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Diversity and community assembly structure in canopy jumping spiders (Araneae: Salticidae) across a land use gradient in Jambi, Sumatra

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Abstract

This study investigates the effects of rainforest transformation to monoculture plantations on the diversity and community assembly structure of arboreal jumping spiders (Araneae: Salticidae) across a land use gradient in Jambi, Sumatra. Spiders were collected via canopy fogging in a nested, replicated design of 32 plots in four land use systems in two landscapes (Bukit Duabelas, Harapan). The four land use systems were: primary degraded lowland rainforest, jungle rubber (extensive rubber agroforestry) monocultures of oil palm (*Elaeis guineensis*) and rubber (*Hevea brasiliensis*). From a total of 912 collected spiders, 677 were identified to 70 different morphospecies.

Roughly 40% of all morphospecies were found exclusively in jungle rubber and/or forest, whereas only half of that were exclusively found in rubber and oil palm combined. Salticid spider abundance did not differ among the land use systems. Salticid species richness was highest in jungle rubber, and lowest in rubber and oil palm, with forest having intermediate species richness, which in turn was not different from any of the other land use systems. Simpson's inverse diversity was significantly higher in forest and jungle rubber, compared with rubber, but was not different from oil palm. Community composition of salticid spiders in forest and jungle rubber was similar, but different from rubber and oil palm, which in turn differed from each other. I also tested the influence of ambient temperature and ambient humidity, mean canopy openness, aboveground plant biomass AGB, stand structural complexity SSCI and the land use intensity index LUI on salticid spider community composition. Among those variables, canopy openness, AGB and LUI had a significant effect on canopy salticids community composition. The three variables only explained 7% of the data variance, strongly suggesting that there are other, possibly more influential environmental factors influencing canopy composition of canopy salticids spiders.

I extracted DNA from legs of up to three individuals from 69 of the 70 identified morphospecies. Two gene regions were sequenced, i.e. the nuclear-encoded large subunit (28S) ribosomal repeat (~750bp) and the ~1 kb mitochondrial encoded cytochrome oxidase I (COI), using the Sanger method. To verify morphology based identification, I used Automatic Barcode Gap Discovery (ABGD). I then calculated phylogenetic diversity PD, Net Relatedness Index NRI and Nearest Taxon Index NTI with single sequences for 55 candidate morphospecies. NRI and NTI are two commonly used metrics in community phylogenetics to determine phylogenetic clustering (indicative of habitat filtering) versus phylogenetic overdispersion (indicative of competitive exclusion) as community assembly mechanisms.

Despite contrasting data in jungle rubber and rubber with respect to NTI and NRI, results indicated that the community assembly in forest is not different from random assembly, while community assembly in oil palms seemed to be strongly influenced by habitat filtering. I discuss the relevance of these findings with regard to the limitations of the used indices.

Overall, my thesis demonstrates that conversion of rainforest and jungle rubber to monocultures of rubber and oil palm (a) had no effect on the abundance on canopy salticids, (b) caused reduction of species richness and Inverse Simpson diversity and (c) entailed shifts in community composition. I found three environmental variables that had a significant effect on community composition and detected differences in the potential community assembly mechanisms between forest and oil palm. Overall, this thesis offers a comprehensive community level analysis of canopy salticids spiders thus far not reported from Southeast Asia.

Introduction

Tropical ecosystems are exceptionally species rich, contain much of the world's biodiversity and are one of the biggest carbon sinks in the world (Sodhi et *al.*, 2004). However, forest conversion to agricultural land use systems is one of the major reasons for worldwide biodiversity loss and proceeds fastest in the tropics (Sodhi et *al.*, 2004; Sala, 2000). Especially in Southeast Asia, deforestation rates are highest among all tropical regions. First major deforestation started around 1800 to expand agricultural areas for rice (*Oryza sativa*) cultivation (Sodhi et *al.*, 2004). Since 1950, commercial timber extraction as well as cultivation of rubber (*Hevea brasiliensis*) and oil palm (*Elaeis guineensis*) were the main drivers of deforestation in Southeast Asia until today (Flint, 1994). By 2010, roughly 70% of the original lowland forest of Sundaland, comprising Malay Peninsula, Borneo, Sumatra and Java were lost by deforestation (Wilcove et *al.*, 2013). The still ongoing forest conversion is feared to result in a loss of 40% of the regions biodiversity by 2100 (Sodhi et *al.*, 2004).

Logging native tree species immediately simplifies the complex canopy structure of tropical rainforests (Okuda et *al.*, 2002). The negative impacts of selective logging on critical parameters like canopy complexity and canopy height are still detected after > 40 years of recovery (Okuda et *al.*, 2002). Tree canopies form an aboveground habitat that is highly threatened and contains a large proportion of the forest's insect and arthropod diversity (Erwin, 1982; Zheng, 2015; Stork & Grimbacher, 2006). Canopy arthropods provide crucial ecosystem functions as they serve as important predators and pollinators (Floren et *al.*, 2011). Furthermore, they constitute the majority of biomass and biodiversity in tropical ecosystems (Fittkau &

Klinge, 1973; Samways, 2005). Studies by Davis & Phillips (2005) and Pfeiffer et *al.* (2008) revealed a significant decrease in species diversity of beetles and ants in oil palm plantations compared to primary forest. However, most studies regarding the effect of forest transformation focused on birds or mammals (Turner & Foster, 2008, Meijaard et *al.*, 2005).

While assessing species richness and abundance of target taxa holds relevant information with regard to community composition, these data are but a snapshot, limited to one point in time. It is often important to understand the processes that lead to the observed community composition. The underlying mechanism is termed community assembly, which is the structuring mechanism behind community succession, leading to a climax community of a given habitat. The two major components of community assembly are competitive exclusion of species and environmental / habitat filtering (MacArthur & Levins, 1964, Diamond, 1975). Community assembly can be measured by molecular biological means, often referred to as community phylogenetics. Community phylogenetics aims to reveal the effects of competitive exclusion and environmental / habitat filtering, based on the phylogenetic relationship that co-occurring species share within a community (Webb et *al.*, 2002, Vamosi et *al.*, 2009). The underlying assumption is, that ecological traits show a phylogenetic signal, i.e. closely related species are assumed to be ecologically more similar than distantly related species. Community assemblages dominantly structured by competitive exclusion consist of distantly related species, resulting in overdispersal on the phylogenetic tree. In contrast, communities structured by environmental / habitat filtering are associated with phylogenetic and phenotypic clustering, as the environment functions as a filter that selects for species of similar traits (Webb et *al.*, 2002). The two most commonly used metrics based on the mean phylogenetic distance of taxa in a community are the Net Relatedness Index (NRI) and the Nearest Taxon Index (NTI). NRI measures the mean pairwise phylogenetic distance of species in a sample in relation to the phylogeny of the local community. NTI measures the phylogenetic distance for every taxon to its closest relative (Webb et *al.*, 2002). Both metrics are below zero with phylogenetic overdispersal (≈ competitive exclusion), above zero with phylogenetic clustering (≈ environmental / habitat filtering) and are zero in randomly assembled communities.

Spiders are very diverse and abundant in rainforest canopies and are among the top predators in arthropod foodwebs (Zheng et *al.*, 2015). Their distribution and assemblage structure are sensitive towards habitat disturbances and alterations in the vegetation structure (Hsieh et *al.*, 2003; Wise, 1993), thus they are useful organisms for biodiversity studies across changing environments. Among the spiders as a whole, the jumping spiders (Araneae: Salticidae) are the family containing the most species (currently 6,188 (World spider catalog, 2020)). Their most remarkable feature are two large anterior median eyes with a spatial acuity much higher than that of other animals of similar size (Land & Nilsson, 2012). This level of visual abilities allows salticids spiders to stalk and catch moving prey with a precise jump that may exceed 20 times their body length (Dalton, 2008). These optical and physical capabilities grant salticids spiders to be some of the most agile arthropod predators in tropical forest canopies. This may also be the reason why salticids spiders and ants seem to compete for similar niche space in Southeast Asian rainforest canopies (Katayama et *al*., 2015). One of the most species rich genera of the Salticidae is *Myrmarachne*, which mimics the morphology of ants from the same region (Yamasaki & Edwards, 2013; Yamasaki & Hahmad 2013, Yamasaki et *al*., 2018). Overall, the Indonesian fauna of jumping spiders comprises 657 described species from 161 genera, constituting >10% of the worldwide species richness of salticids (Ramos 2020; World spider Catalog, 2020). To date, only few studies have addressed the impact of rainforest transformation in Southeast Asia on spider communities in general (Floren & Deeleman-Reinhold, 2005; Floren et *al.*, 2011; Zheng et *al.*, 2015) and investigations on community assembly seems to be limited to Hawaiian and European communities (Gillespie, 2004; Mazzia et *al*., 2015). The general consensus is that anthropogenic disturbance leads to decreased diversity and altered community compositions of arboreal spider communities, including salticid spiders, in Southeast Asia (Floren et *al.*, 2011, Floren & Deeleman-Reinhold, 2005). To the best of my knowledge, detailed studies on the role of habitat transformation on communities of salticid spiders in Southeast Asia are however, lacking, in particular with regards to community assembly.

Hence, the aim of this thesis is to investigate the effect of rainforest conversion to monocultures on the abundance, diversity and community composition of arboreal jumping spiders (Salticidae). Additionally, I aim to explore the role of environmental factors on community composition and shed light on potential differences of community assembly processes, both in rainforests and in monocultures. To do this, I studied the above in a collection of canopy salticids spiders from Jambi Province, Sumatra, Indonesia. The samples were collected along a land use gradient from primary degraded lowland rainforest forest via jungle rubber (a rubber agroforest, with planted rubber trees in a previously logged rainforest) to monocultures of rubber and oil palm. I used the available collection to test two overarching hypotheses (see below).

Hypotheses

(1) Species richness and diversity of canopy jumping spiders decrease across the land use gradient, with highest values in lowland rainforest, intermediate in jungle rubber and lowest in rubber and oil palm monocultures, as a response to changing microclimate and habitat simplification.

(2) Transformation of rainforest to agricultural landscapes strengthens the effect of habitat filtering, resulting in phylogenetic clustering in the community assembly of jumping spiders in oil palm and rubber monocultures.

Methods

Study area

Jumping spiders were collected in 2017 within the frame of the Collaborative Research Centre CRC990 / EFForTS ("Ecological and Socio-economic Functions of Tropical Lowland Rainforest Transformation Systems"). EFForTS investigates the socioeconomic and ecological consequences of rainforest transformation to cash crop dominated landscapes in Jambi province of Indonesia. In this project, scientists from the University of Göttingen (Germany) and the Indonesian universities UNTAD (Tadulako University, Palu), UNJA (Jambi University), IPB (Bogor Agricultural University) cooperate in research and are funded by the German Research Foundation (DFG). Jambi Province covers an area of 50160 km² and faced rapid rainforest transformations to crop land during the last decades. Due to land use policies, focused on economic growth and transmigration programs that resettled about 400000 people from overcrowded regions of Indonesia to Jambi, now primarily occupied in cash-crop production, 55% of Jambi's rainforest was transformed to agricultural land by 2013 (Drescher et *al.*, 2016). In 2014, rubber cultivations spread over more than 650000 ha and oil palm plantations covered about 590000 ha in Jambi Province (Badan Pusat Statistik, 2014). The EFForTS study sites are located in and around the Bukit Duabelas National Park and the Harapan Rainforest forest reserve in Jambi province in Sumatra (Fig.1).

Figure 1 Sampling sites in Jambi Province, Sumatra, Indonesia with two landscapes Bukit Duabelas (B) and Harapan (H) studied. Plot ID's used first letters for landscape (B, H) and land use (F, J, R, O) and the plot number e.g. BJ5 = Bukit Duabelas jungle rubber plot 5. Nature conservation areas 'Bukit Duabelas National Park' and 'Harapan Rainforest Concession' are coloured in brown. From: Berkelmann et *al.*, 2018.

Both landscapes, termed ‘Bukit Duabelas’ (B) and ‘Harapan’ (H) have a nested, replicated mirrored design of core plots across four different land use systems. Each form of land use has four plots of 50 x 50 m in size, resulting in 4 x 4 x 2= 32 plots. Core plots of rubber (*Hevea brasiliensis)* and oil palm (*Elaeis guineensis)* are located in smallholder monoculture plantations. Rubber plantations were established 12 to 21 years before sampling in 2017 and oil palm plantations varied in ages of 13 to 20 years (Drescher et *al.*, 2016). Forest core plots resemble a primary forest, partly degraded by logging activities, according to the definition of Margono et *al.*, 2014. Core plots in jungle rubber were established in smallholder agroforest systems with planted trees of rubber in a previously logged rainforest (Fig.2).

Figure 2. Investigated primary forest (A), jungle rubber agroforest (B), rubber monocultures (C) and oil palm monocultures (D) in Jambi, Sumatra, Indonesia. From Breidenbach et *al.*, 2018.

Spider sampling

Salticid spiders were collected via canopy fogging of three locations in each of the 32 core plots during dry season in June to August of 2017. Canopies were fogged with DECIS 25 (BayerCropScience) insecticide dissolved in petroleum white oil in a 1:9 ratio. Dead arthropods of the target canopies were collected in 8 funnels of 1 m^2 per target canopy. Funnels led to a bottle with EtOH (96%) at the bottom. All specimens were cleaned after sampling and preserved in EtOH at -20°C (Drescher et *al.*, 2016).

Morphospecies identification

From a total amount of 912 jumping spiders (Araneae: Salticidae), 677 individuals were identified to morphospecies with a Stemi 2000-Zeiss binocular microscope. Morphological identification was supported by ‘A Guide to the Spiders of Jambi (Sumatra, Indonesia) - Identification Key to Common Families and Images of the EFForTS collection (Z02)’ (Ramos et *al.*, 2019), containing detailed photography of all jumping spider morphospecies from canopy fogging in the study site in 2013 and comparison to the original morphotypes. 235 juveniles, many newly hatched, were excluded from the analysis as morphological characters for determination were not developed.

Environmental and ecological variables

Environmental and ecological data originate from various EFForTS subprojects which conducted research on the exact same core plots. Temperature (°C) (Meijide et *al.*, 2018), relative humidity (%) (Meijide et *al.*, 2018), aboveground biomass (AGB) (Mg/ha) (Guillaume, 2019), Stand Structural complexity (SSCI) (Ehbrecht 2017), canopy openness (%) (Drescher et *al.*, 2016) and land use intensity index (LUI) (Brinkmann et *al.*, 2019) were tested on their possible influence on jumping spider richness and diversity.

Below-canopy Temperature (°C) and relative humidity (%) were measured for every core plot with a Thermohygrometer (Galltec Mela, Bondorf, Germany), installed at 2m height, from April 2013 to March 2016 (Meijide et *al.*, 2018). Analyses will be executed with mean values for both parameters. Canopy openness (%) of the core plots was measured with a spherical densitometer. Four readings, according to the cardinal directions, were performed in 16 locations in each of the 32 plots. Average values for the four cardinal direction readings were calculated and used as one measurement (Drescher et *al.*, 2016). Aboveground biomass (AGB) (Mg/ha) was calculated with allometric equations, using tree diameter, height and wood specific gravity as parameters. Parameters were measured between August and September 2012, in each core plot for trees and oil palms with a DBH (diameter at breast height) at 1,3m of at least 10cm. (Guillaume, 2019). To quantify the canopy structure, a FARO Focus terrestrial laser scanner (Faro Technologies Inc., Lake Mary, USA) placed on a tripod, at 1.3 m height, (above underwood) centered in each plot, scanned 3D structures of woody components and foliage to provide data for calculations on the stand structural complexity (SSCI). Calculation of the SSCI used the method proposed by Ehbrecht et *al.* (2017). The Land use index (LUI) hints to the extent of land management and was calculated with the method of Blüthgen et *al.* (2012), for core plots of oil palm, rubber and jungle rubber. The LUI comprises information on the quantities of fertilizer (industrial and cow dung), herbicide treatment, liming with $CaCO_3$ and the number of planted trees per hectare (Brinkmann et *al.*, 2019). LUI is zero for forest plots.

Diversity analysis

Analysis of species diversity was conducted in R v3.6.2 (R Core Team 2019), using the working packages vegan, multcomp, GGally and limma (Oksanen et *al.*, 2019; Hothorn et *al.*, 2008; Schloerke, 2018, Ritchie et *al.*, 2015). Mean abundance including undetermined juveniles (individuals per m^2), species richness (S), and the inverse Simpson Index (1/D) (Hill, 1973) were calculated for each plot. One-way analyses of variance (ANOVA) was followed by multiple comparisons with Tukey's HSD using Holm's adjustment (Holm, 1973) to infer significant differences among the four land use types for each index. Data inspection using the Shapiro-Wilk test (Wilk, 1973) indicated that species richness and the inverse Simpson Index meet the requirement of linear models, while abundance required log transformation. Rank abundance curves (Whittaker, 1965; implemented in RankAbund, Hartke 2019) were generated for each land use type to display relative species abundances. Venn's Diagrams were produced to illustrate species overlap between land use systems and landscapes.

