



## Effect of organic farming practices on soil health improvement of coconut farms

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### ABSTRACT

The present study aimed to provide data on what extend of organic management (OF) improve soil health compared to conventional farms (CF). In this study, a total of 24 top soil samples (0–30 cm) were collected from Mo Cay Nam and Mo Cay Bac, Ben Tre, Vietnam, representing organic vs conventional farm soils, respectively to analyze farming systems in terms of the chemical, physical, and biological soil properties. Soil nutrients, soil microbial density, dehydrogenase enzyme activity and soil bacteria diversity were detected using atomic absorption spectrometry, serial dilution and plating; triphenyl formazan detection, and DNA extraction using Invitrogen™ and Qubit™, respectively. Our results indicated that soil bulk density was 11 % lower and soil porosity was 4 % higher, respectively at organic farms compared to the conventional farms. Meanwhile, both soil  $\text{NH}_4^+$  and available phosphorus contents were higher in the organic farming soils (38.9 mg  $\text{kg}^{-1}$  and 69.0 mg  $\text{kg}^{-1}$ , respectively). Total soil bacteria and cellulose-decomposing bacteria were found to be insignificantly lower in conventional farms (CF) as compared to organic farms (OF) (6.01 log CFU  $\text{g}^{-1}$  soil vs 6.26 log CFU  $\text{g}^{-1}$  soil) and (3.82 log CFU  $\text{g}^{-1}$  soil vs 4.18 log CFU  $\text{g}^{-1}$  soil), respectively. The beta diversity of soil bacterial community, along with the bacterial orders *Bacillales*, *Frankiales*, *Elsterales*, *Pseudomonadales*, and *Pedospaerales* exhibited higher with organic farming practices and dehydrogenase enzyme activity in organic farms (OF) was significantly higher (0.61  $\mu\text{g}$  TPF  $\text{g}^{-1}$  soil  $\text{hour}^{-1}$ ) as compared to

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0.47  $\mu\text{g TPF g}^{-1}$  soil  $\text{hour}^{-1}$  in conventional farms (CF). This study demonstrates the benefits of organic management on soil health in coconut plantations and promotes the overall health of coconut orchards.

## 1. Introduction

Considerable population in the world is facing with serious food security which motivate the farming systems involve into more exacerbating methods to compensate the food demand (Petersen et al., 2021). Constant utilization of agricultural lands through conventional agricultural practices caused to severe environmental problems such as soil/water pollution and reduced soil health (Tuomisto et al., 2012). In coconut production in Mekong River Delta in Vietnam, persistent monoculture cultivation, over the long term, poses a notable risk upon the soil physical, chemical, and biological quality, and ineffective resource utilization on a local and global level (Swoboda et al., 2022). Harmful chemical fertilizer usage raised the problems with soil quality and fertility including organic matter loss and elevated soil salinity (Mensik et al., 2018; Mavi et al., 2023). Numerous studies displayed the deleterious impacts of conventional practices including tillage, chemical-based approaches for pest, and disease management through a reduction of soil organic matter, soil structure, diversity and abundance of soil organisms, and soil nutrients (Montgomery and Bikle, 2016). Moreover, conventional farming practices typically stimulate soil microbial activity to have a faster organic matter decomposition process, which in turn significantly reduce soil food webs, earthworm community, and density of soil microbes and soil organic matter (Wardle, 1995; Crittenden et al., 2014; Blakemore, 2018; Mcinga et al., 2020).

Organic farming methods involve a system that excludes synthetic inputs such as fertilizers, pesticides, hormones, and feed additives (USDA, 2012), and become one of the best options for combating against reduced soil health and productivity while promoting sustainable land use. Minimizing the export biomass from farms, particularly coconut husk, can enhance the potassium supply to palms through organic farming practices (Mensik et al., 2018, Magalhaes et al., 2023). Numerous studies on organic farming techniques indicate a predominant influence of biological activity and shifts in microbial community structure, along with their corresponding favored metabolic pathways (Nihad et al., 2023; Purba and Noer, 2023). Organic methods typically promote the growth of microbial diversity and abundance, as well as increase microbial biomass and enzyme activities (Ghabbour et al., 2017; Lori et al., 2017). In particular, research indicates that microbial biomass carbon and nitrogen had 41 % and 51 % higher, respectively, in organic plots, while microbial enzyme activity were higher in organic farm soil compared to conventional farms with a variation between 32 % and 74 % (Lori et al., 2017).

The Mekong Delta region is the primary area for coconut cultivation, with around 130,000 ha dedicated to this crop, constituting approximately 80 % of the country's total coconut acreage. Among the provinces in the Mekong Delta, Ben Tre stands out as a significant coconut hub, boasting the largest coconut plantation area of over 65,000 ha and yielding approximately 540 million fruits/year (Nguyen et al., 2019). Most coconut gardens aged over 20 years old, planted at the spacing of  $7.5 \times 7.5$  m and are mainly managed as monoculture with the application of chemical-based agricultural practices (Bhat et al., 2023).

Conventional farming systems are consistently deteriorating the physical, chemical and biological properties other than causing environmental pollution caused from excess fertilizer applications. The integral consequences on soil health and soil fertility of the two different farming systems including conventional and organic coconut farms in Ben Tre province, Vietnam have not been systematically investigated yet. Additionally, comparative coconut farming studies to determine the most suitable management practice has been neglected in that region. This study evaluated and compared the results of over 3 years of organic coconut farm practices versus that of conventional coconut farming practices for over 20 years on soil health and fertility. We aimed to detect the amendment potential for organic practices in conventional coconut production systems in terms of 1) the chemical, physical and biological soil quality properties, and 2) the composition and diversity of soil bacterial community structure. Our results hold remarkable potential to significantly assist agricultural managers in making decisions regarding management practices that are aligned with climate-smart agriculture (Paustian et al., 2016).

## 2. Material and methods

### 2.1. Study site

Mo Cay Nam district is characterized as a region predominantly involved in organic farming; a practice adopted by approximately 75 % of households with coconut trees aged over 20 years. In Mo Cay Nam district, the coconut plantations are grown with addition of manures as fertilizer without any pesticide application. In order to identify the farmers who practice organic farming in these two sites, a survey was carried out and only farmers who had been engaged in this practice for more than three years were chosen, and data regarding the kind and quantity of organic materials they employed in their main agricultural systems was gathered. The organic coconut farms were practiced by applying only certified organic fertilizer products supplied from Betrimex Viet Nam, and Luong Quoi Coconut Processing Limited Company and as well cow manure ( $20\text{--}40$  kg  $\text{plant}^{-1}$  year $^{-1}$ ), and chicken manure ( $5\text{--}8$  kg  $\text{plant}^{-1}$  year $^{-1}$ ). Moreover, in organic coconut farms farmers have not applied any chemical fertilizers and pesticides during cultivation time. Conversely, Mo Cay Bac district in Ben Tre province exhibits a contrasting profile, with a significant majority of farmers (73.3 %) following conventional and chemical-based agricultural methods for over two decades, same as the age of the coconut trees in this area. Moreover, Mo Cay Nam and Mo Cay Bac are neighboring districts with the baseline original soil that was not significantly

