259 -0.009  0.014 -0.099
```

All fixed factors are significant except DistFromForest (distance from forest). Exchange with area.type (plantation vs. forest area)

```
modSyrphid3 <- glmer.nb(Syrphid.Flies ~
                   area.type + PanColour + FlowersP +
                   (1 | SamplingID) +
```

```
                   offset(log(Sampling.time)),
                 data = pan_data_compact)

summary(modSyrphid3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Negative Binomial(1.246)  ( log )
## Formula: Syrphid.Flies ~ area.type + PanColour + FlowersP + (1 | SamplingID) +
##     offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    558.2    588.1   -271.1    542.2      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.8897 -0.5249 -0.2840  0.0705  7.4954
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.6157   0.7847
## Number of obs: 308, groups:  SamplingID, 77
##
## Fixed effects:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -5.831468   0.336731 -17.318  < 2e-16 ***
## area.typePlantation  0.642463   0.310123   2.072 0.038299 *
## PanColourG          -1.845399   0.567105  -3.254 0.001138 **
## PanColourW           1.029116   0.286960   3.586 0.000335 ***
## PanColourY           0.885739   0.291004   3.044 0.002337 **
## FlowersP             0.011977   0.005303   2.258 0.023928 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) ar.tyP PnClrG PnClrW PnClrY
## ar.typPlntt -0.424
## PanColourG  -0.277  0.002
## PanColourW  -0.577  0.009  0.337
## PanColourY  -0.501 -0.019  0.337  0.656
## FlowersP    -0.544  0.266 -0.009  0.014 -0.098
```

All the fixed effects are now significant, so keep this as the best model.

D.1.4 Butterflies

```
modButterflies1 <- glmer.nb(Butterflies ~
                   DistFromForest + PanColour + FlowersP +
                   DistFromForest*PanColour + DistFromForest*FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)

summary(modButterflies1)
```

Error when making model. Try to remove the least intersting interaction.

```
modButterflies1 <- glmer.nb(Butterflies ~
                   DistFromForest + PanColour + FlowersP +
                   DistFromForest*FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)

summary(modButterflies1)
```

Error when making model. Remove interaction term.

```
modButterflies1 <- glmer.nb(Butterflies ~
                   DistFromForest + PanColour + FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)

summary(modButterflies1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Negative Binomial(7.1503)  ( log )
## Formula:
## Butterflies ~ DistFromForest + PanColour + FlowersP + (1 | SamplingID) +
##     (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    478.3    511.8   -230.1    460.3      299
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.1733 -0.4997 -0.2592 -0.1022  7.6823
## Random effects:
```

```
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.1370   0.3702
##  Date.in    (Intercept) 0.1967   0.4435
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -6.1298373  0.4068172 -15.068  < 2e-16 ***
## DistFromForest  0.0005874  0.0002614   2.248 0.024602 *
## PanColourG     -1.8700821  0.7627016  -2.452 0.014210 *
## PanColourW      1.1047979  0.3267582   3.381 0.000722 ***
## PanColourY      2.0309320  0.3032261   6.698 2.12e-11 ***
## FlowersP       -0.0038802  0.0056705  -0.684 0.493803
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY
## DistFrmFrst -0.532
## PanColourG  -0.255 -0.001
## PanColourW  -0.596 -0.001  0.318
## PanColourY  -0.635  0.001  0.343  0.801
## FlowersP    -0.441  0.246  0.000  0.001 -0.033
```

FlowersP (flower cover) has the higest p value. Remove.

```
modButterflies2 <- glmer.nb(Butterflies ~
                   DistFromForest + PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact)


summary(modButterflies2)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Negative Binomial(7.3553)  ( log )
## Formula: Butterflies ~ DistFromForest + PanColour + (1 | SamplingID) +
##     (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    476.8    506.6   -230.4    460.8      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.1921 -0.4955 -0.2559 -0.1011  7.8625
```

```
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.1288   0.3589
##  Date.in    (Intercept) 0.2233   0.4725
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -6.2581778  0.3697197 -16.927  < 2e-16 ***
## DistFromForest  0.0006333  0.0002617   2.420 0.015517 *
## PanColourG     -1.8702462  0.7626097  -2.452 0.014190 *
## PanColourW      1.1054437  0.3265697   3.385 0.000712 ***
## PanColourY      2.0242508  0.3028513   6.684 2.33e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW
## DistFrmFrst -0.492
## PanColourG  -0.281 -0.001
## PanColourW  -0.656 -0.001  0.318
## PanColourY  -0.715  0.008  0.343  0.801
```

All fixed effects are now significant. Keep this as the best model.

D.1.5 Beetles

```
modBeetles1 <- glmer(Beetles ~
                   DistFromForest + PanColour + FlowersP +
                   DistFromForest*FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBeetles1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Beetles ~ DistFromForest + PanColour + FlowersP + DistFromForest *
##     FlowersP + (1 | SamplingID) + (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    301.4    334.9   -141.7    283.4      299
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.7979 -0.4091 -0.3192 -0.1294  6.6894
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.52551  0.7249
##  Date.in    (Intercept) 0.03106  0.1763
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -5.779e+00  4.476e-01 -12.910   <2e-16 ***
## DistFromForest          -2.061e-04  4.075e-04  -0.506   0.6131
## PanColourG              -1.800e+00  8.126e-01  -2.215   0.0268 *
## PanColourW               2.761e-01  4.058e-01   0.680   0.4963
## PanColourY               7.242e-01  3.741e-01   1.936   0.0529 .
## FlowersP                -4.407e-03  8.910e-03  -0.495   0.6209
## DistFromForest:FlowersP  2.543e-06  1.497e-05   0.170   0.8652
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY FlwrsP
## DistFrmFrst -0.565
## PanColourG  -0.258  0.000
## PanColourW  -0.514 -0.002  0.284
## PanColourY  -0.568  0.044  0.308  0.617
## FlowersP    -0.585  0.554  0.000 -0.003  0.020
## DstFrmFr:FP  0.324 -0.692  0.000  0.002 -0.071 -0.609
```

DistFromForest*FlowersP (interaction between distance from forest and flower cover) has the highest p value. Remove.

