Network complexity of rubber plantations is lower than tropical forests for soil bacteria but not fungi

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Abstract:

Soil microbial communities play a crucial role in ecosystem functioning. Past research has examined the effects of forest conversion on soil microbial composition and diversity, but it remains unknown how networks within these communities respond to forest conversion such as when tropical rainforests are replaced with rubber plantations. Microbial network is viewed as a critical indicator of soil health and quality, and consists of two parts: nodes and edges. In this study, we used the data from Illumina sequencing and metagenome shotgun sequencing to analyze bacterial and fungal community network structure in a large number of soil samples from tropical rainforest and rubber plantation sites in Hainan Island, China. Our results showed only about 5-10% shared network edges (i.e., links between species A and B not only existing in rubber plantation, but also in rainforest) were observed in both bacterial and fungal communities, which indicates that forest conversion altered soil microbial network structure. Meanwhile, the keystone OTU in the communities between rubber plantations and rainforest forest were also completely different, which further proved the above point of view. More edges and more negative correlations of soil bacterial-fungal network were observed in rubber plantation sites (dry season: 4284 total edges, 844 negative; rainy season: 7257 total, 1744 negative) than in rainforest sites (dry season: 3650 total, 149 negative; rainy season: 6018 total, 489 negative) demonstrated that soil bacterial-fungal network structure were more complex and stable in rubber plantation than in rainforest. For bacteria, a larger number of network edges among bacterial networks in samples from tropical rainforest compared to samples from rubber plantations indicates that rainforest bacterial networks were more complex than rubber plantation. However, rubber plantations soil fungal networks showed higher links, suggesting that forest conversion increased fungal network complexity. More edges of network and more links between species and functions were observed in rainy season than in dry season indicating seasonal change had a strong effect on network and function. Further analysis shows soil pH, potassium (AK), total nitrogen (TN) had more links with species of some phyla. In conclusion, forest conversion results in an increase in soil pH, and a decrease in AK and TN, and these changes as well as seasonal variations had a great impact on soil microbial composition, network structure and function.

Keyword: Tropical rainforest, Rubber plantations, Networks, Soil microbial community, Forest conversion

1. Introduction

Soil microbiome is the generic term of massive microorganisms and complex soil environment and it is highly diverse and comprises up to one quarter of Earth’s diversity (Wagg et al., 2019). Soil microbes play a critical role in the maintenance of soil quality and function, and they represent the majority of biodiversity in terrestrial ecosystems (Philippot et al., 2013). A number of studies have investigated the impact of the conversion of tropical forests to rubber plantations on soil microbial composition and diversity (Schneider et al., 2015; Kerfahi et al., 2016, Lan et al., 2017a; 2017b; 2017c; Lan et al., 2020a; 2020b; 2020c). Studies conducted in Indonesia (Schneider et al. 2015), Malaysia (Kerfahi et al. 2016) and South China (Lan et al. 2017a; Lan et al. 2017b; Lan et al. 2017c) have found significant differences between rubber plantations and tropical forests, specifically that the diversity of soil bacteria was higher in rubber plantations than in rainforest. Compared to primary forests, agricultural systems tend to have higher bacterial richness but lower fungal richness (Lan et al., 2017a; Cai et al., 2018; Tripathi et al., 2012; Kerfahi et al., 2016). Compared to Eucalyptus plantations, rubber plantations have higher diversity of both bacteria and fungi (Ma et al., 2019). Song et al. (2019) reported that tropical forest conversion to rubber plantation results in reduced fungal microbial community network complexity, while there are few studies on the impact of forest conversion on soil bacterial community network structure and the drivers leading to the changes of network structure.

The soil microbial network is viewed as a critical indicator of soil health and quality (Kuperman et al., 2014). Microbial network consists of two parts: nodes and edges. Nodes indicate microbes, such as OTU or species, and they can also indicate environmental variables we interested, such as soil pH. Edges (or links) indicate significant correlations between nodes. The number of links related to a node is the node’s degree (Röttjers and Faust, 2018). Usually, the more links of the network has, the more complex the community is. Similarly, the higher the degree of a node (OTU or species), the more important the species is to the network structure (Berry and Widder, 2014). In recent years, microbial network analysis has been used to identify keystone taxa (Banerjee et al., 2018) and provide comprehensive insight into the microbial community structure and assembly (Fuhrman, 2019). The complexity of network structure is understood by calculating the number of edges, and the keystone species of the community are found by estimating the degree of species. The stability of the microbial community is determined by calculating the ratio of positive and negative correlation of the network because a large proportion of positive correlation for microbial community are deemed to be unstable (Coyte et al., 2015).

Previous work has shown that agricultural intensification can reduce microbial network complexity (Banerjee et al., 2019). Logging alters soil fungal network in tropical rainforests, i.e., a better-organized fungal community in the select cut stands when compared with the primary stands (Chen et al., 2019). Soil bacterial networks are less stable under drought than fungal networks (De Vries et al., 2018). While the exact drivers of microbial network structure still remain unknown. Previous study showed that soil nutrients, such as soil phosphorus content, and soil pH, are the main drivers for the network structure of microbial community (Banerjee et al., 2019). Seasonal variation also affects the network structure by changing the keystone species of the community because a keystone species might be present only in a specific season or time period (Banerjee et al., 2018).

Hainan Island is home to a large area of tropical rainforest rich in biodiversity. It is a part of the Indian-Malay rainforest system at the northern edge of the world's rainforest distribution. However, rubber plantations now account for almost a quarter of the total extent of vegetated areas on Hainan Island (Lan et al., 2020a). Previous study conducted in Hainan Island showed forest conversion from rainforest to rubber plantations resulted in shifts in bacterial composition from the Proteobacteria to Chloroflexi, and fungal composition from Basidiomycota to Ascomycota (Lan et al., 2020a). Research also shows microbial (including bacteria and fungi) diversity was higher in rainforest soils than in rubber plantation (Lan et al., 2020a). Therefore we hypothesize that (1) Due to forest conversion from rainforest to rubber plantations results in changes in dominant phyla of microbes in soils, the network structure and related keystone species also changed accordingly. (2) Soil bacterial-fungal network structure were less complex but more stable in rubber plantation than in rainforest due to high species diversity leads to complex network structure and unstable microbiome communities (Coyte et al., 2015). (3) Soil bacterial network in rubber plantation is less complex than rainforest because intensive cropping reduces the complexity of bacterial network although the richness is increased (Karimi et al., 2019).(4) Due to returning litter to the field and applying organic fertilizer in rubber plantation, soil fungal network structure in rubber plantation sites is more complex than in rainforest because organic farming showed a much more complex fungal network than conventional or no-tillage farm systems (Banerjee et al., 2019). By testing these hypotheses, we want to clarify the drivers and mechanisms of microbial community assembly that link forest conversion to differences in soil microbial network structure. This study will provide critical information for understanding and managing microbial communities in tropical forests of China and elsewhere.

2. Methods

2.1 Study site

This study was conducted on Hainan Island (18°10′–20°10′N and 108°37′–111°03′E), south China. The total area of Hainan Island is about 34,000 km^2 (Lopez et al., 2009). Hainan Island is the largest island within the Indo-Burma Biodiversity Hotspot in tropical Asia (Francisco-Ortega et al., 2010) and has a tropical monsoon climate. Hainan Island has a warm and humid climate all year round, with an average annual temperature of 22-26°C. Rainfall is abundant, ranging from 1,000 mm to 2,600 mm yearly, with an average annual precipitation of 1,639 mm. The rainy season occurs from May to October, with a total precipitation of about 1500 mm, accounting for 70-90% of the total annual precipitation. Only 10-30% of the total annual precipitation falls within the dry season, from November to April. The central part of Hainan Island is mountainous and contains old-growth tropical rainforests and monsoon forests. Rubber plantations are found on the plateaus surrounding the central mountainous zone.

2.2 Soil sampling

The tropical rainforests in Hainan are mainly distributed in Bangwangling, Diaoloshan, Wuzhishan, Yinggeling and Jianfengling. Therefore, we selected a tropical rainforest in each of these sites as our study objectives. There are about 530, 000 hectares of rubber plantations in Hainan Island. Five rubber plantations were selected in Wanning, Ledong, Danzhou, Haikou, Qiongzhong, and these five rubber plantation locate in the east, south, west, north and middle of Hainan, respectively. (Figure S1). We selected 25-30 years old rubber trees (i.e., mature rubber plantations) as our study objectives. Management practices, such as latex harvest and the application of fertilizers, are used in rubber plantations. Usually, compound fertilizer (1-1.5 kg per tree) and organic fertilizers (20-25 kg per tree) were applied once or twice a year. More information on the study sites is provided in Table S1. Before soil sampling, we sterilized the soil drill with 75% alcohol. After the removal of the litter layer, by using a 5-cm diameter steel drill, top soil (0 to 20 cm) was collected, then homogenized and passed through a 2-mm mesh sieve. For each site, thirteen soil samples were collected, thus there were a total of 130 samples collected between the rubber plantations and tropical rainforest. Soil sampling was performed twice in 2018, once in January (dry season) and once in July (rainy season).Thus, there were a total of 260 soil samples (130 per forest type). Soil samples were divided into two parts: one was used to analyze soil water contents, soil pH, total nitrogen, total phosphorus (TP), total potassium (TK), nitrate nitrogen (NN), ammonium nitrogen (AN), available phosphorus (AP), potassium (AK). Soil water content (%) was measured gravimetrically. Soil pH was measured in a soil/water suspension (1: 2.5, w/w) using a pH meter. TN was determined using a micro-Kjeldahl digestion followed by steam distillation. TP and TK were measured following digestion with NaOH. NN and AN were determined by steam distillation and indophenol-blue colorimetry, respectively. Soil samples were extracted with NaHCO3 and the extract was then used to measure available soil phosphorus AP via molybdate-blue colorimetry. To measure soil AK, soil was extracted with ammoniumacetate and then the extract was loaded onto an atomic absorption spectrometer with ascorbic acid as a reductant (Chen et al., 2019). Soil properties of the rubber plantation and rainforest sites are shown in Table S2. The other was stored in ultra-low temperature (- 80 ℃) refrigerator for later DNA extraction.