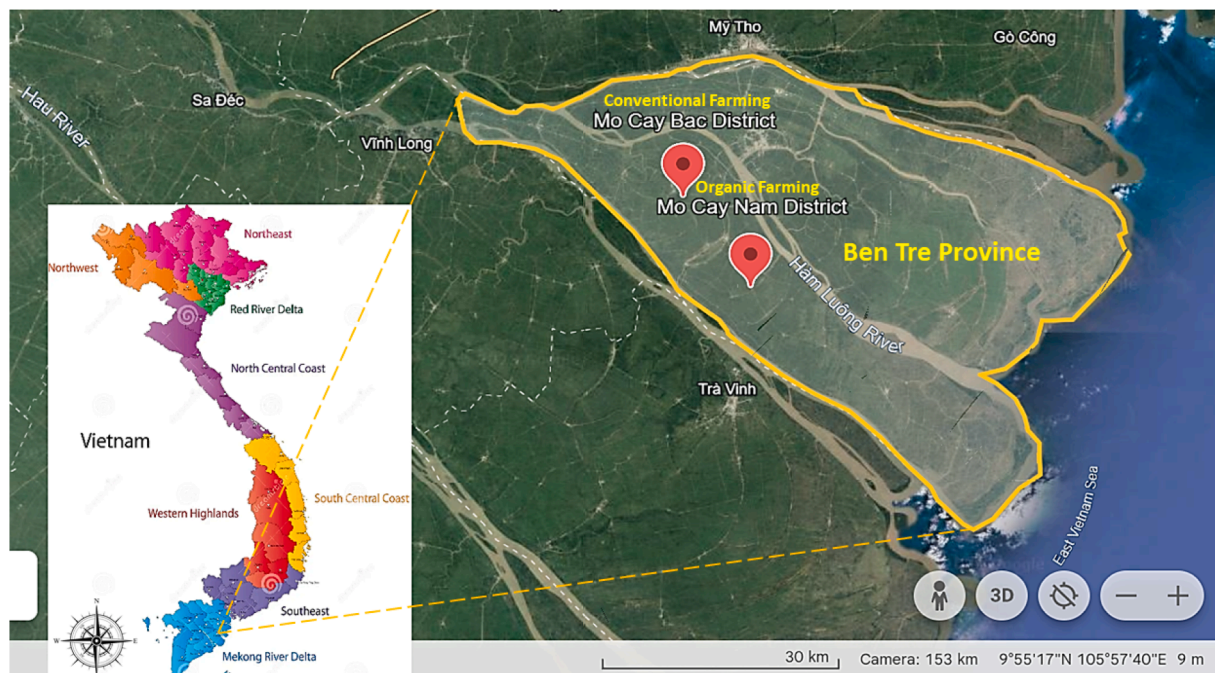


Fig. 1. Map of study site locations of two coconut farming practices adopted at Mo Cay Bac and Mo Cay Nam districts, Ben Tre, Vietnam (Google Earth Pro ver 7.1.8).

different at the beginning (Fig. 1). Therefore, Mo Cay Nam and Mo Cay Bac districts, in Ben Tre province, Vietnam were selected to take soil samples for organic and conventional coconut farms, respectively. Coconuts in these two districts are primarily grown for oil production. However, in the conventional coconut farms, farmers exclusively apply traditional management practices using an average amount of 0.38 N, 0.44 P<sub>2</sub>O<sub>5</sub>, 0.27 K<sub>2</sub>O kg tree<sup>-1</sup> year<sup>-1</sup> synthetic fertilizers including NPK 20–20–15, Urea, Long Thanh Super Phosphate, and KCl. Furthermore, they employ various herbicides, insecticides, and fungicides to manage and control weeds, pests, and related diseases and avoid application of organic materials.

## 2.2. Soil sample collection and analysis

In Ben Tre region 60060 ha is occupied with conventional farming while 17940 ha farm is applied for organic coconut farming. We have selected 12 farms from each coconut farm locations in Mo Cay Nam (organic farm) and Mo Cay Bac (conventional farm) which summed up to 24 farms to represent the Ben Tre region.

From each soil sampling coconut farm illustrating for an individual soil sample, the top 0–30 cm of soil layers from 10 different spots within each coconut farm were collected for an intensive representation of two different farming approaches and combined to constitute one soil sample following a Zig-Zag curve approach using a 5 cm diameter coring soil auger. We obtained one composite soil sample by pooling 10 subsamples collected from each farm plot. This resulted in 12 representative samples for organic farming systems and 12 samples for conventional farming systems. The conventional farm locations have been interpreted as the control samples. Fresh soil samples were carefully sealed in plastic bags, stored in a temperature-controlled cooler box at 4°C, and promptly delivered to the laboratory for comprehensive analysis. At the laboratory, after removing debris and passing through a 2 mm sieve, soil DNA extraction and soil microbiological properties were performed immediately. The remaining samples underwent air-drying, crushing, and sieving through a 2 mm sieve for analysis of soil physical and chemical properties. Two days after soil preparation, physical and chemical properties of soil were analyzed (Houba et al., 1995). In addition, undisturbed soil samples were taken by soil ring sampler, following the procedure of Mtyobile et al. (2019) that 3 ring samples of soil were randomly taken from each coconut farm to measure soil bulk density and porosity.

### 2.2.1. Soil physical properties

The soil's bulk density was assessed using metallic cores of known volume through the cylinder method. Briefly, the procedures are adopted from Mtyobile et al. (2019) and Van et al. (2022). The soil samples were possessed from three sampling points from soil layer 0–10 cm in each coconut farm and placed in plastic trays for the bulk density (BD) analysis in the laboratory. Following collection, soil cores were oven-dried at 105°C for 48 hours. Bulk density (BD) was determined by calculating the ratio of dry soil mass to the volume of the soil cores. The soil's total porosity was subsequently calculated using the bulk density values and particle density (Mtyobile et al., 2019). The particle density of soil is calculated as the ratio of the dry mass (in grams) of soil to the volume of soil particles. The

soil porosity was obtained using the equation:

$$\text{Soil porosity} = [1 - (\text{Soil bulk density} / \text{Particle density})] \times 100$$

### 2.2.2. Soil chemical properties

Soil  $\text{pH}_w$  ( $\text{H}_2\text{O}$ ) and EC were measured in 1:2.5 (w/v) soil slurry (Estefan et al., 2013; Bado et al., 2016). Soil  $\text{NO}_3^-$ -N and  $\text{NH}_4^+$ -N were extracted by 2 M KCl and detected at 540 and 650 nm wavelength, respectively using spectrophotometer (Beckman DU640i UV/Vis, Germany) (Haney et al., 2010). Exchangeable K ( $\text{BaCl}_2$  extractant solution) and total K were detected through atomic absorption spectroscopy (Thermo Scientific™, MA, USA) (Houba et al., 1995; Schaffers and Sykora, 2000). Available phosphorus was determined by the Bray II method and detected at 880 nm wavelength by UV spectrophotometer (Bray and Kurtz, 1945). Total phosphorus was detected by ammonium phosphomolybdate method and measured at 880 nm wavelength (Nagul et al., 2015). Total nitrogen was identified by the Kjeldahl method using semi-micro Kjeldahl Nitrogen Detector (Saez et al., 2013). Soil organic matter (SOM) was analyzed by Walkley and Black (1934).

### 2.2.3. Determination of the soil microbial density

The total number of viable bacteria, fungi, actinomycetes, nitrogen-fixing bacteria, phosphorus-solubilizing bacteria, potassium-solubilizing bacteria, silicate-solubilizing bacteria, and cellulose-decomposing bacteria was estimated using serial dilution and plating techniques (Dubey and Maheshwari, 1999). Briefly, 10 g of soil sample was suspended in 90 mL sterilized PBS (Phosphate-buffered saline), shaken on a shaker for 2 h prior to plating on the agar media. Tryptic soy broth (TSA), potato dextrose agar (PDA), Gause No.1, Burk's N-free, NBRIP, Alexandrov, and soil extract agar (SEA) medium were used for bacteria, fungi, actinomycetes, nitrogen-fixing bacteria, phosphorus solubilizing bacteria, potassium solubilizing bacteria, and silicate solubilizing bacteria, and cellulose decomposing bacteria, respectively. The plates, then, were incubated at 32 °C for microbial growth. The viable counts were taken after 1–4 days of incubation (Mehta and Nautiyal, 2001; Park et al., 2005; Zhang et al., 2023).

### 2.2.4. Determination of dehydrogenase enzyme activity

Dehydrogenase enzyme activity in soil was evaluated following the procedure described in Stevenson (1959) and Burdock et al. (2011). Briefly, six replicates of 1 g of soil (measured on a dry weight basis) were placed in individual 20 mL test tubes. Of those six, three test tubes remained non-sterilized, while the other three underwent sterilization at 121 °C for 20 minutes. To each test tube, one mL of 0.25 M Tris buffer, 50  $\mu\text{L}$  of a 0.04 M glucose solution, and 0.2 mL of a 0.008 M solution of chloride (INT) were mixed successively. Aluminum foil was used to cover test tubes placed in a rack, and the rack was subsequently placed inside the incubator at 30 °C for 6 hours. Afterwards, 10 mL of 99.5 % Ethanol ( $\text{C}_2\text{H}_5\text{OH}$ ) was supplemented to each test tube, and the sample was mixed thoroughly with a vortex machine for 1 minute and filtered via Whatman filter. Lastly, triphenyl formazan content generated by soil microbes in filtrate was quantified by UV–visible spectroscopy at a wavelength of 485 nm (Multiskan™ SkyHigh Microplate Spectrophotometer, SoftMax®Pro 7.0 software). Triple replication was conducted to obtain satisfactory results as micromoles of triphenyl formazan per kilogram of dry soil per hour.

### 2.2.5. DNA extraction, purification and sequencing

**2.2.5.1. Extraction of the total genomic DNA.** Genomic DNA extraction was carried out following the protocols of Thermo Fisher Scientific. DNA concentration extraction was performed utilizing an Invitrogen™ Qubit™ 4 Starter Kit.