Detrended Correspondence Analysis (DCA) indicated no definite linear or unimodal species response (first axis length 3.4). However, abundance data with many zeroes are often best analyzed with unimodal methods (Zheng et *al.*, 2015), so Non-metric Multidimensional scaling (NMDS) and Canonical Correspondence Analysis (CCA) were selected. NMDS ran with five dimensions, 0.098 stress, abundance data and Bray-Curtis dissimilarity, selected by the highest value using the function rankindex implemented in 'vegan', to create a two-dimensional representation of ecological distances among species in the four land use types. Multivariate analysis of variance (MANOVA) was used to test whether land use significantly predicts the species pattern in the NMDS. MANOVA also calculated Wilk's Lambda, which describes the percentage of variance that cannot be explained by a given factor, i.e. land use. CCA was conducted to describe the distribution of jumping spiders constrained to the environmental data. Prior to analysis, linear relationships between environmental variables were tested with standardized data using the function decostand implemented in vegan. Pairwise Pearson Correlations (r) were significant between all environmental variables (Appendix, Figure A1). Based on the almost perfectly linear correlation ($r = 0.94$) between relative humidity and mean temperature, relative humidity was excluded from the environmental constraints used in CCA. A global model containing all explanatory variables was significant under one-way ANOVA, so forward selection was used to rank environmental variables according to their importance

(Blanchet et *al.*, 2008). Forward selection used the alpha significance level and the adjusted coefficient of multiple determination (R^2_a), calculated in the global model, as stopping criteria (Blanchet et *al.*, 2008) and ran for 999 permutations. The variance inflation factor for each constraint indicated intermediate linear dependencies and no redundancy with a maximum value of 3.9 for the forward selection model (Akinwande et *al.*, 2015).

DNA extraction

DNA extraction was carried out for 152 jumping spider individuals from 69 out of 70 identified morphospecies. One morphospecies represented by a single individual was excluded from the genetic analysis as tissue removal would have obstructed future morphological work. For morphospecies represented by at least four individuals, three individuals were used for molecular analysis. Less abundant morphospecies are represented by two replicates or a single individual in the genetic analysis. For DNA extraction, I used both legs of the third leg pair and kept the remaining body as voucher individuals, which are deposited in the collections of the J.F Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Germany, for further examination. DNA extraction of leg tissue was performed with the Agencourt DNAdvance Kit (Beckman Coulter, Krefeld, Germany), following the manufacturers protocol. Legs were individually transferred into 94 µl lysis buffer and manually ruptured with a sterile plastic pestle. Afterwards, 2µl of Chitinase (1mg/ml Sigma-Aldrich, Taufkirchen, Germany) was added and lysate was incubated for 10 minutes on a shaking thermo-block at 37°C. Thereafter, 5µl of Proteinase K (20µg/µl, Genaxxon, Ulm, Germany) was added and samples were incubated for 5 hours on shaking thermo-block at 55°C. The lysed material was transferred without any tissue remains to an AB-1127 plate (ThermoFisher Scientific, Dreieich, Germany) and processed on the automated robot system Biomek 3000 (Beckman Coulter, Krefeld, Germany) using the standard protocol and an elution volume of 100 µl. Two gene regions were amplified and sequenced, i.e. the nuclear-encoded large subunit (28S) ribosomal repeat (~750bp) and the ~1100 bp mitochondrially-encoded cytochrome oxidase I (COI). The Polymerase Chain Reaction (PCR) reaction mix of 25 µl volume contained 2 µl of template DNA, 12.5 µl of SuperHot PCR mastermix (Genaxxon, Ulm, Germany), 1 µl of magnesium chloride (25mM) and 1 µl of each primer (10 pmol/µl; see Table 1 for primer details).

Table 1. Overview of primers used for amplification of the 28S and COI gene regions.

Gene region	Primer name	Primer sequence (5'- 3')	Source
COI	COI_C1-J-1718 "SPID" forward"	GGAGGATTTGGAAATTGATTAGTTCC	Simon et *al.*, 1994
COI	COI_C1-N-2776_reverse	GGATAATCAGAATATCGTCGAGG	Hedin and Maddison, 2001
COI	LCO1490	GGTCAACAAATCATAAAGATATTGG	Folmer et *al.*, 1994
COI	HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	Folmer et *al.*, 1994
28S	28S "O" forward	GAAACTGCTCAAAGGTAAACGG	Hedin and Maddison, 2001
28S	28S "C" reverse	GGTTCGATTAGTCTTTCGCC	Hedin and Maddison, 2001

An alternative PCR reaction mix for samples that failed to amplify were again processed using primers and 12.5 µl KAPA HiFi HotStart ReadyMix (KAPA BIOSYSTEMS, Cape Town, South Africa), 2µl template DNA and 0.75µl for each primer. For COI, both PCR reactions were first performed with the primer pair suggested by Maddison & Simon and repeated with the primer pair proposed by Folmer et *al*. (Tab. 1) for samples that could not be amplified. The PCR cycling conditions had an initial activation step at 95°C for 15 minutes, 35 amplification cycles (denaturation at 95°C for 45 s, annealing at 55°C for 45 s for the ribosomal repeat (28S) and 52°C for 45 s for cytochrome oxidase I (COI), elongation at 72°C for 45 s) and a final elongation step at 72°C for 60 s. PCR products were send for purification and sequencing in forward and reverse direction to SeqLab (Microsynth, Göttingen, Germany).

Sequence analysis

Quality check of sequences was conducted in Geneious Prime 2019 (http://www.geneious.com) and ambiguous positions were corrected using the electropherograms. For the COI gene region, a total of 142 consensus sequences, representing 64 of the 69 morphospecies used in DNA-extraction, were gathered and analyzed. Consensus sequences for the ribosomal repeat region 28S counted 125 sequences and 59 morphospecies in the analysis (See Appendix, Table A3 for an overview of all acquired sequences in this study). Multiple sequence alignment for the nuclear ribosomal 28S consensus sequences was performed with default settings using the 'Clustal Omega' tool in Geneious Prime 2019. Consensus sequences for the coding, mitochondrial cytochrome oxidase I (COI) region were loaded into BioEdit (Hall, T.A., 1999), set into the appropriate protein reading frame, translated and aligned using the ClustalW multiple sequence alignment parameters of 15 for gap opening and 6 for gap extension (Thompson et *al*., 1994).

Automatic Barcode Gap Discovery (ABGD)

The Automatic Barcode Gap Discovery (ABGD) is a procedure that aims to significantly infer the gap between intraspecific- and interspecific diversity, called ‘barcode gap’. Accordingly, genetic pairwise differences are partitioned into hypothetical species, using a range of prior intraspecific divergence to infer a model-based, one-sided confidence limit for the intraspecific and interspecific divergence from sequence data (Puillandre et *al.*, 2011). This barcoding approach was used to check whether the determined morphospecies were congruent with molecular entities. Here, I used the ABGD web version available at (https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html) and the single gene alignments and limited the range of intraspecific variation from Pmin = 0.001 (a single-nucleotide difference) to Pmax = 0.1. Minimum gap width (X) was set to 1.0, the Kimura two parameters model was set to compute the distance matrix and the remaining parameters were set to default. Species grouping for the 28S and COI gene regions were checked for similarities and further compared with the results of morphological identification.

Phylogenetic trees and community structure

Tree reconstruction was done for a set of 55 candidate species determined by the combined results of morphology based identification and ABGD (Appendix, Table A4). Candidate species were represented by one sequence with highest quality per morphospecies, and the new 28S and COI datasets were again aligned using ClustalW in Geneious Prime and BioEdit with the same parameters as mentioned above.

Sequence alignments were loaded in R v3.6.2 (R Core Team 2019) as FASTA files and the best fitting model of sequence evolution was evaluated by the Akaike Information Criterion (AIC) using the modelTest function provided in the R package phangorn (Schliep, 2010). Best model fit for 28S and COI was the Generalised Time-Reversible Model (GTR+I+G) (Tavaré, 1986). Phylogenetic trees were calculated with Baysesian inference in MrBayes 3.2.7 (Huelsenbeck and Ronquist, 2001) using 2 independent runs of 4 chains each, the GTR+I+G model of sequence evolution with nst = 6 and rates = invgamma, MCMC = 2500000 generations and a relative burnin of 25%. Additionally, Maximum Likelihood trees were calculated for comparison with the ‘phangorn' package in R using the same model of sequence evolution as for Bayesian inference and bootstrapping with 5000 replicates. Trees were visualized in FigTree v.1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

Phylogenetic trees for COI produced no resolved phylogeny with the Bayesian inference. Also, Maximum Likelihood trees showed bootstrap values of high uncertainty around 0 at several internal nodes, so 28S phylogenetics were used for further analysis. Investigation of the community assembly structure was done using the packages picante and multcomp (Kembel et *al.*, 2010; Hothorn et *al.*, 2008). Phylogenetic diversity (PD) (Faith, 1992), Net Relatedness Index (NRI) and Nearest Taxon Index (NTI) (Webb et *al.*, 2002) was calculated for all 32 plots using the community matrix of species abundances and the Bayesian inference phylogenetic tree of the 28S gene region only (Appendix, Figure A2).

Phylogenetic diversity (PD) equals the sum of the lengths of all branches on the phylogenetic tree that span the members of a species set (Faith, 1992), i.e. each plot in this study and was calculated with the ‘pd’ function. Additionally, PD gives insight on the evolutionary history of species assemblages and is argued to comprise information on phenotypic variations of species e.g. traits (Faith, 1992; Cadotte, 2008). To investigate phylogenetic clustering and overdispersion of jumping spider communities, NRI and NTI were calculated as standardized effect sizes of the mean pairwise phylogenetic distance (MPD) and of mean nearest taxon distances (MNTD), respectively for each plot. Both metrics were tested against the null model ‘independent swap’, which randomizes the community data with the independent swap algorithm (Gotelli, 2000), while maintaining species occurrence frequency and species richness. Standardised effect sizes of MPD and MNTD were calculated with the functions ‘ses.mpd’ for NRI and ‘ses.mntd’ for NTI using 999 runs and 1000 iterations, respectively. As MPD and MNTD are equivalent to -NRI and NTI, both distances were multiplied by -1. To test if phylogenetic clustering and overdispersion were significant in each of the four land use types, NRI and NTI values for core plots of forest, jungle rubber, rubber and oil palm were combined and t-tests were conducted for each land use type and metric against a null hypothesis of random assembly (mean variance 0). Significant deviances from 0 represent phylogenetic clustering for positive mean values and phylogenetic overdispersion for negative mean values. One-way ANOVAs followed by Holms corrected Tukey’s HSD tests were run to test for significant differences in values of NRI and NTI among the four land use systems.

Results

Diversity and community composition

Morphology based identification of 677 individuals (235 juveniles excluded) resulted in 70 different morphospecies. The majority of morphospecies was present in both investigated landscapes with 41 shared morphospecies. The Bukit Duabelas landscape contained 18 unique morphospecies while the Harapan landscape had 11 exclusive morphospecies (Fig. 3a). Many of these morphospecies found in exclusively one landscape were single findings, i.e. single individuals were found for 11 exclusive morphospecies in the Bukit Duabelas landscape and 5 in the Harapan landscape. With regard to land use systems, 28 morphospecies were found exclusively in jungle rubber and/or forest whereas monocultures of rubber and/or oil palm comprised roughly half of that with 15 species (Fig. 3b). Only six species were present in all of the investigated land use systems.

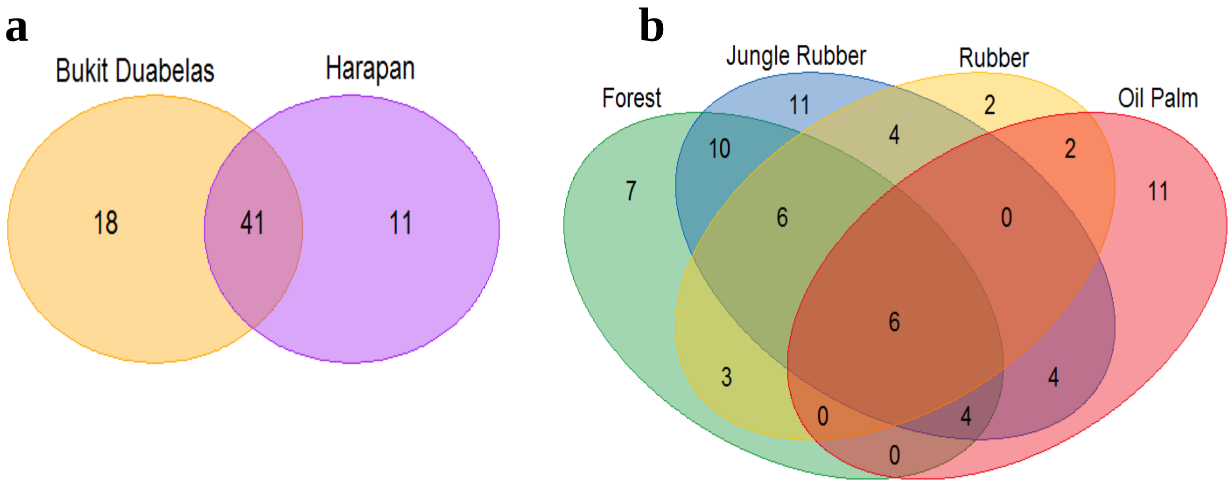

Figure 3 a, b. Venn diagrams showing numbers of arboreal jumping spider morphospecies for the two landscapes Bukit Duableas (yellow) and Harapan (purple) and the four land use systems forest (green), jungle rubber (blue), rubber (yellow) and oil palm (red) in both landscapes in Jambi, Indonesia.

Ranked species abundances of canopy spiders indicated differences among communities from the different the land use systems (Fig. 4). This was confirmed by ANOVA, which revealed significant differences in the shape of rank abundance curves ($F_{[3]} = 17.21$, $p < 0.001$). As per the Akaike Information Criterion AIC, ranked abundances in forest and jungle rubber fitted best to the Mandelbrot model, while the preemption model fit best for rubber, and the Zipf model fitted best for oil palm. Ranked abundance slopes for jungle rubber were significantly different from slopes for rubber and oil palm (both $p < 0.001$), while slopes for forest were only different from rubber ($p < 0.05$, all p values from pairwise Tukey HSD tests after Holm's correction). Slopes from jungle rubber and forest were not different, as were the slopes in oil palm and rubber.

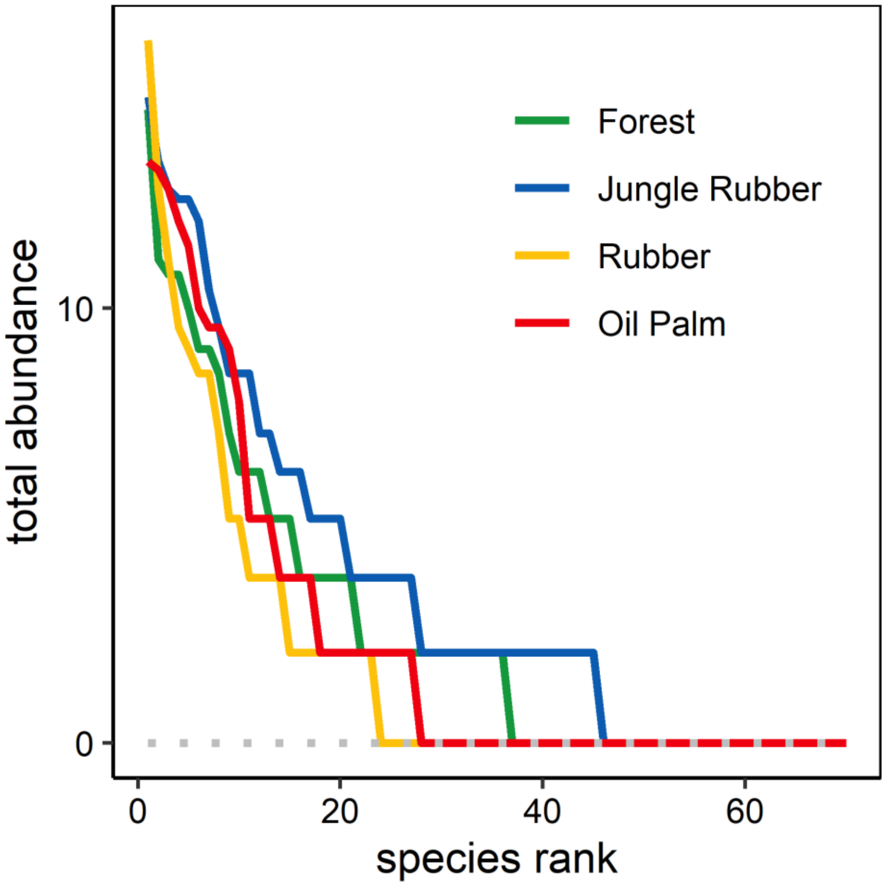

Figure 4. Rank abundance curves of arboreal jumping spiders for four land use systems forest (green), jungle rubber (blue), rubber (yellow) and oil palm (red) in Jambi, Sumatra.