```
modBeetles2 <- glmer(Beetles ~
                   DistFromForest + PanColour + FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBeetles2)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Beetles ~ DistFromForest + PanColour + FlowersP + (1 | SamplingID) +
##     (1 | Date.in) + offset(log(Sampling.time))
```

```
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    299.4    329.2   -141.7    283.4      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.8019 -0.4110 -0.3153 -0.1285  6.7283
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.54314  0.7370
##  Date.in    (Intercept) 0.02681  0.1637
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.8183597  0.4277565 -13.602   <2e-16 ***
## DistFromForest -0.0001548  0.0002932  -0.528   0.5976
## PanColourG     -1.7917499  0.7637398  -2.346   0.0190 *
## PanColourW      0.2853502  0.3819912   0.747   0.4551
## PanColourY      0.7391796  0.3513190   2.104   0.0354 *
## FlowersP       -0.0035018  0.0069309  -0.505   0.6134
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##            (Intr) DstFrF PnClrG PnClrW PnClrY
## DistFrmFrst -0.474
## PanColourG  -0.255  0.000
## PanColourW  -0.508  0.000  0.286
## PanColourY  -0.543 -0.003  0.311  0.621
## FlowersP    -0.462  0.218  0.000 -0.002 -0.027
##  - Rescale variables?
```

FlowersP (flower cover) has the highest p value above. Remove.

```
modBeetles3 <- glmer(Beetles ~
                   DistFromForest + PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBeetles3)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
```

```
## Formula: Beetles ~ DistFromForest + PanColour + (1 | SamplingID) + (1 |
##     Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    297.6    323.8   -141.8    283.6      301
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.7761 -0.4108 -0.3129 -0.1275  6.5439
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.51486  0.7175
##  Date.in    (Intercept) 0.04298  0.2073
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.9226470  0.3807694 -15.554   <2e-16 ***
## DistFromForest -0.0001243  0.0002907  -0.428   0.6688
## PanColourG     -1.7917630  0.7637423  -2.346   0.0190 *
## PanColourW      0.2849484  0.3820235   0.746   0.4557
## PanColourY      0.7339612  0.3511766   2.090   0.0366 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW
## DistFrmFrst -0.432
## PanColourG  -0.287  0.000
## PanColourW  -0.572  0.000  0.286
## PanColourY  -0.623  0.000  0.311  0.621
```

DistFromForest (distance from forest) has the highest p value. Exchange with area.type (plantation area vs. forest area).

```
modBeetles4 <- glmer(Beetles ~
                   area.type + PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBeetles4)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Beetles ~ area.type + PanColour + (1 | SamplingID) + (1 | Date.in) +
```

```
##     offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    297.8    323.9   -141.9    283.8      301
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.7674 -0.4208 -0.3083 -0.1256  6.6612
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.53153  0.7291
##  Date.in    (Intercept) 0.03055  0.1748
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -5.98877    0.36059 -16.608   <2e-16 ***
## area.typePlantation -0.02674    0.37285  -0.072   0.9428
## PanColourG          -1.79176    0.76373  -2.346   0.0190 *
## PanColourW           0.28493    0.38202   0.746   0.4557
## PanColourY           0.73396    0.35118   2.090   0.0366 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) ar.tyP PnClrG PnClrW
## ar.typPlntt -0.313
## PanColourG  -0.303  0.000
## PanColourW  -0.604  0.000  0.286
## PanColourY  -0.658  0.000  0.311  0.621
```

area.type (plantation vs. forest area) has the highest p value. Remove.

```
modBeetles5 <- glmer(Beetles ~
                   PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family = "poisson")


summary(modBeetles5)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## Beetles ~ PanColour + (1 | SamplingID) + (1 | Date.in) + offset(log(Sampling.time))
```

```
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    295.8    318.2   -141.9    283.8      302
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.7660 -0.4242 -0.3084 -0.1261  6.6772
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.53257  0.7298
##  Date.in    (Intercept) 0.02945  0.1716
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -5.9970     0.3424 -17.512   <2e-16 ***
## PanColourG   -1.7918     0.7637  -2.346   0.0190 *
## PanColourW    0.2849     0.3820   0.746   0.4558
## PanColourY    0.7340     0.3512   2.090   0.0366 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##            (Intr) PnClrG PnClrW
## PanColourG -0.319
## PanColourW -0.636  0.286
## PanColourY -0.693  0.311  0.621
```

The only remaining fixed effext is significant. Keep this as the best model.

D.1.6 Moths

```
modMoths1 <- glmer(Moths ~
                   DistFromForest + PanColour + FlowersP +
                   DistFromForest*FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family="poisson")


summary(modMoths1)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Moths ~ DistFromForest + PanColour + FlowersP + DistFromForest *
```

```
##     FlowersP + (1 | SamplingID) + (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    638.6    672.2   -310.3    620.6      299
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.2544 -0.6540 -0.5079  0.4752  3.7330
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.3254   0.5704
##  Date.in    (Intercept) 0.1186   0.3443
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -4.676e+00  3.138e-01 -14.899   <2e-16 ***
## DistFromForest           2.305e-04  3.072e-04   0.750   0.4530
## PanColourG              -4.054e-01  2.393e-01  -1.694   0.0902 .
## PanColourW              -1.189e-01  2.207e-01  -0.539   0.5902
## PanColourY               3.630e-01  1.978e-01   1.836   0.0664 .
## FlowersP                 5.776e-05  6.548e-03   0.009   0.9930
## DistFromForest:FlowersP -7.608e-06  1.141e-05  -0.667   0.5048
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY FlwrsP
## DistFrmFrst -0.652
## PanColourG  -0.305  0.000
## PanColourW  -0.329 -0.003  0.434
## PanColourY  -0.374  0.028  0.484  0.524
## FlowersP    -0.652  0.557  0.000 -0.003  0.011
## DstFrmFr:FP  0.316 -0.657  0.000  0.004 -0.045 -0.572
```

FlowersP (flower cover) has the highest p value. Remove interaction with distance from forest.