**2.2.5.2. Amplicon generation and library preparation.** The sequencing library was prepared using a Meta<sup>VX</sup> Library Preparation Kit. In summary, 20–50 ng of DNA was utilized to produce amplicons covering the V3 and V4 hypervariable regions of the bacterial 16S rRNA gene. The forward primer contained the sequence 'CCTACGGRRBGCASCAGKVRVGAAT' and the reverse primer sequence was 'GGACTACNVGGGTWTCTAATCC' (Vassileva et al., 2023). The ABI GeneAmp 9700 PCR thermocycler (ABI, CA, USA) was then employed to amplify the two distinct hypervariable regions of the bacterial 16S rRNA gene through PCR amplification (Procedures followed the thermal cycling conditions presented in Table S2). Next, the size of PCR products was assessed using 1.5 % agarose gel electrophoresis, where fragments were anticipated to be around 600 base pairs. Finally, detection was performed using a microplate reader (Tecan, Infinite 200 Pro).

**2.2.5.3. Illumina sequencing and data analysis.** Next-generation sequencing was performed using the Illumina Miseq/Novaseq Platform, supplied by Illumina based in San Diego, USA, and facilitated by the company Azenta Life Science in China. This involved double-end sequencing, where the initial reads from both ends were paired to eliminate sequences containing the ambiguous 'N' character, retaining sequences with a length greater than 200 base pairs. Subsequently, quality filtering and chimeric sequence removal were performed. The obtained sequences were clustered into operational taxonomic units (OTUs) using VSEARCH clustering (version 1.9.6), with a sequence similarity threshold set to 97 %. The 16S rRNA reference database was established using Silva, version 138. The RDP (Ribosomal Database Program) classifier with a Bayesian algorithm was employed to analyze the taxonomy of species in the representative sequences. This analysis enabled statistical evaluation of the community composition of each sample across various levels of species classification. The microbial diversity within the soil samples (alpha and beta diversity indices, and rarefaction curves)



**Table 1**

Soil physical, chemical, and biological properties associated with two different coconut farming practices in Ben Tre province, Vietnam.

Soil properties		Conventional farming	Organic farming	F	CV (%)
Soil physical properties	Bulk density ( $\text{g cm}^{-3}$ )	1.20 <sup>a</sup>	1.08 <sup>b</sup>	*	11.6
	Soil porosity ( $\Phi$ , %)	51.3 <sup>b</sup>	53.4 <sup>a</sup>	*	2.72
Soil chemical properties	pH <sub>w</sub> value	5.01	5.06	ns	9.22
	EC value ( $\text{mS cm}^{-1}$ )	0.51 <sup>b</sup>	1.14 <sup>a</sup>	*	6.14
	Total N (%N)	0.12 <sup>b</sup>	0.15 <sup>a</sup>	*	2.16
	Total P (%P <sub>2</sub> O <sub>5</sub> )	0.13 <sup>b</sup>	0.17 <sup>a</sup>	*	19.1
	Total K (%K <sub>2</sub> O)	1.40	1.46	ns	14.6
	Soil Organic Matter (%)	2.99 <sup>b</sup>	3.54 <sup>a</sup>	*	17.0
	Nitrate (NO <sub>3</sub> , $\text{mg kg}^{-1}$ )	4.69 <sup>b</sup>	6.42 <sup>a</sup>	*	26.5
	Ammonium (NH <sub>4</sub> <sup>+</sup> , $\text{mg kg}^{-1}$ )	22.3 <sup>b</sup>	38.9 <sup>a</sup>	*	31.9
	Available phosphorus (P <sub>av</sub> , $\text{mg kg}^{-1}$ )	26.8 <sup>b</sup>	69.0 <sup>a</sup>	*	73.9
	Exchangeable potassium (K <sub>ex</sub> , $\text{meq } 100 \text{ g}^{-1}$ )	0.59 <sup>b</sup>	1.49 <sup>a</sup>	*	55.2
Soil microbial densities ( $\log (\text{CFU g}^{-1} \text{ soil})$ )	Bacteria	6.01 <sup>b</sup>	6.26 <sup>a</sup>	*	4.19
	Actinomycetes	4.55 <sup>a</sup>	4.10 <sup>b</sup>	*	7.56
	Fungi	3.65	3.46	ns	7.96
	Nitrogen fixing bacteria	5.84	6.06	ns	5.58
	Phosphorus solubilizing bacteria	6.45 <sup>a</sup>	5.23 <sup>b</sup>	*	12.9
	Potassium solubilizing bacteria	5.82	5.98	ns	4.31
	Silicate solubilizing bacteria	4.67	4.76	ns	6.29
	Cellulose decomposing bacteria	3.82 <sup>b</sup>	4.18 <sup>a</sup>	*	17.0
Soil enzyme activity	Dehydrogenase ( $\mu\text{g TPF g}^{-1} \text{ soil hour}^{-1}$ )	0.47 <sup>b</sup>	0.61 <sup>a</sup>	*	2.03

Note:

\* means in the same rows with different letters are significantly ( $p < 0.05$ ) different according to *t*-test; ns: non-significant; N: nitrogen; P: phosphorus; K: potassium; N: nitrogen; P<sub>av</sub>: available phosphorus, K<sub>ex</sub>: exchangeable potassium; CFU: Colony forming unit; TPF: triphenyl formazan.

was investigated by calculating Shannon, Chao1, and observed species metrics. The Chao1 metric represents for the species richness while the Shannon metric estimates OTU abundances, and elucidates for both richness and evenness. The detected species metric is the count of unique OTUs found in the sample. For beta diversity analysis of soil samples, both the weighted and unweighted UniFrac approach were used to produce the distance matrix. Microbial diversity was analyzed using sequence abundances by taking Weighted UniFrac into account.

### 2.3. Statistical analysis

The paired *t*-test specifically compared means of paired observations from both farming practices. These statistical analyses offered a comprehensive insight into the interplay between soil properties. The findings are expressed as mean values accompanied by their respective standard deviations (SD) and significant differences were verified by paired *t*-test. Statistical tests were conducted with the Minitab (version 19) software. Pearson's correlation was analyzed using PROC CORR in SAS 9.4 while the principal component analysis (PCA) was conducted by R studio software with the built-in factoextra R package to examine the relationships among soil properties under different practices in coconut farms.

## 3. Results and discussion

### 3.1. Effect of organic and conventional practices on soil physicochemical, and biological properties

#### 3.1.1. Soil physical properties

Organic farming positively influenced on soil bulk density and soil porosity by value of  $1.08 \text{ g cm}^{-3}$  and 53.4 %, respectively as compared to that of conventional farming,  $1.20 \text{ g cm}^{-3}$  and 51.3 %, respectively (Table 1). Bulk density and soil porosity are critical soil physical properties needed for evaluating the degree of soil compaction and the amount of water and air in soil (Mtyobile et al., 2019; Van et al., 2022). These finding indicated that organic farming management reduces the risk of soil compaction. The reduced soil bulk density under organic farming practices is attributed to the increased soil organic matter content (Shepherd, Markus, 2002). According to Karami et al. (2012), the application of diverse organic matter sources could decrease soil bulk density while enhancing soil porosity and water infiltration rate. The lower bulk density and higher porosity of soil under organic farming practices are important for soil, air and nutrient management. This means that higher water, air, and nutrients under organic farming can be easily transferred into deeper layers of soil and stored there for later usage, especially when there is heavy rain compared with conventional farming practices (Williams et al., 2020). Water and nutrient evaporation reduction are also critical for water and nutrient conservation in water and nutrient-limited regions (Williams et al., 2022). These consequences of organic practices could add to the improvement of the soil health system, especially in rain-fed conditions where precipitation is widely varied.

#### 3.1.2. Soil chemical properties

Soil pH (5.01 and 5.06) and total potassium concentration (1.40 and 1.46 for conventional vs organic farming, respectively) did not

significantly differ from each other ( $p < 0.05$ ) (Table 1). This means that within a period of 4 years, organic coconut farm practices did not influence the soil pH and total potassium concentration although soil pH and total potassium concentration were marginally higher in farms under an organic production system (Table 1). However, the organic system showed significantly higher values of soil EC, TN, TP,  $\text{NO}_3^-$ ,  $\text{P-PO}_4^{3-}$ , and exchangeable potassium in comparison to the conventional system.

