ORIGINAL ARTICLE

Effect of land use on soil properties, microbial abundance and diversity of four different crop lands in central Myanmar

Tin Mar Lynn[1,2] · Mostafa Zhran[1,3] · Liu Fang Wang[1] · Tida Ge[1] · San San Yu[2] · Ei Phyu Kyaw[2] · Zaw Ko Latt[2] · Tin Mar Htwe[4]

Abstract

Changing land use systems impact on local edaphic factors and microbial abundance and diversity, however, the information on it in central Myanmar's soils is still lacking. Therefore, soils with four different land uses were analyzed; WAP (soil from perennial tree orchard), PNON (soil from crop rotation of peanut and onion), SESA (soil from mono-crop of sesame) and CHON (soil from mono-crop of onion for 3 years consecutively). Soil organic carbon (SOC), total nitrogen (TN), dissolved organic carbon (DOC), ammonium nitrogen (NH_4^+-N) and pH showed the highest in PNON soil, which suggested crop rotation with high fertilizer input and irrigation had positive effect on the edaphic factors of soil. CHON soil showed the lowest in most soil properties and microbial abundance as a result of intensive use of fertilizer and irrigation, no crop rotation and no input of manures. Microbial community composition showed differences among tested soils and relative abundance of *Chloroflexi* was the highest in CHON soil whereas that of *Basidiomycota* was the highest in WAP soil. The abundances of bacteria and fungi were significantly affected by Olsen *P*, whereas the abundances of archaea were influenced by SOC. Our results suggested crop rotation and manure fertilization (PNON soil) enhanced soil properties and microbial abundance although long-time onion mono-crop (CHON soil) reduced soil fertility. This study can provide information to improve soil quality and sustainability of agro-ecosystems using appropriate agricultural management.

Keywords Crop rotation · Land use · Microbial abundance · Microbial community · Soil fertility

Introduction

Soil is a complex system and soil quality is a comprehensive concept that embraces biological, chemical and physical properties that sustain environmental quality (Wang et al. 2019; Kong et al. 2019) and soil microorganisms' abundance and community, and crop productivity (Sial et al. 2019; van Groenigen et al. 2010). The improvement in soil organic matter (SOM) significantly increase crop productivity (Bennett et al. 2010; Akhtar et al. 2020). SOM can enhance the biological diversity of soil; facilitate nutrient cycles, and increase plant nutrient availability and soil buffering capacity (Wright et al. 2015). Mismanagements in agriculture lead to depletion of SOM and its associated consequences, such as reduced fertility and water maintenance, soil compaction and erosion, increased pest and disease prevalence and intensity (Abawi and Widmer 2000). These problems have become important in developing countries.

The soil microbial biomass, which is up to 1 to 5% of SOM content, is critical to the maintenance of soil function in agricultural soils, because microbes participate in important biological processes which have direct effects on soil fertility and maintenance of soil ecosystem diversity and sustainability (Liu et al. 2008). Bacteria are the most abundant and diverse group of soil microorganisms and play multiple important key roles in soil (Yang et al. 2019), as

✉ Tin Mar Lynn
   tinmarlynn@moe.edu.mm

[1] Key Laboratory of Agro-Ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha 410125, China

[2] Microbiology Division, Biotechnology Research Department, Ministry of Education, Kyaukse, Mandalay Region 100301, Myanmar

[3] Atomic Energy Authority, Nuclear Research Center, Soil & Water Research Department, Abou-Zaabl 13759, Egypt

[4] Ministry of Education, Kyaing Tong Education College, Kyaing Tong, Shan State, Myanmar

well as, fungi and archaea play important roles in soil nutrient cycling.

Myanmar is an agricultural country and 12.6 million hectares of land are using for agriculture. The agricultural sector accounts for 37.8% of the country's GDP and employs 70% of its labor force according to the United Nations Food and Agriculture Organization (https://frontiermyanmar.net/en/myanmar-agriculture-101). Most of the agricultural soils in the low land plain central area of Myanmar are semi-arid soils because of high temperature and low rainfall. Beans, pulses, sesame (*Sesamum indicum*), sunflower and groundnuts or peanut (*Arachis hypogaea* L.) are widely grown as climate-resilient crops in the central dry zone, because they are moderately resistant to drought. About 16% of the cultivated area (3 million ha) is occupied by oilseed crops and they are the third most important crop group in Myanmar agriculture after cereals and pulses (Tun Shwe and Kyu 2017).

Thanaka or Wood apple with scientific name of *Hesperethusa crenulata* Roem (Sapindales: Rutaceae), syn. *Naringi crenulata* and *Limonia acidissima* L. is a common tropical plant species in the Indian subcontinent and Southeast Asia (Wangthong et al. 2010). In Myanmar, the yellowish-white paste made from Thanaka tree's bark is commonly used as traditional skin care for over 1000 years (Kyaw et al. 2018). That skin care is called "Thanaka" in Myanmar Language. And, that Thanaka or wood apple tree prefers hot and dry weather, hence, generally grows in the central dry zone of Myanmar.

Onion (*Allium cepa* L.) is important crops for domestic consumption because most traditional dishes in Myanmar used onion as spices. Onion crop is intensively managed, frequently with short rotations, heavy fertilizer applications, and regular and intensive use of insecticides and fungicides (Wright et al. 2015). Continuous mono-crop cultivation with intensive fertilizer and insecticide usages for long-time may result in decreased soil fertility and steady reductions in crop productivity (Hungria et al. 2009). Therefore, sustainable crop and soil management are important to ensure long-term viability and profitability in the agricultural industry of Myanmar. Crop rotation is used to minimize the problems of continuous mono-cropping (Li et al. 2017) because the plant residues from crop rotation are beneficial for improving soil fertility. Land-use management, one of the most prominent aspects of anthropogenic perturbation in terrestrial ecosystems, has exerted substantial impacts on soil biogeochemical cycling and indigenous microorganisms (Shen et al. 2013).

Most agricultural lands in Myanmar are endangered because of intensified agriculture and poor management which can reduce soil fertility. Improper land use and misguided land management can lead to unproductive farming, and environmental pollution (https://ifdc.org/wp-content/uploads/2018/11/A-Soil-Fertility-and-Fertilizer-Management-Strategy-for-Myanmar-11-16-2018). Some previous studies already reported influence of land use on the microbial abundance and diversity in different soils (Lynn et al. 2017; Keshri et al. 2013); however, there is no information on the effect of land use and soil types on microbial abundance and diversity in arid or semi-arid arable lands in central Myanmar.

Although bean, pulses and oilseed crops are major crops in this area, recently, most of the farmers grow onion because of short cultivation time and higher income. For onion cultivation, intensive fertilizers and irrigation system need to apply and changing land use systems will affect on local edaphic factors, microbial abundance and diversity too. However, the information of that in central dry zone of Myanmar is still lacking. Therefore, studying the effect of land use on soil physicochemical properties and correlation of soil properties with microbial abundance will provide useful information to improve soil fertility, which will lead to enhancing crop production and farmers' profit. To our knowledge, this is the first research for agricultural soils from Myaing Township, Magway Region, Myanmar. The main objective of this study was to look into how land use configures soil physicochemical properties, microbial abundance and community composition in arable soils from the central dry zone in Myanmar. Agricultural soils with different irrigation systems and fertilization managements, which cultivated major crops in that area, were selected to study. Four soils were collected; WAP is soil from wood apple (Thanaka) orchard, PNON is soil from the farmland with crop rotation of peanut and onion, SESA is soil from the farmland with sesame, and CHON is soil from the onion cultivation (mono-cropping).

We hypothesize that (i) differences in soil physicochemical properties derived from changes in land use under different fertilizer managements and different irrigation systems influence soil microbial abundance and diversity and, (ii) intensive agricultural practices in onion mono-crop enhance deterioration in soil fertility and microbial abundance and diversity, however, crop rotation and manure addition will mitigate these deterioration. Soil edaphic factors, microbial abundance (bacteria, archaea and fungi), and their correlation to each other were determined and statistical analyses were performed to identify the key factors affecting microbial abundances and diversity in these four different agricultural lands. Microbial community compositions were also analyzed by high throughput sequencing.

Materials and methods

Study area

The study areas were located at Myaing Towship, Magway Region in a great low land plain of central Myanmar. Full

site details, cultivation history and soil texture were given in Table 1. The annual precipitation is 606.3 mm, the average high annual temperature is 33.7 °C, and the average low annual temperature is 20.1 °C in 2010. During March and April, the mean maximum temperature of about 100 °F (37.8 °C) was found in central Myanmar area (Aung et al. 2017). Due to the high temperature and low rainfall, the central area of Myanmar is dry and most of the farmlands in this area are dry and usually grow beans and oil crops. Mostly, farmers from this area rely on rainfall to grow crops; however, irrigation systems are used to grow onion.

Sample collection

Four soils were collected from this area, WAP (soil from perennial tree orchard under rainfed with a few amount of fertilizer input 5 years ago), PNON (soil from crop rotation of peanut and onion with intensive irrigation and fertilizer input), SESA (soil from mono-crop of sesame under rainfed with medium fertilization) and CHON (soil from mono-crop of onion for 3 years consecutively with intensive irrigation and fertilizer input, chickpeas were planted in this soil 3 years ago). For WAP soil, water and fertilizer applied only when planting started. For PNON and CHON, six times of irrigation and two times of fertilizers (45 days after sowing and 70 days after sowing) were added for one crop of onion although only one time of fertilizer addition at the time of sowing for peanut and chickpea cultivation. Fertilizer usages were shown in supplementary Table 1.