Abundance (N/m²) of arboreal jumping spiders was not affected by land use ($F_{[3,28]} = 1.89$, $p > 0.05$) or landscape ($F_{[1,27]} = 3.77$, $p > 0.05$) (Fig. 5). Jungle Rubber had the highest abundance of jumping spiders with an average of $N_J/m^2 = 0.99 \pm 0.34$ individuals per m², compared to the lowest abundance in rubber plantations ($N_R/m^2 = 0.64 \pm 0.28$, mean ± s.d., respectively). Forest and oil palm had very similar abundances with $N_F/m^2 = 0.75 \pm 0.27$ individuals/m² and $N_O/m^2 = 0.77 \pm 0.35$ individuals/m² each.

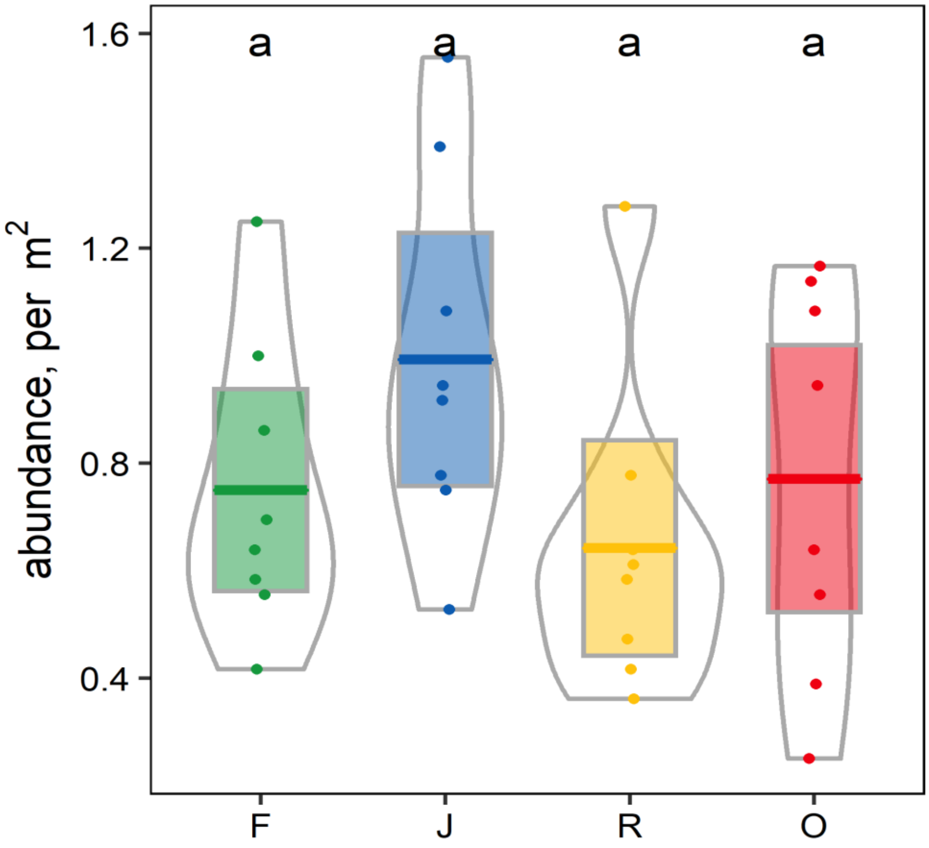

Figure 5. Abundance (individuals/m²) of arboreal jumping spider communities (Salticidae) across four land use systems in Jambi, Sumatra (F = forest, J = jungle rubber, R = rubber, O = oil palm). Boxplots show mean (horizontal line), 95% confidence interval (box), density distribution (grey lines) and raw data (dots). Different letters above boxplots indicate significant differences after multiple comparisons (Holms corrected Tukey HSD, p<0.05).

Species richness (S) of canopy jumping spiders significantly changed with land use ($F_{[3,28]}$ = 12.551,pr(>chi) = 0.0015) but did not significantly differ between landscapes ($F_{[1,27]}$ = 12.523,pr(>chi) = 0.867) (Fig. 3). Overall, species richness per plot ranged from five species in BO3 (Bukit Duabelas oil palm plot 3) to the 18 species in BJ4. (Fig.6). On average, species richness was highest in jungle rubber (S_J = 13 ± 2.5, mean ± s.d.), which was significantly higher than in rubber (S_R = 7 ± 1.41) and oil palm (S_O = 9 ± 2.51). Species richness in forest was intermediate (S_F = 10 ± 1.92) and not significantly different from any of the other land use systems.

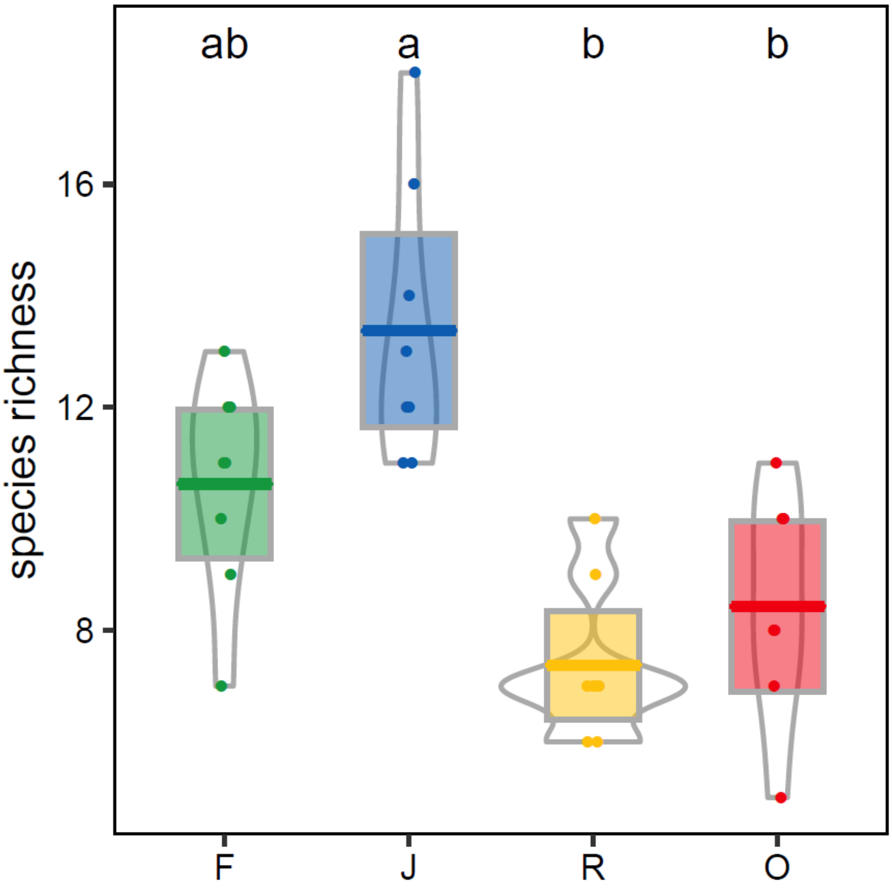

Figure 6. Species richness of arboreal jumping spider communities (Salticidae) across four land use systems in Jambi, Sumatra (F = forest, J = jungle rubber, R = rubber, O = oil palm). Boxplots show mean (horizontal line), 95% confidence interval (box), density distribution (grey lines) and raw data (dots) Different letters above boxplots indicate significant differences after multiple comparisons (Holms corrected Tukey HSD, p<0.05).

Inverse Simpson diversity 1/D was significantly affected by land use ($F_{[3,28]} = 6.90$, $p = 0.0013$) but not by landscape ($F_{[1,27]} = 0.43$, $p = 0.51$). Forest and jungle rubber had the highest Inverse Simpson diversity ($1/D_F = 7.7 \pm 1.5$ and $1/D_J = 8.2 \pm 2.4$, respectively, mean ± s.d.) which was significantly higher than Inverse Simpson diversity in rubber ($1/D_R = 4.6 \pm 1.2$). Inverse Simpson diversity in oil palm ($1/D_O = 6.2 \pm 1.4$) was intermediate and not significantly different from Inverse Simpson diversity in any of the other land use systems (Fig. 7).

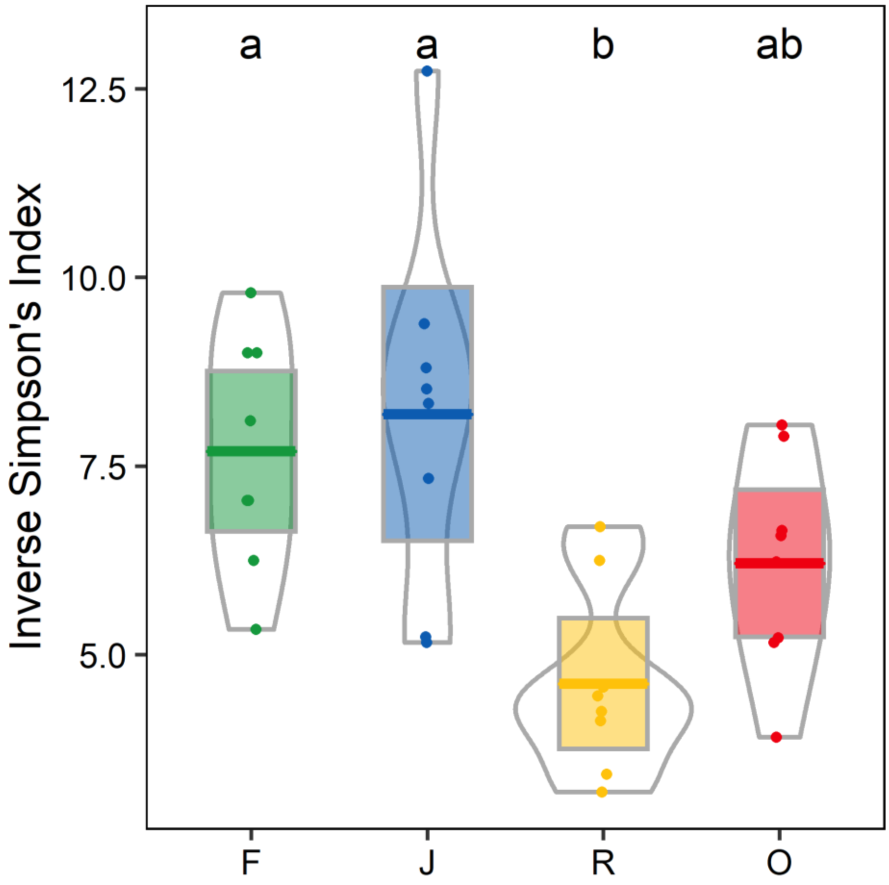

Figure 7. Inverse Simpson's Index of arboreal jumping spider communities (Salticidae) across four land use systems in Jambi, Sumatra (F = forest, J = jungle rubber, R = rubber, O = oil palm). Boxplots show mean (horizontal line), 95% confidence interval (box), density distribution (grey lines) and raw data (dots). Different letters above boxplots indicate significant differences after multiple comparisons (Holms corrected Tukey HSD, $p<0.05$).

Community compositions of arboreal jumping spiders significantly differed between land use systems ($F[_{3,15}] = 13.97$, $p<0.001$) with an unexplained variation of 1.8 % (Wilks' Lambda = 0.018) but not between landscapes ($F[_{1,5}] = 2.21$, $p>0.05$, Wilks' Lambda = 0.674) (Fig. 8). Jumping spider communities of the land use systems separated into three distinct groups with overlapping communities of jungle rubber and forest. Jumping spider communities in oil palm and rubber clearly differ from each other and to communities of forest and jungle rubber. However, communities in rubber, forest and jungle rubber overlap to some extent, which is indicated by six species located in between the cluster of these land use systems (Fig. 3, 8). Common jumping spiders from oil palm plantations are rare in the other land use systems. Jungle rubber and forest contained most of the sampled arboreal jumping spiders with high overlap in species occurrences as already indicated by the Venn's Diagram (Fig. 4).

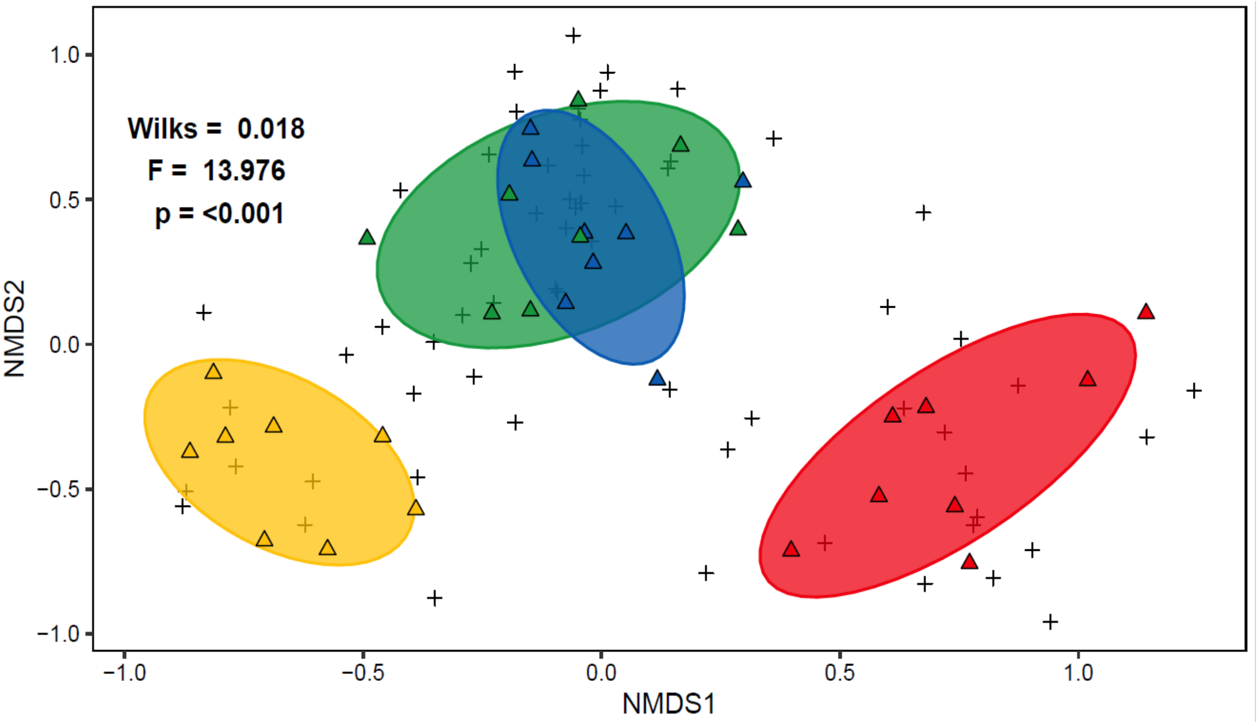

Figure 8. Non-Metric Multi-Dimensional Scaling (NMDS) of arboreal jumping spiders (+) in plots (Δ) of forest (green), jungle rubber (blue), oil palm (red) and rubber (yellow) based on Bray-Curtis dissimilarity (stress = 0.098, k = 5). Ellipses represent 75% confidence intervals for each land use system.

Canonical correspondence analysis (CCA) used environmental constraints to visualize arboreal jumping spider communities in the investigated land use systems on two significant axes. The first axis of the CCA accounted for 3.4% of the variance and separated land use systems across a gradient of land use intensity and canopy openness. The second axis explained 2.1% of variance and used the gradient of aboveground biomass (Fig. 9) to separate land use systems. Results of forward selection analysis indicated that the Land Use Intensity index (LUI, Brinkmann et *al.*, 2019) (F = 2.39, $p<0.001$, $R^2a = 0.0433$ ~ 4,3%), aboveground biomass (Guillaume, 2019) (F = 1.53, $p<0.01$, $R^2a = 0.0157$ ~ 1.57%) and canopy openness (Drescher et *al.*, 2016) (F = 1.46, $p < 0.05$, $R^2a = 0.0157$~ 1.57%) significantly influenced the assemblages of arboreal jumping spiders with a combined explained variance of ~ 7.4%. Temperature and SSCI did not significantly improve the model.

