Using Spider Diversity to Evaluate the Level of Disturbance in the Amazon Rainforest

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Abstract

The Amazon rainforest, one of the world's most biodiverse ecosystems, is under severe threat from anthropogenic activities such as illegal logging, mining, and agriculture. This study introduces the use of spider diversity at the family level as a novel and efficient method for assessing disturbance levels in three habitats within the Madre de Dios region of Peru: primary forest, secondary forest, and grassland. A total of 454 spiders from 15 families were recorded, with significantly higher abundance and diversity in primary forests. Canopy coverage, used as a proxy for disturbance, was strongly correlated with spider diversity, showing a negative relationship between canopy openness and biodiversity. By focusing on family-level identification, this approach simplifies specimens identification while maintaining accuracy in disturbance assessment. The results highlight the potential of spider diversity as an effective tool for evaluating ecosystem disturbance, providing valuable insights for forest management. Long-term studies are recommended to account for seasonal variations.

Introduction

The Amazon rainforest is undeniably one of the most biodiverse ecosystem in the world and providing essential ecosystem service and goods to society (Myers 1997). However, large scale and rapid anthropogenic activities, such as illegal logging and mining, agricultural activities and fires, had been severely threatening the intactness of the Amazon Forest (Vieira et al. 2008; Lapola et al. 2023). Forest has been reduced to many small fragments, reducing the area of the habitat, creating barrier for the passage of animals in the forest and thus restricting the accessibility of resources. Consequently, overall biodiversity in the forest is decreasing. Deforestation and habitat loss could also disrupt the forest dynamics, leading to abrupt mortality in species (Ferreira & Laurance 1997) and drastic reduction in food web complexity in the ecosystem (Pires et al. 2024), all of which are heavily detrimental to an ecosystem. Thus, the impact of human disturbance could be catastrophic on the existing ecosystem.

Biodiversity has always been used as an indicator to assess the health of an ecosystem, as the stability of an ecosystem is often correlated to the level of biodiversity and thus maintaining the sustainability of ecosystem functions and services (Worm et al. 2006; Isbell et al. 2011; Cardinale et al. 2012; Gamfeldt et al. 2013; Pennekamp et al. 2018). The relationship between biodiversity and its impact on ecosystem is often non-linear, the changes in the ecosystem could be exponential as the biodiversity declines (Cardinale et al. 2012). The significance of biodiversity renders it a decent proxy for evaluating the effect of human disturbance on the ecosystem and monitoring

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biodiversity becomes imperative in regulating anthropogenic activities.

Bioindicator refers to taxa or functional groups that can effectively indicate the condition of the environment due to their moderate tolerance to environmental variability (Holt & Miller 2011). Bioindicators can be applied when evaluating the impact of human disturbance in an area or when assessing the restorative effort in a habitat. Their study can prompt decision-making in nature management. Arthropods have readily been used as a bioindicator (Frouz 1999; Maleque et al. 2009; Beiroz et al. 2014), their immense abundance, moderate susceptibility to environmental change and efficient sampling makes them an excellent bioindicator for environmental assessment.

Amongst all arthropods, spiders are the top predators. Their abundance and diversity can directly reflect the effect of both biotic and abiotic impact on the lower trophic levels, making spiders an informative bioindicator (Scott et al. 2006). Moreover, spiders are extremely diverse and abundant in almost all terrestrial habitats, with over 52,000 spider species being described (World Spider Catalog 2024), thus allowing efficient sampling. Spiders have been used as a bioindicator outside of the Neotropics region of the world (Maelfait & Hendrickx 1998; Schwerdt et al. 2018). However, species identification is always time-consuming. In the case of spiders, dissections are often needed to examine the reproductive organ for the confirmation of the spider identity, making juvenile spiders more difficult to identify. Moreover, the distinctive morphology and hunting strategy between families can allow ecologists to identify spiders at family level easily, making spiders diversity a more efficient method for assessing disturbance level of the habitat.

Similar studies using high-level diversity and high-level functionality indicators to evaluate spider assemblages' sensitivity to landscape changes have also been carried out in the Brazilian Amazon (Gonzalez et al. 2021), however, only ground spiders were collected for analysis in the study. Therefore, this study aims to provide a more comprehensive evaluation on the feasibility of using spider diversity at only family level by collecting spiders for the assessment of disturbance levels in the Amazon rainforest to aid forestry management and policy making by collecting spiders both on and above the ground.