Samples were collected on May, 2018 when crops were not planted in soils except for WAP which is the soil from perennial tree orchard. From each soil, three replicate samples were collected, and for each replicate, five soil cores (top 0–10 cm) were collected randomly using a soil sampler, and then, mixing and homogenizing to obtain one replicate. The samples were then sieved through a 2-mm screen and any visible roots or other debris were removed. A portion of each soil sample was stored at 4 °C to analyze some of the soil physicochemical parameters such as SOC, TN, total

phosphate (TP), dissolved organic carbon (DOC), microbial biomass carbon (MBC), Olsen P and pH. And then, part of each soil sample was stored at -20 °C for DNA extraction. The remaining soil sample was air dried before measuring other soil properties.

Soil physicochemical measurements

DOC was extracted with 0.5 M K_2SO_4 and measured using a TOC analyzer (TOC-VWP; Shimadzu, Kyoto, Japan). MBC was determined using the chloroform-fumigation-extraction method (Joergensen et al. 2011). Soil NH_4^+-N and NO_3^--N were extracted using 0.5 M KCl and quantified by a continuous-flow auto-analyzer (Fiastar 5000; Foss Tecator AB, Höganäs, Sweden); Olsen-P was extracted using 0.5 M $NaHCO_3$ and analyzed for P colorimetrically using the ammonium para-molybdate reagent (Olsen and Sommers 1982) at 830 nm on a spectrophotometer. The soil pH was measured using a pH meter after shaking a soil:water (1:2.5 w/v) suspension comprising 10 g of air-dried soil and 25 mL of water. SOC and TN contents were measured by dry combustion using an elemental analyser (Vario MAX C/N, Elementar, Germany). Soil texture (clay, silt, sand %) was determined using a laser particle analyzer (Mastersizer 2000, UK).

DNA extraction and quantitative qPCR

Soil microbial DNA was extracted from 0.5 g of each sample using the Power Soil® DNA Isolation Kit (MoBio, California, USA), following the manufacturer's protocol. The quantity and quality of the extracted DNA were checked using the NanoDrop spectrophotometer (ND-1000; NanoDrop Technologies, Wilmington, DE, USA), and then examined on a 1% (w/v) agarose gel. The extracted DNA was stored at -20 °C for further analysis.

Quantitative polymerase chain reaction (qPCR) was performed to determine the bacteria 16S rRNA gene copies, archaea and fungi. Bacterial 16S rRNA was amplified

Table 1 Information of soil sampling sites and soil texture with standard error of four different soils ($n=3$)

Soils	Sampling sites		Cultivation history	Clay (%)	Silt (%)	Sand (%)	Soil texture
WAP	Latitude	21º 50′ 43" N	Wood Apple orchard (5 years old)	13.58 ± 0.5	70.60 ± 1.7	9.13 ± 1.4	Silt loam
	Longitude	94º 50′ 53″ E					
PNON	Latitude	21º 50′ 51"N	Rotation of Peanut and onion	13.18 ± 0.5	71.28 ± 2.8	10.56 ± 1.4	Silt loam
	Longitude	94º 50′ 19" E					
SESA	Latitude	21º 50′ 44" N	Sesame	10.56 ± 0.5	68.38 ± 2.5	14.35 ± 1.1	Silt loam
	Longitude	94º 50′ 28" E					
CHON	Latitude	21º 51′ 8" N	Onion (Chickpea was cultivated 3 years ago)	19.09 ± 0.2	77.29 ± 0.2	2.23 ± 0.2	Silt loam
	Longitude	94º 50′ 48" E					

In PNON, crop rotation is conventional rotation, common local commercial practice

using the universal primer pair 1396F/1492R (Suzuki et al. 2000). Primers for archaea were U519F and U806R (Shehab et al. 2013) and primers for fungi were nu-ssu-0817 and nu-ssu-1196 (Borneman and Hartin 2000). The PCR mixture (10 μL) contained 5 μL of $2 \times$ SYBR Premix Ex Taq (Takara, Japan), 0.15 μL of each primer, 1 μL of DNA (5 ng μL^{-1}), and 3.7 μL of sterile ddH$_2$O. The qPCR was performed in triplicate using the Roche LightCycler® 480 real-time PCR system (Roche, Switzerland) with the following cycling conditions: for bacteria 16S rRNA gene, 95 °C for 1 min, followed by 40 cycles at 95 °C for 5 s and 60 °C for 30 s; for archaea, 95 °C for 1 min, followed by 40 cycles at 95 °C for 10 s, 54 °C for 30 s and 72 °C for 30 s; and for fungi 95 °C for 1 min, followed by 40 cycles at 95 °C for 10 s, 56 °C for 20 s and 72 °C for 30 s. Series of tenfold dilutions of plasmids that contained cloned genes of bacterial 16S rRNA, archaeal 16S rRNA and fungi 18S rRNA were run in parallel with the template DNA to prepare the respective standard curves for quantification. At the end of each qPCR run, melting curve analysis was performed to check the specificity of the amplification. The qPCR results were used when the amplification efficiency ranged from 90 to 110%, with $R^2 > 0.98$.

High throughput sequencing of 16 s rRNA and ITS region and sequence analysis

16 s rRNA genes for bacteria from four soil samples were amplified with the primers 341F and 806R (Yuan et al. 2018) labeled with unique barcodes at the 5′ end and 3′ end. The PCR conditions were as follows: 95 °C for 3 min, followed by 30 cycles at 95 °C for 15 s, 55 °C for 30 s, and 72 °C for 30 s, and a final extension at 72 °C for 10 min. The ITS1-5F part was amplified using the primer pair as described in Duan et al. (2019). Sequencing was performed on the Illumina HiSeq 2000 platform by Novogene Co., Ltd. (Beijing, China). The sequences were processed using the QIIME 1.9 pipeline (Caporaso et al. 2010). The overlapping paired-end reads were assembled and the primer sequences were removed. The split-sequence libraries were then screened, and all sequences with a quality score of less than 30 were discarded. The chimeras were removed using usearch61 chimera check. After quality filtering, 79,455 sequences for bacterial 16S and 75,531 sequences for fungi ITS were obtained, the correct sequences were processed by the uclust method in QIIME. The sequences with 97% similarity were assigned to the same operational taxonomic unit (OTU) (Edgar 2018). After removing singleton OTUs, 5107 OTUs were obtained in total for 16S bacterial rRNA and 965 OTUs for fungi ITS. All representative OTUs were taxonomically classified using RDP for 16S and unite fungi database for ITS. Alpha diversity was assessed by calculating Shannon index (Shannon 1997) in QIIME. The DNA sequences have

been deposited in the National Center for Biotechnology Information Bioproject database under the Bioproject accession number SRA accession: PRJNA600083.

Statistical analysis

One way analysis of variance (ANOVA) and comparisons of significant differences of soil properties and microbial abundance was performed using Duncan's test ($P < 0.05$) with agricolae R package (De Mendiburu 2014). Correlation of soil properties and microbial abundance were conducted with corrplot in R. Figures except Venn's diagram were illustrated with ggplot2 in R. The contributions of soil type and land use on microbial abundance and community were evaluated with the variance partitioning analysis by the CANOCO 5.0 for window (Microcomputer Power, USA).

Results

Soil physicochemical properties

SOC and TN of PNON were the highest whereas CHON showed the lowest for both and SESA also showed the lowest in TN (Fig. 1). SESA possessed the higher TP and Olsen P than other soils while PNON showed the lowest TP and CHON showed the lowest Olsen P (Fig. 2). DOC, MBC and NH$_4^+$-N were significantly higher in PNON soil than other soils followed by WAP soils. There were no significant differences in the NO$_3^-$-N contents in all soils. The soil pH values were significantly different in all soils ($P < 0.05$), PNON was the highest followed by CHON, WAP and SESA, respectively (Fig. 2). According to clay, silt and sand %, all four soils were silt loam soils.

Correlation between soil physicochemical properties

DOC was significantly and positively correlated with TN, NH$_4^+$-N, pH ($P < 0.001$), SOC ($P < 0.05$) and negatively correlated with TP and Olsen P (Fig. 3). SOC was significantly and positively correlated with TN, NH$_4^+$-N ($P < 0.05$). MBC was apparently dominated by TN and pH ($P < 0.05$). pH was negatively related to TP and Olsen P ($P < 0.01$). Clay (%) and silt (%) were significantly and positively related to C:N ratio.