2.3 DNA extraction and PCR amplification

Microbial DNA was extracted from 0.5 g of soil using the E.Z.N.A.® Soil DNA Kit (Omega Bio-tek, Norcross, GA, U.S.) following the manufacturer’s protocol. The fungal ITS1 hypervariable region was amplified using the PCR primers ITS1F (5'-CTTGGTCATTTAGAGGAAGTAA-3') and ITS2R (5'-GCTGCGTTCTTCATCGATGC-3') (Adams et al., 2013). For bacteria and archaea, the V4 hypervariable region of the bacterial 16S rRNA gene was amplified using the PCR primers 515FmodF (5'-GTGYCAGCMGCCGCGGTAA-3') and 806RmodR (5'-GGACTACNVGGGTWTCTAAT-3') (Walters et al., 2016; Sampson et al., 2016). The PCR reactions were conducted using the following approach: an initial 3 min denaturation at 95°C; followed by 27 cycles of 30s at 95°C, 30s of annealing at 55°C, and 45s of elongation at 72°C; and a 10 min final extension at 72°C.

2.4 Illumina MiSeq sequencing

Amplicons were extracted from 2% agarose gels, purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, U.S.) and quantified using a QuantiFluor™ -ST Fluorometer (Promega, U.S.). Purified amplicons were pooled in an equimolar solution and then sequenced (paired-end, 2 × 250 bp) on an Illumina MiSeq platform according to standard protocols.

Metagenomic shotgun sequencing libraries were prepared and then sequenced by Majorbio, Inc. (Shanghai, China) using the Illumina HiSeq 2000 platform. The NR gene catalog was aligned against the Kyoto Encyclopedia of Genes and Genomes (KEGG) database using BLAST (Version 2.2.28+) and then functionally annotated using KOBAAS 2.0 according to previously described methods (Qin et al., 2010)

2.5 Bioinformatics and data analysis

Raw fastq files were demultiplexed and quality-filtered using QIIME (Caporaso et al., 2010) (version 1.17). Operational Taxonomic Units (OTUs) were clustered with a 97% similarity cut-off using UPARSE (Edgar, 2013), and chimeric sequences were identified and removed using UCHIME. Using the RDP Classifier, the phylogenetic affiliation of each 16S rRNA gene and ITS gene sequence was determined using a confidence threshold of 70% with the SILVA 16S rRNA database and UNITE database, respectively (Amato et al., 2013). The relative abundance was determined for each taxon (Good, 1953), and the Shannon and Simpson diversity indices were calculated based on re-sampled sequence data using MOTHUR (Schloss et al., 2009). For each site, the relative abundance of different taxa (Good, 1953) and the Shannon diversity index were calculated based on re-sampled sequence data using MOTHUR (Schloss et al., 2009). The raw reads were deposited into the NCBI Sequence Read Archive (SRA) database (Accession Number: SRP108394, SRP278296, SRP278319).

2.6 Statistical analysis

For the co-occurrence network analyses, to make the analyses simple, we only use the top 300 most abundant bacterial and fungal OTUs to analyze the network structure of the two forest types, and these OTUs are approximately equal to OTUs with relative abundance greater than 0.05% (Jiao et al., 2016). The networks of each habitat during each sampling period (rainforest and rubber plantations in dry season and rainy season) were constructed with 65 samples each. We also performed the bacterial-fungal community network analysis to investigate soil microbial network complexity of rubber plantation and rainforest across seasons. Interactions consisted of Spearman's rank correlations and co-occurrence networks were constructed using only significant correlations of $\rho > 0.6$ ($P < 0.01$) (Barberan et al. 2012), because this cutoff includes a range of interactions strengths (De Vries et al., 2018). The networks were then visualized in R using the *igraph* package. To reveal the distribution pattern of correlation coefficients, the frequency of the coefficients of $\rho > 0.3$ ($P < 0.01$) were plotted. The Network Analyzer tool in Cytoscape (version 3.4.0) was used to calculate network topology parameters including number of nodes, edges, degree, betweenness, closeness. The number of shared edge and unique edge as well as keystone OTU were calculated to evaluate whether the network structure has changed. Shared network edge is the link (edge) between species A and species B not only existing in rubber plantation network, but also in rainforest network. Unique edge is the link only existing in rubber plantation or rainforest. The number of shared edges and unique edges which were calculated using *igraph* and visualized by using Venn diagrams. Keystone OTU are known to be important for ecosystem structure and function and were selected on the basis of high network degree, high closeness centrality, and low betweenness centrality as defined by Berry and Widder (2014). To evaluate the proportional influence of each phylum on bacterial and fungal network structure, node degrees of each phylum were calculated and bar plots were created. Correlation coefficients between species and functions were calculated based on metagenomics data. Here we used the top 50 most abundant species and top 50 KEGG functions (pathway level 3). Then the species and function correlation network was constructed on the Major bio cloud platform (https://cloud.majorbio.com/). To reveal the relationship between microbial taxon and environment variables, two-way correlation networks were also constructed on the Major bio cloud platform. The topological role of each node in a network was assessed by the Z_i and P_i values, where Z_i represents the nodes connectivity within a module, and P_i measures the degree of a node connected with other modules (Roger and Amaral, 2005). All species can be divided into four groups according to the simplified criteria (Olesen et al., 2007), namely peripherals ($Z_i < 2.5$ and $P_i < 0.62$), connectors ($P_i > 0.62$), module hubs ($Z_i > 2.5$) and network hubs ($Z_i > 2.5$ and $P_i > 0.62$). The Z_i and P_i values were calculated using GIANT package of Cytoscape. The Z_i-P_i plot was created with *ggplot2* in R.

3. Results

3.1 Bacterial and fungal networks

Our results showed that the bacterial-fungal community network were more complex in rubber plantation (4284 edges in dry season, 7257 in rainy season) than in rainforest (3650 in dry season, 6507 in rainy season), and more complex in rainy season than in dry season (Figure 1). Most nodes of bacterial networks (Figure 2) and fungal networks (Figure 3) varied with forest type in both the dry season and rainy season. For bacterial networks, there were 2559 and 2501 edges in tropical rainforest and rubber plantation in dry season respectively, but these two networks only shared 262 edges, accounting only about 10% the total edges (Figure 4A-B). Similarly, these networks only shared 519 edges during the rainy season. For fungal networks, there were only 4 and 5 shared edges (i.e., no more than 5% of the total edges) in dry season and rainy season, respectively (Figure 4C-D).

The number of edges of bacterial and fungal networks were almost equivalent during the dry season. However, in rainy season, there were more edges in the bacterial network in tropical rainforest than in the rubber plantation (Table 1 & Figure 4B). For the network structure of the fungal community, more edges were observed in rubber plantations in rainy season (Table 1 & Figure 4D). Similarly, there were no significant differences in both bacterial and fungal network degree between tropical rainforest sites and rubber plantations in the dry season (Figure 5A, C). In the rainy season, rainforest sites had higher bacterial network degree, while rubber plantations showed higher fungal network degree (Figure 5B, D). For bacterial networks, more nodes (OTUs) with high degree (rubber plantation had 2 nodes with degree greater than 75, rainforest had 8 such nodes) of rainforest were observed during the rainy season (Figure S2B). For fungal networks, 15 nodes of higher degree (degree greater than 25) were observed in rubber plantations, however, only 7 such nodes existed for rainforest sites (Figure S2D). These results indicate rubber plantation fungal network structure was more complex than tropical rainforest during the rainy season, but that the reverse was true for bacteria.

When considering the ratio of positive to negative correlation coefficients, the bacterial-fungal community network revealed that rubber plantations (844 edges in dry season, 1744 edges in rainy season) have more negative links than rainforest (149 edges in dry season, 489 edges in rainy season) indicating network of rubber plantation was more stable than rainforest (Figure 1). More correlations (greater than 0.3, $P < 0.01$) were also calculated to investigate the ratio of positive to negative correlation and the results showed that negative correlations between bacterial and fungal OTUs of rubber plantations were consistently stronger than for tropical rainforest in both dry season and rainy season (Figure 6).

3.2 Keystone taxa

The module hubs and network hubs have been commonly identified as keystone taxa in network. However, for both the bacterial and fungal communities, neither tropical rainforest nor rubber plantation networks possessed module hubs and network hubs (Figure S3-S4). The keystone taxa of bacteria were very different between rubber plantations and tropical rainforest sites in both the dry season and rainy season. For bacteria, there were more keystone taxa in tropical rainforest sites than in rubber plantations in both the dry season and rainy season indicating that the tropical rainforest networks had higher complexity. We found that some groups of Acidobacteria are keystone taxa in tropical rainforest sites but disappeared after forest conversion. There were more Actinobacteria bacteria in rubber plantations than in tropical rainforest sites (Table S3).