Methods

Sampling Sites

The study area was located in Finca Las Piedras, Madre de Dios, Peru. To investigate the effectiveness of spider diversity as an indicator for the assessment of the level of disturbance in the Amazon rainforest, three sites were selected for sampling. (1)Primary Forest (PF), intact forest with a trail system; (2)Secondary Forest (SF), secondary vegetation with 8 years of regeneration; (3)Grassland (GL), adjacent to a pineapple farmland and primarily dominated by grass species. Each habitat represented a different level of disturbance, ranging from the lowest (PF) to the highest level of disturbance (GL) and forming a disturbance gradient. All sampling was conducted between August and September 2024, during the dry season of the Amazon.

Sampling Method

At each habitat, seven 5m x 5m plots were deployed. The location of each plot was randomly generated using QGIS.

To maximize the efficiency of spider sampling and minimize potential biases attributed to the complexity of the habitat (Privet et al. 2020), only visual observation and hand collection method were used. Furthermore, to ensure a more representative spider diversity of the habitat, spiders from the ground, bush and canopy layers were all recorded. The duration for sampling at each plot was 15 minutes. Species were identified and photographed on site, while unknown species were collected for further identification. In addition, both day and night samplings were conducted to ensure both diurnal and nocturnal species were included.

To estimate and quantify the level of disturbance in the habitat, the coverage of the canopy was also measured at each plot by taking a photo at the centre of each plot and analysing it in ImageJ using Hemispherical_2.0 (Beckschäfer 2015).

Results

In total, 454 spiders and 15 families were recorded (115 spiders were recorded in the day and 339 spiders were recorded at night) (Figures 1 & 2). The abundance of spiders recorded in the primary forest was significantly higher than that in the other habitats (Anova : p<0.001) (Figure 3). The number of spiders found in a sampling plot in primary forest (31.43 ± 6.58 individuals) was twice as much as in the secondary forest (16.86 ± 7.76 individuals) and grassland (16.71 ± 4.89 individuals). In terms of species richness and Shannon diversity index, it was significantly different between habitats (Anova : p<0.001)(Figures 4 & 5). Primary forest had the highest

