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SPATIAL AND TEMPORAL VARIABILITY OF SOIL FAUNA UNDER COCONUT CULTIVATION ON LATERITIC SOIL

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ABSTRACT

A recent review has reported that spatial variability has become a limitation in soil fauna studies. The objectives of this study were to quantify the spatial and temporal variability of soil fauna under coconut cultivation on lateritic soil within a short period. The study was conducted in December 2021. In total, 114 pitfall traps were installed through systematic and random methods within the coconut garden located in Perlis, Malaysia. The traps were left in the field for 24 hours. The soil fauna was collected three times within a month and the specimens were identified up to family level. The geostatistical analysis was performed to quantify the spatial and temporal variability. As a result, about 1,608 specimens have been collected and 15 families of soil fauna from 10 orders were identified. The Formicidae (68.5%) and Scolopendridae (0.1%) families were the most and the least abundant soil fauna found in coconut cultivation, respectively. Among those examined soil fauna indices, only abundance showed a significant difference between the sampling time. The spatial and temporal variability of soil fauna were intermediate to high (coefficient of variation = 29.5%–123.8%). The spatial dependency of the examined soil fauna indices ranged from moderate weak to very strong at the distance of 5.5 m to 12.9 m and mainly has been affected by intrinsic factors. The interpolation maps were able to show the changes in the study with low errors. As a conclusion, this study was able to quantify the spatial and temporal variability of soil fauna.

Keywords: *Cocos nucifera*, geostatistic, soil fauna, spatial and temporal pattern

ABSTRAK

Kajian terkini telah melaporkan bahawa kebolehubahan spatial telah menjadi batasan dalam kajian fauna tanah. Objektif kajian ini adalah untuk mengukur kebolehubahan spatial dan

temporal fauna tanah di penanaman kelapa atas tanah laterit dalam tempoh yang singkat. Kajian telah dijalankan pada Disember 2021. Secara keseluruhan, 114 perangkap lubang telah dipasang melalui kaedah sistematik dan rawak di kebun kelapa di Perlis, Malaysia. Perangkap itu dibiarkan di kebun selama 24 jam. Fauna tanah diambil sebanyak tiga kali dalam tempoh sebulan dan spesimen dikenal pasti sehingga peringkat famili. Analisis geostatistik telah dijalankan untuk mengukur kebolehubahan spatial dan temporal. Hasilnya, kira-kira 1,608 spesimen telah dikumpul dan 15 famili fauna tanah daripada 10 order telah dikenalpasti. Famili Formicidae (68.5%) dan Scolopendridae (0.1%), masing-masing merupakan fauna tanah yang paling banyak dan paling sedikit terdapat dalam penanaman kelapa. Di antara indeks fauna tanah yang diperiksa, hanya kelimpahan menunjukkan perbezaan yang signifikan antara masa pensampelan. Kebolehubahan spatial dan temporal fauna tanah adalah sederhana hingga tinggi (pekali variasi = 29.5%–123.8%). Kebergantungan spatial bagi indeks fauna tanah yang diperiksa adalah dari sederhana lemah hingga sangat kuat pada jarak 5.5 m hingga 12.9 m dan terutamanya telah dipengaruhi oleh faktor intrinsik. Peta interpolasi dapat menunjukkan perubahan dalam kajian dengan ralat yang rendah. Sebagai kesimpulan, kajian ini dapat mengukur kebolehubahan spatial dan temporal fauna tanah.

Kata kunci: *Cocos nucifera*, geostatistik, fauna tanah, corak spatial dan temporal

INTRODUCTION

Soil fauna plays an important role in the functioning of ecosystems. Their presence in the soil can be one of the indicators of soil health. The abundance and richness of soil fauna are closely linked with healthy soil conditions and typically used as a reliable indicator of soil health (Cardoso et al. 2013). Soil fauna has been found to have a consistently positive effect on litter decomposition at global and biome levels (Garcia-Palacios et al. 2013). Among the soil fauna, there are many litter-feeding species like the millipedes, which are important consumers of leaves, grasses, and wood litter. This group of soil fauna has a significant influence on the breakdown process of organic matter, thereby influencing the rate of nutrient cycling in the soil systems (Coleman & Wall 2015), and subsequently on the soil properties (Menta & Remelli 2020). Some species of this soil fauna feed, live, reproduce and are highly adapted to specific soil conditions, making them highly sensitive to soil changes (Menta & Remelli 2020). They often move and change in habit according to their environment with their distribution may have a predictable spatial structure (Ettema & Wardle 2002). Collecting soil fauna is cumbersome and time-consuming to identify. Therefore, in many of the studies, it has been practically to collect soil fauna at long-term period like annual or bi-annual based on the study purpose. However, this may neglect important information that can be used to understand the interrelationships with environmental abiotic factors within the landscape in the short-term period like weekly or monthly which rarely being discussed.