Microbial abundance and correlation with soil physicochemical parameters

The number of bacterial 16S rRNA gene copies outnumbered the archaeal 16S rRNA gene copies by one to two orders of magnitude in all soils (Fig. 4). SESA soil showed
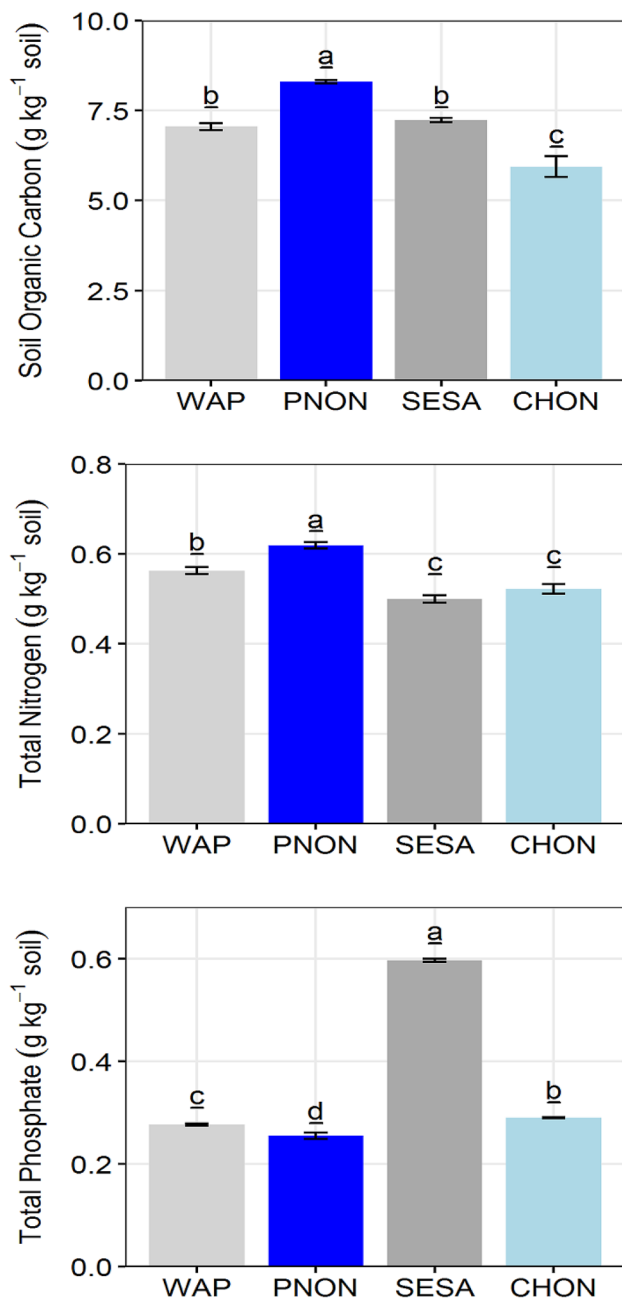
Fig. 1 Basic soil properties of four different soils. Different small letters indicate significant difference ($P < 0.05$). Error bars represent standard error ($n = 3$). WAP–soil from wood apple orchard, PNON–soil from the rotation of peanut and onion, SESA–soil from sesame farmland, CHON–soil from the onion cropping

the highest abundance in bacteria although archaeal abundance was the highest in PNON soil. CHON soil showed the lowest in all bacterial, archaeal and fungal abundance. The ratio of archaea to bacteria was the largest in PNON. For fungal abundance, SESA showed the highest followed by WAP, PNON and CHON, respectively.

The abundance of bacteria was significantly influenced by Olsen-P ($P < 0.01$) and TP ($P < 0.05$) (Fig. 5), however, archaeal abundance was significantly correlated to SOC ($P < 0.001$) and NH_4^+-N content ($P < 0.05$). Moreover, Olsen P content significantly controlled abundance of fungi. On the other side, the ratio of archaea to bacteria was associated with so many soil parameters, SOC and NH_4^+-N ($P < 0.001$), DOC and TN ($P < 0.01$) and, MBC and pH ($P < 0.05$).

Microbial community in four different soils

Phyla *Actinobacteria*, *Proteobacteria*, *Acidobacteria*, and *Chloroflexi* were the most abundant in all soils (Fig. 6a). WAP soil showed the highest in relative abundance of *Proteobacteria* (29.2%) only. Relative abundance of *Actinobacteria* showed the highest in SESA soil (36.9%) followed by WAP (35.4%), CHON (33.7%) and PNON (27.87%), respectively. SESA soil possessed the highest relative abundance in *Firmicutes* and *Verrucomicrobia* while PNON soil described the highest relative abundance in *Planctomycetes* and *Nitrospirae*. CHON soil showed the highest abundance in *Chloroflexi*, *Acidobacteria*, *Bacteroidetes* and *Armatimonadetes* (Fig. 6a). Although *Actinobacteria* and *Proteobacteria* showed the highest abundance in all soils, the highest abundance phylum in soils were different from each other.

For fungi, *Ascomycota* was the most abundant phyla in all soils followed by *Basidiomycota*, *Zygomycota, Glomeromycota* and *Chytridiomycota* (Fig. 6b). Significant differences in fungal composition were observed between soils. High relative abundances of *Basidiomycota* were observed in WAP and CHON soils, while Ascomycota was the richest in PNON soils (95.5%). Higher abundance of *Zygomycota* was also found in CHON soil only. For class level of fugal abundance, *Dothediomycetes* were the richest in PNON soil (38%) although higher abundance of *Sordariomycetes* were found in CHON soil (39.6%) (Fig. 6c).

Influence of soil type and land use on microbial abundance and community

Variance partitioning (partial redundancy analysis RDA) showed that soil type (clay, silt, sand %) explained 28.7% on microbial abundance, while land use explained 19.5% of abundance. The RDA also found strong interactions between soil type and land use (51.8%). Soil type, land use and both of them had significantly dominated microbial abundance ($P < 0.001$) with Monte Carlo permutation test ($P < 0.001$).

For microbial community composition, variance partitioning described that soil type explained 12.8% on microbial abundance, while land use explained 27.4%. Similar to effect on microbial abundance, the RDA also found strong interactions between soil type and land use (59.7%). Soil type, land use and both of them had significantly dominated
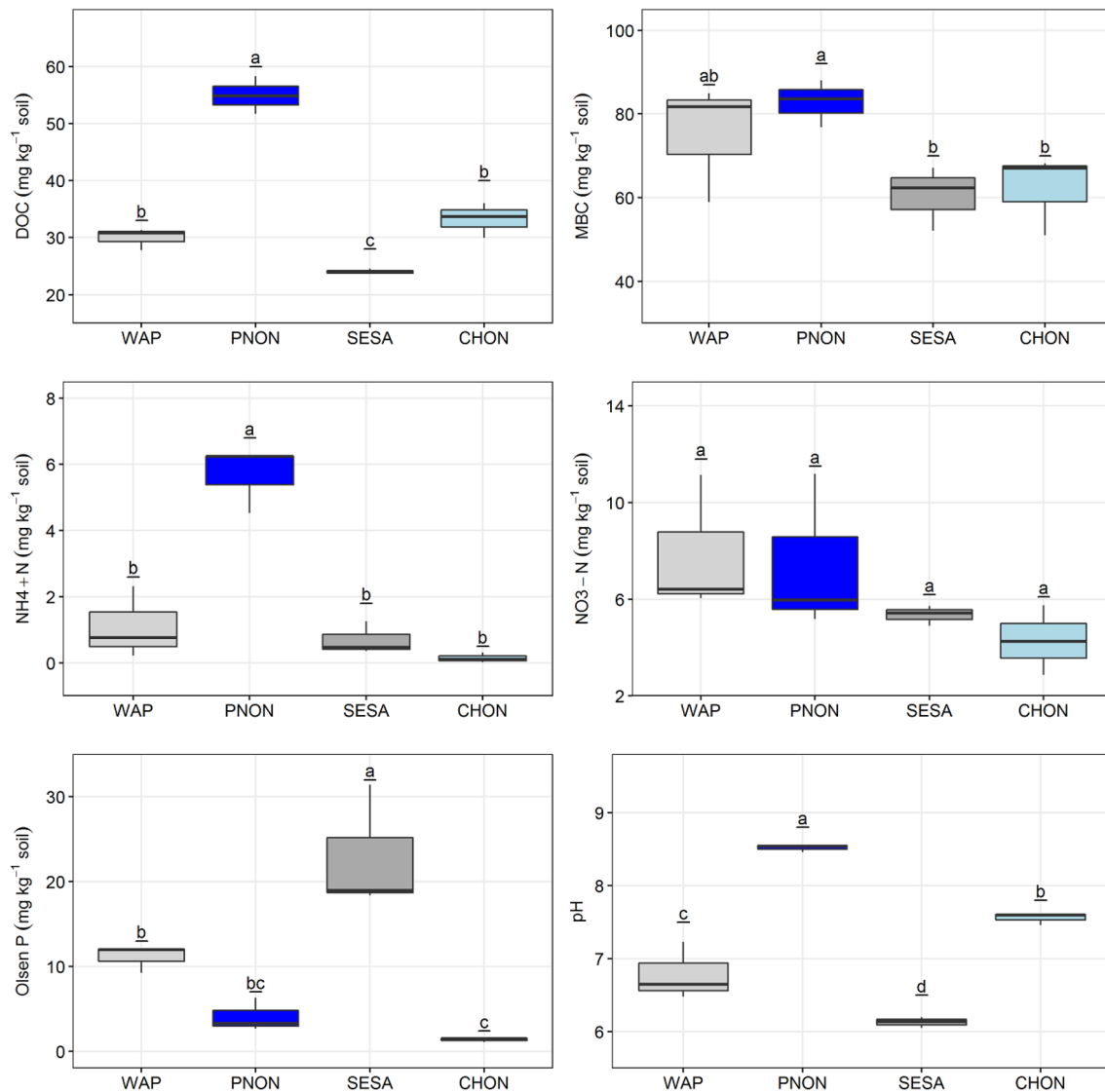
Fig. 2 Physicochemical properties of four different soils. Different small letters indicate significant difference ($P < 0.05$). Error bars represent standard error ($n = 3$). WAP–soil from wood apple orchard, PNON–soil from the rotation of peanut and onion, SESA–soil from sesame farmland, CHON–soil from the onion cropping

on microbial community composition with Monte Carlo permutation test ($P < 0.001$).