In the organic coconut farming model, the values of soil EC, TN, TP, soil organic matter,  $\text{NO}_3^-$ ,  $\text{P-PO}_4^{3-}$ , and exchangeable potassium were  $1.14 \text{ mS cm}^{-1}$ ,  $0.15 \% \text{ N}$ ,  $0.17 \% \text{ P}$ ,  $3.54 \% \text{ SOM}$ ,  $6.42 \text{ mg kg}^{-1} \text{ NO}_3^-$ ,  $38.9 \% \text{ mg kg}^{-1} \text{ NH}_4^+$ ,  $69.0 \% \text{ mg kg}^{-1} \text{ P}$ ,  $1.49 \text{ meq } 100 \text{ g}^{-1}$ , respectively, while in the conventional coconut model they were much lower and obtained values were  $0.51 \text{ mS cm}^{-1}$ ,  $0.12 \% \text{ N}$ ,  $0.13 \% \text{ P}$ ,  $2.99 \% \text{ SOM}$ ,  $4.69 \text{ mg kg}^{-1} \text{ NO}_3^-$ ,  $22.3 \text{ mg kg}^{-1} \text{ NH}_4^+$ ,  $26.8 \text{ mg kg}^{-1} \text{ P}$ ,  $0.56 \text{ meq } 100 \text{ g}^{-1} \text{ K}$ , respectively. This means that by increasing available phosphorus by 158 %, exchangeable potassium by 156 %, soil EC by 124 %,  $\text{NH}_4^+$  by 74 %,  $\text{NO}_3^-$  by 37 %, total phosphorus content by 31 %, and soil organic matter by 18 %, organic coconut farming increases significantly soil chemical properties and make it more favorable to better soil biodiversity. Many of these soil chemical characteristics are linked to the use of organic amendments (Williams et al., 2022; Gopinath et al., 2023; Zhang et al., 2023).

Our research indicated a notable increase in soil organic matter within organic coconut farms compared to conventional ones. This result follows Waring et al. (2022) who indicated that shifting from traditional to organic production systems improved soil organic carbon content. This increment in soil organic matter in organic coconut farms could be due to the addition of organic sources from the coconut tree residues and organic fertilizer additions. Those organic supplements led to a gradually higher accumulation of soil organic matter (Chakraborty et al., 2011; Rahman et al., 2022). Previously, some studies indicated that long-term practices of organic amendments in organic farms strongly had a notable improvement in soil organic matter (Koishi et al., 2020). Similarly, Messmer et al. (2012) found 44 % increase at soil organic matter in the 0–15 cm layer of soil profile over four years for organic farming practices. The primary factor was the enhanced soil fertility in organic farming, creating an optimal growth environment for microorganisms. Organic fertilizers and organic residues from coconut trees provided carbon, nitrogen, phosphorus, and potassium sources that were effectively absorbed, decomposed, and released by soil microorganisms. Contrarily, the chemical fertilizer and pesticide-based farming systems bearing a lower soil organic matter and cellulose-decomposing bacterial population, have diminished organic matter decomposition process, causing less plant available nutrient in the conventional farming soil for plant and soil microorganisms to take up (Karami et al., 2012; Li et al., 2017; Tang et al., 2023).

### 3.1.3. Soil microbial populations

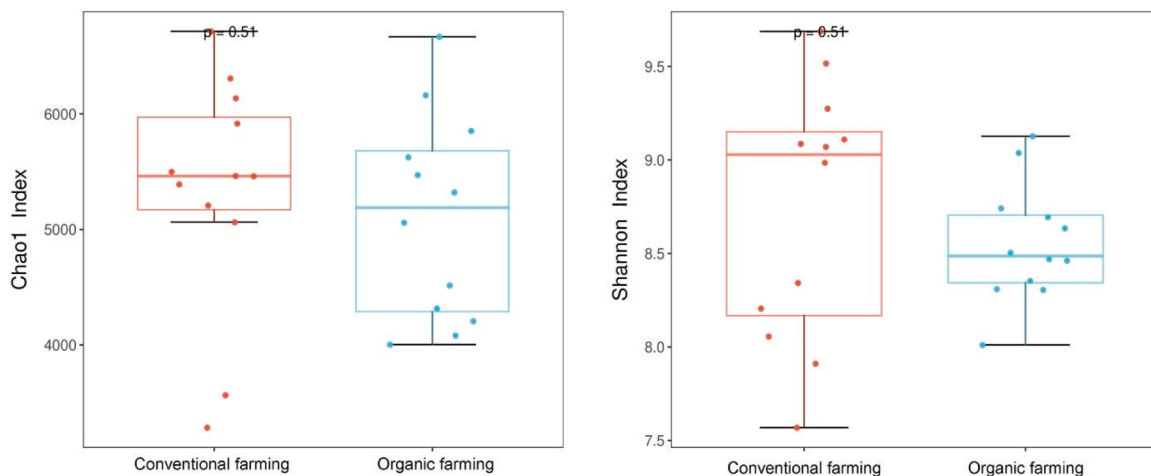
No significant differences between the two types of management were observed for soil fungal populations, and biological nitrogen fixing, potassium solubilizing, and silicate solubilizing soil bacterial populations ( $p > 0.05$ ) (Table 1). One explanation for our findings of no significant difference between two farms with regard of nitrogen fixing bacteria may be that, the time for the organic farm practice was not long enough to change the number of the nitrogen fixing bacteria although the number of nitrogen fixing bacteria in the organic coconut farms was slightly higher ( $9.06 \text{ CFU g}^{-1}$ ) to compare with that of the conventional coconut farms ( $5.84 \text{ CFU g}^{-1}$ ).

However, total cultural bacterial numbers and numbers of cellulose-decomposing bacteria were significantly higher in the soil of the organic farms compared to the conventional farms ( $p < 0.05$ ) (Table 1). The population of cellulose decomposing bacteria in the organic farming coconut system averaging  $4.18 \text{ Log colony forming unit (CFU) (CFU g}^{-1})$ , is  $9.42 \%$  higher and underlines a statistically significant difference compared to the conventional farming system, which is  $3.82 \text{ Log (CFU g}^{-1})$ . The difference is potentially caused by the application of organic fertilizer, which introduced a substantial amount of cellulose into the soil, promoting the activity of soil-borne cellulose-degrading bacterial strains.

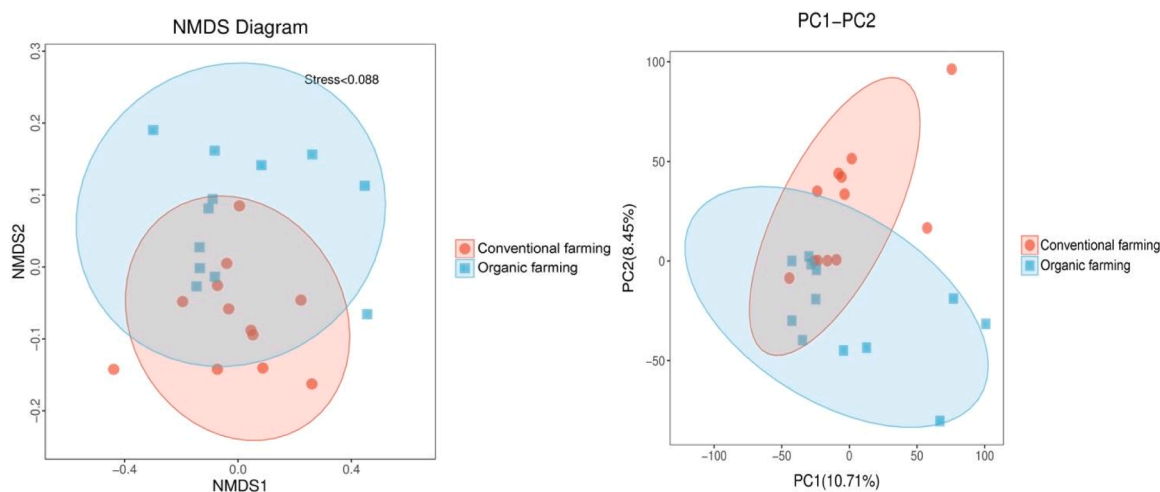
Utilization of these functional bacteria in compost and surface soil has the potential to enhance cellulose degradation (Li et al., 2023; Zhang et al., 2023). When the heterotrophic bacterial population constantly receives organic carbon inputs in the organic coconut farming system, the population of soil bacteria, and cellulose decomposing bacteria increases by using the available source of carbon (Nirukshan et al., 2016). Lazcano et al. (2013) showed similar enhanced numbers of bacterial and fungal populations in organic farming applied with organic manure regularly. Accordingly, the bacterial population responded to the added organic fertilizer coconut farms while the population of fungi were the same in both types of management. However, in the literature fungal populations of agricultural soils have been positively described as impacted by organic amendments (Nakhro and Dkhar, 2010; Swer et al., 2011). In conventional farming, the phosphorus solubilizing bacteria rate averaged  $6.45 \text{ Log (CFU g}^{-1})$ , which was  $23 \%$  higher and displayed a significant difference when compared to the organic coconut farming system with the average phosphorus solubilizing bacteria population of  $5.23 \text{ Log (CFU g}^{-1})$  ( $p < 0.05$ ). Similar observations were made about actinomycetes. This could be attributed to the lower availability of nutrients in conventional farms. Likely, Bao et al. (2021), stated that in less fertile soils, a higher population of actinomycetes, and an increased presence of functional genes are associated with the decomposition of organic matter compared to soils with higher fertility. Thus, such results have been orienting the development of the organic system in coconut farms.