Ecologists study patterns of soil fauna communities through spatial variation to understand the mechanisms that control their distribution (Legendre & Legendre 2012). A spatially explicit approach to soil ecology can enable identification of factors that drive the spatial variability of populations and activities of soil organisms (Ettema & Wardle 2002). In this regard, the spatial variability can be measured using geostatistical method. This method is a promising tool which has been widely used in soil science to capture the spatial variability of nutrients (Shahidin et al. 2018; Kamarudin et al. 2019a, 2019b, 2020) and pest control (Anithakumari et al. 2017) which focuses on specific site management. For some reasons, the application of a geostatistical methods to soil fauna (Fromm et al. 1993; Gholami

et al. 2016) is less discussed although there are numerous studies that have been done on soil fauna. A recent review has been reported that spatial variability has become a limitation of soil fauna studies, suggesting future research on this topic (Beaumelle et al. 2021).

Coconut (*Cocos nucifera*) is one of the most important industrial crops in Southeast Asia, including Malaysia. This crop requires minimal maintenance compared to the other industrial crops such as pineapple, mango, and tomato. Most of the coconut gardens are managed by smallholder farmers and the rest are managed by the estate either as monocrop or intercropping with cocoa, coffee, or fruit crops, or by the plantation. Coconut trees can be grown in a variety of soil conditions, including problematic soils like laterite. Nonetheless, the species diversity of soil fauna in the coconut garden cultivated in the problematic soils has not been well explored. Moreover, compared to the natural forests, agroecosystems like the coconut garden have relatively low in species diversity as well as diversity index of soil fauna, but higher in dominance index (Tang et al. 2006). This is partially because agroecosystems have mono tree species, high soil pH and salinity, and other environmental factors (Tang et al. 2006) like topography and canopy closure (Martius et al. 2004) that can influence ecosystem microclimates. Furthermore, agricultural management practices such as fertilizer application, weeding, pest control and frond arrangement can affect many of the important functional and structural characteristics of ecosystems including the soil fauna and their distribution (Coleman & Wall 2015) by changing the environment surrounding. Furthermore, a study in the palm oil plantation showed that management practice such as application of empty fruit bunch, chemical fertilization and understory vegetation with pruned fronds created spatial complexity in soil fauna feeding activity (Tao et al. 2016). A few studies have been noted to focus on the soil fauna of the coconut garden (Tang et al. 2006), but the limitation on spatial information hinders the management process. In particular, the soil fauna communities are dynamic and vary at different times and spaces. Thus, it is necessary to observe the variability of the soil fauna communities as useful information to explain the ecological patterns in the agroecosystems. Therefore, the aim of this study was to quantify the spatial and temporal variability of soil fauna under coconut cultivation on lateritic soil within a short period.

MATERIALS AND METHODS

Study Sites

This study was conducted in the coconut garden (Figure 1) located at the farm of Universiti Teknologi Mara (UiTM), Perlis Branch, Arau Campus (6°27'11.9" N, 100°16'50.7" E), Perlis, Malaysia. Perlis is in the northern part of Peninsular Malaysia, near to the Malaysian-Thai border and therefore has a tropical monsoon (*Am*) climate according to the Köppen-Geiger Classification System (Kottek et al. 2006). The state has an average annual temperature of 27.4ºC and an average annual precipitation of 1,893.7 mm for the past 30 years (1990–2021). Figure 2 shows the weather conditions during the study period. The total precipitation was 52 mm and the average temperature was 26.9ºC (min = 24.1ºC; max = 31.4ºC).