Discussion

Effect of land use on soil physical and chemical properties

We analyzed soils under four different land use systems. All soils are from conventional agriculture. The soil properties differed significantly among different land use systems (Fig. 1, Fig. 2 and supplementary Fig. S1). Several soil properties such as SOC, TN, DOC, MBC and pH showed the

highest in PNON, which suggested that crop rotation with high fertilizer input and irrigation had positive effect on the physicochemical properties of soil. It was reported that crop rotation could increase the input of organic C in the soil, which led to enhancing soil fertility (Li et al. 2017). Nitrogen linked with SOM was not readily mineralized, hence, comparatively high total N content in soil was the result of high SOM (Kumar et al. 2019). Manure (cow dung) addition into PNON is also one of the reasons for high SOC content.

Soil pH was significantly higher in PNON, and this was compatible with other studies which described soil with crop rotation possessed higher pH than mono-cropping soil (Li et al. 2017). TP and Olsen P content showed the highest in SESA soil which suggested low pH can help to
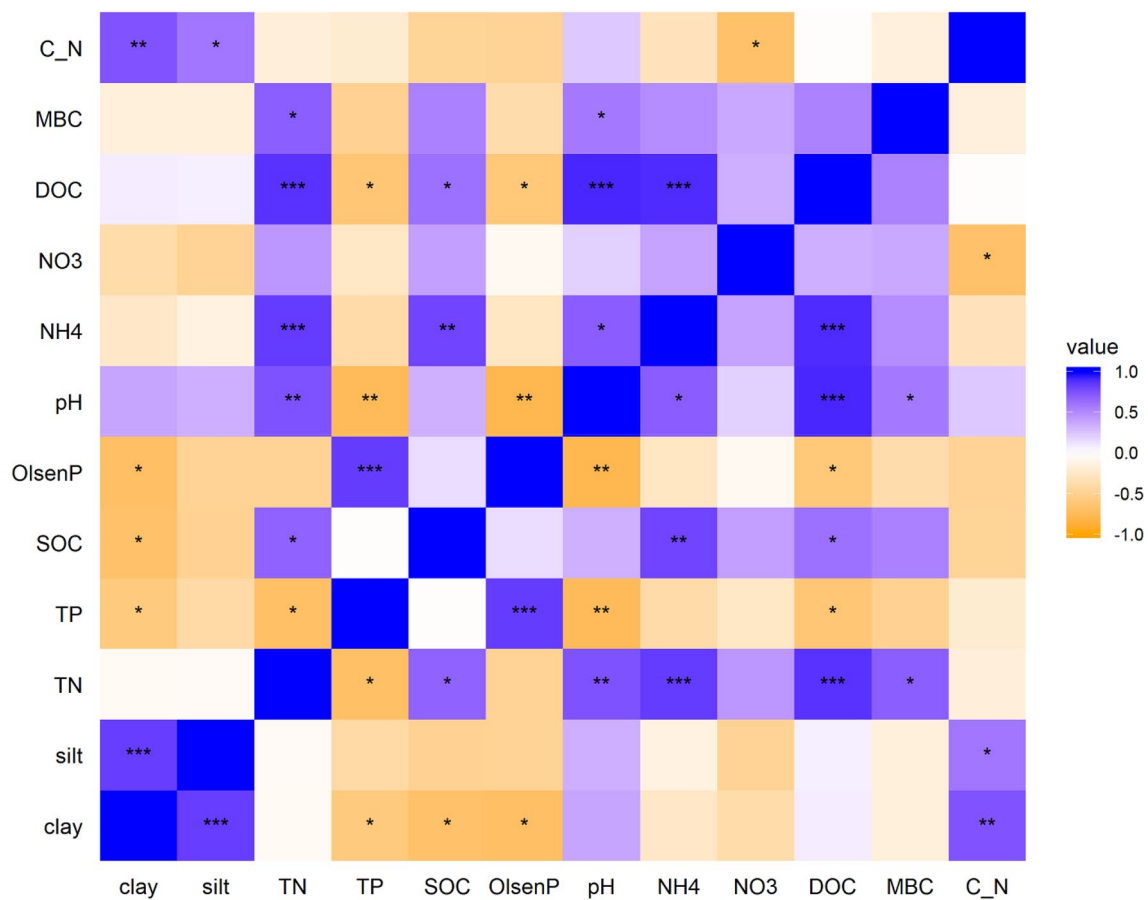
Fig. 3 Correlation (Pearson) between soil physiochemical properties of 4 different soils, C_N–the ratio of carbon to nitrogen. ***Correlation is significant at < 0.001 level, **Correlation is significant at < 0.01 level, *Correlation is significant at < 0.05 level

occupy higher available P. In accordance with our result, it was indicated that higher pH of soil reduced the bioavailability of P to plants and microbes (Kumar et al. 2019). Previous studies outlined that pH is directly or indirectly related to soil moisture, salinity, nutrient availability and many soil characteristics (Luneberg et al. 2018; Lynn et al. 2017).

The significantly lower amounts of SOC, TN and Olsen P in the continual onion rotation were correlated with less SOM. This was in agreement with the previous report in which a positive effect of increased OM on soil TN (Wright et al. 2015). The lower amounts of soil nutrients in the soil following the 3-year onion monoculture was probably due to less plant residues being produced and incorporated into the soil from onion crops (Wright et al. 2015). It was reported that MBC was strongly associated with organic C and total N (Yao et al. 2000). In the present trial, this was also the case; MBC was strongly correlated with SOC, TN and pH. DOC was the lowest in SESA, lower fertilizer input than CHON and PNON and higher tillage than WAP might be the answer for that. DOC was positively associated with pH

and ammonia content and WAP soil occupied the lowest pH (Figs. 2, 3).

Effect of land use on microbial abundance and community

Soil microorganisms are critical to the soil ecosystem because of their significant role in regulating soil nutrients and changes in their abundance caused by different land uses impact changes in soil quality (Konopka 2009). The present analyses indicated that the microbial abundances in the four land uses were significantly different (Fig. 4).

Relative abundance of *Actinobacteria* were higher in all tested soils than other bacterial phyla since *Actinobacteria* are adapted to extreme conditions such as high temperature and high salt concentration because they have spores which can germinate in very low available water (Mohammadipanah and Wink 2015). Other researchers also found that *Actinobacteria* were significantly more abundant in the micro-aggregates of upland soil (Li et al. 2020b) and oligotrophic *Actinobacteria* prefer nutrient-poor environments
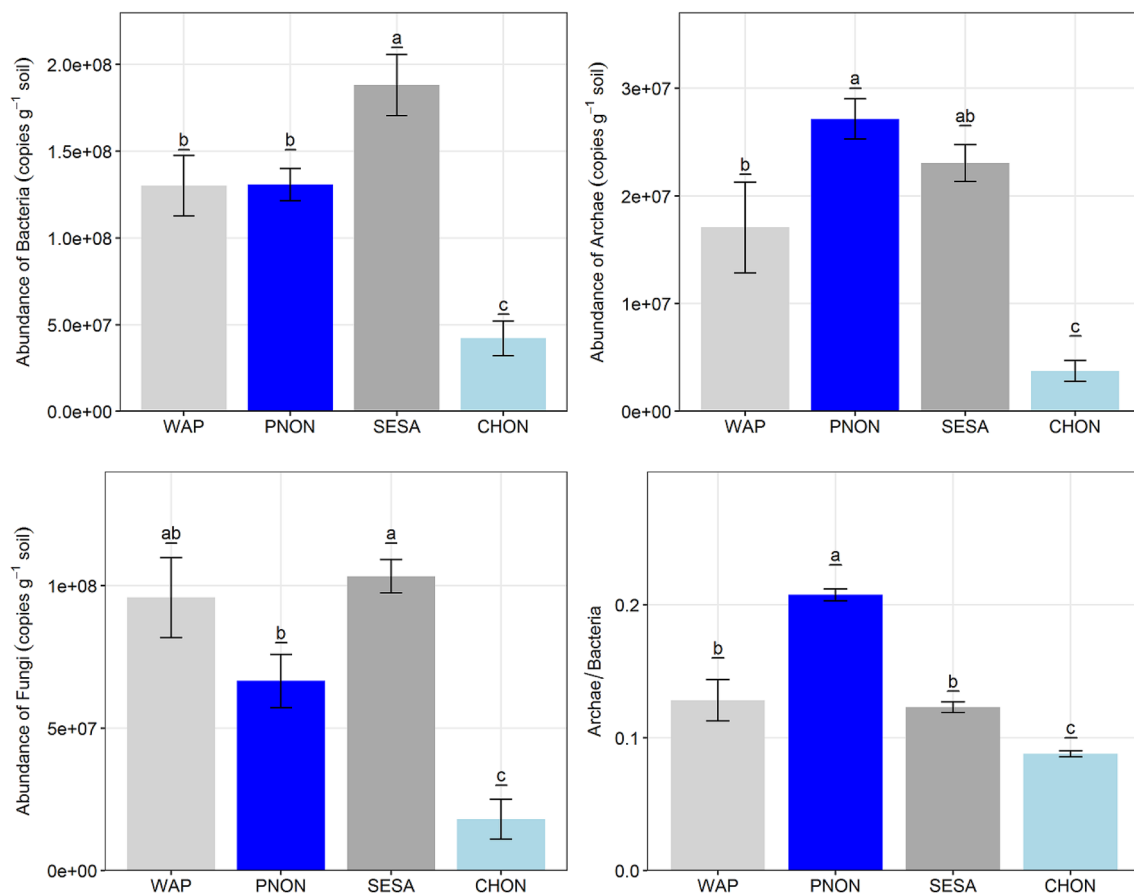
Fig. 4 Abundance of bacteria, Archaea, Fungi and the ratio of Archaea to bacteria in four different soils. Different small letters indicate significant difference ($P < 0.05$). Error bars represent standard error ($n = 3$). WAP–soil from wood apple orchard, PNON–soil from the rotation of peanut and onion, SESA–soil from sesame farmland, CHON–soil from the onion mono-cropping

(Zhong et al. 2020). And also, *Actinobacteria* have beneficial association with plants and also they are important in turnover of SOM because they can decompose polymers (Li and Wu 2018).