Figure 2. Numbers of spider individuals recorded in day and night respectively

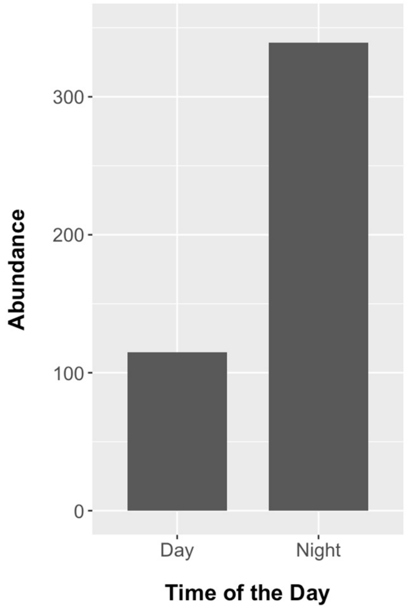

Figure 1. Numbers of spider individuals and families recorded

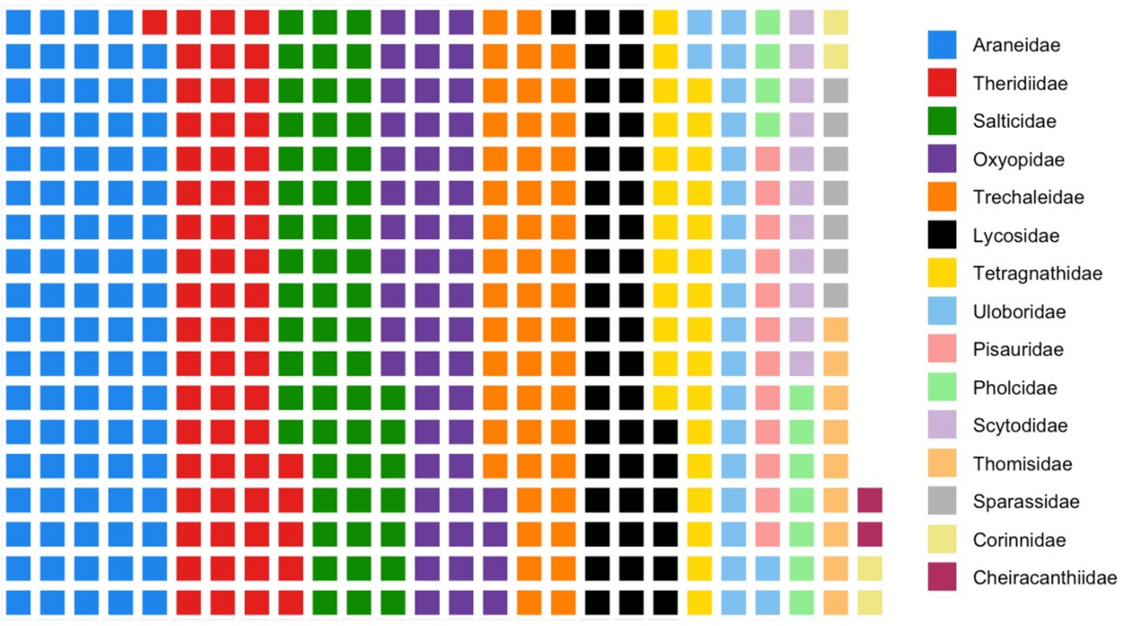

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Figure 3. Average numbers of spider individuals per sampling plot recorded across habitats

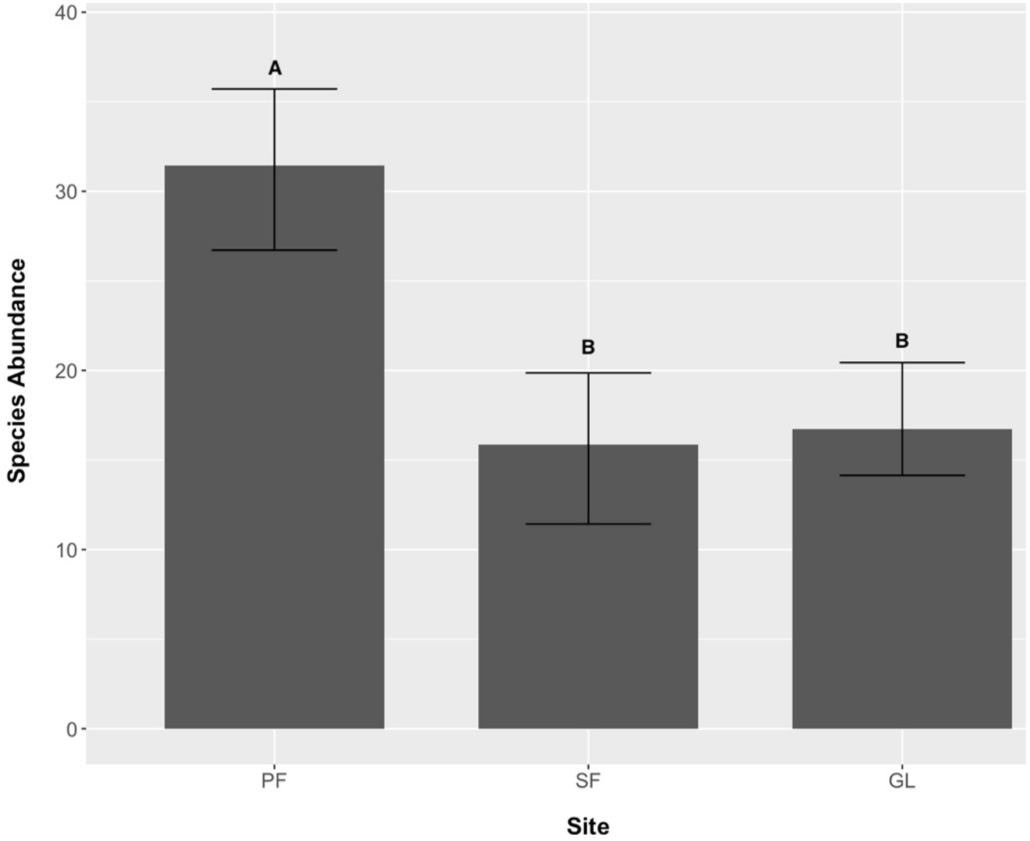

Figure 4. Average numbers of spider families per sampling plot recorded across habitats