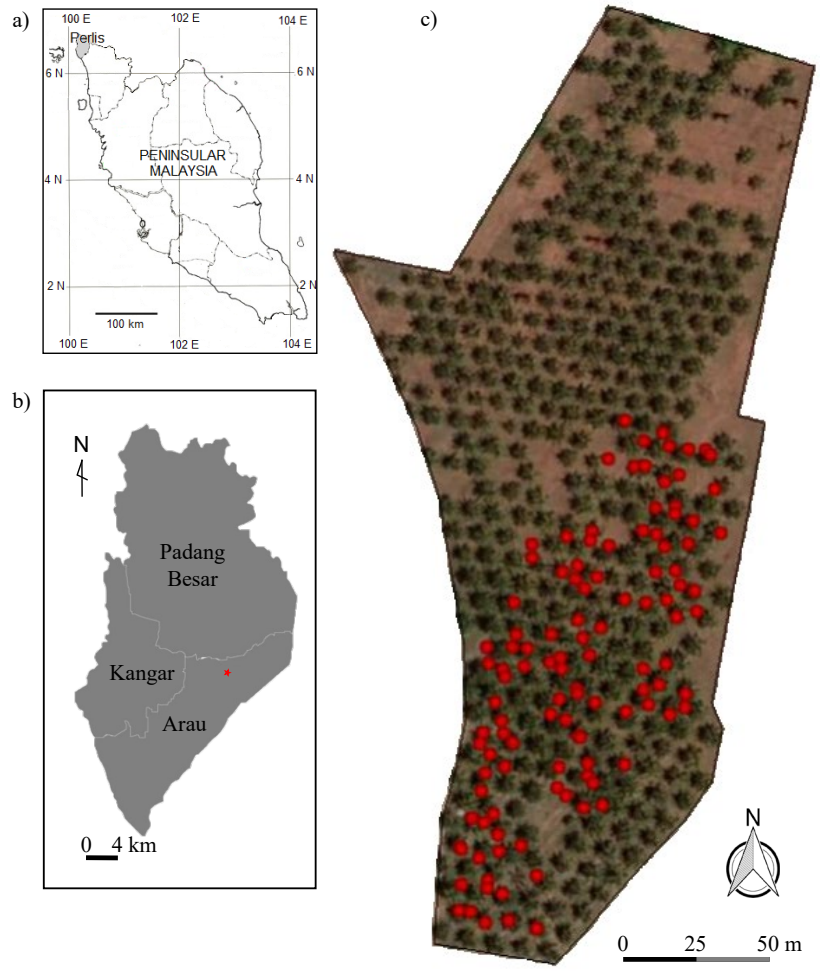

Figure 1. a-b) Location of study site and c) distribution of sampling points (red)

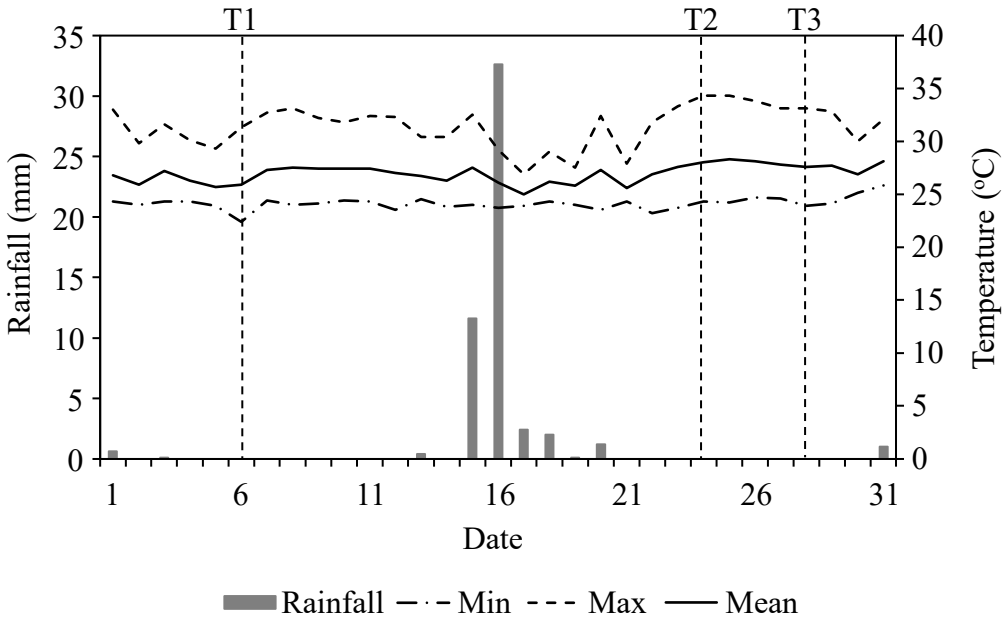

Figure 2. Perlis weather status in December 2021

The UiTM Farm was planted along a coconut garden with various fruit trees like watery rose apple, starfruit, jackfruit, and mango, as well as plantation crops like oil palm, rubber, and paddy. The coconut garden was cultivated in 2005 with hybrid variety of Matag (Malayan Dwaft × Tagnanan Tall) and the trees were planted in a triangular system with a planting distance of 8.23 m × 8.23 m. The trees were now 16 years old at the time of the survey, with about 446 coconut trees planted on 10 acres (4.05 hectares). The soil at the study site is developed from reworked lateritic. Most of the coconut garden area is covered by the Jitra series (Rhodic Hapludults) in the south part and the Terap series (Typic Hapludults) in the north. Both soil series originate from pedimented material formed on pediplains developed on iron-rich shale parent materials. This coconut garden lies on an undulating topography between 2^{o} to 6^{o}.

This coconut garden only received 500 kg of urea (N = 46%) in 2021, approximately 1.1 kg per tree. Undergrowth was controlled using chemical and mechanical applications. Weeds growing between trees are controlled by spraying herbicides, i.e., glyphosate and metsufuron methyl, every three months. Meanwhile, weeds growing between furrows were mowed every two months with a tractor-mounted mower. Coconut leaf drops were placed between the trees every three months.