Chloroflexi and *Acidobacteria* were significantly higher in CHON soil while *Proteobacteria* and *Actinobacteria* showed higher abundance in WAP and SESA soils. In accordance with our result, (Mueller et al. 2015) found that *Acidobacteria* and *Chloroflexi* showed significant positive responses to N addition while *Actinobacteria* and *Proteobacteria*, showed negative responses to high level of N input in arid soil. CHON soil showed the lowest SOC and lowest abundance of *Proteobacteria*. This finding matched with Jenkins et al. (2010) who described *Proteobacteria* as fast-growing copiotrophs which are augmented in C-rich environments.

Ascomycota and *Basidiomycota*, the major fungal groups in all tested soils (Fig. 6b), are saprotrophic fungi which have mutual relationship with plants by providing carbon-based resources and nutrients (Vanegas et al. 2019). Therefore, that finding is reasonable with agricultural soils. It was found that spores of *Basidiomycota* and *Ascomycota* can survive

under high temperature and low moisture (Li et al. 2020a). Other study reported that *Ascomycota* were commonly found to be the dominant root-colonizing fungal group in semi-arid grasslands (Porras-Alfaro et al. 2011) and also found in most soils (Bononi et al. 2020). Although the alpha diversity of bacteria in CHON soils showed the lowest, fungal diversity in CHON was the highest in all tested soils which described fertilizer addition had opposite effect on bacterial and fungal diversity (Supplementary Fig. S2). This finding is partially against our second hypothesis.

Relationships between soil edaphic factors and microbial abundance

Pearson correlation of soil edaphic factors and microbial abundance explained well influence of soil properties on the differences in the abundances of bacterial, archaeal and fungal in four different soils. It was described that changes in land use from natural dry land to agricultural land increased total organic matter and Olsen-P content (Luneberg et al. 2018). Those changes affected on the abundance and
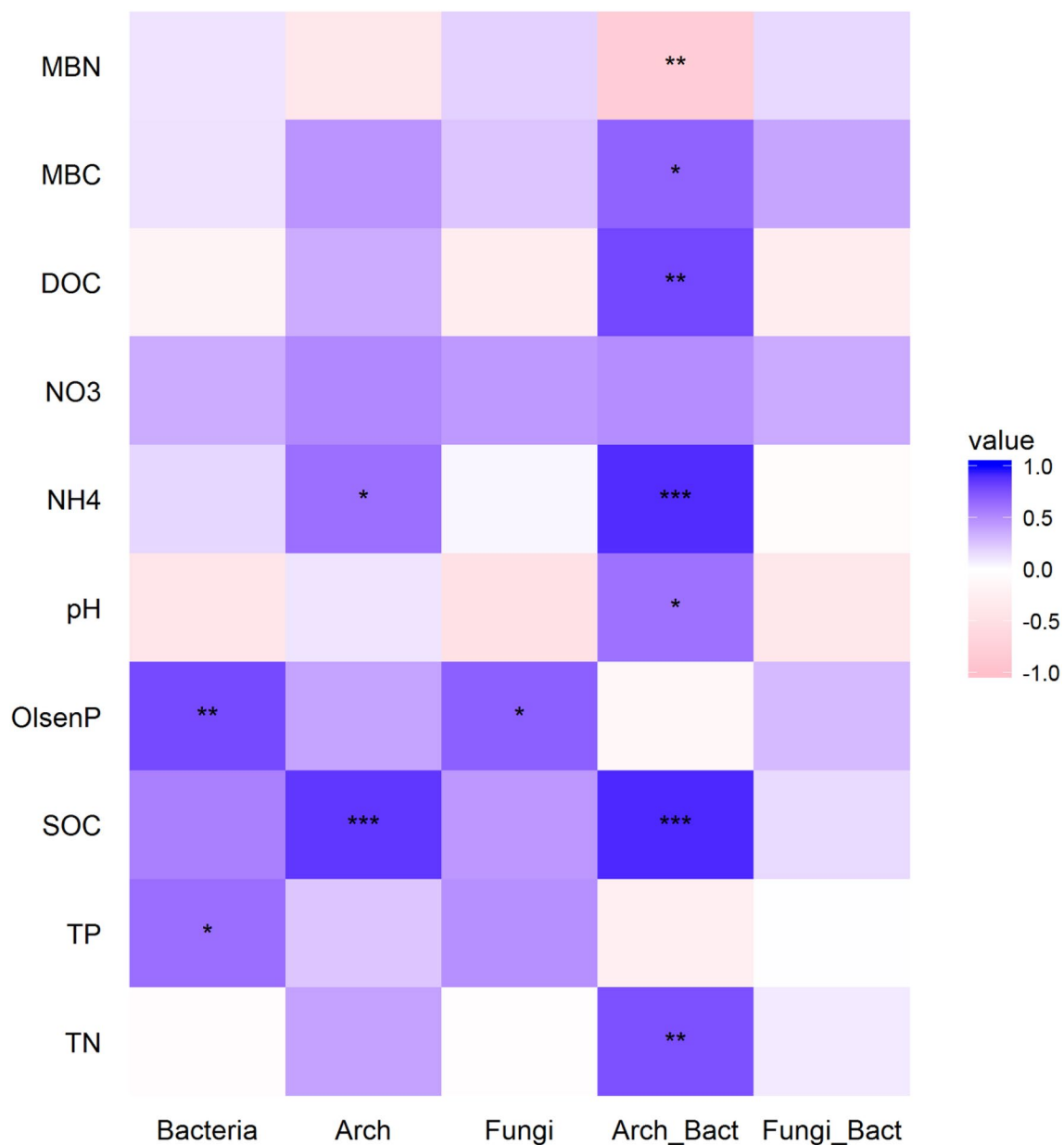
Fig. 5 Correlation analysis of soil physicochemical parameters on microbial abundance in four different semi-arid soils. ***Correlation is significant at < 0.001 level, **Correlation is significant at < 0.01 level, *Correlation is significant at < 0.05 level

diversity of effective bacteria with soil fertility and plant growth promoting activities. Adding fertilizer can stimulate root growth and root exudation leading to higher organic C inputs to soil. Increased SOC can improve soil fertility, soil nutrient and soil microbial abundance (Li et al. 2017).

Our study showed Olsen P strongly influenced on bacterial and fungal abundance (Fig. 5), probably because, microorganisms require P for nucleic acids (DNA and RNA with phosphate backbone), cell membrane synthesis (phospholipid fatty acid) and energy metabolism (Adenosine Tri Phosphate-ATP) (Richardson et al. 2009; Villanueva

et al. 2020). The higher amount of Olsen P can enhance the growth of microorganisms, since they can directly use this form of P (Wu et al. 2017). Intensive use of fertilizer and irrigation, no crop rotation and no input of manures dramatically decreased soil properties and microbial abundance in CHON soil. When poor agricultural practices are applied, such as intensive use of fertilizers and pesticides and monocrop for longer periods, it will lead to loss of microbial abundance and diversity which can cause a reduction in ecosystem flexibility (Lupatini et al. 2013; Figuerola et al. 2015). On the other hand, PNON soil also planted onion