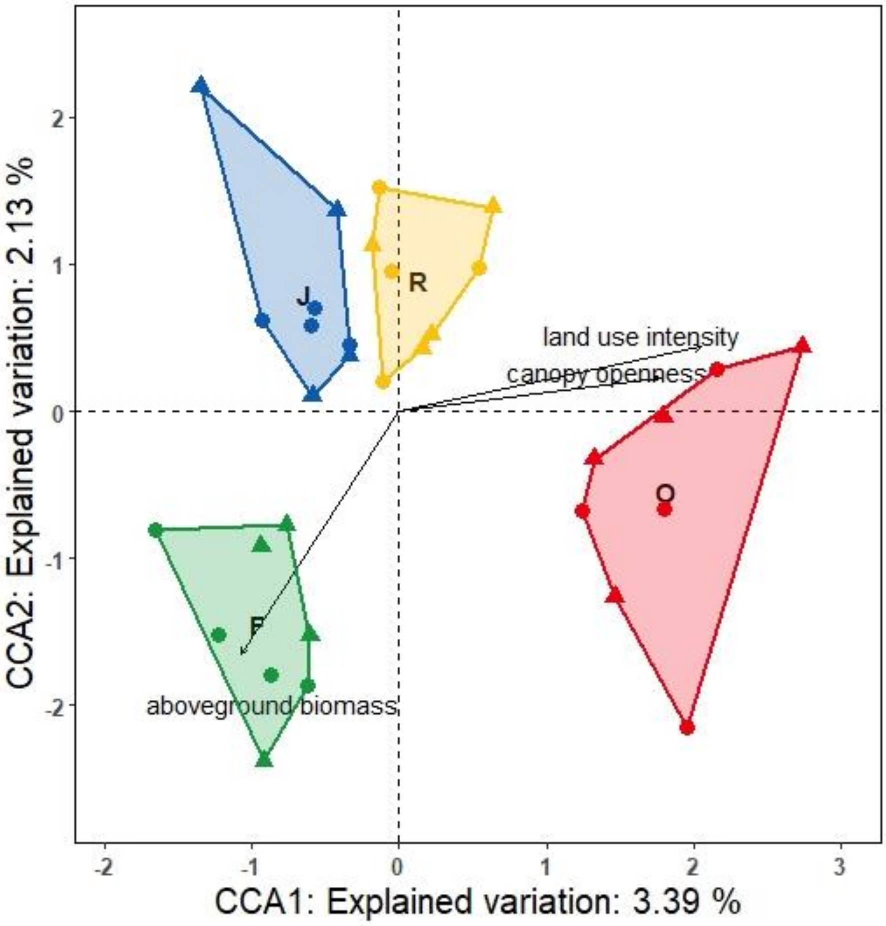

Figure 9. Canonical correspondence analysis (CCA) biplot of relationships between arboreal jumping spider assemblages and environmental constraints in plots of forest (F), jungle rubber (J), rubber (R), oil palm (O) within the two landscapes Bukit Duabelas (circle) and Harapan (triangle). Environmental variables with significant influence on canopy jumping spiders under ANOVA are shown as arrows. Explained variation in % is the adjusted coefficient of multiple determination (R^2a)

Plots of oil palm, with the highest degree of land use intensity and canopy openness among the land use systems are located on the right half of the CCA. In contrast, forest plots with low disturbance, dense canopies and high aboveground biomass locate to the lower left of the CCA biplot. Rubber locates to the upper middle of the ordination as it shows the lowest values for aboveground biomass but is not thoroughly structured by land use intensity and high canopy openness like oil palm. Jungle rubber is intermediate for all three environmental variables and is in the upper left corner of the CCA. However, aboveground biomass, canopy openness and land use intensity solely are not suitable to explain the differences in arboreal jumping spider assemblages with only 7.4% variance explained.

Community phylogenetics

Phylogenetic diversity in arboreal jumping spiders was significantly affected by land use ($F_{[3,28]} = 11.17$, $p<0.001$) but not by landscape ($F_{[1,27]} = 2.32$, $p>0.1$). Highest phylogenetic diversity was found in jungle rubber ($PD_J = 1.8 \pm 0.26$, mean ± s.d.), followed by forest ($PD_F = 1.45 \pm 0.28$) in rubber ($PD_R = 1.14 \pm 0.21$) and oil palm ($PD_O = 1.07 \pm 0.36$) (Fig. 10). Phylogenetic diversity patterns differed from morphological diversity in that oil palm was the land use system with the lowest diversity (Fig. 10) instead of rubber (Fig. 7).

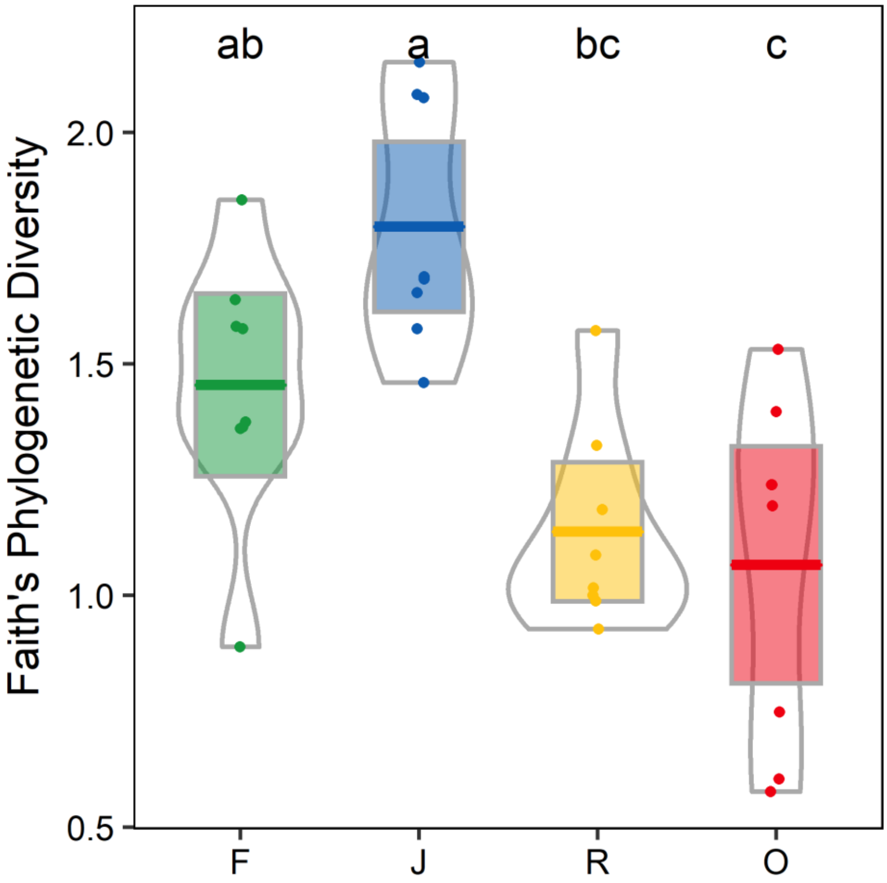

Figure 10. Faith's Phylogenetic Diversity (PD) of arboreal jumping spider communities (Salticidae) among four land use systems in Jambi, Sumatra (F = forest, J = jungle rubber, R = rubber, O = oil palm). Boxplots show mean (horizontal line), 95% confidence interval (box), density distribution (grey lines) and raw data (dots). Different letters above boxplots indicate significant differences after multiple comparisons (Holms corrected Tukey HSD, p<0.05)

Net relatedness NRI was marginally significantly affected by land use ($F_{[3,28]}$ = 20.462, p = 0.059) under ANOVA. Pairwise comparisons, i.e. Tukeys HSD test followed by holms correction indicated a significant difference (p<0.05) between NRI values in rubber (NRI_R = -0.48 ± 0.58, mean ± s.d.) and oil palm (NRI_O = 0.71 ± 1) (Fig. 11). Mean NRI values for forest (0.04 ± 0.88) and jungle rubber (-0.16 ± 0.89) did not differ significantly from the other land use systems. One sided t-tests against 0, suggesting random assembly, were not significant in any of the land use systems. However, average NRI in rubber was found to be marginally significantly below zero, while average NRI in oil palm was marginally significantly above zero (Fig. 11). The nearest taxon index (NTI) showed an overall pattern similar to NRI but revealed significant phylogenetic clustering of arboreal jumping spiders in oil palm (one sided t-test; NTI_O = 0.85 ± 1; t = 2.36, df = 7, p < 0.05). NTI was also significantly higher in oil palm than in the other land use systems. In contrast, jumping spider communities in jungle rubber were overdispersed (NTI_R = -0.78 ± 0.89; t = -2.47; df = 7, p < 0.05). Rubber and forest showed no significant deviance from random expectations. Results for NTI in oil palm and jungle rubber synergize well with the observed pattern of phylogenetic diversity (Fig. 10).

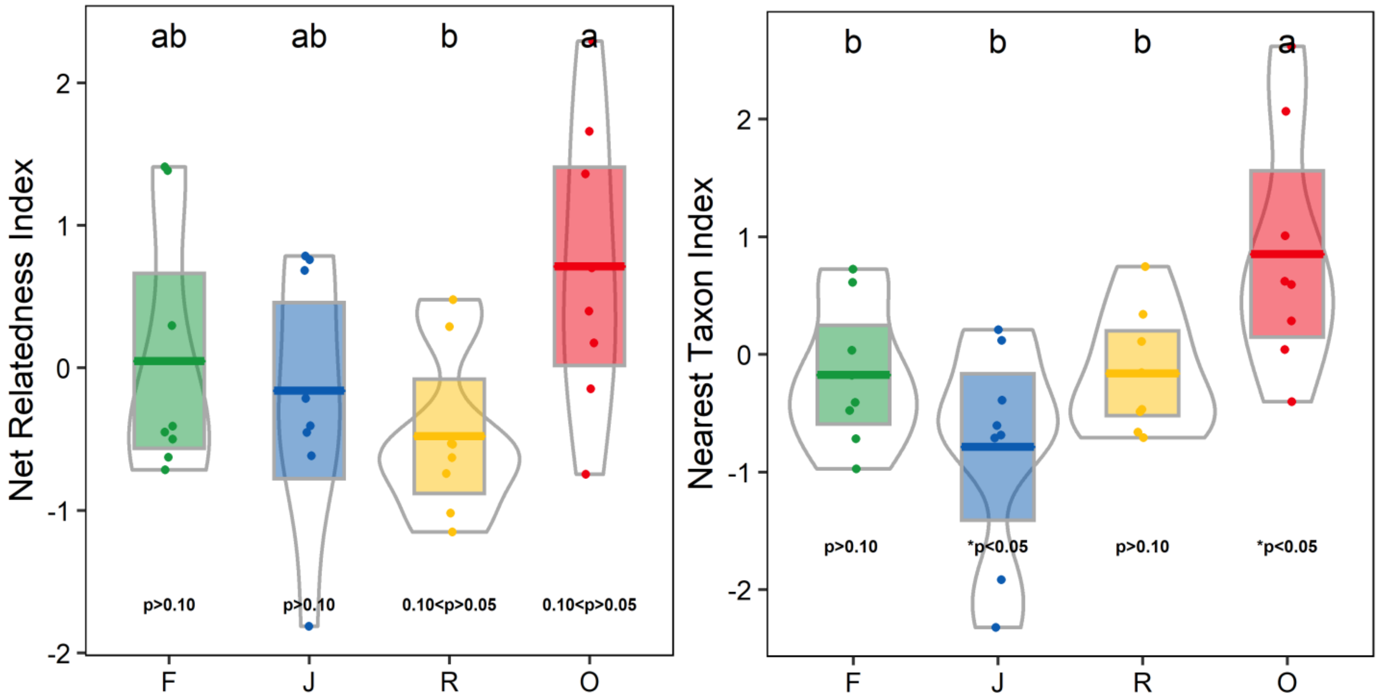

Figure 11. Net Relatedness Index (NRI, left) and Nearest Taxon Index (NTI, right) of arboreal jumping spider communities between land use systems in Jambi, Sumatra (F = forest, J = jungle rubber, R = rubber, O = oil palm). Boxplots show mean (horizontal line), 95% confidence interval (box), density distribution (grey lines) and raw data (dots). Different letters above boxplots indicate significant differences after multiple comparisons (Holms corrected Tukey HSD, p<0.05). One sided t-test results against 0 (random assembly) are shown under each box. Values of NRI and NTI become positive for phylogenetic clustering, negative for phylogenetic overdispersion and 0 in random assemblies.

Discussion

Diversity of arboreal jumping spiders

The results of this study show that the abundance of arboreal jumping spiders is independent of land use (Fig. 5). High frequencies in both monocultures result from a few dominating species, which is confirmed by the steep slopes in the rank abundance curves of rubber and oil palm (Fig. 4). This is in concert with findings by Zheng et *al.* (2015) who found a few very abundant species in rubber plantations of China but no overall decline in spider abundance compared to tropical seasonal rainforests. Additionally, Shochat et *al.* (2004) revealed that human land use alterations lead to increased abundances of one or a few adaptable spider species.

In contrast to my first hypothesis, species richness in forest was not significantly higher than in the monocultures. Instead, jungle rubber showed the highest species richness, which was not different from forest, but significantly higher than oil palm and almost twice that of rubber plantations. This pattern is reminiscent of the intermediate disturbance hypothesis (IDH), which predicts the highest species diversity under intermediate levels of disturbances (Conell, 1978). Jungle rubber plots are characterized by past and current logging activities while preserving an overall forest-like structure and form a heterogeneous transition system between forest and monocultures (Gouyon, 1993; Kotowska et *al.*, 2015). Secondary succession promoted by logging might explain the species rich communities of jumping spiders that can be found in these dynamic habitats. Studies in tropical forests of East Asia revealed a similar effect of intermediate disturbance levels on the diversity of spiders (Tsai et *al.*, 2006; Chen & Tso, 2004). However, IDH did not fit to the patterns of Inverse Simpson Index, as Inverse Simpson is less sensitive to rare species (Hill, 1973). Also, IDH does not explain diversity patterns if all spider families of the same sampling were included (Ramos, in prep.), suggesting that this may be a pattern unique to the salticids.

I could also confirm that forest conversion to monocultures entails shifts in the community composition of jumping spiders (Fig 8.). Differences in habitat complexity are known to be a determinant factor for the structure and diversity of spider communities with the general consensus that complex and diverse habitats promote greater spider diversity (Floren & Reinhold, 2005; Pinkus-Rendon et *al.*, 2006). Canopies of oil palm and rubber form monotonous entities of low complexity (Zheng et *al.*, 2015; Zemp et *al.*, 2019) compared to the canopies of forest or jungle rubber. As a consequence, jumping spider communities in monocultures are fundamentally different in their compositions and comprise less species overall. One important parameter of canopy complexity is described by canopy openness, which significantly impacted jumping spider assemblages in the correspondence analysis (Fig. 9), as expected. Investigated plots of rubber and oil palm showed a significant decrease in canopy cover and contrast the dense canopies with multiple layers in forest and jungle rubber (Drescher et *al.*, 2016). Furthermore, the results show that aboveground biomass, which increases with tree age and height, was significant for the community compositions of salticid spiders. A study conducted in European spruce forests also confirmed the importance of tree age on spider assemblages (Purchart et *al.*, 2013). This synergizes with the results of this study and the investigation of Floren et *al.* (2011), which revealed tree age as an important factor for canopy spiders in Southeast Asian rainforests. Lastly, the land use intensity index LUI, derived from frequencies of fertilization, herbicide spraying and planted oil palms/rubber trees (Brinkmann et *al.*, 2019) was significant for the investigated assemblages of arboreal jumping spiders. However, the statistical effect is biased by the fact that LUI for all forest plots was set to 0 by Brinkmann et *al.* (2019) (Appendix, Table A1), which leaves no variation among forest plots and increases the LUI gradient of the other land use systems relative to forest. Moreover, LUI is not an independent environmental variable per se, as land use change is part of the index as the number of planted palms/trees. A significant correlation with my data is therefore not surprising. However, I decided to keep LUI as an explanatory variable in the light of comparability, as communities of many non-canopy taxa investigated in the ‘EFForTS’ project respond to it (Drescher, pers. comm).

Overall, I assumed a negative effect of habitat simplification and changing temperatures on the diversity of salticid spider communities. Even though the presented results hint to the importance of habitat structure, the low explanatory power averts clear dependencies between the analyzed environmental variables and the diversity of jumping spider communities. Additionally, the expected effect of temperature on salticid spiders could not be proven. This clearly demonstrates the complexity of the investigated systems and moreover that there are more unrevealed environmental factors that lead to the observed changes in community compositions between monocultures and more natural systems.