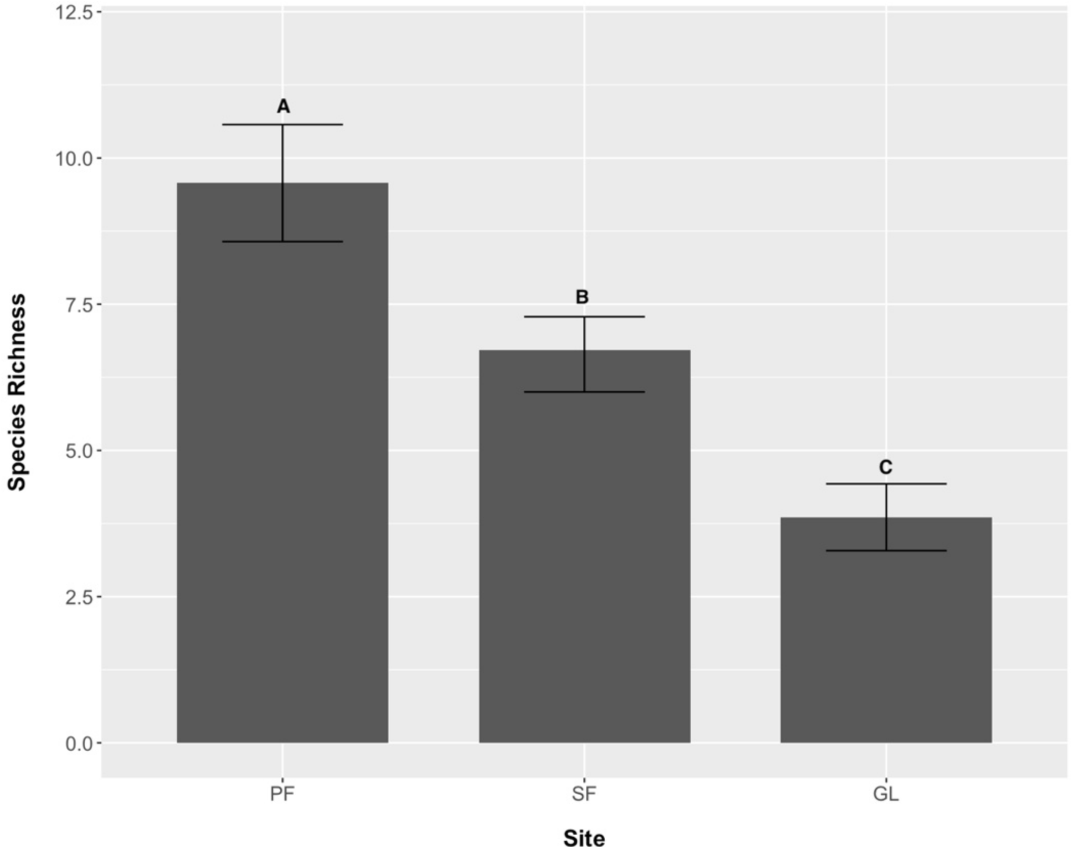

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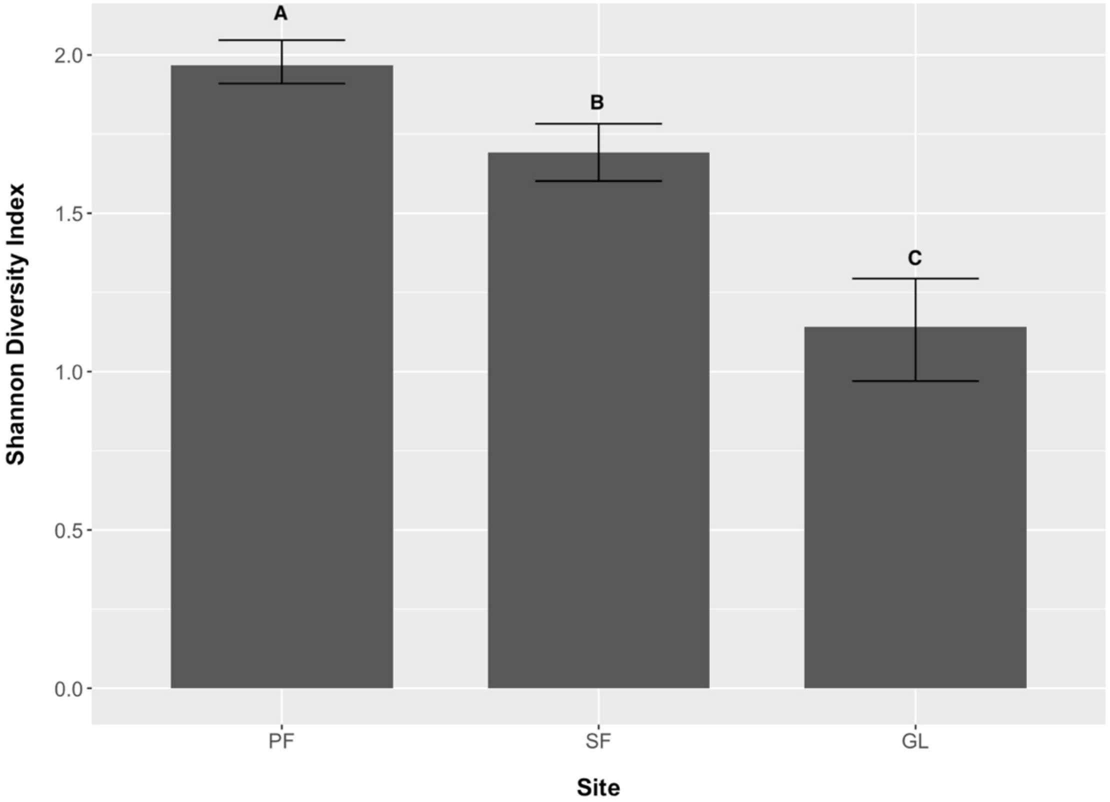
Figure 5. Average Shannon Diversity Index per sampling plot recorded across habitats



species richness (9.57 ± 1.4) and Shannon diversity index (1.97 ± 0.1), followed by secondary forest (species richness: 6.71 ± 0.95; Shannon diversity index: 1.69 ± 0.13) and grassland (species richness: 3.86 ± 0.9; Shannon diversity index: 1.14 ± 0.25).

Canopy coverage was quantified as the percentage of light gap in the canopy which differed significantly between habitats (Anova : p<0.001). Grassland has the highest percentage of light gap in the canopy, whereas primary forest had the smallest percentage (Figure 6). By