Springer

Fig. 6 Relative abundance of different bacterial phylogenetic groups (**a**), fungal group in phylum level (**b**) and fungal group in class level (**c**) from four different soils. WAP–soil from wood apple orchard, PNON–soil from the rotation of peanut and onion, SESA–soil from sesame farmland, CHON–soil from the onion mono-cropping
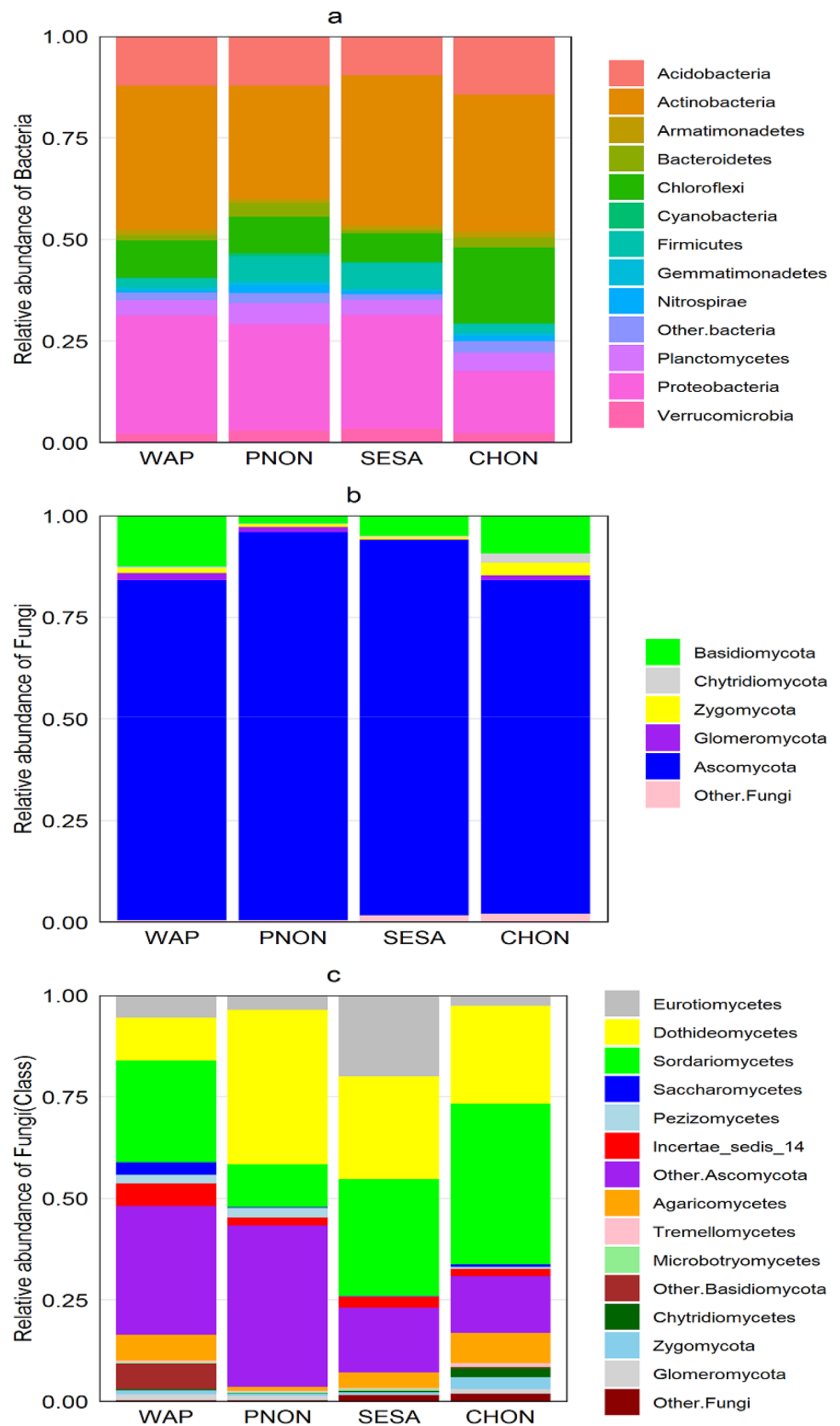
with intensive agrochemical usages; soil physicochemical properties and archaeal abundance are still higher than other soils because of crop rotation and manure addition.

Approximately 0.5–3.8% of the prokaryotes living in moderate aerobic soils are archaea (Ruppel et al. 2007; Belmok et al. 2019), although some studies showed only low ratios or no archaea in some natural soils (Roesch et al. 2007). However, knowledge about the functions of the soil archaea is still scanty. Until now, the recognizable functions of soil archaeal are the nitrification and the methanogenesis (Timonen and Bomberg 2009). The role of archaea in ammonia oxidizing of soil ecosystems might be more important than bacteria, because *AmoA* genes in archaea estimated to be 3000 fold more abundant than bacterial *AmoA* genes in soils (Leininger et al. 2006; Zhao et al. 2020). It was already revealed soil pH affect archaeal abundance and diversity (Timonen and Bomberg 2009). The abundance of bacteria and ammonia oxidizers was also affected by the land use types (Sheng et al. 2013), and low nutrient fertilization in sandy soil decreased the proportion of archaea (Ruppel et al. 2007). It is similar to our result, CHON with low soil quality showed the lowest archaeal abundance. Our study showed abundance of archaea was significantly regulated by SOC and NH_4^+-N. In contrast to this, DOC and nitrate concentrations closely related to the abundance of *AOA* and *AOB* bearing archaea in soil (Meyer et al. 2014).

Fungi play fundamentally important and diverse roles in terrestrial ecosystems, being involved in many of the key processes, such as mycorrhizal symbionts of plants and the main agents for the decomposition of organic material (Anderson et al. 2003). The abundance of fungi and Olsen P and TP content were strongly related suggesting that fungi produced acid and enzymes to solubilize P for plant, and also lower pH in SESA proved that assumption. Interestingly, in contrast to our result, other study reported that the abundance of AM fungi was negatively correlated with soil P content (Koorem et al. 2014). They assumed that different fungi released different organic acids causing reduction of pH, and the negative correlation between fungal biomass and soil pH may be due to the affinity of the fungi towards acidity (Yadav and Tarafdar 2003; Neina 2019). Sufficient organic matter, medium tillage and low pH supply the best condition for highest fungal abundance in SESA soil. Greater fungal abundance associated with higher organic matter soils (Vukicevich et al. 2019), in contrary, another study revealed that fungal abundance decreased with increasing SOC and soil available N (Hu et al. 2013).

MBC in WAP soil was the second highest (75.19 mg kg^{-1} soil) describing that no tillage can enhance microbial growth than mono-cropped soils (SESA and CHON). Fungal abundance showed the highest in WAP soil proving that fungal abundance significantly contributed to microbial biomass. WAP soil has been free from physical disturbance for 5 years

and this can explain the reason for higher fungal abundance because filamentous fungi are more sensitive to physical disturbance than bacteria or archaea (Kumar and Ghoshal 2017). Physical disturbance, mainly tillage, destroyed fungal mycelium networks although bacteria tended to be dominant in soils subjected to intensive tillage and chemical fertilizer application (Garcia-Orenes et al. 2016). Fungal hyphae can produce organic binding agents and entangle soil particles and, in turn enhancing soil aggregation and providing physical protection of SOM (Tisdall et al. 1997). Moreover, fungal residues were degraded slower than bacterial residues, therefore, fungal and bacterial biomass ratio can be used as an indicator of sustainable agro-ecosystems with potential for soil C storage (van Groenigen et al. 2010).

Influence of soil type and land use on microbial abundance and diversity

According to partial RDA analysis, soil type (clay, silt, sand percent) can explain 28.7% and land use (soil physical properties) can explain 19.5% on microbial abundance in four different agricultural soils. Moreover, these two factors can explain together for 51.8% for abundance (Fig. 7a) and 59.7% for community composition (Fig. 7b). These finding support our hypothesis by showing differences in soil physicochemical properties derived from changes in land use under different fertilizer managements and irrigation systems influence the soil microbial abundance and diversity. Mono cropping of onion can significantly decrease the soil physical and chemical properties (Supplementary Figure 1). PNON soil possessed the higher soil quality and microbial abundance than CHON soil even if onion were grown with intensive agricultural management. Therefore, it proved that the crop rotation and manure addition can mitigate the deterioration of soil fertility and it supports our second hypothesis. More researches are needed to give useful information for technical sector to create better agricultural practices.

Conclusions

Physicochemical properties and microbial abundance of soils with four different land use systems were investigated. The soil properties diverged significantly among different land use systems. SOC, TN, DOC, MBC, NH_4^+-N and pH showed the highest in PNON soil with crop rotation with high fertilizer input and irrigation. However, TP and Olsen *P*, fungal abundance were the highest in lowest pH soil, SESA stating the role of fungi in P solubilization in soil. Olsen *P* plays a major role in bacterial and fungal abundance while SOC and NH_4^+-N matter for archaeal abundance. From our result, we can conclude that

Fig. 7 Venn diagrams showing the relative contribution of soil type and land use on microbial abundance (**a**) and community (**b**) obtained from partial redundancy analysis. Only environmental parameters that significantly affected gene abundance and microbial community in the redundancy analysis have been plotted
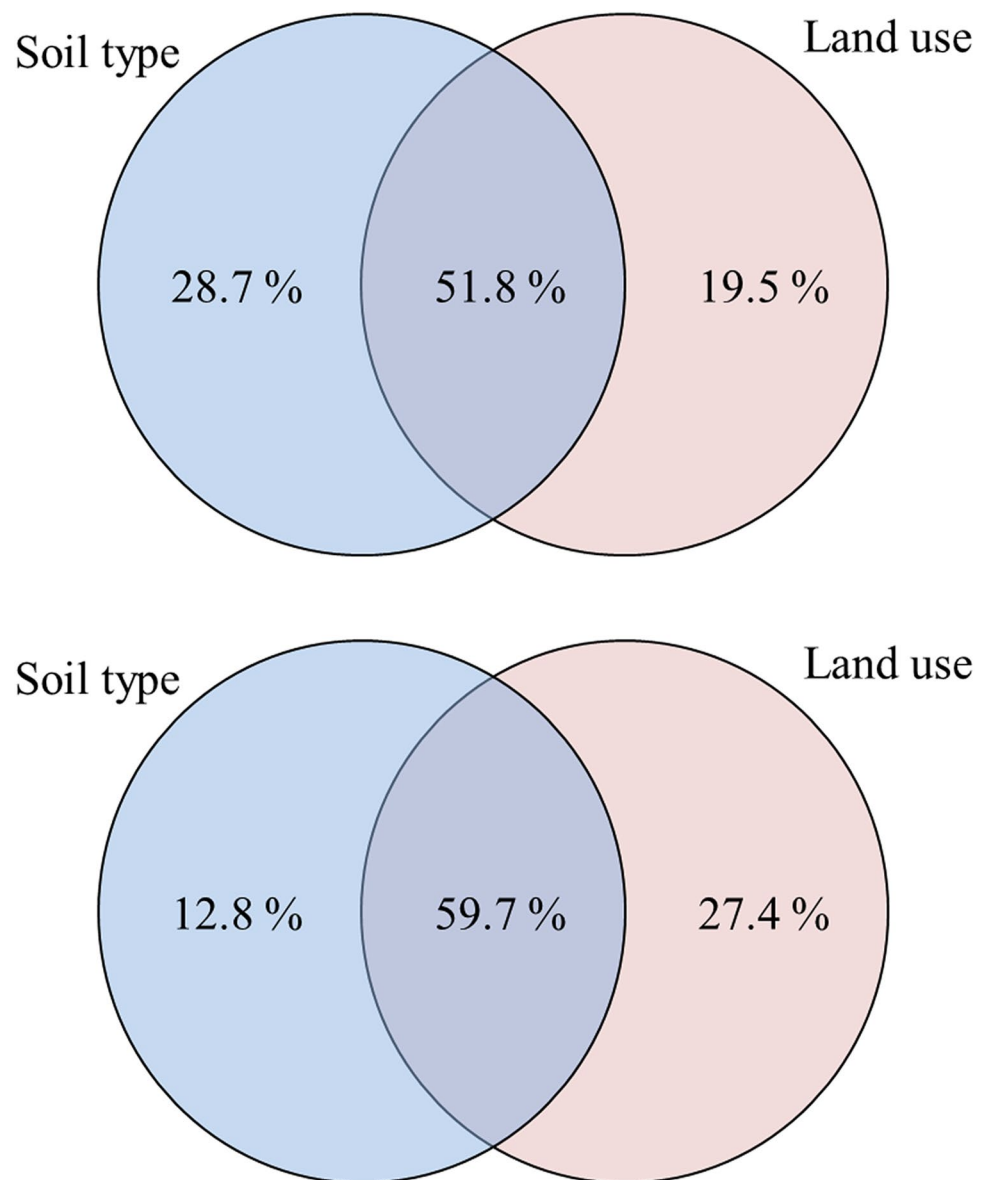
intensive use of fertilizer and irrigation, no crop rotation and no input of manures dramatically decreased soil properties and microbial abundance in mono-crop onion soil. *Chloroflexi* and A*cidobacteria* were significantly higher in CHON soil while *Proteobacteria* and *Actinobacteria* showed higher abundance in WAP and SESA soils. Relative abundance of *Ascomycota* was the highest in all soils followed by *Basidiomycota*. This research has broadened our understanding of the effects of land use on edaphic factors and microbial abundance of semi-arid arable soils and will help the farmers from central Myanmar to maintain and enhance soil fertility and crop yields leading to sustainable agriculture.