Community phylogenetics of arboreal jumping spiders

In my second hypothesis I expected that lowland rainforest transformation to monocultures would result in habitat filtering as the main mechanism in the community assembly of canopy salticids.

Low phylogenetic diversity observed in oil palm and rubber (Fig. 10) suggests that jumping spider communities may have lower phenotypic diversity in monocultures. This is congruent with effects of land use on the phylogenetic diversity in bee and plant communities (Grab et *al.*, 2019; Turley et *al.*, 2016). Conversely, forest and in particular jungle rubber had higher phylogenetic diversity which might hint to less overlap in functional traits and a potential increase in the contribution of species to ecosystem functions via niche complementarity (Srivastava et *al.*, 2012). Results for the nearest taxon index (NTI) revealed phylogenetically clustered communities in oil palm and suggest environmental filtering as the predominant process that structures communities (Fig. 11). The rapidly altered environment in oil palm plantations might function as a filter through which only closely related species can pass (Srivastava et *al.*, 2012). Interestingly, this effect was not observed in rubber plantations and suggests the peculiarity of oil palm plantations which is supported by the clearly different species compositions in oil palm compared to the other land use systems (Fig. 8). On the other hand, NTI for jumping spider communities in jungle rubber suggested phylogenetic overdispersion and therefore competition as the main factor influencing community assembly of salticid spiders. This contradicts the general assumption that frequent disturbances of moderate intensity are associated with low levels of interspecific competition, as proposed in the intermediate disturbance hypothesis IDH (e.g. Connel, 1978; Catford et *al.*, 2012). Communities in forest showed random assemblies based on both NTI and NRI. According to NRI, assemblages in rubber were marginally significant towards phylogenetic overdispersion which hints to competition as the structuring mechanism of community assembly. This contrasts with the findings of habitat filtering in the community assembly of oil palm and my assumption of phylogenetically clustered communities in monoculture plantations. The contradicting results for rubber and jungle rubber demonstrate the difficulty to draw meaningful conclusions on the community assembly based on NRI and NTI. In fact, recent literature shows that both metrics are far from undisputed as measures of community assembly. Narwani et *al.* (2011) criticized the categorical nature of assumptions underlying NRI and NTI. The assumptions that environmental filtering infers phylogenetic and phenotypic clustering while competition infers phylogenetic and phenotypic (over-)dispersion, may be unwarranted, as habitat filtering and competition can interact with each other by additive or opposing effects

(Gerhold et *al.*, 2015; Mayfield & Levine, 2010). Thus, my second hypothesis has to be rejected. Mainly the inexplicable results in rubber accompanied by the recent criticism of NRI and NTI give cause to question the validity of the used indices to answer my research questions, despite the fact that I observed evidence for phylogenetically clustered communities in oil palm plantations.

Conclusion

This thesis reveals how rainforest transformation to monocultures is affiliated with reduced Salticid spider richness and diversity, altered community composition but unchanged abundance. Interestingly, the data indicated a positive effect of intermediate disturbance along the lines of the intermediate disturbance hypothesis. However, as jungle rubber is continuously transformed to land uses of higher revenue, it is unlikely that this type of agroforestry will constitute a conservation refuge for canopy jumping spiders in Jambi Province or elsewhere. Habitat simplification showed an overall minor impact on the observed shifts in salticid spider communities between monocultures and more natural systems and deviations in temperature had no impact at all. Community assembly patterns could not be revealed beyond reasonable doubt. A variety of studies within the EfforTS project have targeted the importance of primary forest and jungle rubber to preserve diversity of various taxa and ecosystem functions in the tropical landscapes of Jambi (Paoletti, 2018, Drescher et al., 2016, Grass et *al.*, 2020). My thesis adds to the previous work in EFForTS by showing the impact of forest transformation on the diversity and community assembly on the most diverse spider family worldwide.

Statement of Authorship

I confirm that the work presented in this thesis titled “Diversity and community assembly structure of canopy jumping spiders (Araneae: Salticidae) across a land use gradient in Jambi, Sumatra”, has been performed and interpreted solely by myself.

Except where specific references are made in the main text of the thesis, this thesis contains no material extracted in whole or part from a thesis, dissertation or research paper presented by me for another degree or diploma. No other person’s work (published or unpublished) has been used without due acknowledgement in the main text of this thesis. This thesis has not been submitted for the award of any other degree or diploma in any other tertiary institution.

I confirm that the printed copies are identical to the electronic ones.

Göttingen, March 24, 2020 ______________________

André Junggebauer

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Appendix

Table A1: Environmental variables for mean temperature (°C), relative humidity (%), Canopy openness (%), SSCI, land use intensity and aboveground biomass (Mg/ha) measured in various EFForTS subprojects for the investigated core plots.

Table A2: Community matrix with counts for all 70 identified morphospecies of jumping spiders (Araneae: Salticidae) in the 32 investigated plots.

Table A3: Overview of (non-)successfully amplified sequences of 152 jumping spider individuals for the 28S and COI gene regions and species / genus identity for each sequence according to the nucleotide database provided by the National Center for Biotechnology Information (NCBI) using the online version of the Basic Local Alignment Search Tool (BLAST).

Table A4: Automatic Barcode Gap Discovery (ABGD) grouping results and the resulting set of 55 jumping spider candidate species used for Bayesian inference tree.

Figure A1: Pearson correlations between all pairs of environmental variables used in the canonical correspondence analysis (CCA) given as values and scatter plots.

Figure A2: Bayesian inference tree for the alignment of the 28S gene region used for calculation of Phylogenetic Diversity (PD), Net Relatedness Index (NRI) and Nearest Taxon Index (NTI).

Table A1. Set of environmental variables measured in various EFForTS subprojects for the investigated core plots among the four land use systems forest (F), jungle rubber (J), oil palm (O) and rubber (R) including temperature (°C) (Meijide et *al.*, 2018), relative humidity (%) (Meijide et *al.*, 2018), canopy openness (%) (Drescher 2016), Stand Structural complexity (SSCI) (unpublished, courtesy of C.D Zemp), land use intensity index (LUI) (Brinkmann et *al.*, 2019) and aboveground biomass (AGB) (Mg/ha) (Guillaume, 2019). Core plots abbreviations read as e.g. Bukit Duabelas (B) forest (F) Core plot 1 (1) = BF1.

Core Plot	**System**	**Mean Temperature [°C]**	**Mean Humidity [%]**	**Canopy Openness [%]**	**SSCI**	**Land Use Intensity**	**Aboveground Biomass [Mg/ha]**
BF1	F	24,5	97,25	2,36	7,96658636	0	230,71
BF2	F	24,48	98,62	3,35	7,2410152	0	262,05
BF3	F	24,42	96,01	2,04	5,98302119	0	305,66
BF4	F	24,85	94,57	2,22	4,69665408	0	370,78
BJ3	J	25,42	91,38	6,39	5,82578912	1,29	129,67
BJ4	J	24,92	94,56	5	7,27426503	1,29	127,73
BJ5	J	25,25	93,32	5,85	7,08820258	1,32	137,9
BJ6	J	25,2	93,09	4,69	8,16455361	1,27	125,63
BO2	O	25,95	88,76	23,41	3,53404987	4,14	72
BO3	O	25,12	92,92	13,29	3,93442672	4,38	98,47
BO4	O	25,45	91,42	12,97	4,23240605	4,95	90,51
BO5	O	25,67	90,86	20,61	3,46767654	2,79	82,35
BR1	R	25,45	91,29	14,49	6,14565827	4,22	77,62
BR2	R	25,53	89,46	12,68	3,91653378	1,67	39,36
BR3	R	25,78	86,9	10,9	3,40427784	4,38	36,19
BR4	R	25,64	89,76	19,43	3,79920161	3,88	46,65
HF1	F	24,88	96,39	2,37	6,01422436	0	364,58
HF2	F	24,91	95,11	2,56	7,20489073	0	320,21

HF3	F	24,67	98,1	2,22	7,44659678	0	362,28
HF4	F	24,92	95,47	3,19	7,89024268	0	430,07
HJ1	J	25,37	91,91	11,39	5,98806891	1,4	100,01
HJ2	J	25,06	93,75	6,85	6,60144309	1,12	103,56
HJ3	J	25,13	91,5	6,76	6,80363883	1,1	116,97
HJ4	J	25,13	93,61	7,48	7,27208404	0,95	103,92
HO1	O	25,35	91,12	15,2	3,6413133	4,23	126,23
HO2	O	25,49	91,28	11,8	2,72193373	3,39	124,91
HO3	O	25,18	91,24	11,95	3,02293422	7,87	104,82
HO4	O	25,39	90,94	15,91	3,46611829	6,04	88,27
HR1	R	25,37	92,25	8,18	5,39099789	3	77,14
HR2	R	25,62	90,01	14,76	6,35352644	1,65	48,2
HR3	R	25,4	91,16	15,72	3,99904595	5,12	69,48
HR4	R	25,59	90,4	11,52	5,14686619	2,51	83,86

Figure A1: Pearson correlation coefficients between all pairs of environmental variables used in the canonical correspondence analysis (CCA) given as values and scatter plots. A perfectly linear relationship between two variables is described by a coefficient of 1.

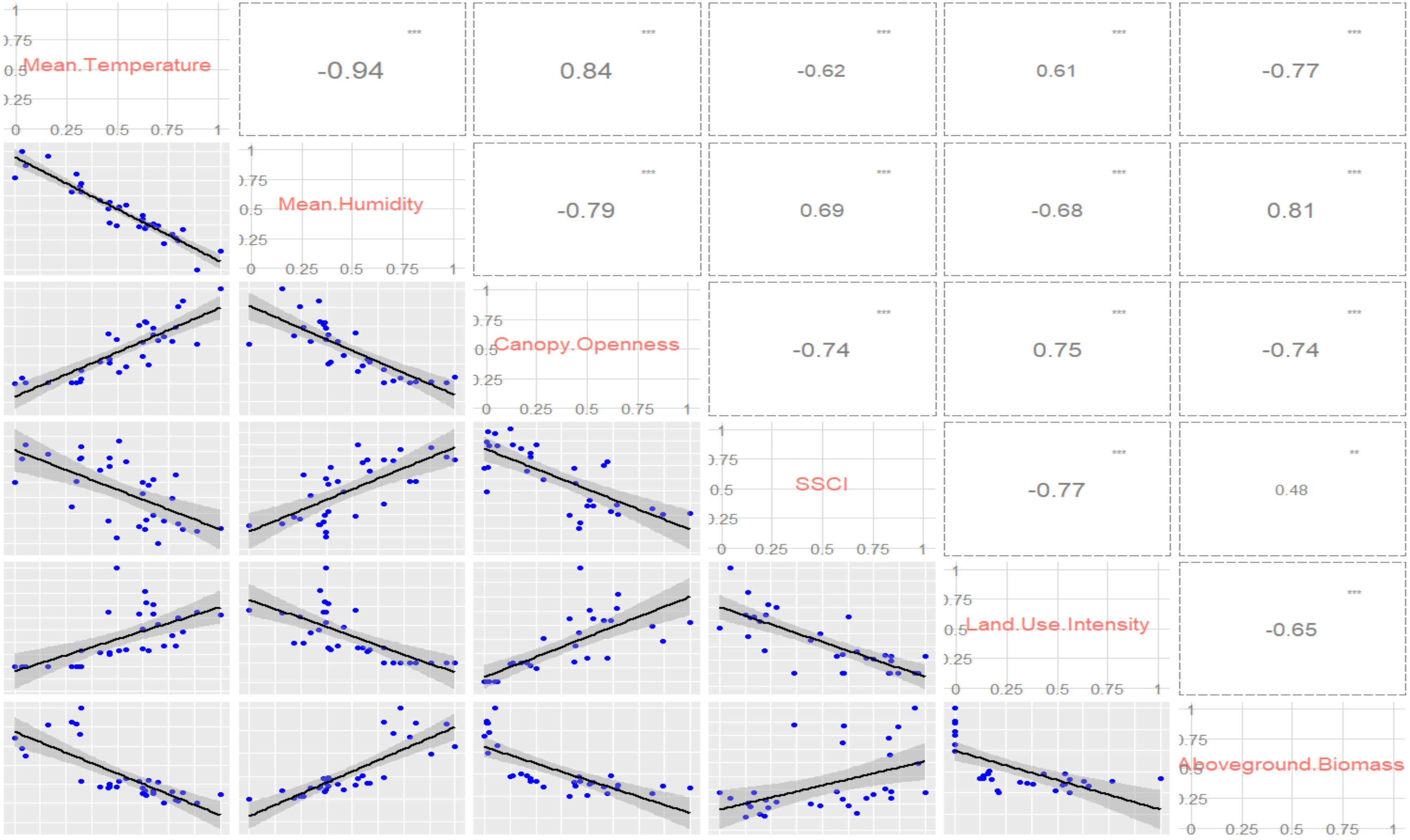

Table A2. Community matrix with counts for all 70 identified morphospecies of jumping spiders in the core plots of four investigated land use systems forest (F), jungle rubber (J), oil palm (O) and rubber (R). Core plots abbreviations read as e.g. Bukit Duabelas (B) forest (F) Core plot 1 (1). The last column ('Sum') gives the sum for each morphospecies across all investigated plots. The penultimate line (Salticid spiders per plot determined to morphospecies) sums up all the individuals used for morphology based identification in each plot, with a total of 677 jumping spiders identified to morphospecies. The last line comprises all 912 collected salticid spiders including undetermined juveniles which was exclusively used to analyze the abundance. A more detailed database is provided in the digital appendix.

Morpho-species	BF 1	BF 2	BF 3	BF 4	BJ 3	BJ 4	BJ 5	BJ 6	BO 2	BO 3	BO 4	BO 5	BR 1	BR 2	BR 3	BR 4	HF 1	HF 2	HF 3	HF 4	HJ 1	HJ 2	HJ 3	HJ 4	HO 1	HO 2	HO 3	HO 4	HR 1	HR 2	HR 3	HR 4	Sum
AraSalt 001	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 002	0	0	2	2	1	2	0	0	5	4	0	0	0	0	0	0	1	4	2	1	0	0	1	3	8	2	1	1	0	0	0	0	**40**
AraSalt 003	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	**4**
AraSalt 005	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**4**
AraSalt 006	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0	0	0	0	0	0	0	0	0	**10**
AraSalt 008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 009	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	0	1	0	0	0	0	0	0	0	0	0	0	0	**13**
AraSalt 010	4	4	2	1	4	6	2	6	0	0	0	1	5	5	2	4	0	3	8	7	9	2	1	1	3	7	1	10	5	3	13	5	**124**
AraSalt 011	0	0	0	0	0	0	11	1	0	0	0	0	1	1	1	0	2	1	0	1	0	0	4	0	0	0	0	0	0	0	2	2	**27**
AraSalt 015	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**2**
AraSalt 017	0	0	0	0	0	3	1	2	2	3	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2	3	4	0	0	0	0	**23**
AraSalt 018	0	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**5**
AraSalt 019	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	**4**
AraSalt 021	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2	2	0	0	0	0	0	0	0	1	0	**7**
AraSalt 022	0	1	0	0	2	2	2	1	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	1	0	0	0	0	0	0	**13**

AraSalt 023	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 024	2	0	0	1	0	5	6	1	1	0	1	0	0	1	0	9	2	1	2	0	2	4	0	0	1	0	0	0	1	1	0	1	**42**
AraSalt 025	1	0	1	0	1	4	9	4	0	0	0	0	0	1	0	1	0	3	2	1	1	0	2	1	0	0	0	2	0	0	0	0	**34**
AraSalt 026	0	0	0	2	0	4	2	0	0	0	1	0	0	0	2	0	2	0	0	0	0	0	0	3	0	0	0	0	0	1	0	0	**17**
AraSalt 027	0	0	1	1	1	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	**11**
AraSalt 028	0	0	1	4	3	3	7	1	0	0	0	0	0	0	0	0	1	2	0	5	0	0	0	4	0	0	0	0	0	0	2	0	**33**
AraSalt 029	0	0	0	0	1	0	1	0	0	0	0	0	3	2	0	1	0	0	1	0	0	0	1	1	0	0	0	0	6	0	4	3	**24**
AraSalt 030	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 032	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	**2**
AraSalt 040	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	**2**
AraSalt 043	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	1	0	0	1	0	0	0	0	0	6	0	0	**13**
AraSalt 045	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	**2**
AraSalt 046	0	0	0	0	0	1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	2	0	0	**10**
AraSalt 047	1	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	2	1	0	1	2	0	1	0	0	0	0	0	0	0	0	**11**
AraSalt 049	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	**2**
AraSalt 050	1	0	0	0	0	0	0	1	0	0	3	0	0	0	0	0	1	0	0	0	1	0	1	0	0	1	2	3	2	0	1	0	**17**
AraSalt 053	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	1	2	0	0	3	0	2	0	0	0	0	**12**
AraSalt 054	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	**4**
AraSalt 055	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**3**
AraSalt 056	0	0	0	0	1	4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	**7**
AraSalt 058	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	**2**
AraSalt 059	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	**6**
AraSalt 060	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	**3**

