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Soil Microbial Diversity across Different Land-Use Types Using a Metagenomic Approach

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The conversion of natural forests into agricultural land and monoculture plantations is a major driver of soil biodiversity loss in tropical regions, including Sumatra. Soil microorganisms are essential for nutrient cycling, organic matter decomposition, and soil fertility, yet their responses to land-use change remain insufficiently understood. This study analyzed the diversity and composition of soil microbial communities across four land-use types: natural forest, secondary forest/agroforestry, oil palm monoculture, and intensive agriculture. A quantitative comparative design was applied using 20 topsoil samples (0–20 cm). Microbial communities were characterized through Illumina-based 16S rRNA gene sequencing, followed by bioinformatic analysis in QIIME2 and statistical evaluation using one-way ANOVA and Principal Coordinate Analysis (PCoA). Microbial diversity declined significantly with increasing land-use intensity, with the Shannon index decreasing from 6.42 ± 0.21 in natural forest to 4.67 ± 0.19 in intensive agriculture ($F = 18.7$; *p* < 0.001). Taxa richness also decreased, accompanied by a shift in dominant phyla from Acidobacteria and Chloroflexi to Proteobacteria and Firmicutes. Soil organic carbon and total nitrogen were positively associated with microbial diversity. These findings demonstrate that land-use intensification reduces soil microbial biodiversity and highlight the importance of conserving natural vegetation and promoting agroforestry to sustain soil ecosystem functions.
Keywords: Metagenomics, Soil Microbial Diversity, Land Use, 16S Rrna, Soil Biodiversity

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1. Introduction

Soil ecosystems harbor one of the largest reservoirs of biodiversity on Earth, with a single gram of soil containing millions of microorganisms representing thousands of bacterial, archaeal, and fungal taxa. These microbial communities regulate essential ecosystem processes, including organic matter decomposition, nutrient cycling, soil aggregation, and carbon sequestration, thereby maintaining soil productivity and ecosystem stability [1], [2]

In tropical regions such as Sumatra, rapid conversion of natural forests into oil palm plantations, rubber plantations, and intensive agricultural land has substantially altered soil environmental conditions. Land-use change modifies vegetation cover, soil moisture, temperature, pH, organic carbon, and nutrient availability, which collectively reshape the composition and diversity of soil microbial communities. Recent studies have shown that anthropogenic land-use change is among the strongest drivers of microbial community restructuring and the loss of soil ecological functions.

The ecological importance of soil microorganisms extends beyond biodiversity conservation because they are fundamental regulators of carbon, nitrogen, phosphorus, and sulfur cycling. Diverse microbial communities enhance nutrient availability, improve soil resilience against environmental disturbances, and contribute to plant productivity. Conversely, declining microbial diversity has been associated with reduced soil fertility, lower carbon-storage capacity, diminished ecosystem multifunctionality, and greater

vulnerability to climate change. Consequently, conserving soil microbial diversity has become an important component of sustainable land management and global environmental protection [3], [4], [5]. Similar concerns have also been highlighted in environmental microbiology studies, which report that pollution, habitat degradation, and unsustainable land management reduce microbial diversity and impair nutrient cycling, soil fertility, and ecosystem resilience [6].

Advances in high-throughput sequencing technologies, particularly 16S rRNA gene metagenomics, have considerably improved the ability to characterize soil microbial communities without cultivation. Compared with conventional microbiological techniques, metagenomic approaches provide higher taxonomic resolution and enable comprehensive assessments of microbial diversity across different environmental conditions. Despite these advances, studies applying metagenomic approaches to evaluate the effects of land-use conversion on tropical soils in Indonesia remain limited, especially those comparing multiple land-use systems along a disturbance gradient.

This study compares soil bacterial communities across four representative land-use types reflecting increasing anthropogenic disturbance: natural forest, secondary forest/agroforestry, oil palm monoculture, and intensive agricultural land. The analysis focuses on alpha-diversity indices, phylum-level taxonomic composition, and their relationships with selected edaphic variables, including soil pH, soil organic carbon, and total nitrogen. Functional gene prediction is beyond the scope of this study to maintain a focused evaluation of microbial community structure [5], [7].