Authors' contributions TML, LFW and MZ did the experiment. TML wrote the draft manuscript. TG, SSY, EPK, ZKL and TMH improved manuscript.

Declarations

Conflict of interest The authors declare that they have no conflict of interest in the publication.

References

Abawi GS, Widmer TL (2000) Impact of soil health management practices on soilborne pathogens, nematodes and root diseases of vegetable crops. Appl Soil Ecol 15(1):37–47

Akhtar K, Wang W, Ren G, Khan A, Enguang N, Khan A, Feng Y, Yang G, Wang H (2020) Straw mulching with inorganic nitrogen fertilizer reduces soil CO2 and N2O emissions and improves wheat yield. Sci Total Environ 741:140488. https://doi.org/10.1016/j.scitotenv.2020.140488

Anderson IC, Campbell CD, Prosser JI (2003) Potential bias of fungal 18S rDNA and internal transcribed spacer polymerase chain reaction primers for estimating fungal biodiversity in soil. Environ Microbiol 5(1):36–47

Aung LL, Zin EE, Theingi P, Elvera N, Aung PP, Han TT, Oo Y, Skaland RG (2017) Myanmar Climate Report. vol ISSN 2387–4201. Norwaygian Meteorological Institute, Norway

Belmok A, Rodrigues-Oliveira T, Lopes FAC, Miranda HS, Krüger RH, Kyaw CM (2019) Long-term effects of periodical fires on archaeal communities from brazilian cerrado soils. Archaea 2019:6957210. https://doi.org/10.1155/2019/6957210

Bennett LT, Mele PM, Annett S, Kasel S (2010) Examining links between soil management, soil health, and public benefits in agricultural landscapes: an Australian perspective. Agr Ecosyst Environ 139(1–2):1–12

Bononi L, Chiaramonte JB, Pansa CC, Moitinho MA, Melo IS (2020) Phosphorus-solubilizing Trichoderma spp. from Amazon soils improve soybean plant growth. Sci Rep-Uk 10(1):2858. https://doi.org/10.1038/s41598-020-59793-8

Borneman J, Hartin RJ (2000) PCR primers that amplify fungal rRNA genes from environmental samples. Appl Environ Microb 66(10):4356–4360

Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, Fierer N, Peña AG, Goodrich JK, Gordon JI, Huttley GA, Kelley ST, Knights D, Koenig JE, Ley RE, Lozupone CA, McDonald D, Muegge BD, Pirrung M, Reeder J, Sevinsky JR, Turnbaugh PJ, Walters WA, Widmann J, Yatsunenko T, Zaneveld J, Knight R (2010) QIIME allows analysis of high-throughput community sequencing data. Nat Methods 7(5):335–336. https://doi.org/10.1038/nmeth.f.303

De Mendiburu F (2014) Agricolae: statistical procedures for agricultural research. R package version 1

Duan Y, Awasthi SK, Chen H, Liu T, Zhang Z, Zhang L, Awasthi MK, Taherzadeh MJ (2019) Evaluating the impact of bamboo biochar on the fungal community succession during chicken manure composting. Biores Technol 272:308–314. https://doi.org/10.1016/j.biortech.2018.10.045

Edgar RC (2018) Updating the 97% identity threshold for 16S ribosomal RNA OTUs. Bioinformatics 34(14):2371–2375. https://doi.org/10.1093/bioinformatics/bty113

Figuerola ELM, Guerrero LD, Turkowsky D, Wall LG, Erijman L (2015) Crop monoculture rather than agriculture reduces the spatial turnover of soil bacterial communities at a regional scale. Environ Microbiol 17(3):678–688

Garcia-Orenes F, Morugan-Coronado A, Zornoza R, Cerda A, Scow K (2016) Changes in soil microbial community structure influenced by agricultural management practices in a mediterranean agro-ecosystem (vol 8, e80522, 2013). PLoS ONE 11(3):e80522

Hu Y, Rillig MC, Xiang D, Hao Z, Chen B (2013) Changes of AM fungal abundance along environmental gradients in the arid and semi-arid grasslands of northern China. PLoS ONE 8(2):e57593–e57593. https://doi.org/10.1371/journal.pone.0057593

Hungria M, Franchini JC, Brandao O, Kaschuk G, Souza RA (2009) Soil microbial activity and crop sustainability in a long-term experiment with three soil-tillage and two crop-rotation systems. Appl Soil Ecol 42(3):288–296

Jenkins SN, Rushton SP, Lanyon CV, Whiteley AS, Waite IS, Brookes PC, Kemmitt S, Evershed RP, O'Donnell AG (2010) Taxon-specific responses of soil bacteria to the addition of low level C inputs. Soil Biol Biochem 42(9):1624–1631. https://doi.org/10.1016/j.soilbio.2010.06.002

Joergensen RG, Wu J, Brookes PC (2011) Measuring soil microbial biomass using an automated procedure. Soil Biol Biochem 43(5):873–876. https://doi.org/10.1016/j.soilbio.2010.09.024

Keshri J, Mishra A, Jha B (2013) Microbial population index and community structure in saline–alkaline soil using gene targeted metagenomics. Microbiol Res 168(3):165–173. https://doi.org/10.1016/j.micres.2012.09.005

Kong D, Liu N, Wang W, Akhtar K, Li N, Ren G, Feng Y, Yang G (2019) Soil respiration from fields under three crop rotation treatments and three straw retention treatments. PLoS ONE 14(9):e0219253. https://doi.org/10.1371/journal.pone.0219253

Konopka A (2009) What is microbial community ecology? ISME J 3:1223. https://doi.org/10.1038/ismej.2009.88

Koorem K, Gazol A, Öpik M, Moora M, Saks Ü, Uibopuu A, Sõber V, Zobel M (2014) Soil nutrient content influences the abundance of soil microbes but not plant biomass at the small-scale. PLoS ONE 9(3):e91998–e91998. https://doi.org/10.1371/journal.pone.0091998

Kumar CM, Ghoshal N (2017) Impact of land-use change on soil microbial community composition and organic carbon content in the dry tropics. Pedosphere 27(5):974–977. https://doi.org/10.1016/S1002-0160(17)60404-1

Kumar S, Suyal DC, Yadav A, Shouche Y, Goel R (2019) Microbial diversity and soil physiochemical characteristic of higher altitude. PLoS ONE 14(3):e0213844

Kyaw MS, Aye MM, Grinnell M, Rabach M (2018) Traditional and ethnobotanical dermatology practices in Myanmar. Clin Dermatol 36(3):320–324. https://doi.org/10.1016/j.clindermatol.2018.03.006

Leininger S, Urich T, Schloter M, Schwark L, Qi J, Nicol GW, Prosser JI, Schuster SC, Schleper C (2006) Archaea predominate among ammonia-oxidizing prokaryotes in soils. Nature 442(7104):806–809

Li J, Bao H, Xing W, Yang J, Liu R, Wang X, Lv L, Tong X, Wu F (2020a) Succession of fungal dynamics and their influence on physicochemical parameters during pig manure composting employing with pine leaf biochar. Biores Technol 297:122377. https://doi.org/10.1016/j.biortech.2019.122377

Li S, Wu F (2018) Diversity and co-occurrence patterns of soil bacterial and fungal communities in seven intercropping systems. Front Microbiol 9:1521. https://doi.org/10.3389/fmicb.2018.01521