Soil Fauna Sampling and Identification

In total, 114 pitfall traps were installed in the southern part of the coconut garden (Figure 1) using systematic and random methods for the soil fauna collection. The pitfall traps have been used extensively to study litter and surface-soil fauna. This method collects surface active soil fauna that fall into the cups filled with preservatives. This method provides comparative estimates when used with caution, although it is difficult to estimate the absolute population (Coleman & Wall 2015). The trap was installed using a 9.5 cm diameter and 12.0 cm deep plastic cup. The cup was placed inside a hole with the opening of the cup remained at the same level to soil surface to avoid water flowing to the cup. Each cup was filled with 100 ml of 75% ethanol to kill and preserve soil fauna. The trap was covered with a 12 × 10 cm plastic plate by hanging it using three wooden sticks to protect the trap from the rain. These traps were left in the garden for 24 hours. The contents were then collected, and the soil fauna were preserved in 75% ethanol for identification following the key to identification from Triplehorn and Johnson (2005). In this study, the soil fauna in 114 traps were collected on each of three occasions: 6th (T1), 24th (T2), and 28th (T3) December 2021. The interval days of samplings were chosen to evaluate how soil fauna might change in the short period of time. All soil fauna collections were screened and identified at the family level. Prior to the geostatistical analysis, the coordinates of each trap were recorded using a handheld GPS receiver (GPSmap 60CSx; Garmin Ltd., KS).

Soil Fauna Indices

In this study, richness was counted based on the total number of family present (Equation 1) and abundance was generated based on the total number of individuals per group family (Equation 2).

$$\text{Richness} = \sum \text{the number of family present} \quad \text{Equation 1}$$

$$\text{Abundance} = \sum \text{the number of individuals per group of family} \quad \text{Equation 2}$$

The diversity index was calculated based on the Shannon-Wiener diversity index (*H'*) (Equation 3) which is the most commonly used in community studies. The Shannon-Wiener diversity index values typically range from 0 to 3.5 (Magurran 1988) where a value of zero indicates that the sample contains only one family and the maximum value indicates that all family of a sample have the same number of individuals.

$$H' = - \sum p_i \log p_i \quad \text{Equation 3}$$

The evenness (Pielou) index was not calculated continuously from the Shannon-Wiener diversity index due to the no diversity found in most locations. Instead, the Simpson's reciprocal index ($1/D$) was calculated (Equation 4). This indicator quantifies biodiversity considering richness and evenness.

$$1/D = 1 / \sum p_i^2 \quad \text{Equation 4}$$

where p_i is the proportion of the total sample represented by family i. The proportion was calculated by dividing the number of individuals in a family i by the total number of samples. The defined minimum value of 1/D is 1, which occurs when a community contains only one family, while higher values of 1/D indicate greater biodiversity in the area.

Statistical Analysis

Analysis of variance (ANOVA) was applied to determine the effects of sampling time on soil fauna indices. Tukey's test ($P<0.05$) was applied to separate the means. All the statistical analyses were done using R version 4.0.2.

Geostatistical Analysis

All computations prior to geostatistical analysis were analyzed with the R version 4.0.2 package gstat (Pebesma 2004). An exploratory data analysis (i.e., minimum, and maximum values, mean, standard deviation (SD), median, median absolute deviation (MAD), skewness, and kurtosis) was explored before fitting the semivariograms. The coefficient variation (CV) was calculated by dividing the SD by the mean and expressed as a percentage. The CV was classified as low (<10%), intermediate (10%–90%) and high (>90%). The Shapiro-Wilk test was applied to test the normal distribution of each data set. The outliers were identified either by using mean ±3SD or median ±2.5MAD for normal and non-normal distributed data sets, respectively.

During the data analysis, all the variables measured at three different sampling times exhibited non-normal distributions ($P<0.05$). The data set has not undergone the transformation process although this method can reduce data distortion. This is because a normal distribution is not a prerequisite, and stationarity is required to use the variogram estimator. Moreover, working with real data is more convenient for interpretation, but precaution is still needed. Therefore, the application of a robust variogram was appropriate to meet this condition.

The semivariogram for data set without and with outliers were constructed using classic (Equation 5) and robust (Equation 6) variogram estimators, respectively.

$$\gamma(h) = 1/(2n(h) \sum [z(i) - z(i+h)]^2 \quad \text{Equation 5}$$

$$\gamma_{CH}(h) = \{1/2n(h) \sum [z(i) - z(i+h)]^{1/2}\}^4/(0.457+0.494/n(h)+0.045/n^2(h)) \quad \text{Equation 6}$$

where $n(h)$ is the number of paired comparisons at lag h and z is the measured values of a target variable at the locations i and $i+h$, respectively.

Half of the maximum sampling distance was used as the active lag distance for the nine bins during the construction of the semivariogram. The number of point pairs in each bin was carefully fitted to exceed the minimum number of 50 point-pairs (minimum = 55 and maximum = 581). A spherical model was fitted to all variables to facilitate the comparison of the sampling times for each selected diversity index (Kamarudin et al. 2019b) although the exponential and linear models showed slightly better fits due to lower residual sums of squares. The nugget, sill, and range were recorded, and the nugget-to-sill ratio was calculated. This nugget-to-sill threshold ratio is very strong (<0.25), moderately strong (0.25–0.50), moderately weak (0.50–0.75) and very weak (>0.75) of spatial dependencies.

Interpolation maps were constructed using the ordinary Kriging method. Leave-one-out cross validation was performed to assess and validate the accuracy of the model estimators based on the mean error (ME) and the root mean squared error (RMSE).