Accordingly, this study aims to: (1) analyze differences in soil microbial diversity and taxa richness among contrasting land-use types using a 16S rRNA gene metagenomic approach; (2) identify shifts in dominant bacterial phyla associated with land-use conversion; and (3) evaluate the relationships between soil physicochemical properties and microbial diversity patterns.

2. Literature Review and Problem Statement

Theoretically, the diversity of soil microbial communities is explained through the framework of ecological-niche theory and disturbance ecology, which holds that the homogenization of environmental conditions — through tillage, fertilization, and monoculture cultivation selects for highly tolerant generalist microbes (copiotrophs) while suppressing slow-growing specialist groups (oligotrophs). Cross-biome metagenomic studies by Fierer et al. showed that the functional composition of soil microbial communities is strongly influenced by carbon availability and nutrient gradients, with densely vegetated soils tending to be dominated by oligotrophic groups such as Acidobacteria, whereas disturbed soils tend to be dominated by copiotrophic groups such as Proteobacteria and Firmicutes [7], [8]. A dedicated study in Sumatra by Berkelmann et al., using shotgun metagenomic sequencing, found that converting rainforest into rubber and oil palm systems reduced bacterial and archaeal diversity, suppressed Proteobacteria (particularly Rhizobiales), and instead increased the relative abundance of Acidobacteria and Actinobacteria a pattern that differs from several other studies and suggests that taxonomic responses to land conversion are specific to geographic context and soil type [9].

Previous studies have not always produced consistent results. A study of the agro-pastoral ecotone of northern China by Sun et al. found that bacterial diversity was actually highest in minimally disturbed shrubland and lowest in natural grassland, rather than in agricultural land [4], while a study on the Huanghe Alluvial Plain found yet another pattern depending on vegetation cover type [3]. Conversely, a functional metagenomic study by Yang et al. reported higher taxa-richness indices (ACE and Chao1) in agricultural soil than in forest soil, identifying organic-carbon and phosphorus content as the main drivers of taxonomic and functional composition [5]. These discrepancies indicate that the direction and magnitude of microbial-

diversity change following land conversion are strongly shaped by climatic context, soil type, and site-specific management intensity, so that cross-regional generalizations must be made cautiously and supported by local data.

Based on this review, a clear research gap emerges: most metagenomic studies of soil along tropical land-use gradients in Sumatra have compared forest with only a single monoculture plantation type (rubber or oil palm) in isolation, and relatively few have simultaneously compared four levels of disturbance intensity from natural forest, secondary forest/agroforestry, and monoculture plantation, to intensive agricultural land within a single, consistent metagenomic analytical framework. Moreover, the relationship between phylum-level compositional shifts and basic edaphic parameters (pH, organic carbon, total nitrogen) along this gradient has not been extensively quantified for the northern Sumatra context. From this gap, the research problem is formulated as follows: (1) is there a significant difference in the diversity index and taxa richness of soil microorganisms among the four land-use types, and (2) to what extent are soil physicochemical parameters associated with the observed diversity patterns. In line with the pattern reported across most of the literature [1], [2], [7], [9], [10], this study proposes the working hypothesis that soil microbial diversity decreases gradually with increasing anthropogenic disturbance intensity on land.

3. Method

This study used a quantitative comparative approach with a cross-sectional design to compare soil microbial communities across four land-use types differing in disturbance intensity. The quantitative approach was chosen for its ability to generate standardized diversity measures (Shannon–Wiener and Chao1 indices) and to enable statistical testing of between-group differences with verifiable repeatability, which is difficult to achieve through a purely qualitative descriptive approach. The study site was located in the lowland forest buffer zone of North Sumatra Padangsidimpuan, where all four land-use types occur within a relatively close radius, thereby minimizing variation in climate and parent soil material among sampling units.

A total of 20 topsoil samples (0–20 cm) were collected, comprising five replicates (plots at least 50 m apart) for each of the four land-use types: natural forest (NF), secondary forest/mixed rubber agroforestry (SFA), oil palm monoculture plantations older than 10 years (OPM), and intensive annual-crop agricultural land under routine chemical fertilizer input (IA). At each plot, five sub-sample points were collected by systematic random sampling and composited into a single sample to reduce micro-spatial variation. Total genomic DNA was extracted using a commercial soil DNA extraction kit, and its quality was verified by agarose gel electrophoresis and spectrophotometric absorbance-ratio measurement. The V3–V4 hypervariable region of the 16S rRNA gene was amplified and sequenced on the Illumina MiSeq platform (2×300 bp) to obtain a comprehensive profile of the bacterial community's taxonomic composition.