### 3.1.4. Soil enzyme activity

Table 1 represents the results of assessing dehydrogenase enzyme activity in organic vs. conventional systems in Mo Cay Bac and Mo Cay Nam districts, Ben Tre province, Vietnam. Numerically, the highest soil enzyme activity dehydrogenase was found in organic farming systems with a value of  $0.61 \text{ } \mu\text{g TPF g}^{-1} \text{ hour}^{-1}$  and  $29.7 \%$  higher while conventional farming systems achieved  $0.47 \text{ } \mu\text{g TPF g}^{-1} \text{ hour}^{-1}$  ( $p < 0.05$ ). This emphasizes that within organic coconut farming systems, a consistent and continuous supply of organic carbon sources as the energy is provided to soil microorganisms, inducing to an elevation in the microbial population, and enhancing the activity of the dehydrogenase enzyme within this soil category (Cardarelli et al., 2023). Similarly Wells et al. (2000) reported an increase in soil dehydrogenase enzyme activity in organic farms especially by bacteria resulting in higher dehydrogenase activity.



**Fig. 2.** A comparison was conducted between the Shannon and Chao1 diversity indices for conventional coconut farms (n = 12) and organic coconut farms (n = 12). Chao1 assesses the species count, while Shannon evaluates the effective species count for alpha diversity. There was no significant difference between conventional and organic coconut farming practices in terms of Chao1 richness (p = 0.51, t-test) and Shannon richness (p = 0.51, t-test).



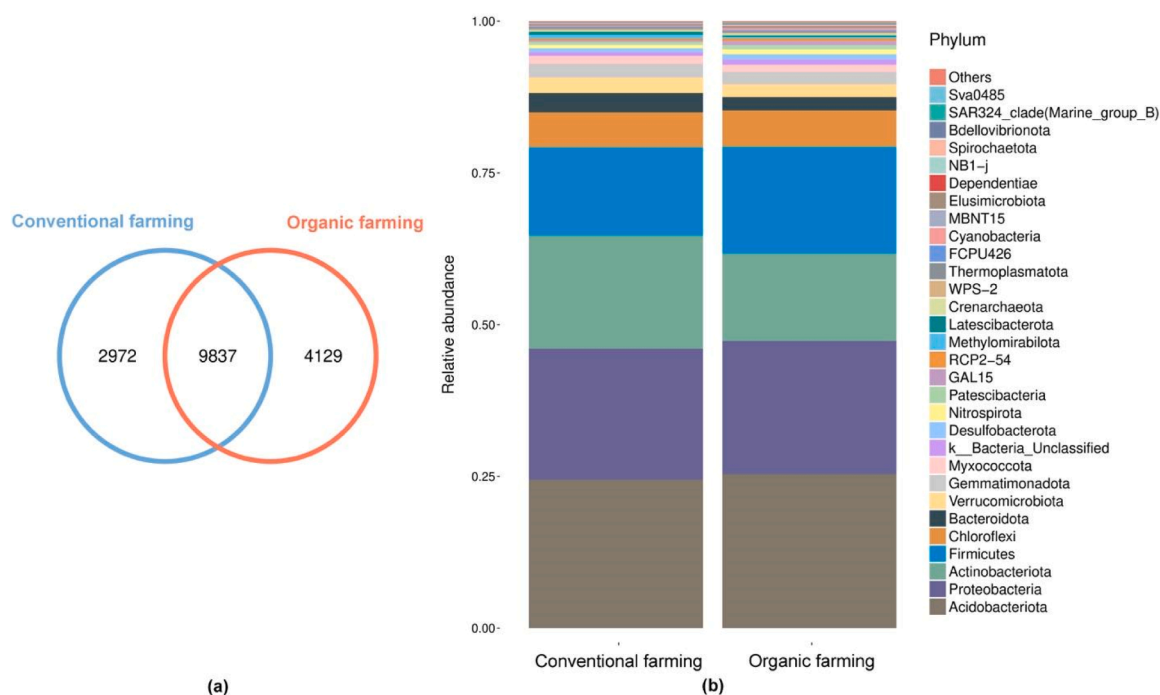
**Fig. 3.** Comparison between the non-metric multidimensional scaling (NMDS) feasibility and Principal Coordinates Analysis (PCoA) analysis for beta diversity of soil bacterial community for conventional coconut farms (n = 12) and organic coconut farms (n = 12). Note: NMDS - Each point represents a sample, and the distance between the points indicates the degree of difference. Stress < 0.2 indicates NMDS can accurately reflect the difference between the groups.

3.1.5. Variation of soil prokaryotic communities

3.1.5.1. Soil alpha and beta diversity indices. In the effort to characterize soil microbiota composition, the chao1 diversity index showed that community richness was consistent between conventional and organic farms, suggesting a comparable number of alpha-diversity (measured by observed richness or evenness of taxa) in both coconut farming systems (Fig. 2). Likewise, the Shannon diversity index showed no difference between the two farming systems (conventional and organic), suggesting a comparable number of alpha diversities in both coconut farming systems (Fig. 2).

The short-term application of organic farming practices in this study has not yet had a positive effect on the richness of soil bacterial species. In natural ecosystems, healthy and disease-free plants benefit from a diverse array of microbes, forming a complex plant-associated microbial community often referred to as the plant's "second genome." This microbial community plays a significant role in enhancing plant growth and productivity (Berendsen et al., 2012; Hacquard, 2016). Our results are consistent with those of Durrer et al. (2021), who concluded that the short-term implementation of organic practices in maize cultivation did not result in significant alterations in the  $\alpha$ -diversity indices of the bacterial community.

Previous studies comparing conventional and organic farming practices on microbial communities have also noted a beneficial



**Fig. 4.** (a) A Venn diagram illustrating the overall number of OTUs found in soil from conventional and organic coconut farming systems, (b) A stacked bar plot displaying the relative abundance of various phyla in the two distinct farming systems. Phyla with relative abundances less than 0.01 % were grouped together and labeled as "others" ( $n = 12$  for each farming system).

impact of short-term organic coconut farming practices on beta diversity (Olden et al., 2004; Constancias et al., 2014; Hartmann et al., 2015; Lupatini et al., 2017). The consistent presence of various organic substrates in the soil, including organic fertilizers, coconut tree residues, and biofertilizer applications, created diverse habitat niches. These niches could be inhabited by a diverse microbial community, leading to an enhancement in soil beta-diversity and the overall structure of the soil microbial community. The reduced heterogeneity, reflected as lower beta diversity in the microbial community of the conventional coconut system, suggests a trend towards increased similarity in the composition of soil bacterial communities across various taxonomic or functional groups (Olden et al., 2004). Other studies have similarly affirmed that soil microorganisms tend to exhibit greater diversity and abundance in organic systems compared to conventional ones across different soil types (Wang et al., 2016; Crowder et al., 2010; Klaus et al., 2013).

Using sequence similarity, the non-metric multidimensional scaling (NMDS) matrix was created from the OTU percentages in each soil sample. This matrix was analyzed to assess the similarity of beta diversity, which represents the variation in community composition (i.e., the observed taxa identities) among samples within a habitat across different soil samples (Fig. 3). NMDS ordination revealed distinct beta diversity associated with organic coconut farm practices (Fig. 3). Furthermore, principal coordinate analysis (PCoA) was utilized to illustrate the clustering outcomes of bacterial soil samples based on the Bray–Curtis distance. The soil samples from organic coconut farming system were distributed in different quadrants as compared with the soil samples from the conventional coconut farming system, indicating that these soil samples from two different farming practices had substantial environmental heterogeneity and significant separation of the soil communities (Fig. 3). The farming method played a significant role in influencing the taxonomic and phylogenetic variabilities of the microbial communities. Specifically, the organic coconut farming system exhibited a greater impact on community variability compared to conventional coconut farming. Our research suggests that maintaining a steady organic coconut farming system has beneficial effects on microbial community variability. Specifically, it promotes more diverse communities in organic systems compared to conventional ones.