AraSalt 061	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	**2**
AraSalt 063	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	**6**
AraSalt 065	0	0	0	0	0	0	0	0	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	6	4	0	0	0	0	0	0	**14**
AraSalt 066	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	**7**
AraSalt 067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	**1**
AraSalt 069	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	13	2	1	0	0	0	0	0	0	0	0	**19**
AraSalt 073	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 074	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 077	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 078	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**3**
AraSalt 080	0	0	0	0	1	0	1	0	0	2	6	0	0	0	0	0	0	0	1	0	0	0	0	2	6	3	0	2	0	0	0	1	**25**
AraSalt 081	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 082	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	**3**
AraSalt 083	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	**6**
AraSalt 084	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	**3**
AraSalt 086	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	5	0	0	0	0	**10**
AraSalt 087	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	**6**
AraSalt 090	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	**2**
AraSalt 091	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	**1**
AraSalt 092	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	3	2	0	0	0	0	0	0	0	0	1	0	0	0	**9**
AraSalt 095	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	**2**
AraSalt 098	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 099	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**

AraSalt 100	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**2**
AraSalt 102	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	**2**
AraSalt 104	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	**2**
AraSalt 106	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**2**
AraSalt 107	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 108	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 109	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**3**
AraSalt 110	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
AraSalt 111	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1**
Salticid spiders per plot determined to morpho-species	18	18	10	18	18	44	48	26	18	11	23	9	14	13	10	18	14	24	26	24	23	33	19	20	28	25	13	34	24	15	26	13	677
Abundance of all Salticid spiders collected (including juveniles)	21	25	15	20	19	50	56	34	20	14	34	9	17	15	13	22	23	31	45	36	33	39	27	28	39	41	23	42	26	28	46	21	912

Table A3: Sequencing results for 152 jumping spider individuals for the 28S and COI gene regions. Abbreviations in Voucher-ID read as e.g. Bukit Duabelas (B), forest (F), core plot (2), fogging location (3), fogging year (2017), Araneae (Ara), Salticidae (Salt), morphospecies 005 (005), replicate number a particular morphospecies (3) = BF2.3.2017AraSalt005.3. Successful amplifications are shown by the length of the amplicons in base pairs (bp) for both gene regions COI and 28S, respectively. Each sequence was compared with the nucleotide database provided by the National Center for Biotechnology Information (NCBI) using the online version of the Basic Local Alignment Search Tool (BLAST) available at https://blast.ncbi.nlm.nih.gov/Blast.cgi.

family	Morphospecies	Genus (BLAST)	Voucher-ID	COI [bp]	BLAST hit [species]	BLAST hit [Acc.no.]	BLAST hit % identity	28S [bp]	BLAST hit [species]	BLAST hit [Acc.no.]	BLAST hit % identity	region
Salticidae	AraSalt005	---	BF2.3A.2017AraSalt005.3	---	---	---	---	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt069	---	HJ2.1A.2017AraSalt069.2	---	---	---	---	805	*Simaetha sp.*	JX145746.1	92.83	Harapan
Salticidae	AraSalt102	---	HJ1.3A.2017AraSalt102.2	---	---	---	---	---	---	---	---	Harapan
Salticidae	AraSalt106	---	BF2.3A.2017AraSalt106.1	---	---	---	---	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt107	---	BF2.3A.2017AraSalt107.1	---	---	---	---	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt108	---	BF1.3A.2017AraSalt108.1	---	---	---	---	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt110	---	BO4.1A.2017AraSalt110.1	---	---	---	---	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt009	*Anarrhotus* (Plexippinae)	HJ1.2A.2017AraSalt009.3	1070	*Anarrhotus fossulatus*	EU815605.1	96	766	*Anarrhotus fossulatus*	EU815492.1	99.87	Harapan

Salticidae	AraSalt010	*Anarrhotus* (Plexippinae)	HJ1.1A.2017AraSalt010.1	910	*Anarrhotus fossulatus*	EU815605.1	95.82	---				Harapan
Salticidae	AraSalt017	*Anarrhotus* (Plexippinae)	HO4.2A.2017AraSalt017.1	1076	*Anarrhotus fossulatus*	EU815605.1	95.79	714	*Anarrhotus fossulatus*	EU815492.1	99.87	Harapan
Salticidae	AraSalt017	*Anarrhotus* (Plexippinae)	HO2.1A.2017AraSalt017.2	1060	*Anarrhotus fossulatus*	EU815605.1	95.79	714	*Anarrhotus fossulatus*	EU815492.1	99.86	Harapan
Salticidae	AraSalt017	*Anarrhotus* (Plexippinae)	HO2.3A.2017AraSalt017.3	1092	*Anarrhotus fossulatus*	EU815605.1	95.89	714	*Anarrhotus fossulatus*	EU815492.1	99.86	Harapan
Salticidae	AraSalt003	*Bathippus* (Euphoyrina)	BJ5.3.2017AraSalt003.2	678	*Zora spinimana*	KY270091.1	87.42	826	*Bathippus pahang*	KC615401	99.63	Bukit Duabelas
Salticidae	AraSalt002	*Bavia* (Hisponinae)	BJ4.1.2017AraSalt002.1	710	*Bavia cf. aericeps*	EU815603	94.12	802	*Bavia cf. aericeps*	EU815490	96.40	Bukit Duabelas
Salticidae	AraSalt002	*Bavia* (Hisponinae)	BF4.2A.2017AraSalt002.2	1113	*Bavia cf. aericeps*	EU815603	92,29	824	*Bavia cf. aericeps*	EU815490	96,66	Bukit Duabelas
Salticidae	AraSalt002	*Bavia* (Hisponinae)	BF4.2A.2017AraSalt002.3	976	*Bavia cf. aericeps*	EU815603	92.34	818	*Bavia cf. aericeps*	EU815490	96.66	Bukit Duabelas
Salticidae	AraSalt090	*Carrhotus* (Heliophaninae)	BJ4.1.2017AraSalt090.1	1102	*Carrhotus sp.*	AY297408.1	90.33	814	*Carrhotus xanthogramma*	JN817037.1	98.49	Bukit Duabelas
Salticidae	AraSalt090	*Carrhotus* (Heliophaninae)	HJ2.3A.2017AraSalt090.2	1091	*Carrhotus sp.*	AY297408.1	90.26	799	*Carrhotus xanthogramma*	JN817037.1	98.98	Harapan
Salticidae	AraSalt043	*Cytaea* (Euphorinae)	HR2.2A.2017AraSalt043.2	1044	*Cytaea oreophila*	KC615665.1	99.08	760	*Cytaea oreophila*	KC615422.1	98.68	Harapan
Salticidae	AraSalt043	*Cytaea (Euphorinae)*	HR2.3A.2017AraSalt043.3	685	*Selenops sp.*	HM575969.1	87.79	759	*Cytaea oreophila*	KC615422.1	98.39	Harapan
Salticidae	AraSalt043	*Emathis (Euophryinae)*	HF2.1A.2017AraSalt043.1	699	*Evarcha arcuata*	KY269941.1	88.91	814	*Emathis gombak*	KC615424.1	98.87	Harapan

Salticidae	AraSalt010	*Epeus* (Plexippinae)	HJ1.3A.2017AraSalt010.2	694	*Epeus alboguttatus*	NC_042829.1	91.03	696	*Epeus sp.*	AY297248.1	98.56	Harapan
Salticidae	AraSalt010	*Epeus* (Plexippinae)	HJ1.3A.2017AraSalt010.3	922	*Epeus alboguttatus*	NC_042829.1	90.63	---	---	---	---	Harapan
Salticidae	AraSalt015	*Epeus* (Plexippinae)	BR3.3A.2017AraSalt015.1	1101	*Epeus sp.*	AY297378.1	93.78	818	*Epeus sp.*	AY297248.1	100	Bukit Duabelas
Salticidae	AraSalt015	*Epeus* (Plexippinae)	BJ3.2.2017AraSalt015.2	1106	*Epeus sp.*	AY297378.1	94.09	796	*Epeus sp.*	AY297248.1	99.73	Bukit Duabelas
Salticidae	AraSalt003	equivocal (likely new sequence)	BJ6.2.2017AraSalt003.1	1113	*Myrmarachne japonica*	JN817283	87,01	827	*Bathippus pahang*	KC615401	99.25	Bukit Duabelas
Salticidae	AraSalt005	equivocal (likely new sequence)	BJ6.2.2017AraSalt005.1	1089	*Noegus aff. Rufus*	AY297372.1	87.30	768	*Heratemita alboplagiata*	AF327934	91.25	Bukit Duabelas
Salticidae	AraSalt005	equivocal (likely new sequence)	BF1.1A.2017AraSalt005.2	1022	*Myrmarachne endoi*	LC193964.1	87.31	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt006	equivocal (likely new sequence)	HF4.2A.2017AraSalt006.1	684	*Cocalus sp.*	KU893267.1	88.73	794	*Gelotia cf. bimaculata*	KM033158.1	94.71	Harapan
Salticidae	AraSalt008	equivocal (likely new sequence)	HJ2.3A.2017AraSalt008.1	1097	*Cf. Thorelliola sp.*	AY297393.1	89.76	753	*Hakka himeshimensis*	JN817058.1	95.64	Harapan
Salticidae	AraSalt009	equivocal (likely new sequence)	BF3.3A.2017AraSalt009.1	714	*Myrmarachne spissa*	KY587560.1	89.02	788	*Pancorius sp.*	JX145780.1	98.26	Bukit Duabelas
Salticidae	AraSalt009	equivocal (likely new sequence)	BF3.3A.2017AraSalt009.2	683	*Myrmarachne robusta*	MK154679.1	89.93	759	*Pancorius sp.*	JX145780.1	99.85	Bukit Duabelas
Salticidae	AraSalt011	equivocal (likely new sequence)	BJ5.1.2017AraSalt011.2	723	*Sitticus floricola*	KY269335.1	90.87	707	*Heratemita alboplagiata*	AF327934	89.92	Bukit Duabelas

Salticidae	AraSalt011	equivocal (likely new sequence)	BJ5.1.2017AraSalt011.3	714	*Sitticus floricola*	KY269335.1	90.87	792	*Heratemita alboplagiata*	AF327934	90.49	Bukit Duabelas
Salticidae	AraSalt011	equivocal (likely new sequence)	BJ5.1.2017AraSalt011.1	686	*Sitticus floricola*	KY269335.1	90.87	760	*Heratemita alboplagiata*	AF327934	90.52	Bukit Duabelas
Salticidae	AraSalt018	equivocal (likely new sequence)	BF3.2A.2017AraSalt018.1	1105	*Myrmarachne sp.*	JX145681.1	89.07	822	*Junxattus daiqini*	KC615553.1	95.94	Bukit Duabelas
Salticidae	AraSalt018	equivocal (likely new sequence)	BF4.1A.2017AraSalt018.2	1080	*Myrmarachne sp.*	JX145681.1	88.96	826	*Junxattus daiqini*	KC615553.1	95.79	Bukit Duabelas
Salticidae	AraSalt019	equivocal (likely new sequence)	BF2.3A.2017AraSalt019.1	694	*Ligurra latidens*	KY017896.1	87.50	813	*Emathis gombak*	KC615424.1	100	Bukit Duabelas
Salticidae	AraSalt019	equivocal (likely new sequence)	BF2.2A.2017AraSalt019.2	---	---	---	---	816	*Emathis gombak*	KC615424.1	99.87	Bukit Duabelas
Salticidae	AraSalt022	equivocal (likely new sequence)	BJ5.3.2017AraSalt022.1	695	*Sitticus floricola*	KX537297.1	88.91	801	*Viciria praemandibularis*	JX145757.1	99.62	Bukit Duabelas
Salticidae	AraSalt022	equivocal (likely new sequence)	BJ4.1.2017AraSalt022.2	720	*Sitticus floricola*	KX537297.1	88.91	819	*Viciria praemandibularis*	JX145757.1	99.88	Bukit Duabelas
Salticidae	AraSalt022	equivocal (likely new sequence)	BJ4.1.2017AraSalt022.3	700	*Sitticus floricola*	KX537297.1	88.91	826	*Viciria praemandibularis*	JX145757.1	99.63	Bukit Duabelas
Salticidae	AraSalt023	equivocal (likely new sequence)	BJ5.2.2017AraSalt023.1	679	*Myrmarachne sp.*	MF804727.1	88.77	792	*Schenkelia modesta*	EU815487.1	98.94	Bukit Duabelas
Salticidae	AraSalt027	equivocal (likely new sequence)	BJ3.3.2017AraSalt027.1	711	*Ptocasius weyersi*	KU893272.1	93.00	794	*Telamonia masinloc*	AY297256.1	98.67	Bukit Duabelas

Salticidae	AraSalt027	equivocal (likely new sequence)	BF3.3A.2017AraSalt027.2	712	*Ptocasius weyersi*	KU893272.1	93.00	806	*Anarrhotus fossulatus*	EU815492.1	98.93	Bukit Duabelas
Salticidae	AraSalt027	equivocal (likely new sequence)	HO2.3A.2017AraSalt027.3	712	*Ptocasius weyersi*	KU893272.1	92.98	801	*Anarrhotus fossulatus*	EU815492.1	98.67	Harapan
Salticidae	AraSalt028	equivocal (likely new sequence)	BJ5.3.2017AraSalt028.1	1057	*Soesilarishius ruizi*	KC615713.1	88.17	788	*Plexippinae* sp.	JX145803.1	98.91	Bukit Duabelas
Salticidae	AraSalt028	equivocal (likely new sequence)	BJ5.3.2017AraSalt028.2	1061	*Soesilarishius ruizi*	KC615713.1	88.18	785	*Plexippinae* sp.	JX145803.1	98.78	Bukit Duabelas
Salticidae	AraSalt032	equivocal (likely new sequence)	BO4.3A.2017AraSalt032.1	1091	*Telamonia masinloc*	AY297385.1	90.42	807	*Siler sp.*	KY888734.1	99.71	Bukit Duabelas
Salticidae	AraSalt032	equivocal (likely new sequence)	HO4.1A.2017AraSalt032.2	1091	*Telamonia masinloc*	AY297385.1	90.42	798	*Siler sp.*	KY888734.1	99.71	Harapan
Salticidae	AraSalt045	equivocal (likely new sequence)	HJ3.2A.2017AraSalt045.1	1091	*Evaracha hoyi*	AY297379.1	89.73	770	*Hakka himeshimensis*	JN817058.1	95.40	Harapan
Salticidae	AraSalt045	equivocal (likely new sequence)	HJ3.2A.2017AraSalt045.2	1077	*Evaracha hoyi*	AY297379.1	89.73	813	*Hakka himeshimensis*	JN817058.1	95.77	Harapan
Salticidae	AraSalt046	equivocal (likely new sequence)	HR2.2A.2017AraSalt046.1	1062	*Mantisatta longicauda*	AY297399.1	87.46	772	*Plexippinae sp.*	JX145803.1	98.87	Harapan
Salticidae	AraSalt047	equivocal (likely new sequence)	BJ5.2.2017AraSalt047.1	714	*Myrmarachne cf. melanocephala*	KY587558.1	89.30	765	*Ballus chalybeius*	EF514398.1	89.40	Bukit Duabelas