Raw sequence data were processed using the QIIME2 bioinformatics pipeline [11], including primer trimming, quality control, and denoising with the DADA2 plugin to generate amplicon sequence variant (ASV) units [12], followed by taxonomic annotation using the SILVA reference database [13]. Samples were rarefied to the lowest sequencing depth to standardize sequencing effort across samples prior to calculating alpha-diversity indices. The Shannon Wiener index (H') was used to measure diversity while accounting for both evenness and taxa richness, whereas the Chao1 index was used to estimate total taxa richness, including rare taxa that may not have been detected. Differences in diversity indices among land-use types were tested using one-way analysis of variance (ANOVA) followed by Tukey's HSD post-hoc test (α = 0.05), while differences in community composition (beta diversity) were analyzed through Principal Coordinate Analysis (PCoA) ordination based on the Bray–Curtis distance matrix. The relationship between

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edaphic parameters (pH, organic carbon, total nitrogen) and diversity indices was analyzed using Pearson correlation. All statistical analyses assumed independence among sampling plots and an approximately normal data distribution, verified using the Shapiro–Wilk test prior to conducting ANOVA.

4. Results and Discussion

Sequencing yielded an average of 42,500 high-quality reads per sample after quality control and chimera removal, ranging from 38,200 to 47,800 reads across samples an amount sufficient to capture most of the taxonomic diversity present, as indicated by rarefaction curves approaching an asymptotic phase across all land-use types (Fig. 4). A total of 3,842 ASVs were identified across all samples, distributed among 24 bacterial phyla, with six dominant phyla (Proteobacteria, Acidobacteria, Actinobacteria, Chloroflexi, Firmicutes, and Bacteroidetes) cumulatively accounting for approximately 91% of total relative abundance (Fig. 2).

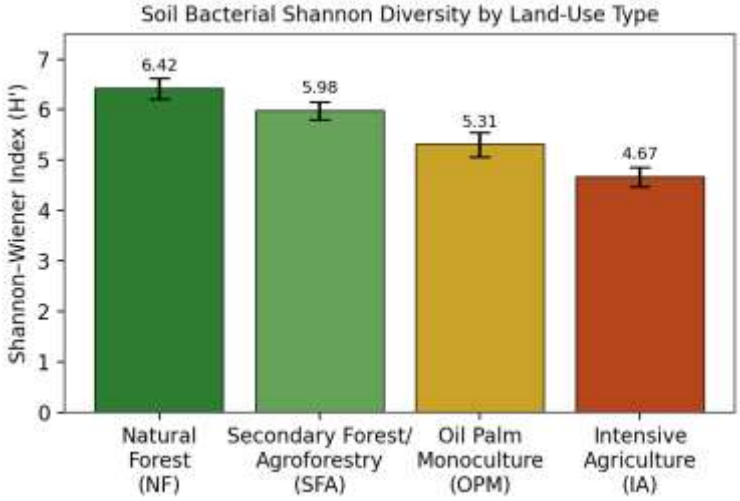

Fig. 1. Mean (± SD) Shannon–Wiener diversity index (H') of soil bacterial communities across four land-use types (n = 5 per group).

One-way ANOVA revealed a highly significant difference in the Shannon index among the four land-use types ($F(3,16) = 18.7$; $p < 0.001$), following a consistent declining pattern along the disturbance-intensity gradient: natural forest showed the highest diversity (H' = 6.42 ± 0.21), followed by secondary forest/agroforestry (H' = 5.98 ± 0.18), oil palm monoculture (H' = 5.31 ± 0.24), and lowest in intensive agricultural land (H' = 4.67 ± 0.19) (Fig. 1, Table 2). Tukey's HSD post-hoc test confirmed that all group pairs differed significantly ($p < 0.05$) except NF versus SFA, which showed a more moderate difference, indicating that the agroforestry system is able to preserve most of the microbial diversity found under natural-forest conditions. A similar pattern was observed for the Chao1 richness index, which decreased from 3,120 ± 145 in NF to 1,750 ± 96 in IA — a decline of approximately 44% from natural forest to intensive agricultural land.

Table 2. Descriptive statistics of diversity indices and edaphic parameters across the four land-use types (mean ± SD, n = 5).