```
modMoths2 <- glmer(Moths ~
                   DistFromForest + PanColour + FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family="poisson")


summary(modMoths2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
```

```
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Moths ~ DistFromForest + PanColour + FlowersP + (1 | SamplingID) +
##     (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    637.1    666.9   -310.5    621.1      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.2245 -0.6544 -0.5066  0.4801  3.8524
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.3331   0.5772
##  Date.in    (Intercept) 0.1114   0.3338
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -4.601e+00  2.875e-01 -16.005   <2e-16 ***
## DistFromForest  9.175e-05  2.225e-04   0.412   0.6801
## PanColourG     -4.055e-01  2.357e-01  -1.720   0.0854 .
## PanColourW     -1.183e-01  2.174e-01  -0.544   0.5863
## PanColourY      3.554e-01  1.946e-01   1.826   0.0678 .
## FlowersP       -2.739e-03  5.266e-03  -0.520   0.6030
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF PnClrG PnClrW PnClrY
## DistFrmFrst -0.558
## PanColourG  -0.328  0.000
## PanColourW  -0.355 -0.001  0.434
## PanColourY  -0.382 -0.003  0.484  0.525
## FlowersP    -0.536  0.144  0.000  0.000 -0.029
```

DistFromForest (distance from forest) has the highest p value. Exchange with area.type (plantation area vs. forest area).

```
modMoths3 <- glmer(Moths ~
                   area.type + PanColour + FlowersP +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family="poisson")


summary(modMoths3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Moths ~ area.type + PanColour + FlowersP + (1 | SamplingID) +
##     (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    636.9    666.7   -310.4    620.9      300
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.2250 -0.6554 -0.5030  0.4895  3.8490
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.3278   0.5725
##  Date.in    (Intercept) 0.1138   0.3374
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -4.611479   0.278898 -16.535   <2e-16 ***
## area.typePlantation  0.186754   0.313494   0.596   0.5514
## PanColourG          -0.405451   0.235699  -1.720   0.0854 .
## PanColourW          -0.118323   0.217448  -0.544   0.5863
## PanColourY           0.355090   0.194639   1.824   0.0681 .
## FlowersP            -0.002419   0.005443  -0.444   0.6568
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) ar.tyP PnClrG PnClrW PnClrY
## ar.typPlntt -0.518
## PanColourG  -0.338  0.000
## PanColourW  -0.366 -0.001  0.434
## PanColourY  -0.391 -0.008  0.484  0.525
## FlowersP    -0.605  0.294  0.000 -0.001 -0.031
```

FlowersP (flower cover) has the highest p value. Remove.

```
modMoths4 <- glmer(Moths ~
                   area.type + PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family="poisson")
```

```
summary(modMoths4)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Moths ~ area.type + PanColour + (1 | SamplingID) + (1 | Date.in) +
##     offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    635.1    661.2   -310.5    621.1      301
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.2355 -0.6575 -0.5048  0.5000  3.7902
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.3195   0.5652
##  Date.in    (Intercept) 0.1290   0.3591
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -4.6878     0.2256 -20.776   <2e-16 ***
## area.typePlantation   0.2283     0.3079   0.742   0.4583
## PanColourG           -0.4054     0.2357  -1.720   0.0854 .
## PanColourW           -0.1184     0.2175  -0.544   0.5862
## PanColourY            0.3522     0.1945   1.811   0.0702 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) ar.tyP PnClrG PnClrW
## ar.typPlntt -0.450
## PanColourG  -0.418  0.000
## PanColourW  -0.453  0.000  0.434
## PanColourY  -0.506  0.000  0.485  0.525
```

area.type has the highest p value. Remove.

```
modMoths5 <- glmer(Moths ~
                   PanColour +
                   (1 | SamplingID) + (1 | Date.in) +
                   offset(log(Sampling.time)),
                 data = pan_data_compact, family="poisson")
```

```
# Have a look at the model
summary(modMoths5)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## Moths ~ PanColour + (1 | SamplingID) + (1 | Date.in) + offset(log(Sampling.time))
##    Data: pan_data_compact
##      AIC      BIC   logLik deviance df.resid
##    633.6    656.0   -310.8    621.6      302
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.2457 -0.6559 -0.5100  0.4787  3.7420
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 0.3202   0.5658
##  Date.in    (Intercept) 0.1364   0.3693
## Number of obs: 308, groups:  SamplingID, 77; Date.in, 13
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -4.6158     0.2030 -22.738   <2e-16 ***
## PanColourG   -0.4055     0.2357  -1.720   0.0854 .
## PanColourW   -0.1183     0.2175  -0.544   0.5863
## PanColourY    0.3522     0.1945   1.811   0.0702 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##            (Intr) PnClrG PnClrW
## PanColourG -0.464
## PanColourW -0.503  0.434
## PanColourY -0.563  0.485  0.525
```

The only remaining fixed factor is not significant.

D.2 Models based on manual observation data

D.2.1 All pollinators

```
# Make full model
modVisPollinatorsFull <- glmer(Total ~ DistFromForest + FlowerCover + timeofday +
                          (1 | SamplingID) + (1 | Date),
```