For fungi, more keystone taxa were observed in rubber plantations than in tropical rainforest sites during both the dry season and rainy season, indicating the rubber plantation networks were more complex. Most keystone taxa belong to Ascomycota suggesting member of this group are very import for network structure. In addition to forest conversion, seasonal changes also affect the keystone taxa of the fungal community network. There were more Basidiomycota OTUs in the dry season, but more Ascomycota in rainy season (Table S4).

3.3 Influencing factors of microbial composition and network structure

Two-ways correlation network analysis of the 300 most abundant OTUs and environmental variables revealed elevations (106 degree), AK (104), soil pH (86) were main drivers of bacterial community composition (Figure S5A). For fungi, elevation had the highest degree (61), followed by AK (51) (Figure S5B). Relationship between OTU abundance and soil pH revealed the soil pH negatively correlated with species of Acidobacteria, but positively correlated with species of Chloroflexi and species of Ascomycota (Figure S6). AK positively correlated with species of Planctomycetes Verrucomicrobia and Basidiomycota, however negatively correlated with Chloroflexi and Ascomycota. In words, AK, soil pH were important driver for microbial composition.

Total degree of each phylum were used to reveal the influence of each phylum on network structure (Figure 7). For bacteria, Proteobacteria, Actinobacteria and Acidobacteria had a large influence on network structure. Acidobacteria and Planctomycetes contributed more to rainforest networks than rubber plantation networks. However, Actinobacteria and Chloroflexi showed the opposite. For fungi, Ascomycota and Basidiomycota had large influence of network structure. Both Ascomycota and Basidiomycota had stronger influence on rainforest networks than rubber plantation networks. The influence of Ascomycota was stronger during the rainy season than in the dry season, indicating seasonal change also had impact on fungal community networks. Degree of each phylum of bacterial and fungal network also revealed seasonal change had effects on network degree (Figure S7).

3.4 Interaction between species and functions

Two-way network analysis of the 50 most abundant species (all belong to bacteria groups, metageomic data) and the 50 most abundant KEGG functions revealed the interaction between microbial composition and functions. The results showed that soil network structure in at rainforests sites (460 edges in dry season, 1750 in rainy season) was more complex than rubber plantations (223 in dry season, 451 in rainy season) (Figure 8) indicating that more links between microbial species and functions were observed in soils of rainforest sites. Both rubber plantations and rainforest networks were more complex in the rainy season than in dry season. We also found that metabolism was the most important function in soil microbial network. Surprisingly, species of Actinobacteria negatively correlated function in rubber plantations.

4. Discussion

4.1 Forest conversion reduces soil bacterial network complex

Land-use changes increasingly threaten biodiversity, particularly in tropical forests (Gibson et al., 2011). However, we still have little understanding of how soil networks response to forest conversion, such when rainforests are converted to rubber plantations. Our results showed that forest conversion had large effects on both soil bacterial and fungal networks. More edges (Table 1) and higher degree (Figure 4) of tropical rainforest bacterial networks were observed, especially during the rainy season, which indicates that the rainforest bacterial network was more complex than the rubber plantation network. This consistent with previous observations that soil bacterial networks were more complex in natural systems than in crop soil (Karimi et al., 2019). Further study showed that soil networks become more connected as nature restoration progresses (Morriën et al., 2017). The observed decrease in network complexity and cohesion supports the hypothesis that cropping may enhance the isolation of bacterial taxa (Karimi et al., 2019), which results in lower connection of the network. In addition, at the microscale, the structure of tilled soils is more homogeneous, and the soil pores are less connected than in soils under without tillage (Pagliai et al., 2004), such as rainforest soil. In nature, soil ecosystems are highly heterogeneous since soil microbial biodiversity hot spots can form spatial and temporally within soil aggregates (Bach et al., 2018). This spatial heterogeneity likely plays an important role for the interactions among microbes and the mechanisms by which more complex and diverse communities drive various nutrient cycling processes on small spatial scales (Wagg et al., 2018).

A large number of studies employing microbial network analysis have enriched our understanding of microbial co-occurrence patterns in various soil ecosystems, however, very little is known of whether differences in the structure of microbial networks have consequences for microbiome functioning (Wagg et al., 2018). Our results demonstrated that more species related with metabolism in natural system than in the agricultural system, especially in the rainy season. This is in line with a previous study conducted in Sumatra, Indonesia, which found that the transformation of forest to rubber results in a 10-16% decrease in community metabolism (Barnes et al., 2014). Fewer interactions between microbial species (most of them are bacteria) and functions in rubber plantations demonstrated that forest conversion reduced soil bacterial network complex.

4.2 Forest conversion increased soil fungal network complexity

Surprisingly, rainforest bacterial networks were characterized by fewer edges (Table 1) and lower degree (Figure 4), which means that rubber plantation bacterial networks were more complex than the native forest. Our results were not consistent with a study conducted in Xishuangbanna (Song et al., 2019) which showed that tropical forest conversion reduced fungal network complex, but consistent with previous observations which found that fungal community networks were better organized disturbed forest compared to primary forest (Chen et al., 2019). Banerjee et al. (2019)'s observation showed that organic agricultural fields harbored much more complex fungal networks with many more keystone taxa than conventional managed fields. Forest conversion resulted in shifts in fungal composition from Basidiomycota to Ascomycota (Figure S8), as seen in previous investigations (Lan et al., 2020a; Lan et al., 2020b). Previous work showed that Basidiomycota species show higher drought sensitivity than Ascomycota species (Taniguchi et al., 2018), this would result in a shift in richness and abundance of Basidiomycota species (Figure S8). Many Basidiomycota species are capable of long-distance dispersal (Egidi et al. 2019, Geml et al., 2012), which may result in a decrease in fungal network. This possibly explained why Ascomycota OTUs contribute more to the network structure than Basidiomycota (Figure 6). Overall, reduction in abundance and richness of Basidiomycota species led to an increase in fungal links in rubber plantations.

4.3 Forest conversion enhanced the stability of soil network

Microbial community's ability to resist and recover from disturbances were defined as stability of communities (De Vries and Ashley, 2013).The positive to negative ratio of network links indicates the balance between facilitative and inhibitive relationships within a network (Karimi et al., 2017). Theoretical studies, for example, predict that ecological networks that consist of weak interactions are more stable than those with strong interactions (Neutel et al., 2002, Coyte et al., 2015), and that compartmentalization and presence of negative interactions increase the stability of networks under disturbances (Coyte et al., 2015, Rooney et al., 2006, Stouffer & Bascompte 2011). In our study, more negative correlations were detected in rubber plantation, indicating the network structure of rubber plantation soils was more stable than rainforest soils (De Vries et al., 2018). Forest conversion from rainforest to rubber plantations resulted in shifts in bacterial composition from Proteobacteria to Chloroflexi, and fungal composition from Basidiomycota to Ascomycota (Lan et al., 2020a). Proteobacteria and Basidiomycota belong to copiotrophic microorganism, while Chloroflexi and Ascomycota belong to oligotrophic microorganism (Yang et al., 2019; Lan et al., 2020a). This indicated forest conversion resulted in shits in soil microbial composition from *k*-strategists tend to be *r*-strategists (De Vries et al., 2013). R-strategists are quickly-growing and less resistant but more resilient to disturbances. However, growth is not the only mechanism that could maintain community stability because the response of microorganisms to disturbance are very complex.

4.4 Main drivers for soil microbial composition and network structure

Forest conversion results in the loss of plant diversity, plant biomass and increasing soil pH (Lan et al., 2017a, 2017b). Rubber plantations had a significantly higher pH, which explains the relative decrease in the abundance of Acidobacteria (Lan et al., 2017a). Our results demonstrate that keystone taxa of soil microbes change after forest conversion (Table 1). We found that many OTUs of Acidobacteria fit our criteria as keystone species for rainforest sites, which is consistent with previous findings (Banerjee et al., 2018). Unexpectedly, OTU11388 and OTU11373, both Acidobacteria, were observed in rainforest soils in both the dry and rainy seasons, indicating Acidobacteria were very important for rainforest soil bacterial networks (Figure 6 and table S3). Higher AK concentration resulted in a higher abundance and more taxa of of Actinobacteria (Figure 9), which suggests that Actinobacteria contributed more in rubber plantation than in rainforest (Figure 6). Indeed, forest conversion reduced the abundance of Actinobacteria OTUs (Figure S9). Due to the human disturbance in rubber plantations, the soil will inevitably be slightly polluted with herbicides and domestic garbage. Previous study showed member of Actinobacteria were observed in contaminated soil (Jiao et al., 2016).

Forest conversion also increases land use intensity (Brinkmann et al., 2019), including the application of fertilizer and herbicide. Herbicide application also caused significant decreases in root colonization and spore biomass of arbuscular mycorrhizal fungi in tropical agriculture (Zaller et al., 2014). Soil nutrient concentration shows a decline around the roots of rubber plantations compared to those from rainforests (Sahner et al., 2015). Our observation is no exception, for instance, AK and TN concentration was significant lower in rubber plantation than in samples from rainforest sites (Table S2). Higher concentration of AK reasonably explained the higher contribution of Basidiomycota on the network structure (Figure 8B) due to AK positive association with Basidiomycota.