RESULTS

Soil Fauna Indices

The results of soil fauna indices in this part were shown on the temporal (i.e, time) basis of T1, T2 and T3. A total of 15 families of soil fauna were successfully identified from 10 taxonomic order: Araneae, Blattodea, Coleoptera, Hemiptera (Heteroptera), Hymenoptera, Opisthopora, Orthoptera, Polydesmida, Scolopendromorpha and Thysanoptera (Figure 3). The number of families found during sampling on T1, T2 and T3 were 13, 14 and 14 families, respectively. A total of 1,608 specimens of soil fauna were collected at this study site. The number of individuals collected on T1, T2 and T3 were 495, 526 and 587 specimens, respectively. Among those examined soil fauna indices, only abundance showed a significant difference ($P < 0.05$) between the sampling time. Among the specimens' collection, the families of Formicidae (n = 1,101) and Scolopendridae (n = 2) showed the most and the lowest abundant number of individuals, respectively (Figure 3). On the other hand, the families of Blattidae, Lumbricidae and Scolopendridae were rarely discovered within the study period.

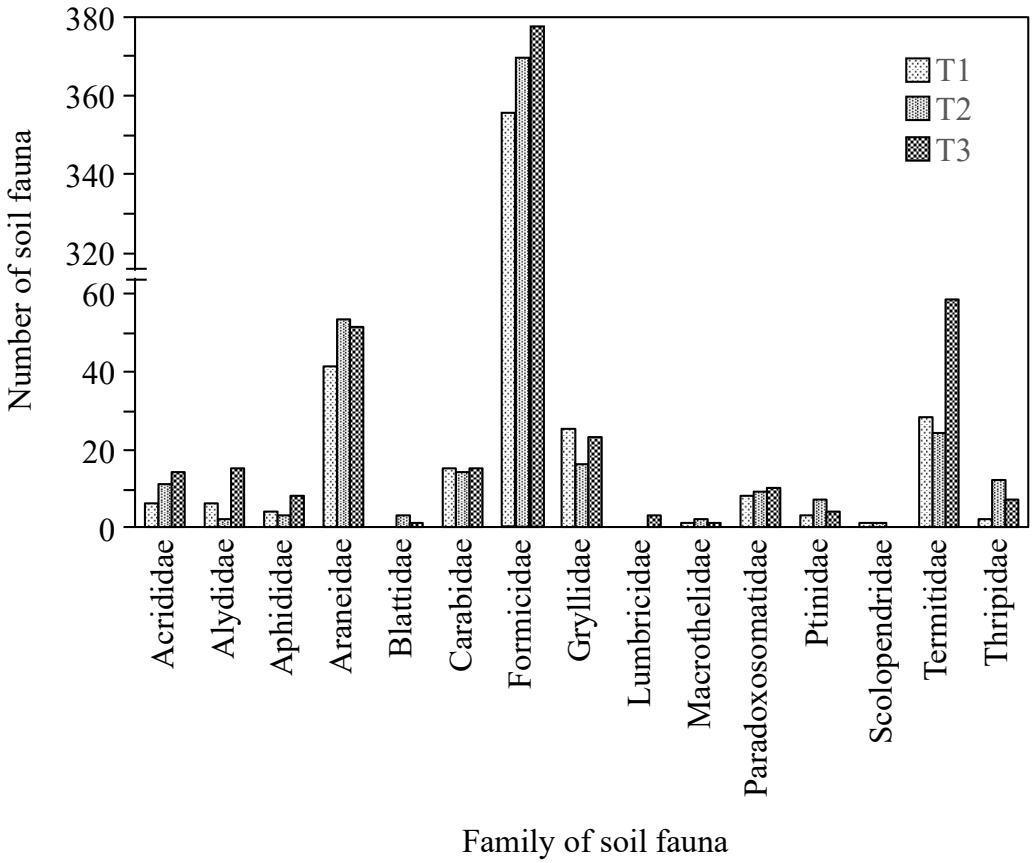

Figure 3. Total number of soil fauna collected at the coconut garden

The Shannon-Wiener diversity index and reciprocal index show the increasing pattern during the sampling. In general, the temporal Shannon-Wiener index on T1, T2, and T3 were 1.15, 1.23, and 1.39, respectively, while the temporal reciprocal index on T1, T2, and T3 were 1.89, 1.97, and 2.30, respectively.