In the organic coconut farms, use of only organic fertilizers contributes to increasing the organic matter content in the soil, and the absence of chemical spraying could protect the microbial community in the soil. These are two main factors that contribute to the difference in soil properties between the two groups of coconut farming practices, because adding organic matter is a prerequisite, an important component, related to all physical, chemical and biological properties of the soil (Fageria, 2012; Lori et al., 2017), suggesting that organic farming helps increase from 32 % to 84 % carbon and N in microbial biomass as well as the activity of dehydrogenase, urease and protease enzymes compared to the conventional farming system. In addition, many studies have evaluated the impact of organic fertilizers from different sources on soil microbial communities showed that the use of organic fertilizers helped to increase biomass and respiratory activity of soil microorganisms, thereby increasing soil chemical properties through the mineralization of their organic matter (Ridder et al., 2010). Riaz et al. (2017) stated that the provision of organic fertilizers to the soil enhanced the soil microbial community in numbers and diversity, which is important for nutrient cycling and pest control arising from the soil environment, especially organic farming stimulated an increase of the numbers of cellulose decomposing bacteria, which is significant



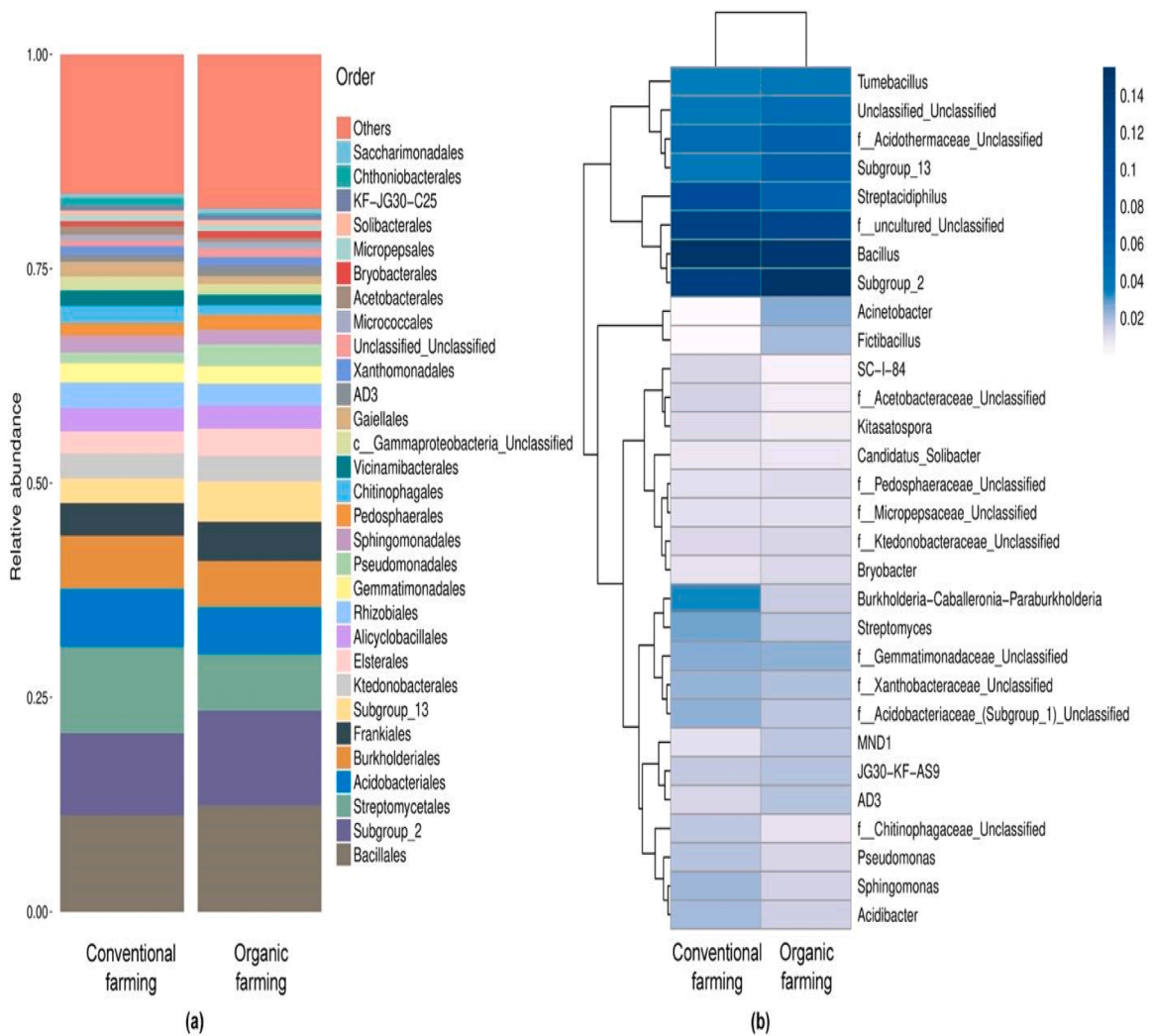


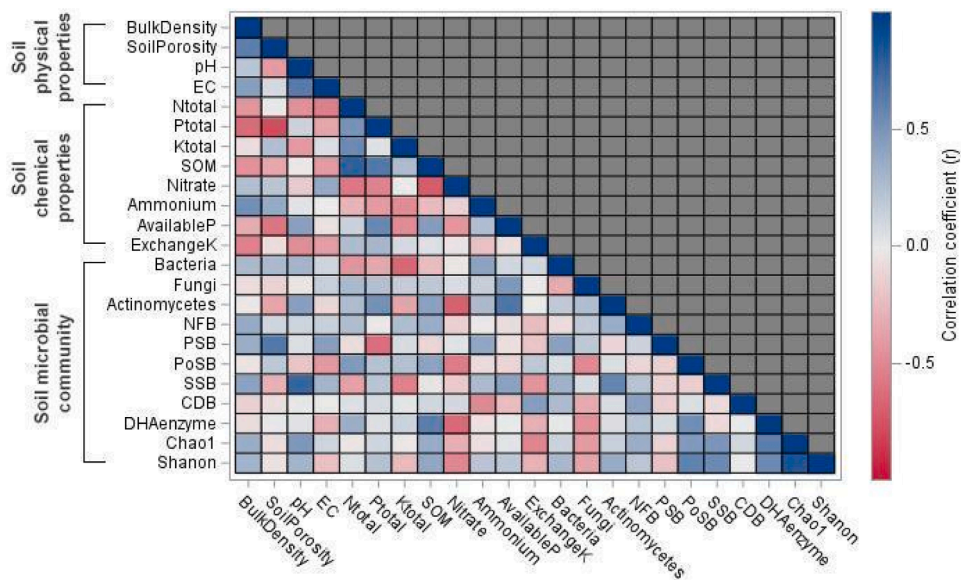
Fig. 5. (a) Relative abundance of the top 30 bacterial orders in the two different soil samples (Group 1: conventional coconut farming practices, and Group 2: Organic coconut farming practices), (b) Heat map analysis of the top 30 bacterial Genera in the two different soil samples.

in maintaining soil fertility through the nutrient conversion cycle for crops (Bramble et al., 2024; Ratul et al., 2018).