Spatiotemporal heterogeneity can be a major driver of the abundance and distribution of keystone taxa in soil which is a highly heterogeneous and multifaceted environment (Mills et al., 1993, Power et al., 1996; Mouquet et al., 2013). Seasonal variability determines the structural and compositional properties of microbiomes in an environment, and as such, a keystone species might be present only in a specific season or time period (Banerjee et al., 2018). It was interesting that more bacterial OTUs were identified as connectors during the rainy season than in the dry season. Connectors have been characterized as generalists (Olesen et al., 2007), and generalists drive covariation among communities in a network (Chen et al., 2019). Previous observation demonstrated that some keystone taxa that were found in the dry season disappeared during the rainy season (Lan et al., 2018). Seasonal changes possibly explained the keystone taxa was observed in rainy season but not in dry season.

4.5 Possible impact of forest conversion on microbial community function

Forest conversion results in a decrease in abundance of Proteobacteria and increase of Actinobacteria. Most species of Proteobacteria was positively correlated with metabolic function, while most of Actinobacteria was negatively associated with metabolic function (Figure 8). Therefore, the changes in the abundance of these two phyla results in a reduction of microbial community function after forest conversion. Due to metabolic function of a specific species usually affected by environmental conditions (Louca et al., 2018), some species are not correlated with any function in the dry season, but correlated with metabolic function in the rainy season, indicating there some microorganisms do not participate in the metabolic process in dry season, especially for the rubber plantations. In conclusion, forest conversion as well as seasonal variation had a great impact on soil microbial community functions.

5. Summary

Our knowledge about land-use impacts on soil ecosystems is mostly limited to biodiversity and ecosystem functions, leaving uncertainty about how soil networks change after forest conversion. This study is the most comprehensive report on changes in network structure that occur when tropical rainforests are converted into rubber forest. Our study showed that forest conversion altered both bacterial and fungal soil networks, reduced bacterial network complexity and enhanced fungal network complexity, especially during the rainy season. One possible reason maybe that forest conversion changed soil pH and other soil properties, which altered bacterial composition, subsequent network structure as well as functions. Our study demonstrates the impact on forest conversion for soil network structure, which has important implications for ecosystem functions, such as metabolic function, and health of soil ecosystems in tropical regions.

Code availability

Not applicable

Authors' contributions

Guoyu Lan: Conceptualization, Methodology, Writing, Reviewing and Editing; Chuan Yang, Rui Sun, Bangqian Chen, Xicai Zhang and Zhixiang Wu: Investigation

Competing interests

The authors declared that they have no conflicts of interest to this study.

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References

Adams RI, Miletto M, Taylor JW, Bruns T D. Dispersal in microbes: fungi in indoor air are dominated by outdoor air and show dispersal limitation at short distances, ISME J., 7(7):1262-1273, 2013

Amato, K.R., Yeoman, C.J., Kent, A., Carbonero, F., Righini, N., Estrada, A.E., Gaskins, H.R., Stumpf, R.M., Yildirim, S., Torralba, M., Gillis, M., Wilson, B.A., Nelson, K.E., White, B.A., Leigh, S.R., Habitat degradation impacts primate gastrointestinal microbiomes, ISME J., 7: 1344-1353, 2013

Bach, E. M., Williams, R. J., Hargreaves, S. K., Yang, F. & Hofmockel, K. S. Greatest soil microbial diversity found in micro-habitats, Soil Biol. Biochem., 118: 217-226, 2018

Banerjee, S., Schlaeppi, K., van der Heijden, M.G.A. Keystone taxa as drivers of microbiome structure and functioning, Nat. Rev. Microbiol., 16: 567-576, 2018;

Banerjee, S., Walder, F., Büchi, L., Meyer, M., Held, A.Y., Gattinger, A., Keller, T., Charles, R., van der Heijden, M.G.A. Agricultural intensification reduces microbial network complexity and the abundance of keystone taxa in roots, ISME J. 2019; 13:1722-1736.

Barberan, A., Bates, S.T., Casamayor, E.O., Fierer, N. Using network analysis to explore co-occurrence patterns in soil microbial communities, ISME J., 6:343-351,2012

Barnes, A. D. Jochum, M., Mumme, S., Haneda, N. F., Farajallah, A., Widarto, T. H. & Brose, U. Consequences of tropical land use for multitrophic biodiversity and ecosystem functioning, Nat Commun., 5: 5351, 2014

Berry D, Widder S. Deciphering microbial interactions and detecting keystone species with co-occurrence networks, Front Microbiol., 5:1–14, 2014;.

Brinkmann N., Schneider D. , Sahner J., Ballauff J.,Edy N., Barus H., Irawan B., Budi S.W., Qaim M.,Danie R., Polle, A.. Intensive tropical land use massively shifts soil fungal communities, Sci. Rep., 9:3403, 2019

Cai, Z.Q., Zhang, Y. H, Yang, C.,Wang, S. Land-use type strongly shapes community composition, but not always diversity of soil microbes in tropical China, Catena 165: 369-380, 2018;

Caporaso, J.G., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F.D., Costello, E.K., Fierer, N., Peña, A.G., Goodrich, J.K., Gordon, J.I., QIIME allows analysis of high-throughput community sequencing data, Nat. Methods, 7: 335-336, 2010

Chen, J., Xu, H., He, D., Li, Y.D., Luo, T.S., Yang, H.G., Lin, M.X., 2019. Historical logging alters soil fungal community composition and network in a tropical rainforest, For. Ecol. Manage., 433 (5): 228-239, 2019

Coyte, K. Z., Schluter, J. Foster, K. R. The ecology of the microbiome: networks, competition, and stability, Science, 350: 663-666,2015;

De Vries, Ashley, S. Controls on soil microbial community stability under climate change. Front.Microbiol., 4: 265, 2013

De Vries, V. F. T., Griffiths, R. I., Mark, B., Hayley, C., Mariangela, G., Soon, G. H., et al. Soil bacterial networks are less stable under drought than fungal networks, Nature Commun. 9(1): 3033, 2018

Edgar, R.C. UPARSE: Highly accurate OTU sequences from microbial amplicon reads, Nat. Methods 10:996-998, 2013

Egidi, E., Delgado-Baquerizo, M., Plett, J.M., Wang, J. Eldridge, D. J., Bardgett, R.D., Maestre, F.T., Singh, B.K. A few Ascomycota taxa dominate soil fungal communities worldwide. Nat. Commun. 10: 2369,2019;

Francisco-Ortega, J., Wang, Z.S., Wang, F.G., Xing, F.W., Liu, H., Xu, H., Xu, W.X., Luo, Y.B., Song, X.Q., Gale, S., Boufford, D.E., Maunder, M., An, S.Q., Seed plant endemism on Hainan Island: a framework for conservation actions, Bot. Rev. 76: 346-376,2010

Fuhrman, J. A. Microbial community structure and its functional implications. Nature 459: 193-199, 2009

Galicia, L., García-Oliva, F. The effects of C, N and P additions on soil microbial activity under two remnant tree species in a tropical seasonal pasture, Appl. Soil Ecol. 2004; 26:(1) 31-39

Geml, J.,Timling, I.,Robinson, C. H., Lennon, N., Nusbaum, H.C., Brochmann, C.; Noordeloos, M.E.; Taylor, D. L. An arctic community of symbiotic fungi assembled by dispersers: phylogenetic diversity of ectomycorrhizal basidiomycetes in Svalbard based on soil and sporocarp DNA, J. Biogeogr., 39: 74-88,2012;

Gibson L., Lee, T. M., Koh, L. P., Brook, B.W., Gardner, T.A., Barlow, J., Peres, C.A., Bradshaw, C. J. A., Laurance, W.F., Lovejoy T.E., Sodhi, N.S. Primary forests are irreplaceable for sustaining tropical biodiversity, Nature, 478, 378-381, 2011

Good, I. L. 1953. The population frequencies of species and the estimation of population parameters, Biometrika, 40: 237-264,1953

Jiao, S., Liu, Z.S., Lin, Y.B., Yang, J., Chen, W.M., Wei, G.H. Bacterial communities in oil contaminated soils: biogeography and co- occurrence patterns. Soil Biol. Biochem. 98:64-73, 2016

Karimi, B., Dequiedt, S., Terrat, S., Jolivet, C., Arrouays, D., Wincker, P., Cruaud, C., Bispo, A., Prévost-Bouré, N.C., Ranjard, L. Biogeography of soil bacterial networks along a gradient of cropping intensity. Sci. Rep., 9(1) 3812, 2019.