measuring the spearman correlation coefficient between Shannon diversity index and the percentage of the light gap in the canopy of the sampling plots, a strong negative correlation was shown (R=-0.85, p=8.1e-07) (Figure 7). It suggested that the thinner the canopy, the lower the lower the diversity is. In addition, the UPGMA clustering analysis using Bray-Curtis Dissimilarity Index shown distinctive clustering between habitats (Figure 8), suggesting high similarity in species composition within the habitat.

Figure 6. Average percentage of light gap in the canopy per sampling plot across habitats

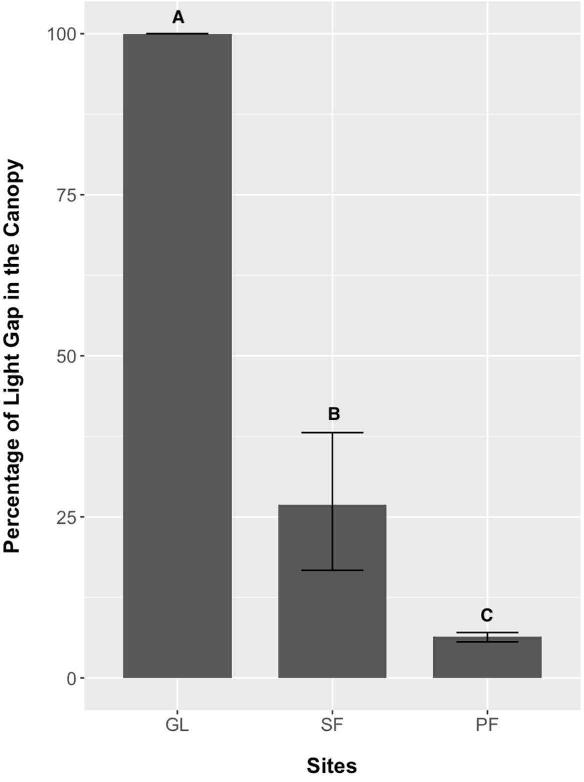


Figure 7. Graph showing correlation between Shannon Diversity Index and percentage of light gap in the canopy