```
                        data=manual_data_noNA, family="poisson")


summary(modVisPollinatorsFull)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Total ~ DistFromForest + FlowerCover + timeofday + (1 | SamplingID) +
##     (1 | Date)
##    Data: manual_data_noNA
##      AIC      BIC   logLik deviance df.resid
##    444.3    459.3   -216.2    432.3       84
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.06763 -0.59546 -0.05775  0.16166  0.67106
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 1.733    1.316
##  Date       (Intercept) 1.144    1.070
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.2906413  1.7569038  -3.011   0.0026 **
## DistFromForest  0.0001058  0.0006986   0.151   0.8797
## FlowerCover    -0.0356659  0.0284140  -1.255   0.2094
## timeofday      14.9788782  3.7210436   4.025 5.69e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF FlwrCv
## DistFrmFrst -0.422
## FlowerCover -0.241  0.098
## timeofday   -0.880  0.110 -0.023
```

DistFromForest (distance from forest) has the highest p value. Exchange with AreaType (forest area vs. plantation area)

```
modVisPollinators2 <- glmer(Total ~ AreaType + FlowerCover + timeofday +
                                 (1 | SamplingID) + (1 | Date),
                               data=manual_data_noNA, family="poisson")


summary(modVisPollinators2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
```

```
##  Family: poisson  ( log )
## Formula: Total ~ AreaType + FlowerCover + timeofday + (1 | SamplingID) +  
##     (1 | Date)
##    Data: manual_data_noNA
##      AIC      BIC   logLik deviance df.resid 
##    443.6    458.6   -215.8    431.6       84 
## Scaled residuals: 
##      Min       1Q   Median       3Q      Max 
## -1.05914 -0.58652 -0.05816  0.16132  0.68497 
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 1.7440   1.3206  
##  Date       (Intercept) 0.9621   0.9809  
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
## 
## Fixed effects:
##                    Estimate Std. Error z value Pr(>|z|)    
## (Intercept)        -5.68956    1.69348  -3.360  0.00078 ***
## AreaTypePlantation  0.74480    0.82023   0.908  0.36386    
## FlowerCover        -0.03237    0.02851  -1.135  0.25634    
## timeofday          15.22854    3.71202   4.102 4.09e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) ArTypP FlwrCv
## ArTypPlnttn -0.355              
## FlowerCover -0.259  0.134       
## timeofday   -0.902  0.103 -0.010
```

AreaType has the highest p value. Remove.

```
modVisPollinators3 <- glmer(Total ~ FlowerCover + timeofday +
                              (1 | SamplingID) + (1 | Date),
                            data=manual_data_noNA, family="poisson")


summary(modVisPollinators3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Total ~ FlowerCover + timeofday + (1 | SamplingID) + (1 | Date)
##    Data: manual_data_noNA
##      AIC      BIC   logLik deviance df.resid 
##    442.3    454.8   -216.2    432.3       85 
```

```
## Scaled residuals:
##      Min       1Q   Median      3Q     Max
## -1.07228 -0.60329 -0.06003  0.16085  0.65872
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 1.720    1.312
##  Date       (Intercept) 1.215    1.102
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -5.18020    1.59377  -3.250  0.00115 **
## FlowerCover -0.03607    0.02828  -1.275  0.20217
## timeofday   14.91940    3.69362   4.039 5.36e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) FlwrCv
## FlowerCover -0.220
## timeofday   -0.923 -0.035
```

Flower cover has the highest p value. Remove.

```
modVisPollinators4 <- glmer(Total ~ timeofday +
                              (1 | SamplingID) + (1 | Date),
                            data=manual_data, family="poisson")


summary(modVisPollinators4)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Total ~ timeofday + (1 | SamplingID) + (1 | Date)
##    Data: manual_data
##
##      AIC      BIC   logLik deviance df.resid
##    459.0    469.1   -225.5    451.0       89
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.0890 -0.6087 -0.0050  0.1678  0.6136
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
```

```
##  SamplingID (Intercept) 1.629    1.276   
##  Date       (Intercept) 1.047    1.023   
## Number of obs: 93, groups:  SamplingID, 93; Date, 8
## 
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)    
## (Intercept)   -5.388      1.467  -3.674 0.000239 ***
## timeofday     14.303      3.503   4.084 4.43e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation of Fixed Effects:
##           (Intr)
## timeofday -0.957
```

The one remaining fixed effect is significant. Keep this as the best model.

D.2.2 Bees

```
modVisBeesFull <- glmer(Bee ~ DistFromForest + FlowerCover + timeofday +
                       (1 | SamplingID) + (1 | Date),
                     data=manual_data_noNA, family="poisson")


summary(modVisBeesFull)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Bee ~ DistFromForest + FlowerCover + timeofday + (1 | SamplingID) +  
##     (1 | Date)
##    Data: manual_data_noNA
## 
##      AIC      BIC   logLik deviance df.resid 
##      288      303     -138      276       84 
## 
## Scaled residuals: 
##     Min      1Q  Median      3Q     Max 
## -0.8890 -0.4418 -0.2741  0.1101  0.8893 
## 
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 2.087    1.445   
##  Date       (Intercept) 1.158    1.076   
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
## 
```

```
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -8.4901858  2.4110113  -3.521 0.000429 ***
## DistFromForest  0.0002632  0.0007165   0.367 0.713357
## FlowerCover    -0.0261603  0.0352209  -0.743 0.457634
## timeofday      19.1444162  5.0790915   3.769 0.000164 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) DstFrF FlwrCv
## DistFrmFrst -0.391
## FlowerCover -0.235  0.129
## timeofday   -0.917  0.138 -0.004
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## convergence code: 0
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
##  - Rescale variables?
```

DistFromForest (distance from forest) has the highest p value. Exchange distance from forest with area type.