Salticidae	AraSalt047	equivocal (likely new sequence)	HF2.1A.2017AraSalt047.2	662	*Myrmarachne cf. melanocephala*	KY587558.1	88.89	---	---	---	---	Harapan
Salticidae	AraSalt049	equivocal (likely new sequence)	BR4.1A.2017AraSalt049.1	1096	*Myrmarachne endoi*	LC193957.1	90.64	785	*Anarrhotus fossulatus*	EU815492.1	98.40	Bukit Duabelas
Salticidae	AraSalt049	equivocal (likely new sequence)	HF4.1A.2017AraSalt049.2	1078	*Hyllus tuberculatus*	EU815622.1	90.49	801	*Schenkelia modesta*	EU815487.1	98.54	Harapan
Salticidae	AraSalt054	equivocal (likely new sequence)	HF3.3A.2017AraSalt054.1	689	*Ligurra latidens*	KY017896.1	91.17	810	*Heratemita alboplagiata*	AF327934.1	92.42	Harapan
Salticidae	AraSalt054	equivocal (likely new sequence)	HF2.2A.2017AraSalt054.2	710	*Ligurra latidens*	KY017896.1	91.07	813	*Heratemita alboplagiata*	AF327934.1	92.42	Harapan
Salticidae	AraSalt055	equivocal (likely new sequence)	BO5.1A.2017AraSalt055.1	687	*Ptocasius weyersi*	KU893272.1	93.00	791	*Anarrhotus fossulatus*	EU815492.1	98.92	Bukit Duabelas
Salticidae	AraSalt055	equivocal (likely new sequence)	BJ6.2.2017AraSalt055.2	664	*Ptocasius weyersi*	KU893272.1	93.28	801	*Anarrhotus fossulatus*	EU815492.1	98.67	Bukit Duabelas
Salticidae	AraSalt061	equivocal (likely new sequence)	HJ3.2A.2017AraSalt061.1	1104	*Eris militaris*	AF328000.1	89.23	801	*Folibiatus sp. Malaysia*	KC615575.1	95.00	Harapan
Salticidae	AraSalt061	equivocal (likely new sequence)	HR3.2A.2017AraSalt061.2	1077	*Eris militaris*	AF328000.1	89.23	794	*Folibiatus sp. Malaysia*	KC615575.1	95.26	Harapan
Salticidae	AraSalt063	equivocal (likely new sequence)	HR1.3A.2017AraSalt063.1	1075	*Myrmarachne assimilis*	AY297412.1	88.43	820	*Cocalus murinus*	EF419019.1	89.93	Harapan
Salticidae	AraSalt063	equivocal (likely new sequence)	BR3.3A.2017AraSalt063.2	1068	*Myrmarachne assimilis*	AY297412.1	88.33	800	*Cocalus murinus*	EF419019.1	89.93	Bukit Duabelas

Salticidae	AraSalt063	equivocal (likely new sequence)	BR3.1A.2017AraSalt063.3	1065	*Myrmarachne assimilis*	AY297412.1	88.75	804	*Cocalus murinus*	EF419019.1	89.93	Bukit Duabelas
Salticidae	AraSalt069	equivocal (likely new sequence)	HJ2.1A.2017AraSalt069.1	1071	*Orcevia keyserlingi*	KC615739.1	87.69	799	*Simaetha sp.*	JN817061.1	93.01	Harapan
Salticidae	AraSalt069	equivocal (likely new sequence)	HJ2.1A.2017AraSalt069.3	1085	*Myrmarachne sp.*	EU815616.1	87.31	812	*Simaetha sp.*	JX145746.1	92.73	Harapan
Salticidae	AraSalt077	equivocal (likely new sequence)	HF3.3A.2017AraSalt077.1	686	*Myrmarachne formicaria*	KM893989.1	90.44	799	*Telamonia vlijimi*	JN817061.1	97.19	Harapan
Salticidae	AraSalt078	equivocal (likely new sequence)	BF4.1A.2017AraSalt078.1	1082	*Agobardus cf. anormalis*	KC615636.1	90.37	790	*Telamonia vlijimi*	JN817061.1	98.45	Bukit Duabelas
Salticidae	AraSalt078	equivocal (likely new sequence)	BF4.2A.2017AraSalt078.2	1097	*Myrmarachne endoi*	LC193956.1	99.68	798	*Philodromus cespitum*	JN817023.1	86.52	Bukit Duabelas
Salticidae	AraSalt080	equivocal (likely new sequence)	BO3.1A.2017AraSalt080.1	702	*Myrmarachne japonica*	JN817283.1	89.87	803	*Telamonia vlijimi*	JN817061.1	98.58	Bukit Duabelas
Salticidae	AraSalt080	equivocal (likely new sequence)	BO4.2A.2017AraSalt080.3	702	*Myrmarachne cf. Melanocephala*	KY587558.1	90.02	799	*Telamonia vlijimi*	JN817061.1	98.46	Bukit Duabelas
Salticidae	AraSalt102	equivocal (likely new sequence)	HJ1.3A.2017AraSalt102.1	1081	*Cheliceroides longipalpis*	NC_041120.1	90.09	753	*Laufeia concava*	KC615554.1	94.18	Harapan
Salticidae	AraSalt066	equivocal (only one sequence with equivocal similarity)	HR1.2A.2017AraSalt066.1	1089	*Mantisatta longicauda*	AY297399.1	87.23	---	---	---	---	Harapan

Salticidae	AraSalt066	equivocal (only one sequence with equivocal similarity)	HR1.2A.2017AraSalt066.2	1075	*Mantisatta longicauda*	AY297399.1	87.34	---	---	---	---	Harapan
Salticidae	AraSalt066	equivocal (only one sequence with equivocal similarity)	HR1.2A.2017AraSalt066.3	1108	*Mantisatta longicauda*	AY297399.1	87.05	---	---	---	---	Harapan
Salticidae	AraSalt073	equivocal (only one sequence with equivocal similarity)	HJ1.2A.2017AraSalt073.1	1098	*Cosmophasis micarioides*	EU815580.1	90.02	---	---	---	---	Harapan
Salticidae	AraSalt080	equivocal (only one sequence with equivocal similarity)	BO4.2A.2017AraSalt080.2	706	*Myrmarachne cf. Melanocephala*	KY587558.1	90.24	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt098	equivocal (only one sequence with equivocal similarity)	BJ3.3.2017AraSalt098.1	1112	*Agorius sp.*	LC431809.1	94.11	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt099	equivocal (only one sequence with equivocal similarity)	BJ4.1.2017AraSalt099.1	714	*Mogrus cognatus*	MK154720.1	90.27	---	---	---	---	Bukit Duabelas

Salticidae	AraSalt100	equivocal (only one sequence with equivocal similarity)	BJ4.2.2017AraSalt100.1	1123	*Myrmarachne endoi*	LC193956.1	87.13	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt028	equivocal (only one sequence with equivocal similarity)	BJ4.2.2017AraSalt028.3	1062	*Soesilarishius ruizi*	KC615713.1	88.50	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt046	equivocal (only one sequence with equivocal similarity)	HR2.2A.2017AraSalt046.2	1062	*Mantisatta longicauda*	AY297399.1	87.40	---	---	---	---	Harapan
Salticidae	AraSalt046	equivocal (only one sequence with equivocal similarity	HR1.2A.2017AraSalt046.3	1065	*Mantisatta longicauda*	AY297399.1	87.38	---	---	---	---	Harapan
Salticidae	AraSalt047	equivocal (only one sequence with equivocal similarity)	HF3.3A.2017AraSalt047.3	---				826	*Ballus chalybeius*	EF514398.1	89.26	Harapan
Salticidae	AraSalt050	equivocal (only one sequence with equivocal similarity)	BO4.2A.2017AraSalt050.3	1067	*Myrmarachne foenisex*	JX145679.1	94.80	---	---	---	---	Bukit Duabelas

Salticidae	AraSalt053	equivocal (only one sequence with equivocal similarity)	HO4.2A.2017AraSalt053.1	1084	*Phintella aequipeiformis*	LC105669.1	91.28	---	---	---	---	Harapan
Salticidae	AraSalt001	equivocal (only one sequence)	BF1.3A.2017AraSalt001.1	---				781	*Plexippinae sp.*	JX145803.1	99.32	Bukit Duabelas
Salticidae	AraSalt084	equivocal (only one sequence)	HO3.2A.2017AraSalt084.1	1104	*Myrmarachne endoi*	LC193956.1	99.78	---	---	---	---	Harapan
Salticidae	AraSalt095	equivocal (only one sequence)	BF4.2A.2017AraSalt095.1	1083	*Agobardus cf. anormalis*	KC615636.1	90.31	---	---	---	---	Bukit Duabelas
Salticidae	AraSalt095	equivocal (only one sequence)	HR4.3A.2017AraSalt095.2	1073	*Agobardus cf. anormalis*	KC615636.1	90.31	---	---	---	---	Harapan
Salticidae	AraSalt083	*Heratemita* (Marpissinae)	HO4.2A.2017AraSalt083.1	699	*Cheliceroides longipalpis*	NC_0441120.1	88.55	810	*Heratemita alboplagiata*	AF327934.1	99.33	Harapan
Salticidae	AraSalt083	*Heratemita* (Marpissinae)	BO4.2A.2017AraSalt083.2	686	*Cheliceroides longipalpis*	NC_0441120.1	88.36	815	*Heratemita alboplagiata*	AF327934.1	99.33	Bukit Duabelas
Salticidae	AraSalt083	*Heratemita* (Marpissinae)	BO4.2A.2017AraSalt083.3	689	*Cheliceroides longipalpis*	NC_0441120.1	88.28	822	*Heratemita alboplagiata*	AF327934.1	99.33	Bukit Duabelas
Salticidae	AraSalt092	*Heratemita (Marpissinae)*	BJ6.1.2017AraSalt092.1	1067	*Heratemita alboplagiata*	AF327991.1	89.20	791	*Heratemita alboplagiata*	AF327934.1	97.99	Bukit Duabelas
Salticidae	AraSalt092	*Heratemita* (Marpissinae)	BF4.2A.2017AraSalt092.2	1067	*Heratemita alboplagiata*	AF327991.1	89.20	791	*Heratemita alboplagiata*	AF327934.1	97.99	Bukit Duabelas
Salticidae	AraSalt059	*Maleius* (Euophryinae)	HJ2.2A.2017AraSalt059.1	1086	*Maileus cf. fuscus*	KC615743.1	97.40	814	*Maileus cf. fuscus*	KC615560.1	99.60	Harapan
Salticidae	AraSalt059	*Maleius* (Euophryinae)	BJ3.1.2017AraSalt059.2	1089	*Maileus cf. fuscus*	KC615743.1	97.30	807	*Maileus cf. fuscus*	KC615560.1	99.73	Bukit Duabelas

Salticidae	AraSalt059	*Maleius* (Euophryinae)	HJ2.3A.2017AraSalt059.3	709	*Sitticus rupicola*	MG047861.1	90.88	812	*Maileus cf. fuscus*	KC615560.1	99.73	Harapan
Salticidae	AraSalt006	*Mintonia* (Spartaeinae)	HF4.2A.2017AraSalt006.2	1081	*Spartaeinae sp.*	AY297363.1	87.62	818	*Mintonia cf. melinauensis*	KM033160	99.86	Harapan
Salticidae	AraSalt006	*Mintonia* (Spartaeinae)	HF4.2A.2017AraSalt006.3	1081	*Spartaeinae sp.*	AY297363.1	87.46	818	*Mintonia cf. melinauensis*	KM033160	99.46	Harapan
Salticidae	AraSalt056	Myrmarachne (Myrmarachnidae)	BJ4.1.2017AraSalt056.1	1064	*Myrmarachne wanlessi*	LC193969.1	95.79	779	*Jessica osoriana*	KR558908.1	84.88	Bukit Duabelas
Salticidae	AraSalt056	Myrmarachne (Myrmarachnidae)	BJ4.1.2017AraSalt056.2	1066	*Myrmarachne wanlessi*	LC193969.1	95.79	727	*Jessica osoriana*	KR558908.1	84.94	Bukit Duabelas
Salticidae	AraSalt056	Myrmarachne (Myrmarachnidae)	BJ4.1.2017AraSalt056.3	1074	*Myrmarachne wanlessi*	LC193969.1	95.79	787	*Jessica osoriana*	KR558908.1	84.77	Bukit Duabelas
Salticidae	AraSalt021	Myrmarachne (Myrmarachnidae)	HF2.1A.2017AraSalt021.1	1047	*Myrmarachne wanlessi*	LC193969.1	93.20	789	*Opisthoncus kochi*	EU815468.1	87.05	Harapan
Salticidae	AraSalt021	Myrmarachne (Myrmarachnidae)	HJ2.2A.2017AraSalt021.2	1063	*Myrmarachne wanlessi*	LC193969.1	93.20	---				Harapan
Salticidae	AraSalt021	Myrmarachne (Myrmarachnidae)	HJ3.2A.2017AraSalt021.3	1058	*Myrmarachne wanlessi*	LC193969.1	93.20	749	*Opisthoncus kochi*	EU815468.1	86.65	Harapan
Salticidae	AraSalt024	*Myrmarachne* (Myrmarachnidae)	BJ4.1.2017AraSalt024.1	1065	*Myrmarachne cornuta*	LC193952.1	99.13	803	*Mymrarachne cornuta*	MK716316.1	98.00	Bukit Duabelas
Salticidae	AraSalt024	*Myrmarachne* (Myrmarachnidae)	BJ4.1.2017AraSalt024.2	1055	*Myrmarachne cornuta*	LC193952.1	98.92	795	*Mymrarachne cornuta*	MK716316.1	97.98	Bukit Duabelas

Salticidae	AraSalt024	*Myrmarachne* (Myrmarachnidae)	BJ4.1.2017AraSalt024.3	1074	*Myrmarachne cornuta*	LC193952.1	99.03	733	*Mymrarachne cornuta*	MK716316.1	97.40	Bukit Duabelas
Salticidae	AraSalt025	*Myrmarachne* (Myrmarachnidae)	BJ5.2.2017AraSalt025.1	699	*Myrmarachne formicaria*	MG045726.1	91.86	789	*Myrmarachne japonica*	JN817063.1	91.38	Bukit Duabelas
Salticidae	AraSalt025	*Myrmarachne* (Myrmarachnidae)	BJ5.2.2017AraSalt025.2	723	*Myrmarachne formicaria*	MG045726.1	91.86	760	*Myrmarachne japonica*	JN817063.1	91.57	Bukit Duabelas
Salticidae	AraSalt025	*Myrmarachne* (Myrmarachnidae)	BJ5.2.2017AraSalt025.3	715	*Myrmarachne formicaria*	MG045726.1	91.86	772	*Myrmarachne japonica*	JN817063.1	91.14	Bukit Duabelas
Salticidae	AraSalt040	*Myrmarachne* (Myrmarachnidae)	HO3.2A.2017AraSalt040.1	1021	*Myrmarachne sp.*	JX145681.1	92.43	798	*Myrmarachne japonica*	JN817063.1	95.22	Harapan
Salticidae	AraSalt040	*Myrmarachne* (Myrmarachnidae)	HR1.2A.2017AraSalt040.2	720	*Myrmarachne japonica*	JN817283.1	93.02	757	*Myrmarachne japonica*	JN817063.1	95.90	Harapan
Salticidae	AraSalt050	*Myrmarachne* (Myrmarachnidae)	HO3.2A.2017AraSalt050.1	1060	*Myrmarachne cornuta*	LC193953.1	98.79	778	*Myrmarachne cornuta*	MK716316.1	97.97	Harapan
Salticidae	AraSalt050	*Myrmarachne* (Myrmarachnidae)	BJ6.1.2017AraSalt050.2	1059	*Myrmarachne cornuta*	LC193953.1	98.57	771	*Myrmarachne cornuta*	MK716316.1	97.72	Bukit Duabelas
Salticidae	AraSalt058	*Myrmarachne* (Myrmarachnidae)	HR1.2A.2017AraSalt058.1	686	*Myrmarachne sp.*	KP978606.1	91.68	788	*Myrmarachne japonica*	JN817063.1	93.77	Harapan
Salticidae	AraSalt058	*Myrmarachne* (Myrmarachnidae)	HR3.1A.2017AraSalt058.2	1035	*Myrmarachne sp.*	JX145681.1	93.90	800	*Myrmarachne sp.*	JX145755.1	98.36	Harapan
Salticidae	AraSalt067	*Myrmarachne* (Myrmarachnidae)	HO3.2A.2017AraSalt067.1	1102	*Myrmarachne assimilis*	LC193951.1	93.31	723	*Myrmarachne japonica*	JN817063.1	97.32	Harapan
Salticidae	AraSalt074	*Myrmarachne* (Myrmarachnidae)	BO2.2A.2017AraSalt074.1	1099	*Myrmarachne foenisex*	JX145679.1	95.01	687	*Myrmarachne evidens*	JX145752.1	98.40	Bukit Duabelas