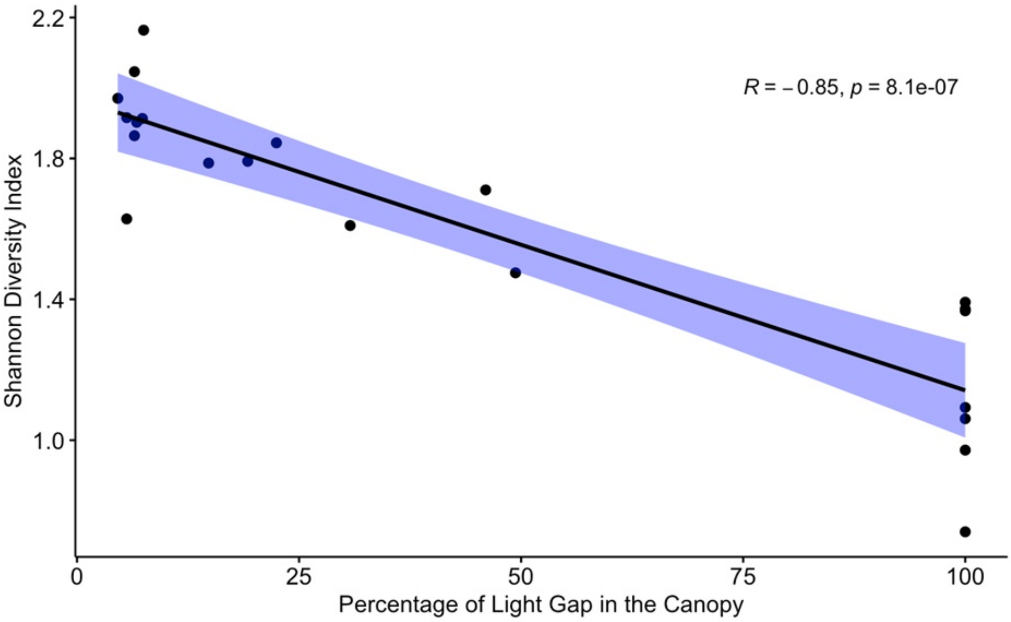
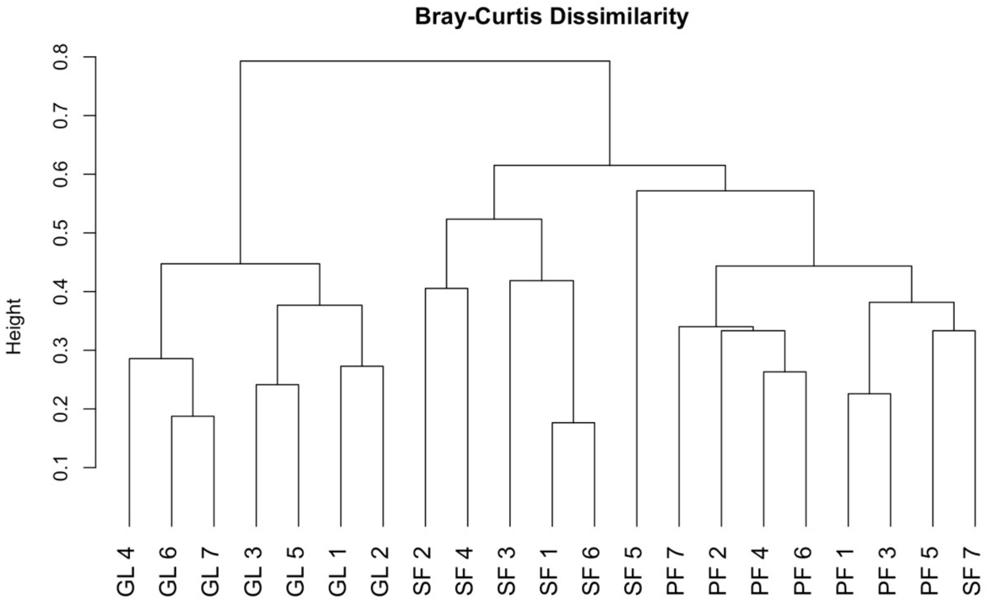