```
modVisBees2 <- glmer(Bee ~ AreaType + FlowerCover + timeofday +
                       (1 | SamplingID) + (1 | Date),
                     data=manual_data_noNA, family="poisson")


summary(modVisBees2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Bee ~ AreaType + FlowerCover + timeofday + (1 | SamplingID) +
##     (1 | Date)
##    Data: manual_data_noNA
##
##      AIC      BIC   logLik deviance df.resid
##    287.4    302.4   -137.7    275.4       84
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.8808 -0.4395 -0.2766  0.1124  0.9584
##
```

```
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 2.105    1.451
##  Date       (Intercept) 1.077    1.038
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
##
## Fixed effects:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -8.82166    2.36909  -3.724 0.000196 ***
## AreaTypePlantation  0.83916    0.91846   0.914 0.360897
## FlowerCover        -0.02239    0.03548  -0.631 0.527937
## timeofday          19.37001    5.08152   3.812 0.000138 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) ArTypP FlwrCv
## ArTypPlnttn -0.346
## FlowerCover -0.247  0.142
## timeofday   -0.927  0.128  0.009
```

Flower cover has the highest p value. Remove

```
modVisBees3 <- glmer(Bee ~ AreaType + timeofday +
                       (1 | SamplingID) + (1 | Date),
                     data=manual_data, family="poisson")


summary(modVisBees3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Bee ~ AreaType + timeofday + (1 | SamplingID) + (1 | Date)
##    Data: manual_data
##
##      AIC      BIC   logLik deviance df.resid
##    297.0    309.6   -143.5    287.0       88
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9055 -0.4549 -0.2912  0.1371  0.9834
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
```

```
##  SamplingID (Intercept) 1.921    1.386
##  Date       (Intercept) 1.082    1.040
## Number of obs: 93, groups:  SamplingID, 93; Date, 8
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -8.7486     2.1569  -4.056 4.99e-05 ***
## AreaTypePlantation    0.8680     0.8981   0.966 0.333816
## timeofday            18.4172     4.7642   3.866 0.000111 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) ArTypP
## ArTypPlnttn -0.338
## timeofday   -0.949  0.132
```

Area type has the highest p value. Remove.

```
modVisBees4 <- glmer(Bee ~ timeofday +
                       (1 | SamplingID) + (1 | Date),
                     data=manual_data, family="poisson")


summary(modVisBees4)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Bee ~ timeofday + (1 | SamplingID) + (1 | Date)
##    Data: manual_data
##
##      AIC      BIC   logLik deviance df.resid
##    295.8    305.9   -143.9    287.8       89
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9283 -0.4594 -0.2807  0.1443  0.9461
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 1.850    1.360
##  Date       (Intercept) 1.335    1.156
## Number of obs: 93, groups:  SamplingID, 93; Date, 8
##
```

```
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -8.143      2.025  -4.021 5.78e-05 ***
## timeofday     17.925      4.673   3.836 0.000125 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr)
## timeofday -0.965
```

The one remaining fixed effect is significant. Keep this as the best model.

D.2.3 Syrphid flies

```
modVisSyrphidsFull <- glmer(Syrphid ~ DistFromForest + FlowerCover + timeofday +
                                 (1 | SamplingID) + (1 | Date),
                               data=manual_data_noNA, family="poisson")


summary(modVisSyrphidsFull)
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## Syrphid ~ DistFromForest + FlowerCover + timeofday + (1 | SamplingID) +
##     (1 | Date)
##    Data: manual_data_noNA
##
##      AIC      BIC   logLik deviance df.resid
##    137.5    152.5    -62.7    125.5       84
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.4066 -0.3190 -0.2900 -0.2537  1.2885
##
## Random effects:
##  Groups     Name        Variance  Std.Dev.
##  SamplingID (Intercept) 2.1553790 1.46812
##  Date       (Intercept) 0.0005876 0.02424
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
##
## Fixed effects:
```

```
##                  Estimate Std. Error   z value Pr(>|z|)    
## (Intercept)    -3.4990406  0.0021241 -1647.286  < 2e-16 ***
## DistFromForest  0.0003231  0.0002471     1.308    0.191    
## FlowerCover    -0.0142265  0.0021175    -6.718 1.84e-11 ***
## timeofday       3.3750973  0.0021240  1589.059  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation of Fixed Effects:
##             (Intr) DstFrF FlwrCv
## DistFrmFrst -0.006              
## FlowerCover  0.000 -0.082       
## timeofday    0.000 -0.002  0.000
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## convergence code: 0
## Model failed to converge with max|grad| = 0.0339097 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

DistFromForest has the highest p value. Exchange distance from forest with area type.

```
modVisSyrphids2 <- glmer(Syrphid ~ AreaType + FlowerCover + timeofday +
                               (1 | SamplingID) + (1 | Date),
                             data=manual_data_noNA, family="poisson")


summary(modVisSyrphids2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Syrphid ~ AreaType + FlowerCover + timeofday + (1 | SamplingID) +  
##     (1 | Date)
##    Data: manual_data_noNA
## 
##      AIC      BIC   logLik deviance df.resid 
##    137.1    152.1    -62.5    125.1       84 
## 
## Scaled residuals: 
##     Min      1Q  Median      3Q     Max 
## -0.4168 -0.3177 -0.2924 -0.2461  1.3151 
## 
## Random effects:
##  Groups     Name        Variance  Std.Dev. 
```

```
##  SamplingID (Intercept) 2.115e+00 1.4542694
##  Date       (Intercept) 1.039e-07 0.0003224
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
##
## Fixed effects:
##                      Estimate Std. Error   z value Pr(>|z|)
## (Intercept)        -3.625981   0.002151 -1685.981  < 2e-16 ***
## AreaTypePlantation  0.571901   0.002151   265.926  < 2e-16 ***
## FlowerCover        -0.010921   0.002136    -5.112 3.19e-07 ***
## timeofday           3.550462   0.002151  1650.968  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) ArTypP FlwrCv
## ArTypPlnttn  0.000
## FlowerCover -0.001  0.000
## timeofday    0.000  0.000  0.000
## convergence code: 0
## Model failed to converge with max|grad| = 0.0328701 (tol = 0.002, component 1)
```

All fixed effects are now significant. Keep this as the best model.