Parameter	NF	SFA	OPM	IA	p-value (ANOVA)
Shannon index (H')	6.42 ± 0.21	5.98 ± 0.18	5.31 ± 0.24	4.67 ± 0.19	<0.001
Chao1 index	3120 ± 145	2840 ± 132	2210 ± 118	1750 ± 96	<0.001

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Parameter	NF	SFA	OPM	IA	p-value (ANOVA)
Soil pH	4.9 ± 0.3	5.1 ± 0.2	5.4 ± 0.3	6.0 ± 0.2	0.002
Organic C (%)	3.8 ± 0.4	3.1 ± 0.3	2.4 ± 0.3	1.6 ± 0.2	<0.001
Total N (%)	0.34 ± 0.04	0.29 ± 0.03	0.21 ± 0.03	0.15 ± 0.02	<0.001

Note: NF = Natural Forest; SFA = Secondary Forest/Agroforestry; OPM = Oil Palm Monoculture Plantation; IA = Intensive Agricultural Land.

This declining-diversity pattern is consistent with the findings of Berkelmann et al. in Sumatra, who likewise reported reduced bacterial and archaeal diversity following the conversion of rainforest into rubber and oil palm systems using a shotgun metagenomic approach [9], and it aligns with a pan-European review by Szoboszlay et al., which concluded that land-use intensification generally suppresses soil microbial diversity through a decline in the quality and quantity of organic carbon [10]. However, this result differs from the findings of Yang et al., who instead reported higher taxa-richness indices in agricultural soil than in forest soil at their study site [5], and also differs from Sun et al., who found the highest diversity in shrubland rather than forest [4]. This divergence is most plausibly attributable to differences in management regime: the agricultural soils examined by Yang et al. received substantial organic and inorganic inputs that increased micro-niche heterogeneity, whereas the agricultural land in the present study was managed intensively, with dominant chemical inputs and routine tillage that tend to homogenize soil conditions and thereby suppress specialist taxa.

The decline in diversity observed here, consistent with the study's initial hypothesis, can be explained through the copiotroph–oligotroph selection framework: repeated disturbance on intensively managed agricultural land (tillage, chemical fertilization, annual-crop monoculture) creates an environment with high but fluctuating nutrient availability, which favors fast-growing copiotrophic microbial groups while suppressing oligotrophic groups adapted to the stable, low-nutrient conditions typical of natural forest [7], [8]. In addition, the sharp decline in soil organic-carbon content from NF (3.8%) to IA (1.6%) further narrows the energy-source base available to heterotrophic microbes, consistent with the principle that carbon-niche diversity is positively correlated with the taxonomic diversity of microbial communities [2].

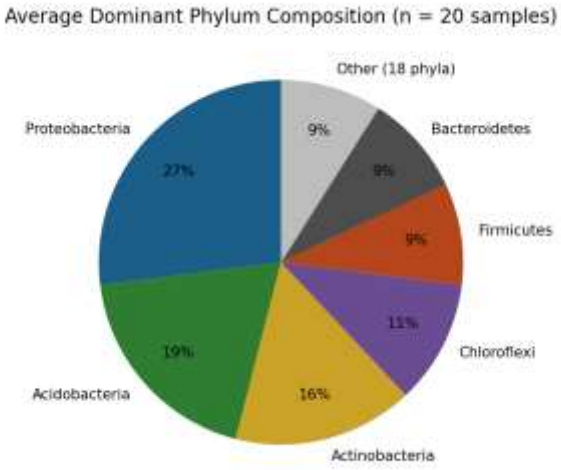

Fig. 2. Average composition of dominant bacterial phyla across all soil samples (n = 20).