Karimi, B., Dequiedt, S., Terrat, Sébastien, Jolivet, C. , Arrouays, D. , & Wincker, P. , Cruaud C., Bispo A., Prévost-Bouré N. C., Ranjard L. Biogeography of soil bacterial networks along a gradient of cropping intensity, Sci Rep., 9(1): 3812, 2019

Karimi, B., Maron, P.A., Chemidlin-Prevost Boure, N., Bernard, N., Gilbert, D., Ranjard, L. Microbial diversity and ecological networks as indicators of environmental quality, Environ. Chem. Lett., 15: 265-281, 2017

Kerfahi, D., Tripathi, B.M., Dong, K., Go, R., Adams, J.M. Rainforest conversion to rubber plantation may not result in lower soil diversity of bacteria fungi and nematodes, Microb. Ecol., 72: 359-371, 2016

Kuperman, R.G., Siciliano, S.D., Römbke, J., Oorts, K., Deriving site-specific soil clean-up values for metals and metalloids: rationale for including protection of soil microbial processes, Integr. Environ. Assess. Manage., 10 (3):388-400, 2014

Lan, G.Y., Li, Y., Wu, Z.X., Xie, G.S. Impact of tropical forest conversion on soil bacterial diversity in tropical region of China, Eur. J. Soil Biol., 83: 91-97, 2017c

Lan, G.Y., Li, Y.W., Jatoi, M.T., Tan, Z.H., Wu, Z.X., Xie, G.S. Change in soil microbial community compositions and diversity following the conversion of tropical forest to rubber plantations in Xishuangbanan southwest China, Trop. Conserv. Sci., 10: 1-14, 2017b

Lan, G.Y., Li, Y.W., Wu, Z.X., Xie GS. Soil bacterial diversity impacted by conversion of secondary forest to rubber or eucalyptus plantations—a case study of Hainan Island, south China, For Sci., 63:87-93, 2017a

Lan, G.Y., Li,Y.W., Lesueur, D., Wu, Z.X., Xie, G.S. Seasonal changes impact soil bacterial communities in a rubber plantation on Hainan Island China, Sci. Total Environ., 626c: 826-834, 2018

Lan, G.Y., Wu, Z.X., Li, Y.W., Chen, B.Q. The drivers of soil bacterial communities in rubber plantation at local and geographic scales, Arch. Agron. Soil. Sci., 66(3): 358-369, 2020c

Lan, G.Y., Wu, Z.X., Sun, R., Yang, C., Chen, B.Q., Zhang, X. Tropical rainforest conversion into rubber plantations results in changes in soil fungal composition, but underling mechanisms of community assembly remain unchanged, Geoderma, 375: 114505, 2020b

Lan, G.Y., Wu, Z.X., Sun, R., Yang, C., Chen, B.Q., Zhang, X.C. Forest conversion changed the structure and functional process of tropical forest soil microbiome, Land. Degrad. Dev. 2020a. DOI: 10.1002/ldr.3757

Lopez, S., Rousset, F., Shaw, F.H., Ruth, G., Shaw, R.G., Ophélie, R. Joint effects of in? breeding and local adaptation on the evolution of genetic load after fragmentation, Conserv. Biol., 23: 1618-1627, 2009

Louca, S., Polz, M.F., Mazel, F., Albright, M.B.N., Huber, J.A., O'Connor, M.I., Ackermann, M., Hahn, A.S., Srivastava, D.S., Crowe, S.A., Doebeli, M., Parfrey, L.W. Function and functional redundancy in microbial systems. Nat. Ecol. Evol., 2: 936-943, 2018

Ma, H., Zou, W., Yang, J., Hogan, J. A., Chen, J. Dominant tree species shape soil microbial community via regulating assembly processes in planted subtropical forests. Forests, 10(11): 978, 2019

Mills, L.S., Soulé, M.E., Doak, D.F. The keystone- species concept in ecology and conservation, BioScience, 43: 219-224, 1993

Morriën, E., Hannula, S., Snoek, L. et al. Soil networks become more connected and take up more carbon as nature restoration progresses, Nat. Commun., 8: 14349, 2017

Mouquet, N., Gravel, D., Massol, F., Calcagno, V. Extending the concept of keystone species to communities and ecosystems, Ecol. Lett., 16:1-8, 2013

Neutel, A. M., Heesterbeek, J. A. P., de Ruiter, P. C. Stability in real food webs: weak links in long loops, Science, 296:1120-1123, 2002

Olesen, J.M., Bascompte, J., Dupont, Y.L., Jordano, P. The modularity of pollination networks, Proc. Nat. Acad. Sci. USA, 104: 19891-19896, 2007

Pagliai, M., Vignozzi, N., Pellegrini, S. Soil structure and the effect of management practices. Soil Tillage Res. 79: 131-143, 2004

Philippot, L., Spor, A., He´nault, C., Bru, D., Bizouard, F., Jones, C. M., Sarr, A., Maron, P.A. Loss in microbial diversity affects nitrogen cycling in soil Laurent, ISME J., 7:1609-1619, 2013

Power M, Tilman D, Estes J, Menge B, Bond W, Mills S, Daily G, Castilla J, Lubchenco J, Paine R, Power M, Tilman D, Estes J, Menge B, Bond W, Mills L, Daily G, Castilla J, Lubchenco J, Paine R. Challenges in the quest for keystones, Bioscience. 46: 609-620,1996

Qin, J., Li, R., Raes, J., Arumugam, M., Burgdorf, K.S., Manichanh, C., Nielsen,T., Pons, N., Levenez, F., Yamada T. A human gut microbial gene catalogue established by metagenomic sequencing, Nature, 464: 59-65, 2010

Roger, G., Amaral, L.A.N., Functional cartography of complex metabolic networks, Nature, 433: 895,2005

Rooney, N., McCann, K., Gellner, G., Moore, J. C. Structural asymmetry and the stability of diverse food webs, Nature, 442, 265-269, 2006

Röttjers, L, Faust, K. From hairballs to hypotheses–biological insights from microbial networks, FEMS Microbiol. Rev., 10:1093, 2018

Sahner, J. , Budi, S. W. , Barus, H. , Edy, N. , Meyer, M. , Corré, MD, Polle, A. Degradation of root community traits as indicator for transformation of tropical lowland rain forests into oil palm and rubber plantations, PloS One, 10(9): e0138077, 2015

Sampson, T.R., Debelius J W, Thron T, Janssen, S., Shastri, G.G., Ilhan, Z.E., Challis, C., Schretter, C.E., Rocha, S., Gradinaru, V., Chesselet, M.F., Keshavarzian, A., Shannon, K. M., Krajmalnik-Brown, R., Wittung-Stafshede, P., Knight, R., Mazmanian, S.K. Gut microbiota regulate motor deficits and neuroinflammation in a model of Parkinson's disease. Cell, 167(6): 1469-1480, 2016

Schloss, P.D., Westcott, S.L., Ryabin, T., Hall, J.R., Hartmann, M., Hollister, E.B., Lesniewski, R.A, Oakley, B.B., Parks, D.H., Robinson, C.J. Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. Appl Environ Microbiol. 75: 7537-7541, 2009

Schneider, D., Engelhaupt, M., Allen, K., Kurniawan, S., Krashevska, V., Heinemann, M., Scheu, S. Impact of lowland rainforest transformation on diversity and composition of soil prokaryotic communities in Sumatra Indonesia, Front. Microbiol., 6: 296,2015;

Song H., Singh, D., Tomlinson, K.W., Yang, X.D., Ogwu, M.C., Slik, J. W. F., Adams, J.M. Tropical forest conversion to rubber plantation in southwest China results in lower fungal beta diversity and reduced network complexity, FEMS Microbiol. Ecol., 95, 7: fiz092, 2019

Stouffer, D. B., Bascompte, J. Compartmentalization increases food-web persistence, Proc. Natl. Acad. Sci. USA. 108:3648-3652, 2011

Taniguchi, T., Kitajima, K., Douhan, G.W., Yamanaka, N., Allen, M.F. A pulse of summer precipitation after the dry season triggers changes in ectomycorrhizal formation, diversity, and community composition in a Mediterranean forest in California, USA. Mycorrhiza. 28(7): 665-677, 2018

Tripathi, B. M., Kim, M., Singh, D., Lee-Cruz, L., Lai-Hoe, A., Ainuddin, A. N., Adams, J. M. Tropical soil bacterial communities in Malaysia: pH dominates in the equatorial tropics too, Microb Ecol., 64: 474-484,2012

Wagg, C., Schlaeppi, K., Banerjee, S., Kuramae, E.E., van der Heijden, M.G.A. Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning, Nat Commun., 10:4841, 2019

Walters, W., Hyde, E. R., Berg-Lyons, D., Ackermann, G., Humphrey, G., Parada, A., Gilbert, J. A., Jansson, J. K., Caporaso, J. G., Fuhrman, J. A., Apprill, A., Knight, R. Improved bacterial 16S rRNA gene (V4 and V4-5) and fungal internal transcribed spacer marker gene primers for microbial community surveys, mSystems, 1(1): e00009-15, 2016

Yang, W., Zhang, D., Cai, X., Xia, L , Luo, Y.Q., Cheng, X., An, S.Q. Significant alterations in soil fungal communities along a chronosequence of *spartina alterniflora* invasion in a Chinese yellow sea coastal wetland. Sci. Total Environ., 693(25): 133548., 2019.

Zaller, J. G., Heigl, F., Ruess, L., Grabmaier, A. Glyphosate herbicide affects belowground interactions between earthworms and symbiotic mycorrhizal fungi in a model ecosystem, Sci Rep., 4:5634,2014

Figure legend

Figure 1 The soil bacterial-fungal community network of rubber plantation and rainforest in dry season and rainy season. Red solid circles indicate fungi, and green solid circle indicate bacteria. Red lines indicate positive correlation between OTUs, and green indicate negative correlation. Absolute value of correlation coefficient ρ > 0.6, $P < 0.01$

Figure 2 Soil bacterial network structure of rubber plantations and tropical rainforest in dry and rainy seasons. Red lines indicate positive correlation between OTUs, and green indicate negative correlation. Absolute value of correlation coefficient ρ > 0.6, $P < 0.01$

Figure 3 Soil fungal network structure of rubber plantations and tropical rainforest in dry and rainy season. Red lines indicate positive correlation between OTUs, and green indicate negative correlation. Absolute value of correlation coefficient ρ > 0.6, $P < 0.01$

Figure 4 Number of shared and unique edges of soil bacterial and fungal networks in rubber plantations and tropical rainforests in the dry and rainy season. The number where the two circles cross is number of shared edges. Numbers in red circle presents the unique edges in rainforest, while in blue circle present the unique edges in rubber plantations.