Figure 8. UPGMA clustering analysis using Bray-Curtis Dissimilarity Index



Discussion

The result from the study have shown a distinctive difference in terms of spider diversity along the disturbance gradient. The significantly higher abundance in primary forest was twice the number than secondary forest and grassland, it suggested a much higher carrying capacity in the primary forest than the other habitats which also inferred a higher abundance of other organisms in the primary forest. Both species richness and the Shannon diversity index shown a distinctive difference between habitats, primary forest had the highest diversity followed by secondary forest and grassland. It strongly supports the use of spider diversity at family level as an indicator for the assessment of disturbance levels.

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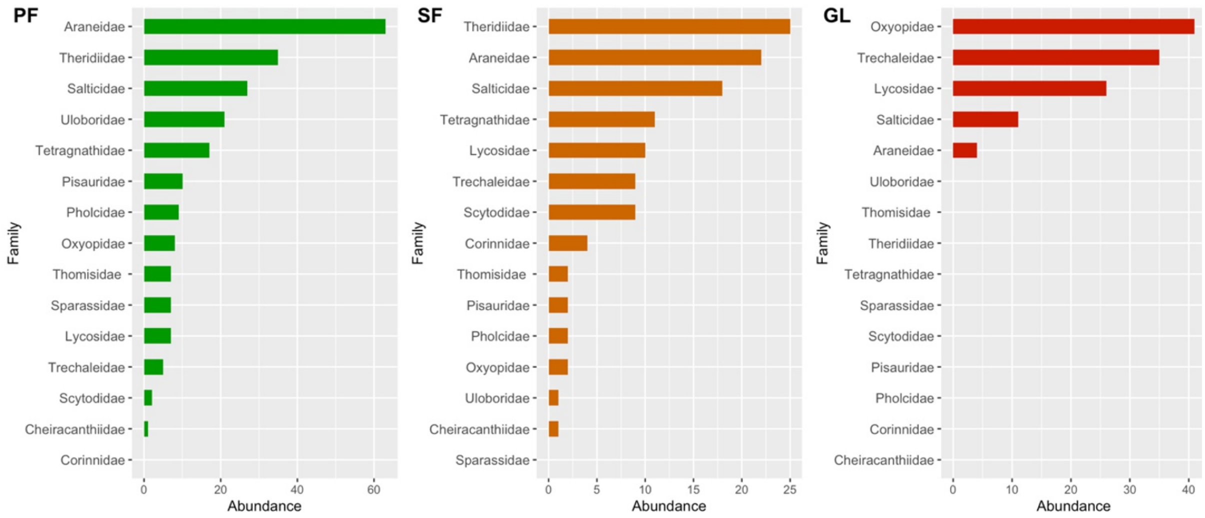
The UPGMA clustering analysis base on Bray-Curtis Dissimilarity Index have shown three big clusters, plots within each habitat were clusters together which suggested a distinctive species composition between habitats. However, two plots from the secondary forest were clustered together with plots in the primary forest, indicating a higher similarity between secondary and primary forest. It highlighted the effect of reforestation and its importance in enhancing biodiversity in disrupted habitat.

When looking at the dominant spider families in each habitat (Figure 9), primary and secondary forest were dominated by web-builder, whereas grassland was dominated by ground-dwelling spiders. It also explains the higher similarity in terms of species composition between secondary and primary forest. The complex vegetation structure in primary and secondary forest provides attachment surface for the construction of their web and facilitate predation. Also, the denser canopy coverage in primary and secondary forest provides refuge and reduces the chance of being preyed. Both advantages increase the chances of survival and hence its abundance which explained the discrepancy of dominant spider family between habitats.

Using canopy coverage as a proxy for disturbance, the correlation between canopy coverage and spider diversity also suggested a distinctive difference in spider diversity along the disturbance gradient, which further support the use of spider diversity at family level as an indicator for the assessment of disturbance levels.

All the evidence from this study points toward potential use of spider diversity as an indicator of disturbance. However, it is important to note that samplings were only done during Aug. Therefore, effect for seasonal variation was not accounted for and further long-term study should be conducted to fill the knowledge gap.

Figure 9. Number of spider families in each habitat



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