Exploratory Data Analysis

The results of soil fauna indices in this part were shown at the spatial (i.e., space) basis calculated on T1, T2 and T3. The exploratory data analysis of 114 sampling points (i.e., spatial) at each sampling time is summarized in Table 1. The number of families at each sampling point within three sampling times was found at least 1 (minimum) to 3 (maximum) families; given the median±MAD ranging from 1.00±0.00 to 2.00±1.48 and the CV showed intermediate (range = 36.62%–39.13%) variation. The abundance at each sampling point within the three sampling times showed a narrow range of 1 to 13 individuals; given the median±MAD ranging from 4±3 to 5±2 and the CV showed intermediate (range = 49.06%–56.31%) variation. Due to the low diversity at each sampling point (i.e., number of families between 1 and 3), the diversity index showed a value ranging from 0 to 1.08, given the median±MAD in the range of 0.00±0.00 to 0.39±0.58 and the CV showed high (range = 103.73%–123.76%) variation. The reciprocal index at the sampling point within three sampling times ranged from 1.00 to 2.88; given the median±MAD in the range of 1.00±0.00 to 1.30±0.45 and the CV showed intermediate (range = 39.54%–32.95%) variation. All the data have positive skewness ranging from 0.31 to 1.16 indicating that all data sets are a right-skewed distribution. Meanwhile the kurtosis, a shape of a probability distribution, showed both positive and negative values indicating the data set had heavy-tailed and light-tailed

distributions, respectively. For this reason, all data sets at the three sampling times exhibited non-normal distributions ($P < 0.05$) as they had outliers except for the richness and diversity index at T3.

Table 1. Exploratory data analysis of biological diversity indices of soil fauna at the spatial basis (i.e., space) calculated on T1, T2 and T3 (i.e., time)

Attributes	T1				T2				T3			
	Richness	Abundance	Diversity index	Reciprocal index	Richness	Abundance	Diversity index	Reciprocal index	Richness	Abundance	Diversity index	Reciprocal index
Mean	1.43	4.34	0.25	1.31	1.51	4.61	0.29	1.34	1.59	5.15	0.32	1.39
SD	0.53	2.45	0.31	0.40	0.55	2.26	0.31	0.40	0.62	2.62	0.33	0.46
Median	1.00	4.00	0.00	1.00	1.00	4.00	0.00	1.00	2.00	4.50	0.39	1.30
MAD	0.00	2.97	0.00	0.00	0.00	1.48	0.00	0.00	1.48	2.22	0.58	0.45
Minimum	1.00	1.00	0.00	1.00	1.00	1.00	0.00	1.00	1.00	1.00	0.00	1.00
Maximum	3.00	12.00	0.96	2.33	3.00	13.00	1.05	2.78	3.00	13.00	1.08	2.88
Skewness	0.65	0.97	0.54	0.78	0.45	0.97	0.31	0.83	0.56	0.86	0.37	1.16
Kurtosis	-0.84	0.54	-1.50	-1.03	-0.90	1.40	-1.50	0.09	-0.59	0.33	-1.19	1.30
CV	37.18	56.31	123.76	30.86	36.62	49.06	107.79	29.54	39.13	50.84	103.73	32.95
Normality test	$1.14E^{-14}$	$7.99E^{-07}$	$1.40E^{-13}$	$3.92E^{-13}$	$5.71E^{-14}$	$2.05E^{-05}$	$2.33E^{-12}$	$3.08E^{-11}$	$7.57E^{-13}$	$5.18E^{-06}$	$3.27E^{-11}$	$3.62E^{-11}$
Outliers	47	1	47	47	55	10	55	55	0	4	0	4

Abbreviation: SD = standard deviation; MAD = median absolute deviation; CV = coefficient of variation

Semivariogram

Due to the presence of outliers, most of the diversity indices in this study were fitted using a robust variogram estimator, except the richness and diversity index on T3, which were fitted using a classic variogram estimator. A spherical model fitted to the theoretical model showed a residual sum of squares of less than 5.38. Some of the fitted models exhibited nuggets up to 2 with a nugget-to-sill ratio ranging from 0 to 0.62. The richness shows a strong spatial dependence with a spatial range of 5.5 m and 13.0 m on T1 and T2, respectively, and a moderately weak spatial dependence with a spatial range of 11.2 m on T3. The abundance shows a moderately strong spatial dependence with spatial range of 5.5 m on T1 while a very strong spatial dependence with spatial range of 10.9 and 10.2 m on T2 and T3, respectively. The diversity index shows a very strong spatial dependence with a range of 5.5 m and 12.0 m on T1 and T2, respectively, and a moderately weak spatial dependence with a range of 12.1 m on T3. The reciprocal index shows a strong spatial dependence with ranges of 5.5 m, 12.3 m and 5.5 m on T1, T2 and T3, respectively (Table 2; Figure 4).