Figure 5 Network degree of soil bacterial and fungal community of rubber plantations (blue) and tropical rainforest (red) in dry season and rainy season.

Figure 6 Frequency distributions of correlations in bacterial (a: dry season, b: rainy season) and fungal (c: dry season, d: rainy season) networks of rubber plantations and tropical rainforest in the dry season and rainy season. (Absolute correlation coefficient greater than 0.3, $P < 0.01$) Correlations in rainforest networks are red, correlations in rubber plantation networks are blue.

Figure 7 Proportional influence of different phylum on bacterial and fungal network structure in both dry season and rainy. The influence was the number of degrees of nodes belonging to a particular phylum. (a: bacteria in dry season, b: bacteria in rainy season, c: fungal in dry season, d: fungal in rainy season).

Figure 8 Network of the top 50 most abundant species (based on metagenomics data) and top 50 most frequent KEGG functions (pathway level 3) of rubber plantations and tropical rainforest sites in dry season and rainy season. (A: rubber in dry season; B: rainforest in dry season; C: rubber in rainy season; D: rainforest in rainy season) The size of the node indicates the species/function abundance. A red line indicates positive correlation between species/functions, and green indicates negative correlation. Absolute value of correlation coefficient > 0.6, $P < 0.01$

Table 1 Topological properties of soil microbial (bacterial and fungi) network structure in rubber plantation and tropical rain forest in dry season and rainy season

	Bacteria				Fungi			
	Rubber Dry	**Rainforest Dry**	**Rubber Rainy**	**Rainforest Rainy**	**Rubber Dry**	**Rainforest Dry**	**Rubber Rainy**	**Rainforest Rainy**
No. of nodes	291	287	296	296	220	235	243	244
No. of edges	2448	2559	4248	5019	791	769	1250	905
No. of positive edges	2052	2508.00	3385	4901	760	764	1195	897
No. of negative edges	396	51	863	118.00	31	5	55	8
Connectance	0.06	0.06	0.09	0.11	0.02	0.02	0.03	0.02
Average degree	16.82	17.83	16.67	33.91	16.67	6.54	10.28	7.41
Average betweenness	100.61	93.52	31.23	42.57	208.90	185.03	170.99	266.31
Average of shortest path length	2.92	2.92	2.56	2.45	4.00	3.626	3.81	5.27
Diameter	6.00	7.00	7.00	6.00	10.00	12.00	9.00	15.00
Cluster of coefficient	0.46	0.451	0.51	0.54	0.59	0.457	0.49	0.51
No of clusters	11.00	14.00	5.00	5.00	94.00	75.00	62.00	67.00
Degree centralization	0.12	0.11	0.17	0.18	0.08	0.08	0.10	0.10
Betweenness centralization.	0.0066	0.0067	0.0053	0.0049	0.02	0.03	0.121	0.04
Closeness centralization.	0.35	0.35	0.40	0.41	0.31	0.351	0.291	0.26
Neighborhood Connectivity	21.12	21.79	34.69	40.68	10.45	9.28	13.78	9.44
Topological coefficient	0.26	0.26	0.26	0.27	0.33	0.36	0.37	0.50

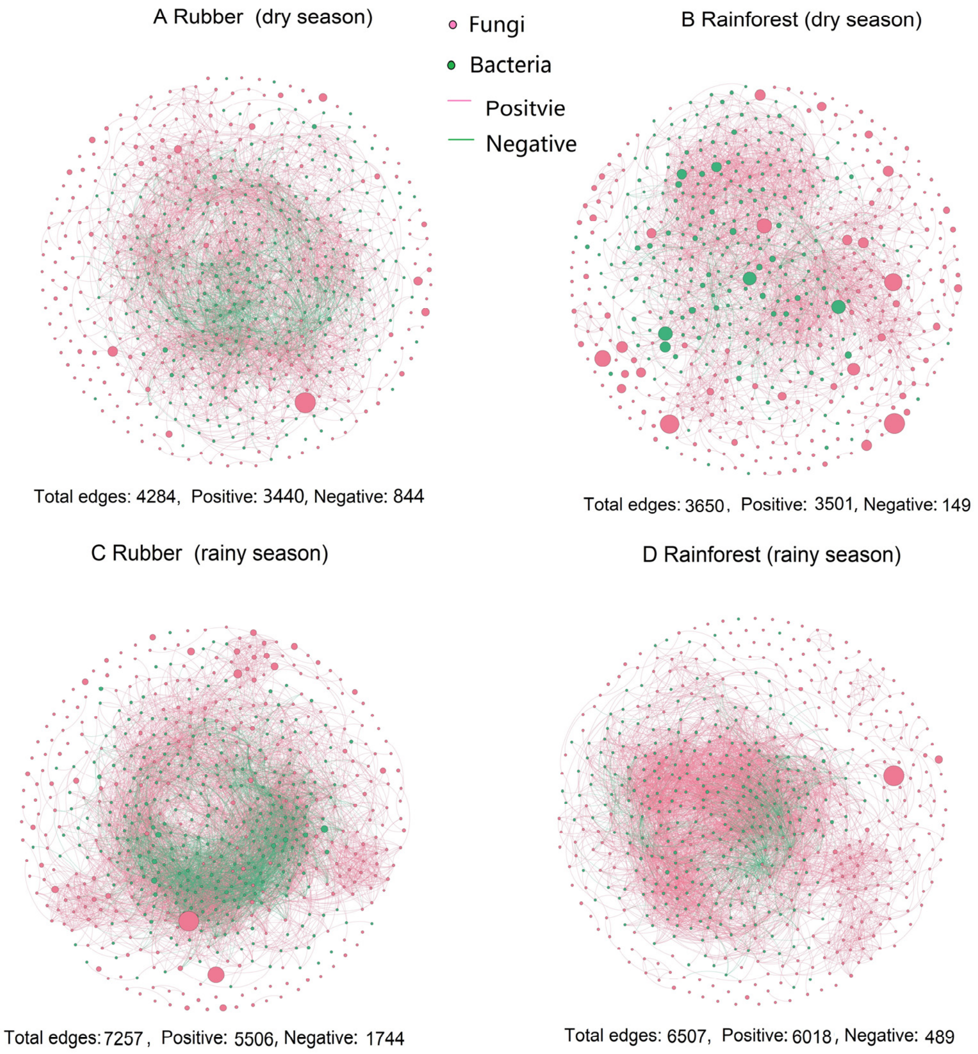


Figure 1 The soil bacterial-fungal community network of rubber plantation and rainforest in dry season and rainy season. Red solid circles indicate fungi, and green solid circle indicate bacteria. Red lines indicate positive correlation between OTUs, and green indicate negative correlation. Absolute value of correlation coefficient $\rho > 0.6$, $P < 0.01$.

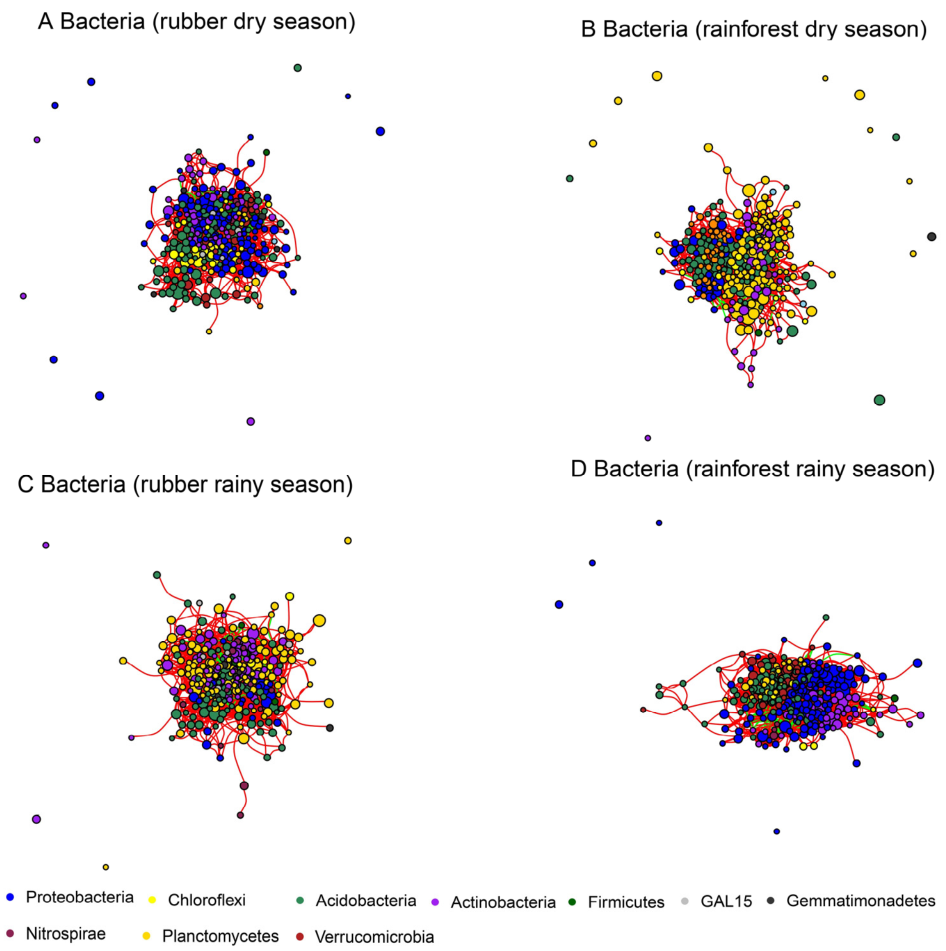


Figure 2 Soil bacterial network structure of rubber plantations and tropical rainforest in dry and rainy season. Red line indicates positive correlation between OTUs, and green indicates negative correlation. Absolute value of correlation coefficient $\rho > 0.6$, $P < 0.01$