D.2.4 Butterflies

```
modVisButterfliesFull <- glmer(Butterfly ~ DistFromForest + FlowerCover + timeofday +
                              (1 | SamplingID) + (1 | Date),
                            data=manual_data_noNA, family="poisson")
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(modVisButterfliesFull)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## Butterfly ~ DistFromForest + FlowerCover + timeofday + (1 | SamplingID) +
##     (1 | Date)
##    Data: manual_data_noNA
##      AIC      BIC   logLik deviance df.resid
##    244.9    259.9   -116.4    232.9       84
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.5867 -0.4021 -0.3229  0.2629  0.8697
## Random effects:
```

```
##  Groups     Name        Variance Std.Dev.
##  SamplingID (Intercept) 3.224    1.796
##  Date       (Intercept) 0.000    0.000
## Number of obs: 90, groups:  SamplingID, 90; Date, 8
##
## Fixed effects:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -5.4622426  2.1365326  -2.557   0.0106 *
## DistFromForest  0.0003799  0.0004003   0.949   0.3426
## FlowerCover    -0.0289867  0.0384798  -0.753   0.4513
## timeofday      10.7500926  4.6602102   2.307   0.0211 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF FlwrCv
## DistFrmFrst -0.366
## FlowerCover -0.356  0.292
## timeofday   -0.920  0.140  0.052
```

Flower cover has the highest p value. Remove flower cover.

```
modVisButterflies2 <- glmer(Butterfly ~ DistFromForest + timeofday +
                                 (1 | SamplingID) + (1 | Date),
                               data=manual_data, family="poisson")


summary(modVisButterflies2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Butterfly ~ DistFromForest + timeofday + (1 | SamplingID) + (1 |
##     Date)
##    Data: manual_data
##      AIC      BIC   logLik deviance df.resid
##    249.2    261.9   -119.6    239.2       88
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.5728 -0.3890 -0.3161  0.2655  0.8268
## Random effects:
##  Groups     Name        Variance  Std.Dev.
##  SamplingID (Intercept) 3.308e+00 1.8187521
##  Date       (Intercept) 3.104e-08 0.0001762
## Number of obs: 93, groups:  SamplingID, 93; Date, 8
##
```

```
## Fixed effects:
##                   Estimate Std. Error   z value Pr(>|z|)    
## (Intercept)    -5.9377361  0.0014498 -4095.475   <2e-16 ***
## DistFromForest  0.0004392  0.0002331     1.884   0.0595 .  
## timeofday      10.5727903  0.0014497  7293.237   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) DstFrF
## DistFrmFrst -0.004       
## timeofday    0.000 -0.002
```

Distance from forest is not significant. Exchange distance from forest with area type.

```
modVisButterflies3 <- glmer(Butterfly ~ AreaType + timeofday +
                             (1 | SamplingID) + (1 | Date),
                           data=manual_data, family="poisson")


summary(modVisButterflies3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Butterfly ~ AreaType + timeofday + (1 | SamplingID) + (1 | Date)
##    Data: manual_data
##      AIC      BIC   logLik deviance df.resid 
##    248.5    261.2   -119.3    238.5       88 
## Scaled residuals: 
##     Min      1Q  Median      3Q     Max 
## -0.5961 -0.3999 -0.3199  0.2639  0.8414 
## Random effects:
##  Groups     Name        Variance  Std.Dev. 
##  SamplingID (Intercept) 3.160e+00 1.7776669
##  Date       (Intercept) 1.295e-07 0.0003599
## Number of obs: 93, groups:  SamplingID, 93; Date, 8
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)   
## (Intercept)          -5.9110     1.9397  -3.047  0.00231 **
## AreaTypePlantation    0.7137     0.5155   1.385  0.16619   
## timeofday            10.6456     4.5638   2.333  0.01967 * 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##             (Intr) ArTypP
```

```
## ArTypPlnttn -0.285
## timeofday   -0.969  0.140
```

Area type is not significant. Remove area type.

```
modVisButterflies4 <- glmer(Butterfly ~ timeofday +
                              (1 | SamplingID) + (1 | Date),
                            data=manual_data, family="poisson")

summary(modVisButterflies4)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Butterfly ~ timeofday + (1 | SamplingID) + (1 | Date)
##    Data: manual_data
##      AIC      BIC   logLik deviance df.resid
##    248.4    258.6   -120.2    240.4       89
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.5233 -0.4075 -0.3250  0.2914  0.6557
## Random effects:
##  Groups     Name        Variance  Std.Dev.
##  SamplingID (Intercept) 3.355e+00 1.8315479
##  Date       (Intercept) 3.002e-08 0.0001733
## Number of obs: 93, groups:  SamplingID, 93; Date, 8
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -5.306      1.917  -2.768  0.00564 **
## timeofday      9.928      4.655   2.133  0.03293 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
##           (Intr)
## timeofday -0.978
```

The remaining fixed effect is significant. Keep this as the best model.

Appendix E

This appendix presents the difference in number of individuals trapped between the two areas, highlighting the morphospecies within different groups having the most noticeable difference.

Bees

There was no bee morphospecies that had a noticeable difference in the number of individuals trapped between the two areas.

Beetles

There was only one beetle morphospecies that had a noticeable difference in the number of individuals trapped between the two areas. “A64”, within family Carabidae was found five times in the forest area, but never in the plantation area.

Figure E.1: Morphospecies A64. 11 mm long

Syrphid flies

For the syrphid flies, three morphospecies had a noticeable difference in the number of individuals trapped between the two areas. Both “A124” and “A30” had four representatives in the forest area, and none in the plantation. “A35” had 14 representations in the forest area, and five in the plantation.