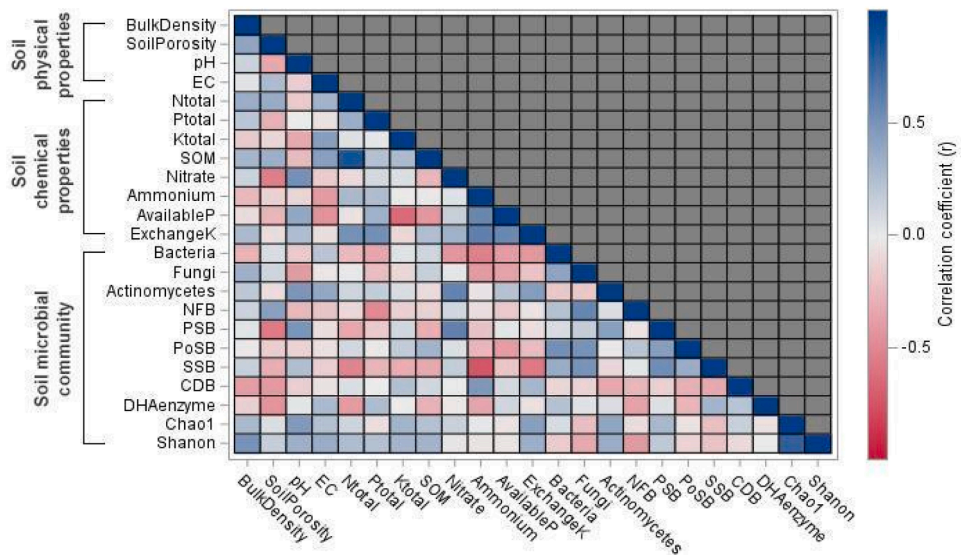
**3.1.5.2. Composition of soil bacterial community structure.** In total, 26,775 bacterial OTUs (operational taxonomic unit) were identified, with 2972 OTUs (11.1 %) exclusively found in soil from conventional coconut fields and 4129 OTUs (15.42 % of total OTUs) in soil from organic coconut fields (Fig. 4a) which is 38.9 % higher than conventional farming system. Additionally, 9837 OTUs (73.84 %) were shared between soils from fields managed with both organic and conventional practices. The taxonomic diversity of the prokaryotic community was influenced by the different farming methods. The findings revealed that classified sequences were associated with the top 30 bacterial phyla across both farming practice groups (Fig. 4b). Distinct patterns of variation at the phylum level were evident between the groups practicing organic coconut farming and those practicing conventional coconut farming. Organic coconut farming practices improved the relative abundances of 10 soil bacterial phyla including Acidobacteriota (25.39 %), Proteobacteria (21.96 %), Firmicutes (17.59 %), Chloroflexi (5.99 %), k\_Bacteria\_Unclassified (0.89 %), Desulfobacterota (0.84 %), Nitrospirota (0.84 %), Patescibacteria (0.68 %), GAL 15 (0.67 %), and RCP2-54 (0.48 %) as compared to the soil samples collected from the traditional coconut farming practices in which only 4 soil bacterial phyla including Actinobacteriota (18.61 %), Verrucomicrobiota (2.56 %), Gemmatimonadota (2.28 %), and Myxococcota (1.27 %) were stimulated to increase (Fig. 4b).

The most abundantly identified bacteria phyla in both organic and conventional coconut farms was found to be Acidobacteriota, Proteobacteria, Actinobacteriota, Firmicutes, Chloroflexi, Bacteroidota, Verrucomicrobiota, and Gemmatimonadota. Further analysis indicated that Acidobacteriota, Proteobacteria, Firmicutes (Bacillota), and Chloroflexi were the top four phyla that increased significantly in soil samples in the organic coconut farm group. These top four soil bacterial phyla are considered as beneficial bacteria in soil with different functionality for soil ecology (Kalam et al., 2020). Initially, Acidobacteriota thrive and proliferate in acidic and

a) Organic farming



b) Conventional farming



**Fig. 6.** Pearson’s correlations among soil physio-biochemical properties under organic (a) and conventional (b) coconut production; *Note: Correlation coefficient (r) > 0 indicates positive association. Gradient color map represents the power of association between variables; darker blue indicating positively stronger relationship, deeper red indicating negatively stronger relationship.* SOM: Soil organic matter; NFB: Nitrogen fixing bacteria; PSB: phosphorus solubilizing bacteria; PoSB: Potassium solubilizing bacteria; CDB: Cellulose decomposing bacteria; DHA: Dehydrogenase activity, SSB: Silicate solubilizing bacteria.

nutrient-poor environments, so they are characterized as oligotrophic bacteria (Kielak et al., 2016). Proteobacteria includes *Rhizobium* sp., *Agrobacterium* sp. benefits for plant and soil (Rahimlou et al., 2021). Firmicutes (Bacillota) contains notable genera of Bacillota including Bacilli, order Bacillales and are gram-positive and obligate anaerobic bacteria possessing spore-forming, and cocci- or rod-shaped characteristics. They can be used as bioremediation and phytoremediation of heavy metals and organic chemical pollutants in soils (Hashmi et al., 2013) other than bio-fertilizer, and biocontrol agents. The Chloroflexota encompass a bacterial phylum comprising aerobic thermophiles that utilize oxygen and thrive in elevated temperatures; anoxygenic phototrophs, which utilize light for photosynthesis (such as green non-sulfur bacteria), as well as anaerobic halo-respirers that utilize halogenated organic compounds (like toxic chlorinated ethenes and polychlorinated biphenyls) as electron acceptors (Ward et al., 2009).

Inversely, the most significantly predominant phylum stimulated in conventional farming soil samples was Actinobacteriota

(18.61 %), which has specialized metabolism inhabiting competitive and nutrient limited environments. Actinobacteria can survive much better than other groups of soil microbes and play multifunctional roles (Mitra et al., 2022). Numerous actinobacteria play roles in solubilizing and mobilizing nutrients, particularly phosphates and iron. Additionally, they serve as supportive bacteria in mycorrhizal symbiosis and biological nitrogen fixation (Boukhatem et al., 2022).

When comparing organic and conventional coconut farming methods, it was evident that the organic coconut farming approach led to a notable rise in the relative abundance of seven soil bacterial orders out of 30 prevalent genera including Bacillales, Subgroup\_2, Frankiales, Subgroup\_13, Elsterales, Pseudomonadales, Pedosphaerales, and AD3 (Fig. 5a). Treatment with conventional coconut farming practices caused an increment of abundance of Streptacidiphilus, Burkholderia-Caballeronia-Paraburkholderia, Streptomyces, Acidobacteriaceae (Subgroup\_1) Unclassified, Chitinophagaceae Unclassified, Pseudomonas, Sphingomonas, and Acidobacter, and reduced abundance of the potentially favorable Acinetobacter and Fictibacillus (Fig. 5b).

We found that the relative abundance of Bacillales, Frankiales, Elsterales, Pseudomonadales, and Pedosphaerales significantly increased with organic farming practices. When farming practices are altered, the diversity of the bacterial community changes, leading to variations in its functionality within soil ecological systems (Knelman et al., 2012; Eo and Park, 2016; Zhang et al., 2016). The variation in the diversity of the bacterial community was primarily influenced by changes in the relative abundance of specific bacterial orders. This change enhances the functional productivity of the bacterial community in coconut planting soil (Gopal et al., 2009; Cardoso et al., 2021) and potentially reduce the relative abundance of pathogens and their pathogenic effects (Pirttilae et al., 2021; Wei et al., 2023). Murillo et al. (2023) observed that numerous *Bacillus* spp. within the Bacillales order, originating from the avocado rhizosphere, exhibited the capability to boost plant growth and alleviate symptoms of *Fusarium* wilt in *A. thaliana* when introduced into the soil which clearly indicates the potential of these strains and their metabolites as biocontrol agents against avocado pathogens and biofertilizers.

Diagne et al. (2013) and Nouioui et al. (2019) indicated that nitrogen-fixing bacteria *Frankia* (Frankiales) reduced the negative impacts of abiotic and biotic stresses. Introducing *Frankia* through inoculation notably enhances plant growth, biomass, shoot and root nitrogen content, as well as the survival rate after transplantation in fields of actinorrhizal plants (Narayananamy et al., 2020).

Elsterales were identified as advantageous genera that could potentially enhance the growth of tobacco plants (Chen et al., 2022). *Pseudomonas* from the Pseudomonadales order is present both in the rhizosphere and within the plant itself, contributing to soil and plant defense mechanisms. The *Pseudomonas* spp are known to regulate plant pathogens and effectively manage diseases through direct and indirect means. *Pseudomonas* spp. can serve as plant growth-promoting rhizobacteria (PGPR), aiding in nitrogen fixation, phosphorus and potassium solubilization, and production of phytohormones, lytic enzymes, volatile organic compounds, antibiotics, and secondary metabolites under stress conditions (Oleńska et al., 2020).