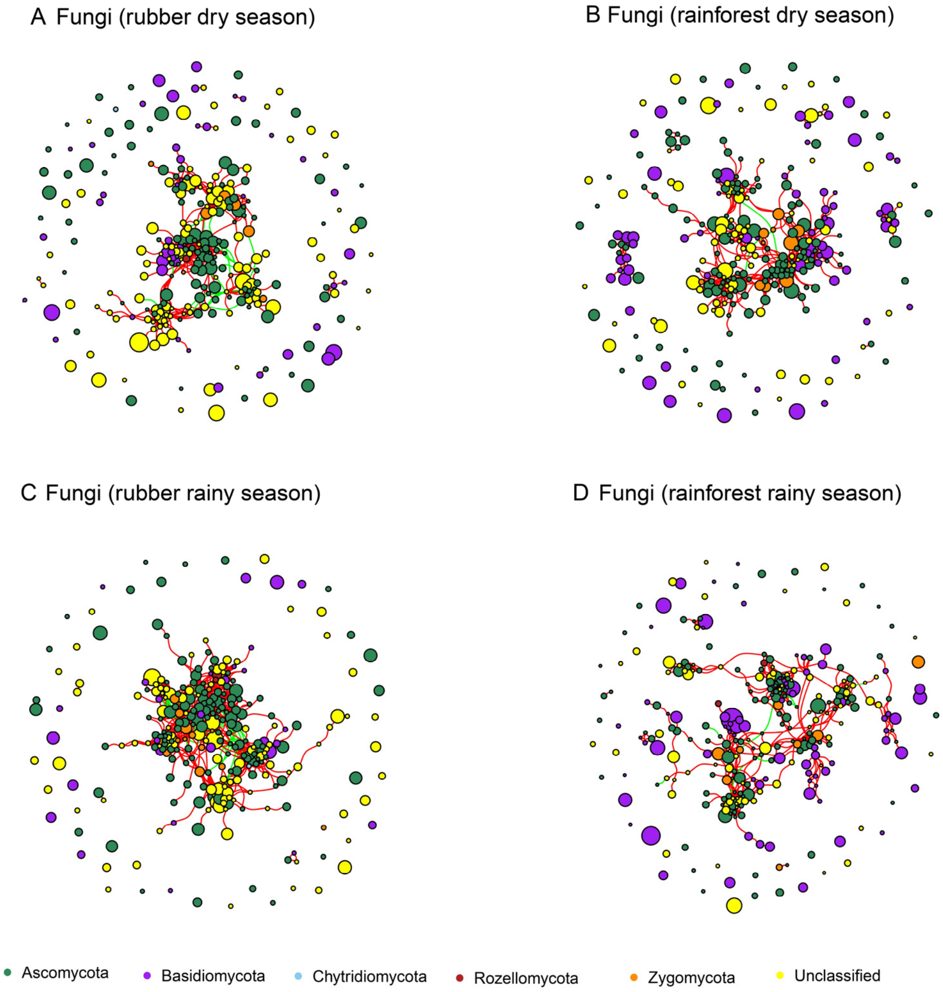
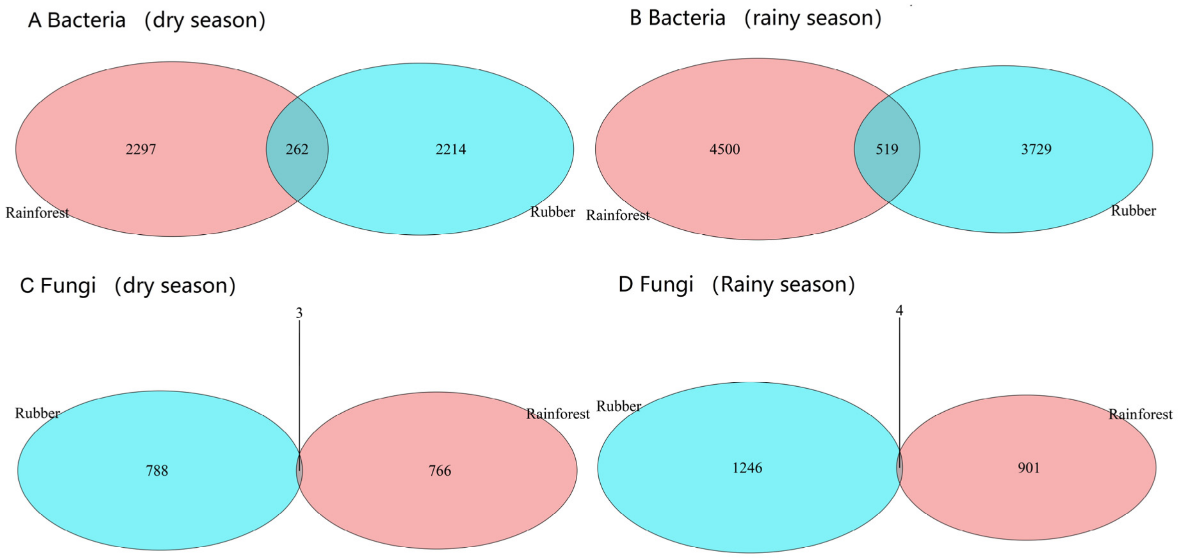


Figure 3 Soil fungal network structure of rubber plantations and tropical rainforest in dry and rainy season. Red line indicates positive correlation between OTUs, and green indicates negative correlation. Absolute value of correlation coefficient $\rho > 0.6$, $P < 0.01$



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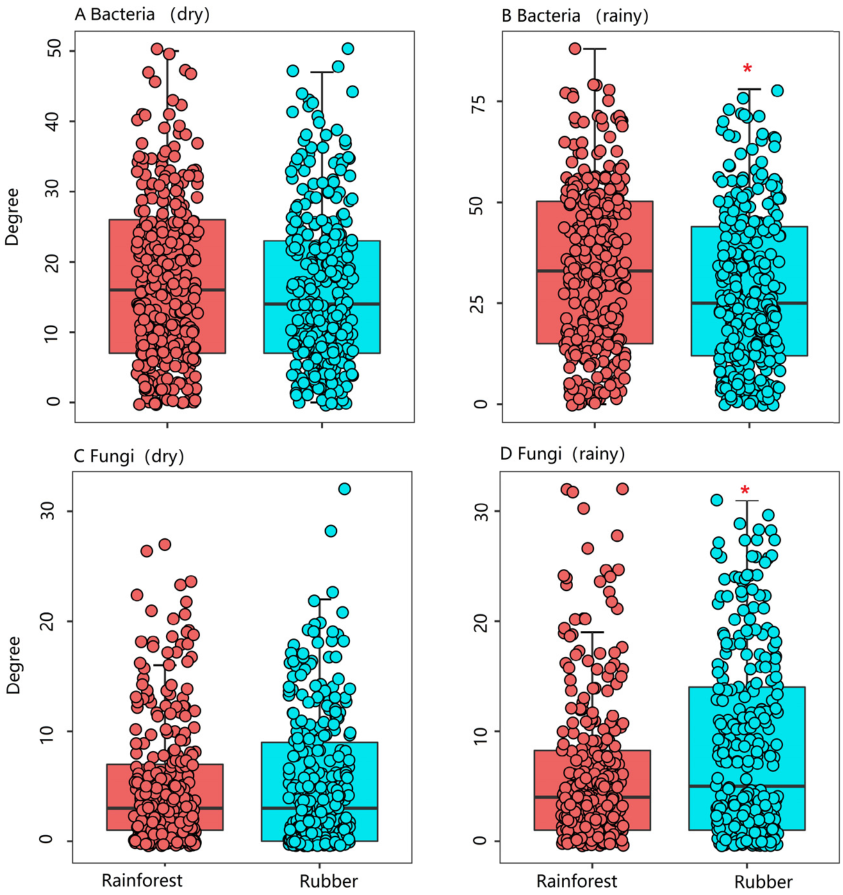