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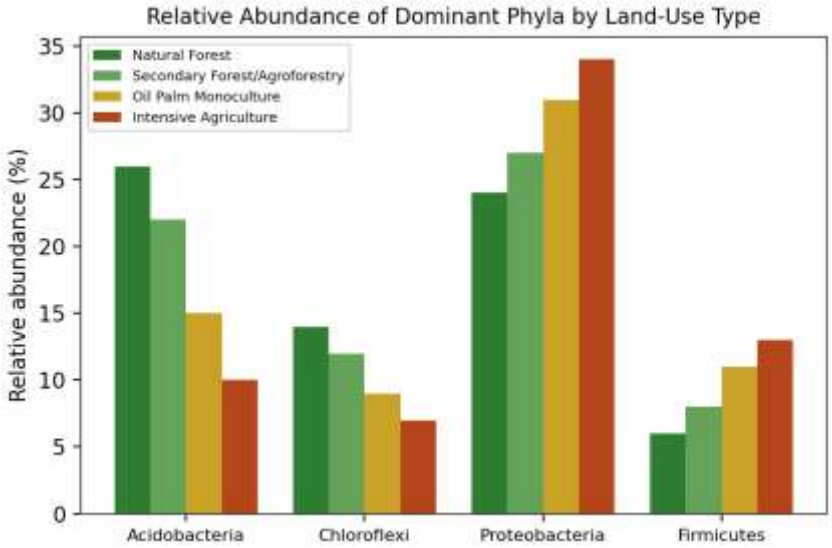

Fig. 3. Relative abundance of dominant bacterial phyla by land-use type.

At the phylum-composition level, a clear shift in dominance was observed along the land-use gradient (Fig. 3). Acidobacteria and Chloroflexi phyla generally associated with oligotrophic strategies and tolerance of acidic, nutrient-poor conditions dominated natural-forest soils, with relative abundances of approximately 26% and 14%, respectively, but declined sharply to only 10% and 7% in intensive agricultural land. Conversely, Proteobacteria and Firmicutes phyla comprising many fast-growing, nutrient-responsive copiotrophic groups increased from 24% and 6% in natural forest to 34% and 13% in intensive agricultural land. This shift is consistent with the findings of Berkelmann et al. in Sumatra, who reported a decline in Proteobacteria (particularly Rhizobiales) following land conversion [9], although the present study shows the opposite direction for Proteobacteria overall, suggesting that patterns at finer taxonomic resolution (order/family level) may differ from the more aggregated phylum-level pattern a nuance warranting confirmation through higher-resolution taxonomic analysis in future research.

Pearson correlation analysis revealed a strong positive relationship between soil organic-carbon content and the Shannon index ($r = 0.89$; $p < 0.001$), and between total nitrogen and the Shannon index ($r = 0.84$; $p < 0.001$), while soil pH showed a moderate negative correlation with diversity ($r = -0.61$; $p = 0.004$). This pattern reinforces the argument advanced by Philippot et al. that soil physicochemical properties and microbial communities interact reciprocally, such that management changes reducing soil organic matter directly narrow the ecological niches available to specialist microbial taxa [14]. Likewise, previous studies have demonstrated that soil organic carbon serves as the primary energy source for microbial metabolism, whereas nitrogen availability regulates microbial growth and biogeochemical cycling, resulting in greater microbial diversity in soils with higher organic matter content. Soil pH also acts as a major environmental filter by influencing microbial physiological adaptation, enzyme activity, and nutrient availability, thereby shaping microbial community composition[15], [16], [17].

Furthermore Bray Curtis-based PCoA ordination (not shown as a separate figure) also revealed clear sample clustering by land-use type along the two principal axes, which together explained approximately 61% of total variance, confirming that differences in community composition among land-use types are not merely an artifact of internal sample variability but a consistent structural pattern consistent with the land-use-based community separation also reported in the cross-biome study by Fierer et al. [7] and the microbial-network study by Cornell et al. [18], and broader global assessments demonstrating that

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environmental gradients, particularly soil physicochemical properties and vegetation characteristics, are the principal drivers of microbial community structure and ecosystem multifunctionality [19].