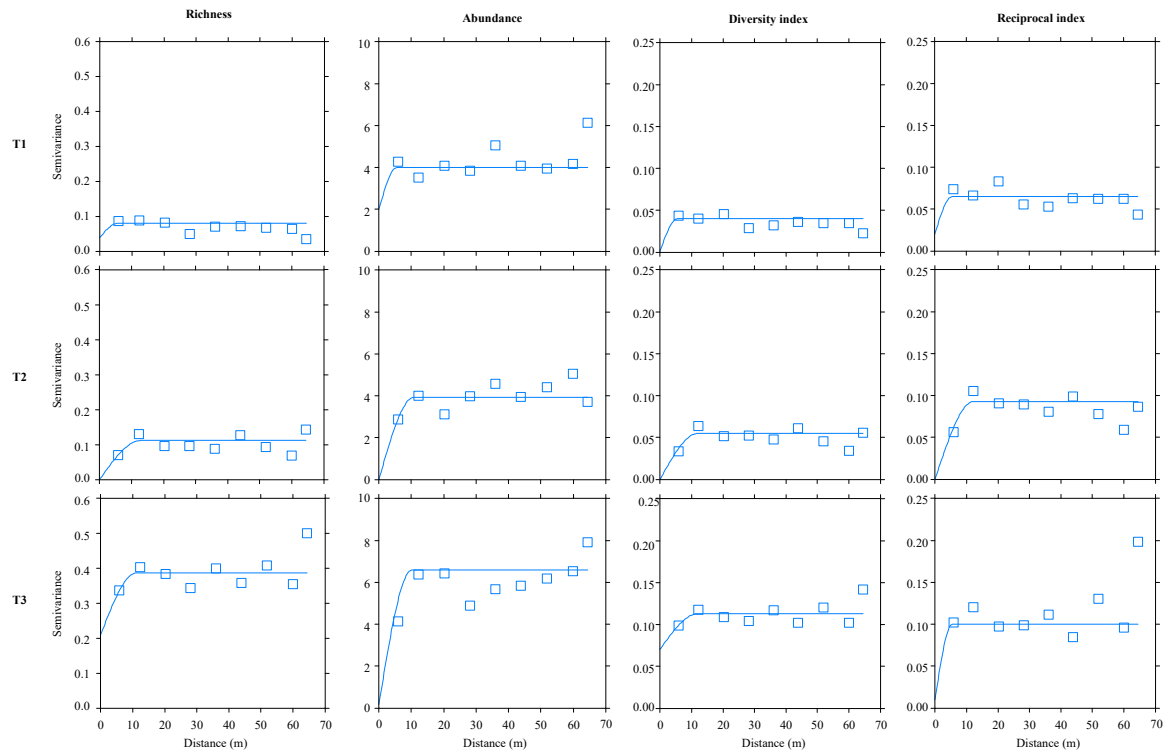

Figure 4. Semivariogram of examined diversity indices of soil fauna at the study site

Interpolation Map

The interpolation maps were successfully generated at low ME (range = -7.35E^{-03}–1.42E^{-02}) and RSME (range = 0.32–2.94). Through these interpolation maps, changes in spatial and temporal variability of soil fauna can be observed. The number of families at the sampling sites can be observed in the richness map. At least one family of soil fauna was found around the sampling area, with two families scattered in the northeast of the sampling area on T1. On T2, two families of soil fauna were found widely distributed within the sampling area and three families were rarely seen at the study site. On T3, the two families dominated areas (a few points with three families) were in the southern part of the sampling area, with one or two families in the central and northern parts. The same pattern is seen in the diversity index. Meanwhile, the number of soil fauna across the sampling area can be observed on an abundance map. The number of individuals of soil fauna were found in at least one to four specimens in the south, at least five specimens in the central part, and six or seven specimens in the northern part on T1. On T2, most areas have one to five specimens except in the northeast and southwest parts where 6 to 12 specimens were found. Meanwhile, on T3, most areas have six specimens except in the central part of the sampling area where 7 to 12 specimens were found. On the other hand, the reciprocal index showed the same pattern on T1 and T3 with one family while T2 shows more than one family at certain points compared to T1 and T3.

Figure 5. Interpolation maps of the examined diversity indices of soil fauna at the study site

DISCUSSION

The diversity indices of soil fauna in the coconut garden were well explored. A lower number of presented soil fauna may indicate an unhealthy soil condition which can result in severe effects, including degradation of soil and reduction of agricultural productivity capacity (Nuria et al. 2008; Teh et al. 2018). Therefore, their presence is beneficial to the agroecosystems (Eriksen-Hamel & Whalen 2007). Generally, the total number of 15 families and 1,608 specimens from 10 orders collected in this coconut garden was lower than Tang et al. (2006) and Araujo et al. (2018) studies. Tang et al. (2006) collected 5,378 specimens from 27 orders at the coconut farm in China due to the different methods of Tullgren and Bearmann. While Araujo et al. (2018) collected 34,982 specimens from 16 orders in a coconut farm located in northeastern Brazil using the pitfall trap method. This difference might be mainly caused by management practice due to use of organic fertilizer (i.e., cow manure) and the soil type of Fluvic Neossol in Araujo et al. (2018) study. Organic fertilizer has been known to be good to increase soil organic matter and enhance soil fauna (Zhou et al.

2022) compare than synthetic fertilizer. While the soil type of Fluvic Neossol generally known as alluvial soil has different soil characteristics than the soil type in this study which may affect the present of soil fauna (Burton et al. 2022). Although the soil properties were not analysed in this study, the Jitra series soil often has fine and medium subangular blocky structures, high clay content with moderate nutrient contents and low organic matter (DOA 2018) which made it less fertile than alluvial soil.