Figure E.2: Three morphospecies of syrphid flies captured in the pan traps. Based on comparison of trapped individuals between the two areas. All three presented morphospecies showed a preference for the forest areas. Photograph was not taken at standardised distance. Length is presented below for size reference. A30 = 6 mm, A35 = 6 mm, A124 = 12 mm. Photo: K.H

Wasps

Wasps can in many cases be excellent pollinators (Willmer, 2011), but due to limited knowledge of tropical wasp taxonomy and time constraints, they were not included as pollinators in this study. Nine morphospecies had a noticeable difference in the number of individuals trapped between the two areas. “A113” was found nine times in the forest area, and one in the plantation. “A114” was found six times in the plantation area, and one in the forest area. “A128” was found seven times in the forest area, and two times in the plantation. “A49” was found eight times in the forest area, and zero in the plantation. “A5” was found six times in the plantation area, and zero times in the plantation. “A55” was found 18 times in the forest area, and seven times in the plantation. “A112” was found seven times in the plantation and two times in the forest area. “A202” was found 13 times in the plantation area, and two in the plantation. “A276” was found 11 times in the plantation area and none in the forest

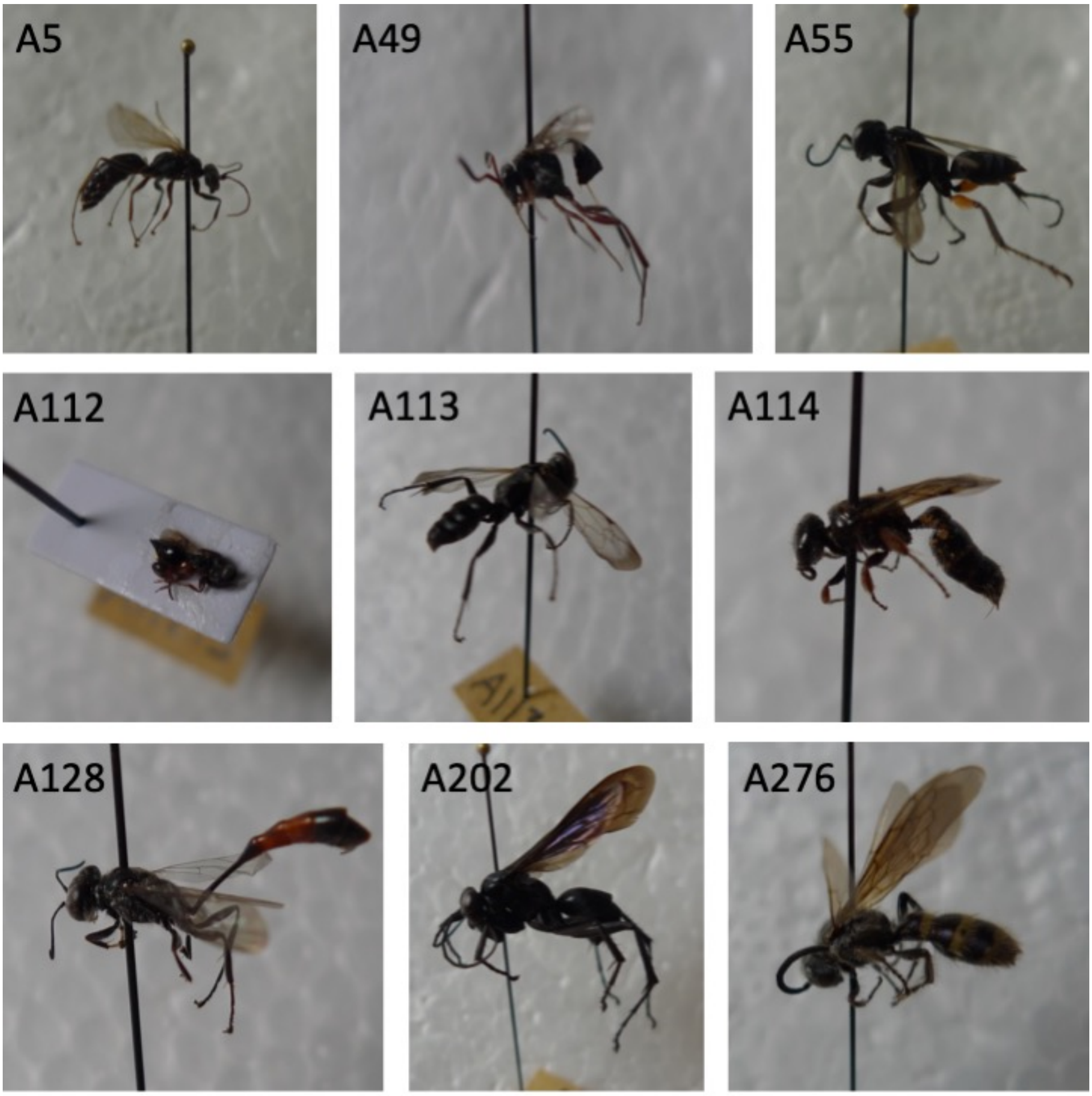


Figure E.3: Nine morphospecies of wasps captured in the pan traps. Based on comparison of trapped individuals between the two areas these individuals showed a preference for either forest or plantation area. Photograph is not taken at standardised distance. Length is presented below for reference. A5 = 10 mm, A49 = 6 mm, A55 = 11 mm, A112 = 3 mm, A113 = 9 mm, A114 = 7 mm, A128 = 11 mm, A202 = 11 mm, A276 = 9 mm. Photo: K.H

Flies (not syrphid)

As for wasps, several families within the flies, besides the syrphid flies are recognized as viable pollinators (Willmer, 2011), but due to insufficient knowledge of taxonomy for tropical flies, all other flies than syrphid flies were noted as non-pollinators. There were six morphospecies that had a noticeable difference in the number of individuals trapped between the two areas. Morphospecies “A111”, within family Dolichopodidae, had 562 representatives in the forest area, and 273 in the plantation. “A42” possibly within family Muscidae, had 321 representatives in the forest area, and 174 in the plantation area. “A46”, possibly within genus Musca, had 56 representatives in the forest area, and 13 in the plantation. “A152”, possibly within family Anthomyiidae, had 136 representatives in the plantation area, and 56 in the forest. “A194”, possibly within family Muscidae, had 238 representatives in the plantation area, and 12 in the forest. “A43” within family Calliphoridae, had 174 representatives in the plantation area, and 76 in the forest.