Li TZ, Liu TT, Zheng CY, Kang CS, Yang ZC, Yao XT, Song FB, Zhang RZ, Wang XR, Xu N, Zhang CY, Li W, Li SM (2017) Changes in soil bacterial community structure as a result of incorporation of Brassica plants compared with continuous planting eggplant and chemical disinfection in greenhouses. PLoS ONE 12(3):e0173923

Li X, Zhang H, Sun M, Xu N, Sun G, Zhao M (2020b) Land use change from upland to paddy field in Mollisols drives soil aggregation and

associated microbial communities. Appl Soil Ecol 146:103351. https://doi.org/10.1016/j.apsoil.2019.09.001

Liu Z, Liu G, Fu B, Zheng X (2008) Relationship between plant species diversity and soil microbial functional diversity along a longitudinal gradient in temperate grasslands of Hulunbeir, Inner Mongolia. China Ecol Res 23(3):511–518. https://doi.org/10.1007/s11284-007-0405-9

Luneberg K, Schneider D, Siebe C, Daniel R (2018) Drylands soil bacterial community is affected by land use change and different irrigation practices in the Mezquital Valley. Mexico, Sci Rep-Uk, p 8

Lupatini M, Suleiman AKA, Jacques RJS, Antoniolli ZI, Kuramae EE, de Oliveira Camargo FA, Roesch LFW (2013) Soil-borne bacterial structure and diversity does not reflect community activity in Pampa biome. PLoS ONE 8(10):e76465–e76465. https://doi.org/10.1371/journal.pone.0076465

Lynn TM, Liu Q, Hu YJ, Yuan HZ, Wu XH, Khai AA, Wu JH, Ge TD (2017) Influence of land use on bacterial and archaeal diversity and community structures in three natural ecosystems and one agricultural soil. Arch Microbiol 199(5):711–721

Meyer A, Focks A, Radl V, Welzl G, Schoning I, Schloter M (2014) Influence of land use intensity on the diversity of ammonia oxidizing bacteria and archaea in soils from grassland ecosystems. Microb Ecol 67(1):161–166

Mohammadipanah F, Wink J (2015) Actinobacteria from arid and desert habitats: diversity and biological activity. Front Microbiol 6:1541. https://doi.org/10.3389/fmicb.2015.01541

Mueller RC, Belnap J, Kuske CR (2015) Soil bacterial and fungal community responses to nitrogen addition across soil depth and microhabitat in an arid shrubland. Front Microbiol 6:891–891. https://doi.org/10.3389/fmicb.2015.00891

Neina D (2019) The role of soil pH in plant nutrition and soil remediation. Appl Environ Soil Sci 2019:5794869. https://doi.org/10.1155/2019/5794869

Olsen SR, Sommers LE (1982) Phosphorus. In: AL KDP (ed) methods of soil analysis part 2 American Society of Agronomy, Soil Science Society of America, Madison, pp 403–430

Porras-Alfaro A, Herrera J, Natvig DO, Lipinski K, Sinsabaugh RL (2011) Diversity and distribution of soil fungal communities in a semiarid grassland. Mycologia 103(1):10–21. https://doi.org/10.3852/09-297

Richardson AE, Barea JM, McNeill AM, Prigent-Combaret C (2009) Acquisition of phosphorus and nitrogen in the rhizosphere and plant growth promotion by microorganisms. Plant Soil 321(1–2):305–339

Roesch LF, Fulthorpe RR, Riva A, Casella G, Hadwin AKM, Kent AD, Daroub SH, Camargo FAO, Farmerie WG, Triplett EW (2007) Pyrosequencing enumerates and contrasts soil microbial diversity. Isme J 1(4):283–290

Ruppel S, Torsvik V, Daae FL, Ovreas L, Ruhlmann J (2007) Nitrogen availability decreases prokaryotic diversity in sandy soils. Biol Fert Soils 43(4):449–459

Shannon CE (1997) The mathematical theory of communication. 1963. MD Comput 14(4):306–317

Shehab N, Li D, Amy GL, Logan BE, Saikaly PE (2013) Characterization of bacterial and archaeal communities in air-cathode microbial fuel cells, open circuit and sealed-off reactors. Appl Microbiol Biot 97(22):9885–9895

Shen JP, Cao P, Hu HW, He JZ (2013) Differential response of archaeal groups to land use change in an acidic red soil. Sci Total Environ 461:742–749

Sheng R, Meng DL, Wu MN, Di HJ, Qin HL, Wei WX (2013) Effect of agricultural land use change on community composition of bacteria and ammonia oxidizers. J Soil Sediment 13(7):1246–1256

Sial TA, Liu J, Zhao Y, Khan MN, Lan Z, Zhang J, Kumbhar F, Akhtar K, Rajpar I (2019) Co-application of milk tea waste and npk fertilizers to improve sandy soil biochemical properties and

wheat growth. Molecules 24(3):423. https://doi.org/10.3390/molecules24030423

Suzuki MT, Taylor LT, DeLong EF (2000) Quantitative analysis of small-subunit rRNA genes in mixed microbial populations via 5′-nuclease assays. Appl Environ Microb 66(11):4605–4614

Timonen S, Bomberg M (2009) Archaea in dry soil environments. Phytochem Rev 8(3):505–518

Tisdall JM, Smith SE, Rengasamy P (1997) Aggregation of soil by fungal hyphae. Soil Res 35(1):55–60. https://doi.org/10.1071/S96065

Shwe T, Kyu KL (2017) Groundnuts: producing the good oil for myanmar. Aciar project: SMCN/2011/047 'Increasing productivity of legume-based farming systems in the central dry zone of Myanmar.' Mypulses 2:28–29

van Groenigen K-J, Bloem J, Bååth E, Boeckx P, Rousk J, Bodé S, Forristal D, Jones MB (2010) Abundance, production and stabilization of microbial biomass under conventional and reduced tillage. Soil Biol Biochem 42(1):48–55. https://doi.org/10.1016/j.soilbio.2009.09.023

Vanegas J, Muñoz-García A, Pérez-Parra KA, Figueroa-Galvis I, Mestanza O, Polanía J (2019) Effect of salinity on fungal diversity in the rhizosphere of the halophyte Avicennia germinans from a semi-arid mangrove. Fungal Ecol 42:100855. https://doi.org/10.1016/j.funeco.2019.07.009

Villanueva L, von Meijenfeldt FAB, Westbye AB, Yadav S, Hopmans EC, Dutilh BE, Damsté JSS (2020) Bridging the membrane lipid divide: bacteria of the FCB group superphylum have the potential to synthesize archaeal ether lipids. ISME J. https://doi.org/10.1038/s41396-020-00772-2

Vukicevich E, Lowery DT, Bennett JA, Hart M (2019) Influence of groundcover vegetation, soil physicochemical properties, and irrigation practices on soil fungi in semi-arid vineyards. Front Ecol Evol 7:118

Wang W, Akhtar K, Ren G, Yang G, Feng Y, Yuan L (2019) Impact of straw management on seasonal soil carbon dioxide emissions, soil water content, and temperature in a semi-arid region of China. Sci Total Environ 652:471–482. https://doi.org/10.1016/j.scitotenv.2018.10.207

Wangthong S, Palaga T, Rengpipat S, Wanichwecharungruang SP, Chanchaisak P, Heinrich M (2010) Biological activities and safety of Thanaka (Hesperethusa crenulata) stem bark. J Ethnopharmacol 132(2):466–472. https://doi.org/10.1016/j.jep.2010.08.046

Wright PJ, Falloon RE, Hedderley D (2015) Different vegetable crop rotations affect soil microbial communities and soilborne diseases of potato and onion: literature review and a long-term field evaluation. New Zeal J Crop Hort 43(2):85–110

Wu XH, Ge TD, Yan WD, Zhou J, Wei XM, Chen L, Chen XB, Nannipieri P, Wu JS (2017) Irrigation management and phosphorus addition alter the abundance of carbon dioxide-fixing autotrophs in phosphorus-limited paddy soil. Fems Microbiol Ecol 93(12):fix154

Yadav RS, Tarafdar JC (2003) Phytase and phosphatase producing fungi in arid and semi-arid soils and their efficiency in hydrolyzing different organic P compounds. Soil Biol Biochem 35(6):745–751. https://doi.org/10.1016/S0038-0717(03)00089-0

Yang Y, Wang P, Zeng Z (2019) Dynamics of bacterial communities in a 30-year fertilized paddy field under different organic-inorganic fertilization strategies. Agronomy 9(1):14

Yao H, He Z, Wilson MJ, Campbell CD (2000) Microbial biomass and community structure in a sequence of soils with increasing fertility and changing land use. Microb Ecol 40(3):223–237

Yuan J, Zhao J, Wen T, Zhao M, Li R, Goossens P, Huang Q, Bai Y, Vivanco JM, Kowalchuk GA, Berendsen RL, Shen Q (2018) Root exudates drive the soil-borne legacy of aboveground pathogen infection. Microbiome 6(1):156. https://doi.org/10.1186/s40168-018-0537-x

Zhao J, Meng Y, Drewer J, Skiba UM, Prosser JI, Gubry-Rangin C (2020) Differential ecosystem function stability of ammonia-oxidizing archaea and bacteria following short-term environmental perturbation. Msystems 5(3):e00309-00320. https://doi.org/10.1128/mSystems.00309-20%JmSystems

Zhong Z, Zhang X, Wang X, Fu S, Wu S, Lu X, Ren C, Han X, Yang G (2020) Soil bacteria and fungi respond differently to plant diversity and plant family composition during the secondary succession of abandoned farmland on the Loess Plateau, China. Plant Soil. https://doi.org/10.1007/s11104-019-04415-0

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.