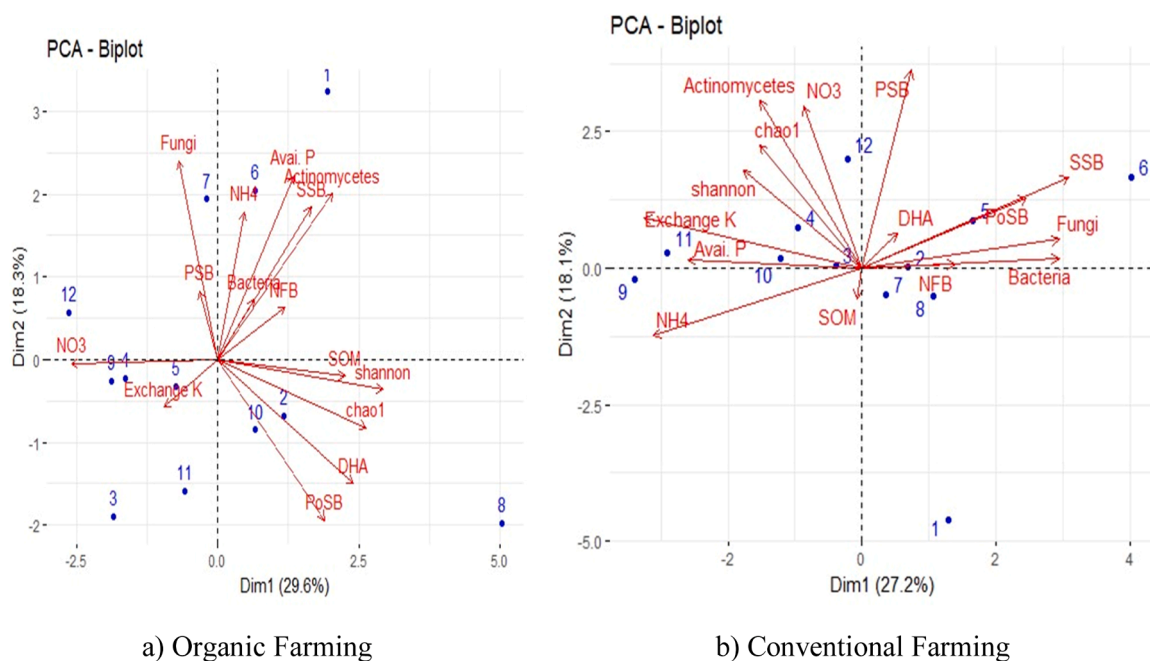
These findings imply that organic coconut farming methods may enhance soil health conditions, fostering an environment conducive to the growth of potentially beneficial microorganisms.

### 3.2. Relationship among soil physio-biochemical properties in organic and conventional coconut productions

The correlations of soil physical, chemical, and biological properties varied between two coconut farming systems. Regression revealed predominant of significant correlations in coconut farms applying organic practices, as compared to the conventional system (Fig. 6). Adopting organic farming practices significantly led to the improvements in soil organic matter, soil porosity, electrical conductivity, total nitrogen, phosphorous, exchangeable potassium and their available forms, soil microbial density including the soil bacteria, and cellulose decomposing bacteria. Both management practices revealed significant correlations between soil organic matter and total nitrogen indicating the nitrogen is sourced from the soil organic matter. Porosity is an important soil quality indicator associated with water penetration and nutrient element transfer in the rhizosphere (Pagliai et al., 2004). Under organic management, the soil organic matter and soil porosity were found significantly related to total phosphorous, available phosphorous, and phosphorous solubilizing bacteria which was not indicated in coconut farm implementing conventional system which is supported by Girma et al. (2020) too. The presence of phosphorus bacteria under organic management system provided higher available phosphorus and total P so on. Highly correlated covariates in organic farming include total nitrogen and soil organic matter, Chao1, and Shannon indices which are later found also in our PCA analysis, silicate solubilizing bacteria and pH.

In our study, reduction in total phosphorus in the soil was primarily influenced by the abundance of phosphorus-solubilizing bacteria, subsequently leading to an enhancement in available phosphorus. Notably, the increase in soil organic matter under organic practices was identified as the primary contributing factor to the augmentation of dehydrogenase enzyme abundances which aligns well with a meta-analysis conducted by Lori et al. (2017). In conventional coconut production, no significant correlation was found to be associated with the improvement in soil physical properties as well as soil microbial richness and abundance indices except for the relatively high correlation between actinomycetes and phosphorus solubilizing bacteria with nitrate. Also, potassium solubilizing bacteria have been found to be relatively highly correlated with the abundance of bacteria and fungi. However, in this study we found that the soil EC of the conventional coconut farm soils was significantly lower than that in the organic coconut farm soils, meaning that an acidification process has been happening in conventional farming soils due to the intensive application of chemical fertilizer, and soil acidification causes an important negative impact on soil bacterial abundance and diversity (Li et al., 2023). Moreover, Santos et al. (2020) reported that the soluble salts as a major component of soil acidification with effects on plant growth and microbial activity. The incorporation of intensive tillage, chemical fertilizer, pesticide, and herbicide applications, as commonly seen in conventional farming systems, had adverse effects on soil physical and chemical properties, posing a serious threat to soil microbial communities (Dubey et al., 2019; Lupatini et al., 2017).

PCA results demonstrate the positive effect of organic management on soil organic matter, actinomycetes abundance, potassium



**Fig. 7.** PCA of soil physio-biochemical parameters under organic (a) and conventional (b) coconut production. *SOM*: Soil organic matter; *NFB*: Nitrogen fixing bacteria; *PSB*: phosphorus solubilizing bacteria; *PoSB*: Potassium solubilizing bacteria; *CDB*: Cellulose decomposing bacteria; *DHA*: Dehydrogenase activity. *SSB*: Silicate solubilizing bacteria.

solubilizing bacteria, and dehydrogenase activity in contrast to conventional farming practices, which is emphasized in Table 1. Moreover, Chao1 and Shannon indices are similar in both farming systems. These two diversity indices were positively correlated to the soil organic matter in the organic coconut farming system and positively related to the abundance of actinomycetes in the conventional coconut farming system. High demand for dissolved potassium by coconut trees in the soil can lead to competition for available potassium sources with microbial communities. Hence, the activity of potassium-solubilizing bacteria is vital in coconut-cultivated soil to generate sources of dissolved potassium for such bacterial group's growth and survival. While the high correlation of nitrogen fixing bacteria exists with silicate solubilizing bacteria, available potassium, actinomycetes, and ammonium in organic farming contributing to Dim 1, in conventional farming we found more correlation among dehydrogenase enzyme activities with potassium solubilizing bacteria, silicate solubilizing bacteria, nitrogen fixing bacteria and fungi corresponding mostly to Dim 2 (Fig. 7). It's also noteworthy that previous studies by Lu et al. (2023) have demonstrated that the potassium requirement of coconut trees exceeds the available potassium. Additionally, incorporation of coconut husks residues in organic farming practices greatly contribute to improved supply of available potassium to coconut palms. These further underscores the significance of potassium in the growth and yield of coconut trees (Mensik et al., 2018, Magalhaes et al., 2023). Many previous studies also mentioned that many factors positively respond to organic farming including soil enzyme activity, soil nutrients, diversity of microbial community (García et al., 2008; Wang et al., 2016).

#### 4. Conclusions

Our study highlighted that short-term organic coconut farming application significantly contributes to a great deal of soil characteristics such as soil porosity, EC, soil organic matter, total nitrogen, total phosphorus, available phosphorus, exchangeable potassium, total heterotrophic bacteria, and population of cellulose decomposing bacteria in coconut orchards. Continuously, the organic-based practices of coconut farms depicted a higher dehydrogenase enzyme activity compared to conventional farming. Our results indicate that implementing organic farming techniques may influence microbial composition and attract beneficial bacteria to coconut farm soil. In addition, in organic coconut farms, a strong correlation has been observed between soil organic matter with total nitrogen, phosphorus, and dehydrogenase enzyme activity. Subsequent research is needed to investigate the potential benefits of combined applications of organic farming systems and intercropping plants for enhancing the beneficial effects on soil fertility and at the same time increasing the quality of coconut production in Mekong Delta Region, Vietnam. These findings suggest that adoption of organic farming methods provide significant benefits to soil quality and environmental health through exclusion of chemical fertilizer and pesticide applications and continuously added organic supplies.



## CRediT authorship contribution statement

**Lasar Hendra Gonsalve:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software. **Lesueur Didier:** Writing – review & editing, Writing – original draft, Resources, Methodology, Investigation, Funding acquisition, Data curation, Conceptualization. **Baii Shahla Hosseini:** Writing – review & editing, Writing – original draft, Supervision, Project administration, Methodology, Investigation, Funding acquisition, Data curation, Conceptualization. **Tran Huu-Tuan:** Writing – review & editing, Writing – original draft, Visualization, Validation. **Nguyen Huu-Thien:** Writing – review & editing, Writing – original draft, Visualization, Methodology. **Do Thanh-Luan:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology. **Nguyen Nghia Khoi:** Writing – review & editing, Writing – original draft, Supervision, Project administration, Methodology, Funding acquisition, Data curation, Conceptualization. **Robotjazi Javad:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Data curation. **Vo Vy Thao Duyen:** Writing – review & editing, Writing – original draft, Visualization, Software, Data curation. **Tecimen Hüseyin Barış:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Data curation.

## Declaration of Competing Interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Nghia Khoi Nguyen reports financial support was provided by The Australian Centre for International Agricultural Research (ACIAR), Australia under grant No. 009-Nghia Nguyen-Vietnam. Nghia Khoi Nguyen reports a relationship with ACIAR, Australia that includes: funding grants. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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## Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.eti.2025.104067](https://doi.org/10.1016/j.eti.2025.104067).

## Data availability

Data will be made available on request.

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