Others

Representatives of the category defined as “others” hosted all morphospecies belonging

Figure E.4: Six morphospecies of flies captured in the pan traps. Based on comparison of trapped individuals between the two areas these individuals showed a preference for either forest or plantation area. Photograph is not taken at standardised distance. Length is presented below for reference. A42 = 7 mm, A43 = 7 mm, A46 = 9 mm, A111 = 3 mm, A152 = 6 mm, A194 = 4mm. Photo: K.H to other insect groups than those defined above. In addition to morphospecies possibly within those groups, but who was not recognized belonging to them when sorted. There were three morphospecies that had a noticeable difference in the number of individuals trapped between the two areas. “A47”, a planthopper, was found 23 times in the forest area, and only once in the plantation. “A48”, a representative of order Hemiptera, was found 21 times in the forest area, and only once in the plantation. “A222”, resembling a moth, possibly within order Lepidoptera but with characteristics making placement in a certain group difficult, hence placed in “others”, were found 13 times in the plantation area and none in the forest area.

Figure: Three morphospecies of “others” captured in the pan traps. Based on comparison of trapped individuals between the two areas these individuals showed a preference for either forest or plantation area. Photograph is not taken at standardised distance. Length is presented below for reference. A47 = 5 mm, A48 = 12 mm, A222 = 4mm. Photo: K.H

Table E.1: Number individual representatives within bees, beetles and syrphid flies trapped in pan traps in the two areas

Bees			*Beetles*			*Syrphid flies*		
Morpho ID	**Forest**	**Plantation**	**Morpho ID**	**Forest**	**Plantation**	**Morpho ID**	**Forest**	**Plantation**
A1	3	0	A115	2	0	A101	1	0
A129	1	0	A138	1	0	A124	4	0
A132	1	0	A151	1	0	A130	1	0
A145	1	3	A183	1	0	A219	1	0
A155	2	0	A185	1	0	A220	1	0
A17	1	0	A191	1	0	A223	3	0
A186	1	0	A213	2	0	A229	1	0
A198	0	3	A214	1	0	A24	1	0
A199	0	1	A216	2	0	A241	1	0
A215	1	0	A228	3	0	A26	2	0
A218	1	0	A239	0	1	A263	0	1
A248	1	0	A243	1	2	A266	1	0
A249	1	0	A244	1	1	A278	0	1
A252	1	1	A245	1	1	A289	0	1
A260	0	1	A251	0	1	A290	0	1
A269	1	0	A253	0	2	A30	4	0
A288	0	1	A257	0	1	A31	0	2
A58	2	0	A261	0	1	A33	1	0
A59	2	0	A262	0	1	A34	16	24
A65	2	0	A273	0	1	A35	14	5
A67	1	0	A274	0	1	A37	1	3
A69	1	0	A279	0	1	A38	3	0
A71	1	0	A280	0	3	A39	1	0
A76	1	0	A285	0	1	A45	39	47
A90	0	2	A50	1	0	A53	1	0
A91	1	0	A64	5	0			
			A70	1	0			
			A74	0	0			
			A75	2	0			
			A83	1	0			
			A89	0	2			

Table E.2: Number individual representatives within wasps, flies and ”others” trapped in pan traps in the two areas

Wasps						***Flies (not syrphid)***			***Other***		
Morpho ID	**Forest**	**Plantation**	**Morpho ID**	**Forest**	**Plantation**	**Morpho ID**	**Forest**	**Plantation**	**Morpho ID**	**Forest**	**Plantation**
A112	2	7	A217	1	0	A111	562	273	A119	1	0
A113	9	1	A22	0	1	A137	1	4	A120	1	0
A114	6	1	A224	4	0	A148	4	1	A123	2	0
A115	1	0	A255	0	1	A149	1	0	A139	1	0
A116	4	0	A256	0	2	A150	3	0	A145	1	2
A117	1	0	A267	1	0	A152	56	136	A163	1	0
A118	2	0	A268	1	1	A156	0	3	A181	1	0
A125	1	0	A272	1	0	A157	1	0	A183	0	1
A126	2	1	A276	0	11	A193	0	1	A188	1	0
A127	2	1	A277	0	1	A194	12	238	A190	1	2
A128	7	2	A286	0	1	A195	0	1	A204	0	1
A134	2	1	A36	2	0	A208	0	1	A206	0	1
A136	1	0	A44	13	13	A219	0	2	A222	0	13
A140	1	0	A49	8	0	A225	0	1	A234	1	0
A141	1	5	A5	6	0	A226	1	0	A240	1	0
A142	1	0	A54	2	4	A230	1	0	A247	1	0
A143	2	0	A55	18	7	A231	2	0	A250	1	0
A144	2	1	A56	4	2	A234	1	0	A264	1	0
A146	1	0	A57	1	0	A254	0	2	A271	1	0
A153	3	0	A62	2	0	A259	0	1	A275	0	1
A154	18	17	A63	5	3	A265	1	0	A281	0	1
A183	2	3	A68	2	1	A40	22	24	A287	0	1
A184	3	2	A7	2	2	A42	321	174	A47	23	1
A189	1	0	A72	1	1	A43	76	174	A48	21	1
A190	0	4	A73	2	1	A46	56	13	A66	14	13
A192	2	0	A78	1	0	A53	1	0	A70	1	0
A196	4	2	A79	1	0				A77	2	0
A200	0	1	A80	1	0						
A201	0	2	A81	15	17						
A202	2	13	A82	1	0						
A205	1	0	A9	6	9						