Salticidae	AraSalt081	Myrmarachne (Myrmarachnidae)	BO4.3A.2017AraSalt081.1	1106	*Myrmarachne wanlessi*	LC193969.1	95.79	807	*Opisthoncus kochi*	EU815468.1	85.25	Bukit Duabelas
Salticidae	AraSalt086	*Myrmarachne (Myrmarachnidae)*	HO4.1A.2017AraSalt086.1	1061	*Myrmarachne foenisex*	JX145679.1	94.90	732	*Myrmarachne foenisex*	JX145753.1	97.95	Harapan
Salticidae	AraSalt086	*Myrmarachne (Myrmarachnidae)*	HO4.2A.2017AraSalt086.2	1063	*Myrmarachne foenisex*	JX145679.1	94.90	752	*Myrmarachne foenisex*	JX145753.1	97.99	Harapan
Salticidae	AraSalt086	*Myrmarachne (Myrmarachnidae)*	BO4.1A.2017AraSalt086.3	1053	*Myrmarachne foenisex*	JX145679.1	94.77	735	*Myrmarachne foenisex*	JX145753.1	97.94	Bukit Duabelas
Salticidae	AraSalt091	Myrmarachne (Myrmarachnidae)	HO3.1A.2017AraSalt091.1	1113	*Myrmarachne endoi*	LC193956.1	99.68	771	*Philodromus cespitum*	JN817023.1	86.67	Harapan
Salticidae	AraSalt104	*Myrmarachne* (Myrmarachnidae)	HR3.1A.2017AraSalt104.1	1078	*Agobardus cf. anormalis*	KC615636.1	90.37	790	*Telamonia vlijimi*	AY297256.1	98.27	Harapan
Salticidae	AraSalt104	*Myrmarachne* (Myrmarachnidae)	BJ4.1.2017AraSalt104.2	1106	*Myrmarachne assimilis*	LC193951.1	93.42	803	*Myrmarachne japonica*	JN817063.1	97.11	Bukit Duabelas
Salticidae	AraSalt060	*Omoedus* (Euophryinae)	BJ4.1.2017AraSalt060.1	1094	*Omoedus ephippigerus*	KC615765.1	99.70	823	*Omodeus ephippigerus*	KC615587.1	99.50	Bukit Duabelas
Salticidae	AraSalt060	*Omoedus* (Euophryinae)	HJ1.3A.2017AraSalt060.2	1080	*Omoedus ephippigerus*	KC615765.1	96.46	823	*Omodeus ephippigerus*	KC615587.1	96.15	Harapan
Salticidae	AraSalt060	*Omoedus* (Euophryinae)	BF2.1A.2017AraSalt060.3	1115	*Omoedus ephippigerus*	KC615765.1	95.75	821	*Omodeus ephippigerus*	KC615587.1	99.75	Bukit Duabelas
Salticidae	AraSalt100	*Orcevia* (Euophyrinae)	BF2.1A.2017AraSalt100.2	1085	*Orcevia keyserlingi*	KC615739.1	89.86	777	*Orcevia keyserlingi*	KC615555.1	94.78	Bukit Duabelas
Salticidae	AraSalt029	*Phaeacius* (Spartaeinae)	BR1.2A.2017AraSalt029.1	1053	*Phaeacius cf. fimbriatus*	DQ665759.1	91.16	815	*Phaeacius* sp.	KM033167.1	99.73	Bukit Duabelas
Salticidae	AraSalt029	*Phaeacius* (Spartaeinae)	BR1.3A.2017AraSalt029.2	1049	*Phaeacius cf. fimbriatus*	DQ665759.1	91.37	813	*Phaeacius* sp.	KM033167.1	99.73	Bukit Duabelas

Salticidae	AraSalt029	*Phaeacius* (Spartaeinae)	BR1.3A.2017AraSalt029.3	1063	*Phaeacius cf. fimbriatus*	DQ665759.1	91.26	799	*Phaeacius* sp.	KM033167.1	99.86	Bukit Duabelas
Salticidae	AraSalt087	*Phintella* (Heliophaninae)	HF4.1A.2017AraSalt087.1	1058	*Phintella sp.*	AY297397.1	90.42	791	*Phintella sp.*	AY297268.1	91.03	Harapan
Salticidae	AraSalt053	*Phintella* (Heliophaninae)	HJ3.2A.2017AraSalt053.2	696	*Phintella arenicolor*	JN817285.1	91.62	743	*Phintella sp.*	KY888722.1	91.32	Harapan
Salticidae	AraSalt053	*Phintella* (Heliophaninae)	HJ3.3A.2017AraSalt053.3	1059	*Phintella aequipeiformis*	LC105669.1	91.40	788	*Phintella sp.*	KY888722.1	93.26	Harapan
Salticidae	AraSalt087	*Phintella* (Heliophaninae)	HF1.2A.2017AraSalt087.2	1059	*Phintella sp.*	AY297397.1	90.60	787	*Phintella sp.*	AY297268.1	91.02	Harapan
Salticidae	AraSalt087	*Phintella* (Heliophaninae)	BJ4.1.2017AraSalt087.3	1059	*Phintella sp.*	AY297397.1	90.39	799	*Phintella sp.*	AY297268.1	90.90	Bukit Duabelas
Salticidae	AraSalt109	*Phintella* (Heliophaninae)	BR1.3A.2017AraSalt109.1	699	*Phintella vittata*	MK392822.1	99.83	798	*Phintella vittata*	KY888722.1	99.87	Bukit Duabelas
Salticidae	AraSalt030	*Portia* (Spartaeinae)	BJ6.1.2017AraSalt030.1	1080	*Portia taiwanica*	KM033214.1	89.74	797	*Portia labiata*	EF419041.1	99.86	Bukit Duabelas
Salticidae	AraSalt026	*Telamonia* (Plexippinae)	BJ4.3.2017AraSalt026.1	1063	*Telamonia dimidiata*	JX145703.1	96.38	787	*Telamonia masinloc*	AY297256.1	99.20	Bukit Duabelas
Salticidae	AraSalt026	*Telamonia* (Plexippinae)	BF4.2A.2017AraSalt026.2	1044	*Telamonia dimidiata*	JX145703.1	98.97	787	*Telamonia dimidiata*	JX145788.1	99.62	Bukit Duabelas
Salticidae	AraSalt026	*Telamonia* (Plexippinae)	BF4.1A.2017AraSalt026.3	1057	*Telamonia dimidiata*	JX145703.1	98.97	789	*Telamonia dimidiata*	JX145788.1	99.62	Bukit Duabelas
Salticidae	AraSalt065	*Telamonia* (Plexippinae)	HO2.1A.2017AraSalt065.1	1057	*Telamonia cf. festiva*	JX145701.1	99.38	788	*Telamonia vlijimi*	EF419019.1	99.48	Harapan

Salticidae	AraSalt065	*Telamonia* (Plexippinae)	HO2.1A.2017AraSalt065.2	1051	*Telamonia cf. festiva*	JX145701.1	99.54	766	*Telamonia vlijimi*	JN817061.1	99.74	Harapan
Salticidae	AraSalt065	*Telamonia* (Plexippinae)	HO2.1A.2017AraSalt065.3	698	*Telamonia dimidiata*	MK154812.1	91.48	803	*Telamonia vlijimi*	JN817061.1	99.36	Harapan
Salticidae	AraSalt082	*Thiania* (Euophyrina)	BO4.2A.2017AraSalt082.1	700	*Thiania bhamoensis*	MK392826.1	100	791	*Thiania bhamoensis*	EF419049.1	100	Bukit Duabelas
Salticidae	AraSalt082	*Thiania* (Euophyrina)	HO2.1A.2017AraSalt082.2	706	*Thiania bhamoensis*	MK392826.1	82	810	*Thiania cf. Suboppressa*	KC615599.1	96.94	Harapan
Salticidae	AraSalt082	*Thiania* (Euophyrina)	HO4.2A.2017AraSalt082.3	697	*Thiania bhamoensis*	MK392826.1	100	795	*Thiania bhamoensis*	EF419049.1	100	Harapan

Table A4: Grouping results of ABGD for COI and 28S with merged morphospecies and the resulting set of unique candidate species used in the calculation for the Bayesian inference tree for 28S (Appendix, Figure A2). ABGD grouped eight morphospecies considered as different in morphology based identification, into four unique morphospecies by the inferred barcode gap for 28S and COI (yellow). New candidate species after ABGD grouping results (024, 027, 056, 086) are shown underlined in the table. Full Voucher-ID's e.g. (BF1.3A.2017AraSalt001.1) (see Appendix, Table A3) are abbreviated to the morphospecies number for clarity.

Morphospecies grouping for 28S (Initial Partition with prior maximal distance P=2.78e-03)	Morphospecies grouping for COI (Initial Partition with prior maximal distance P=1.67e-03)	Morphological morphospecies merged to a single candidate species	Candidate species used for Bayesian inference tree
Group[1] n: 1 ;**id: 001.1**	**Group[1] n: 1 ;**id: 002.1	024 + 050 = 024	001
Group[2] n: 3 ;**id: 002.1 002.2 002.3**	**Group[2] n: 2 ;**id: 002.2 002.3	27 + 55 = 027	002
Group[3] n: 2 ;**id: 003.1 003.2**	**Group[3] n: 2 ;**id: 003.1 003.2	056 + 081 = 056	003
Group[4] n: 1 ;**id: 005.1**	**Group[4] n: 2 ;**id: 005.1 005.2	074 + 086 = 086	005
Group[5] n: 1 ;**id: 006.1**	**Group[5] n: 1 ;**id: 006.1		006
Group[6] n: 2 ;**id: 006.2 006.3**	**Group[6] n: 1 ;**id: 006.2		008
Group[7] n: 3 ;**id: 008.1 045.1 045.2**	**Group[7] n: 1 ;**id: 006.3		009
Group[8] n: 3 ;**id: 011.1 011.2 011.3**	**Group[8] n: 1 ;**id: 008.1		010
Group[9] n: 2 ;**id: 018.1 018.2**	**Group[9] n: 1 ;**id: 009.1		011
Group[10] n: 3 ;**id: 019.1 019.2 043.1**	**Group[10] n: 1 ;**id: 009.2		015
Group[11] n: 2 ;**id: 021.1 021.3**	**Group[11] n: 5 ;**id: 009.3 010.1 017.1 017.2 017.3		017
Group[12] n: 3 ;**id: 022.1 022.2 022.3**	**Group[12] n: 2 ;**id: 010.2 010.3		018
Group[13] n: 5 ;**id: 024.1 024.2 024.3 050.1 050.2**	**Group[13] n: 3 ;**id: 011.1 011.2 011.3		019
Group[14] n: 3 ;**id: 025.1 025.2 025.3**	**Group[14] n: 2 ;**id: 015.1 015.2		021
Group[15] n: 3 ;**id: 029.1 029.2 029.3**	**Group[15] n: 2 ;**id: 018.1 018.2		022
Group[16] n: 1 ;**id: 030.1**	**Group[16] n: 1 ;**id: 019.1		023

Group[17] n: 2 ;**id: 032.1 032.2**	**Group[17] n: 3** ;id: 021.1 021.2 021.3	024
Group[18] n: 2 ;**id: 043.2 043.3**	**Group[18] n: 3** ;id: 022.1 022.2 022.3	025
Group[19] n: 2 ;**id: 047.1 047.3**	**Group[19] n: 1** ;id: 023.1	026
Group[20] n: 2 ;**id: 053.2 053.3**	**Group[20] n: 5** ;id: 024.1 024.2 024.3 050.1 050.2	027
Group[21] n: 2 ;**id: 054.1 054.2**	**Group[21] n: 3** ;id: 025.1 025.2 025.3	028
Group[22] n: 4 ;**id: 056.1 056.2 056.3 081.1**	**Group[22] n: 1** ;id: 026.1	029
Group[23] n: 1 ;**id: 058.1**	**Group[23] n: 2** ;id: 026.2 026.3	030
Group[24] n: 3 ;**id: 059.1 059.2 059.3**	**Group[24] n: 4** ;id: 027.1 027.2 027.3 055.1	032
Group[25] n: 3 ;**id: 060.1 060.2 060.3**	**Group[25] n: 3** ;id: 028.1 028.2 028.3	040
Group[26] n: 2 ;**id: 061.1 061.2**	**Group[26] n: 4** ;id: 029.1 029.2 029.3 043.3	043
Group[27] n: 3 ;**id: 063.1 063.2 063.3**	**Group[27] n: 1** ;id: 030.1	045
Group[28] n: 3 ;**id: 069.1 069.2 069.3**	**Group[28] n: 1** ;id: 032.1	046
Group[29] n: 2 ;**id: 078.2 091.1**	**Group[29] n: 1** ;id: 032.2	047
Group[30] n: 3 ;**id: 082.1 082.2 082.3**	**Group[30] n: 1** ;id: 040.1	049
Group[31] n: 3 ;**id: 083.1 083.2 083.3**	**Group[31] n: 1** ;id: 040.2	053
Group[32] n: 3 ;**id: 087.1 087.2 087.3**	**Group[32] n: 1** ;id: 043.1	054
Group[33] n: 2 ;**id: 090.1 090.2**	**Group[33] n: 1** ;id: 043.2	056
Group[34] n: 1 ;**id: 100.2**	**Group[34] n: 2** ;id: 045.1 045.2	058
Group[35] n: 1 ;**id: 102.1**	**Group[35] n: 2** ;id: 046.2 046.3	059
Group[36] n: 1 ;**id: 109.1**	**Group[36] n: 2** ;id: 047.1 047.2	060
Group[37] n: 1 ;**id: 009.1**	**Group[37] n: 2** ;id: 049.1 049.2	061

Group[38] n: 1 ;**id: 009.2**	**Group[38] n: 5** ;id: 050.3 074.1 086.1 086.2 086.3	063
Group[39] n: 4 ;**id: 009.3 017.1 017.2 017.3**	**Group[39] n: 1** ;id: 053.1	065
Group[40] n: 1 ;**id: 010.2**	**Group[40] n: 1** ;id: 053.2	067
Group[41] n: 2 ;**id: 015.1 015.2**	**Group[41] n: 1** ;id: 053.3	069
Group[42] n: 1 ;**id: 023.1**	**Group[42] n: 2** ;id: 054.1 054.2	077
Group[43] n: 1 ;**id: 026.1**	**Group[43] n: 4** ;id: 056.1 056.2 056.3 081.1	078
Group[44] n: 2 ;**id: 026.2 026.3**	**Group[44] n: 1** ;id: 058.1	080
Group[45] n: 5 ;**id: 027.1 027.2 027.3 055.1 055.2**	**Group[45] n: 1** ;id: 058.2	082
Group[46] n: 3 ;**id: 028.1 028.2 046.1**	**Group[46] n: 3** ;id: 059.1 059.2 059.3	083
Group[47] n: 2 ;**id: 049.1 049.2**	**Group[47] n: 1** ;id: 060.1	086
Group[48] n: 3 ;**id: 065.1 065.2 065.3**	**Group[48] n: 1** ;id: 060.2	087
Group[49] n: 1 ;**id: 077.1**	**Group[49] n: 1** ;id: 060.3	090
Group[50] n: 2 ;**id: 078.1 104.1**	**Group[50] n: 2** ;id: 061.1 061.2	091
Group[51] n: 2 ;**id: 080.1 080.3**	**Group[51] n: 3** ;id: 063.1 063.2 063.3	092
Group[52] n: 1 ;**id: 040.1**	**Group[52] n: 3** ;id: 065.1 065.2 065.3	100
Group[53] n: 1 ;**id: 040.2**	**Group[53] n: 2** ;id: 067.1 104.2	102
Group[54] n: 1 ;**id: 058.2**	**Group[54] n: 3** ;id: 069.1 069.2 069.3	104
Group[55] n: 2 ;**id: 067.1 104.2**	**Group[55] n: 1** ;id: 077.1	109
Group[56] n: 2 ;**id: 074.1 086.2**	**Group[56] n: 2** ;id: 078.1 104.1	
Group[57] n: 2 ;**id: 086.1 086.3**	**Group[57] n: 2** ;id: 078.2 091.1	
Group[58] n: 2 ;**id: 092.1 092.2**	**Group[58] n: 3** ;id: 080.1 080.2 080.3	
	Group[59] n: 2 ;id: 082.1 082.3	

	Group[60] n: 1 ;id: 082.2
	Group[61] n: 3 ;id: 083.1 083.2 083.3
	Group[62] n: 3 ;id: 087.1 087.2 087.3
	Group[63] n: 1 ;id: 090.1
	Group[64] n: 1 ;id: 090.2
	Group[65] n: 2 ;id: 092.1 092.2
	Group[66] n: 1 ;id: 100.2
	Group[67] n: 1 ;id: 102.1
	Group[68] n: 1 ;id: 109.1

Figure A2: Bayesian inference tree for the 28S alignment of 55 candidate species of jumping spiders (aligned tip labels) with Bayesian posterior probabilities given for each node. Full Voucher-ID's e.g. (BF1.3A.2017AraSalt001.1) (see Appendix. Table A3.) are abbreviated to the morphospecies number (e.g. 001) for clarity. Morphospecies of ant-mimicking salticid spiders (*Myrmarachne)* (see Appendix Table A3) are highlighted (yellow) on the tree.