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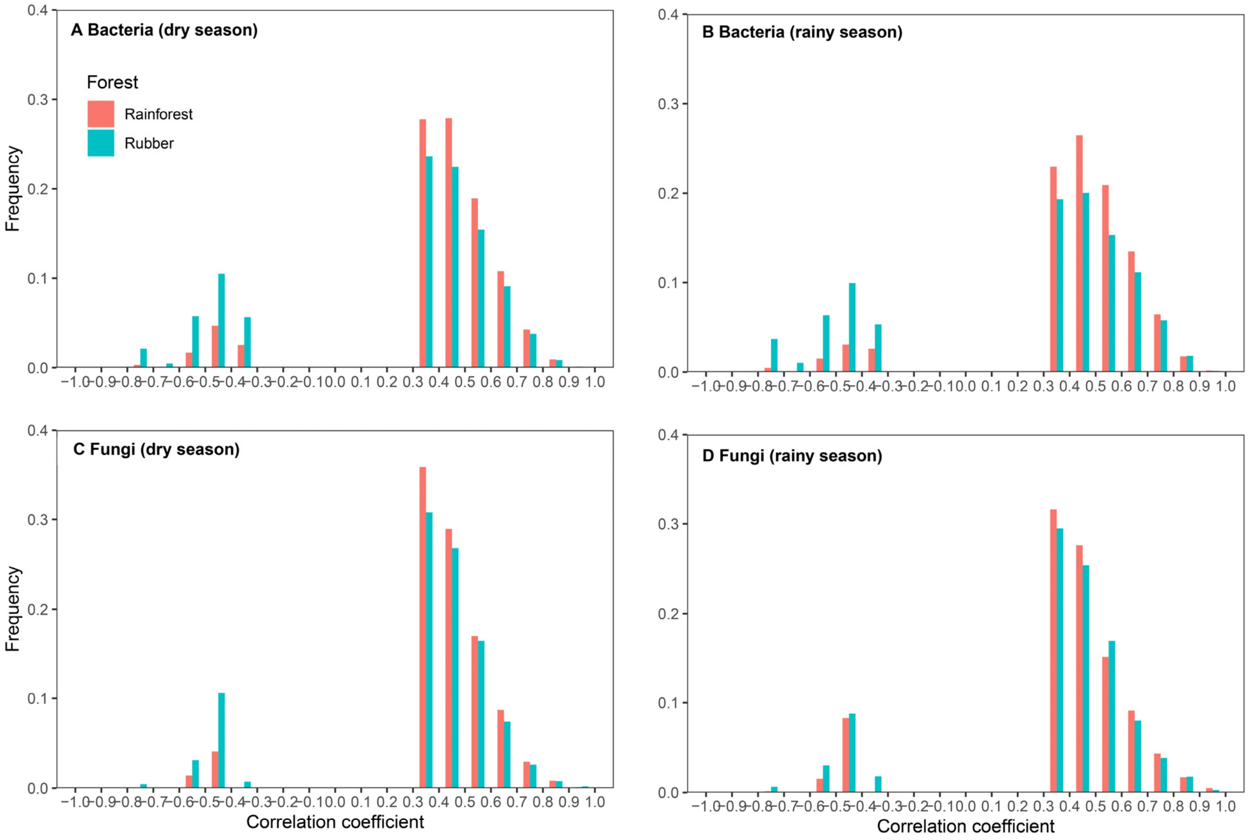

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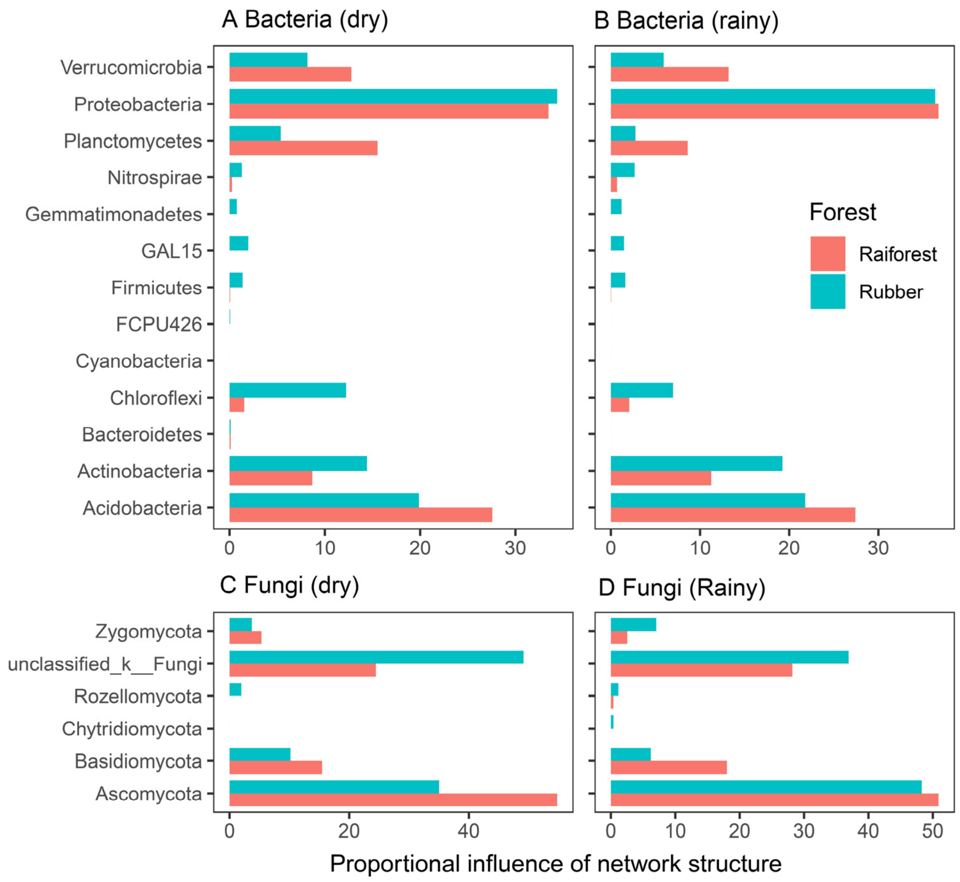

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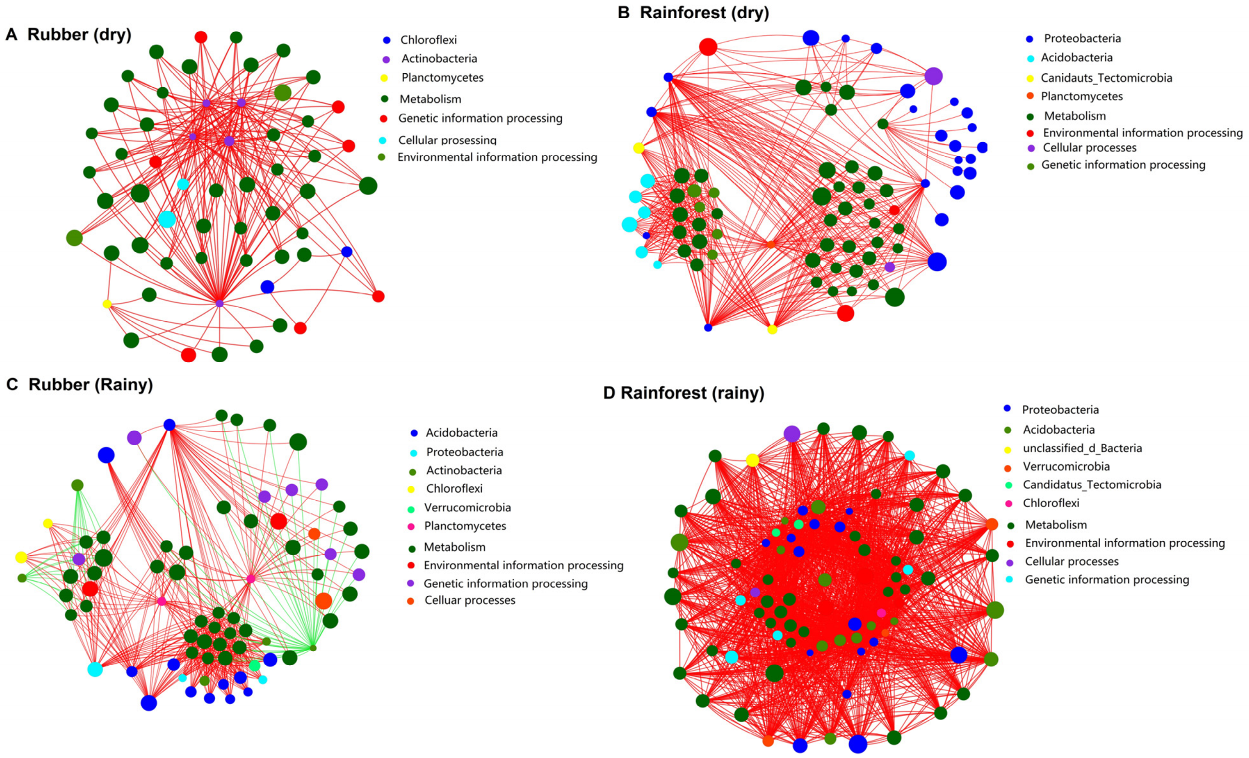

Figure 8 Network of the top 50 abundant species (based on metagenomics data) and top 50 abundant KEGG function (pathway level 3) of rubber plantations and tropical rainforest in dry season and rainy season. (A: rubber in dry season; B: rainforest in dry season; C: rubber in rainy season; D: rainforest in rainy season) The size of the node indicates the species/function abundance. Red line indicates positive correlation between species/functions, and green indicates negative correlation. Absolute value of correlation coefficient > 0.6, $P < 0.01$