Similar to other studies, the Formicidae family has the most abundant soil fauna found in the coconut garden (Araujo et al. 2018). The presence of the Formicidae group provides insight into the presence of other organisms, since many Formicidae members can maintain obligate interactions through trophic and symbiotic with plants and other animals (Bakhtiar & Maryati 2009). Moreover, many ant (Formicidae group) pores can be found at 0–15 cm of soil depth of Jitra series (DOA 2018). This shows that the Formicidae can live in a wide range of habitats (Colorado & Chavez 2023) including in this problematic soil.

The spatial variability of soil fauna at the study site was well explored. The number of families (1-3 families) and individual (1-13 specimens) found at each sampling point were relatively low and directly low the Shannon-Wiener diversity index (0.00-1.08) as well as Simpson's reciprocal index (1.00-2.88). The low collection of soil fauna at each sampling point may be due to the short period of traps being installed at the study site (Hohbein & Conway 2018). Although the Shannon-Wiener diversity index within the sampling area varies in the range of 0 to 1 and similar to Araujo et al. (2018), the taxa levels were different where they identified the soil fauna up to morphospecies, one level lower than this study.

Generally, a very strong spatial dependency is associated with intrinsic factors (e.g., topography, food sources, vegetation, temperature and rainfall) while a very weak spatial dependency is associated with extrinsic factors (e.g., management activities like weeding control, agrochemicals application, harvesting and frond arrangement). Meanwhile, moderate strong or weak spatial dependency is associated with both intrinsic and extrinsic factors weighted to the dominant factor. However, the moderate weak spatial dependency obtained by the richness and diversity index on T3 shown in this study was due to a high nugget value (>50% of sill). This high nugget value can be associated with measurement error and/or existence variance at a smaller scale or at lag 0 (Kamarudin et al. 2019b). In this study, a strong spatial can be found within 5.5 m to 13.0 m for both spatial and temporal variability. In other words, the same family and/or the abundance of soil fauna can be found within this range. These strong spatial dependencies might be affected by the soil and microclimate at the study site. This can be supported by the significant difference found between sampling time on abundance which may be caused by the temperature (Ma et al. 2021). However, in the geostatistical analysis, the semivariogram is strongly influenced by the sampling design (Ettema & Wardle 2002) and spatial sampling has to regard the extent, the sampling interval, and the support (area or volume of an individual sample) (Legendre & Legendre 2012). Thus, these parameters must be chosen based on the scientific question as well as physical and practical limitations.

The spatial dependency of soil fauna indices (i.e., richness, abundance, diversity index and reciprocal index) varies horizontally in both spatial and temporal. This can be explained because soil biodiversity is shaped by the co-action of numerous factors (Martius et al. 2004) including environment and management. These factors act at different spatial scales (or time), and may interact, while ecological processes are scale-dependent and hierarchically structured. Some studies show the correlation between gradients in site and soil properties,

including bulk density, aggregation, texture, oxygen concentration, pH, moisture, soil organic matter content, inorganic nitrogen availability, precipitation levels and vegetation dynamics. Soil often has high variation in nutrient contents even on a small scale which may affect the distribution of vegetation (Kamarudin et al. 2020). This also may affect the distribution of soil fauna found in this study like the one in the interpolation maps. The interpolation maps successfully showed the distribution of richness (family), abundance, diversity index and reciprocal index. Most of the maps looked similar within the area and over the sampling time except abundance. This might be due to no significant difference ($P \geq 0.05$) over the slope and sampling time except abundance. The distribution obtained in the interpolation maps showed the distribution of soil fauna in the small-scale heterogeneity indicated by many small patches which reflecting hot and cold spots (Ettema & Wardle 2002).

CONCLUSION

As a conclusion, 15 families from 10 orders have been identified in the coconut cultivation area with a total specimen of 1,608 within three times of sampling (average = 536 soil fauna). Among the identified group, Formicidae (68.5%) and Scolopendridae (0.1%) families were the most and the least abundant of soil fauna found in coconut cultivation, respectively. Among those examined soil fauna indices, only abundance showed a significant difference ($P<0.05$) between the sampling time. Meanwhile, the geostatistical analysis reveals that all examined variables had strong spatial dependency (CV = 29.5–123.8) from 5.5 m to 13.0 m except richness and diversity index on the third day of sampling due to the high nugget value (>50% of sill). The interpolation maps were able to show the temporal and spatial distribution of species richness, abundance, diversity index and reciprocal index. For the future study, it is recommended to associate the distribution of soil fauna with the soil properties and microclimate data.

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Conflict of Interest
The authors declare that they have no conflict of interest.

Ethics Declarations
No ethical issue required for this research.

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This manuscript has no associated data.

Authors' Contributions
KNK and MAMS conceived this research, designed experiments and performed experiments; KNK, MAMS, MIK and IMU participated in the data analysis and interpretation of the data;

KNK, MIK and IMU wrote the paper and participated in the revisions of it. All authors read and approved the final manuscript.

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