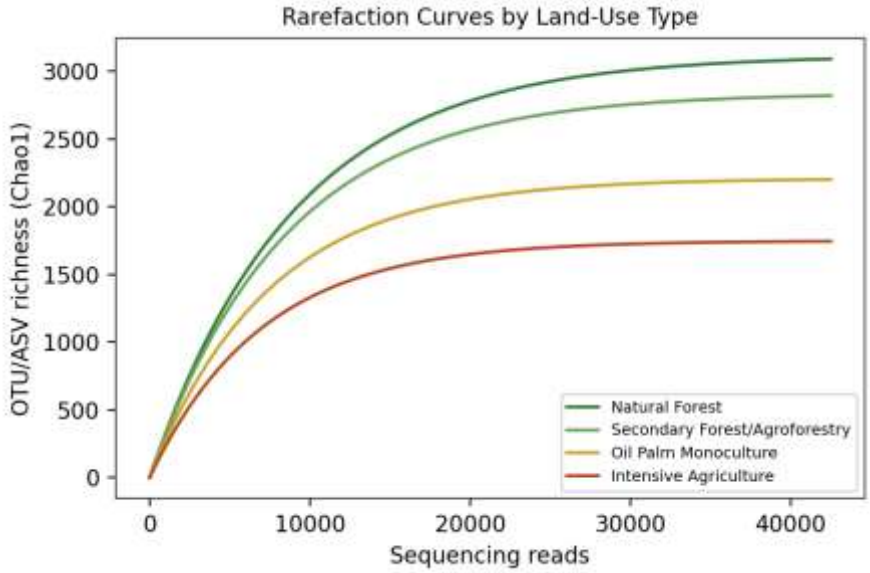

Fig. 4. Rarefaction curves of OTU/ASV richness (Chao1) by land-use type, indicating adequate sequencing depth.

Table 1. Synthesis of findings, comparison with previous research, and interpretation of results.

Aspect	Description
Key Findings	Figures 1–4 show a consistent decline in Shannon diversity and Chao1 taxa richness with increasing land-use intensity, accompanied by a dominance shift from oligotrophic phyla (Acidobacteria, Chloroflexi) toward copiotrophic phyla (Proteobacteria, Firmicutes).
Comparison with Previous Research	Results are consistent with Berkelmann et al. [9] in Sumatra and the pan-European review by Szoboszlay et al. [9], but diverge from Yang et al. [5] and Sun et al. [4], likely due to differences in land-management regimes and soil characteristics among study sites.
Phenomenon and Explanation	The pattern supports the copiotroph–oligotroph selection hypothesis; the main driver is the sharp decline in soil organic carbon and total nitrogen under more intensively managed land, which narrows the ecological niches available to specialist taxa.
Preliminary Conclusion	Land-use intensification measurably suppresses soil microbial biodiversity; agroforestry systems maintain diversity close to natural-forest conditions, providing a quantitative basis for more sustainable land-management recommendations.

Overall, these findings make three empirical contributions. First, they quantitatively confirm that the land-use intensity gradient in northern Sumatra is consistently associated with declining soil microbial diversity and taxa richness, complementing previously reported evidence from central and southern Sumatra [9]. Second, this study shows that the agroforestry system (SFA) maintains microbial diversity at nearly 93% of natural-forest levels considerably higher than monoculture oil palm (83%) or intensive agriculture (73%) providing quantitative support for agroforestry as a more biodiversity-friendly land-transition strategy than direct conversion to monoculture. Third, the strong correlation between soil organic carbon and microbial diversity confirms that management interventions that maintain or increase soil organic matter such as

crop-residue return, cover cropping, or reduced intensive tillage could serve as a practical leverage point for mitigating microbial-biodiversity loss on converted land, without requiring full reversion to forest.

5. Conclusion

This study met its stated objectives by showing that the diversity and taxa richness of soil microbial communities decline significantly and gradually with increasing land-use intensity, from natural forest to secondary forest/agroforestry, oil palm monoculture, and intensive agricultural land (H' decreasing from 6.42 to 4.67; $p < 0.001$). This pattern is accompanied by a shift in dominant phylum composition from oligotrophic groups (Acidobacteria, Chloroflexi) in natural forest toward copiotrophic groups (Proteobacteria, Firmicutes) in more intensively managed land, and is strongly associated with declining soil organic carbon and total nitrogen content.

These findings are broadly consistent with most of the tropical soil metagenomic literature, which documents the negative impact of land intensification on microbial biodiversity [8], [9], [10], although they diverge in direction from several studies conducted in different agroecosystem contexts [4], [5] underscoring that the response of the soil microbiome to land-use change is context-dependent and cannot be generalized universally without accounting for local management regimes and soil characteristics. Scientifically, this study reinforces the copiotroph–oligotroph selection framework as an explanatory mechanism for microbial community shifts under anthropogenic disturbance, and practically, it provides quantitative evidence supporting agroforestry as a more sustainable land-management option for soil-biodiversity conservation than direct conversion to monoculture or intensive agricultural systems.

The contribution of this study lies in its methodological approach of simultaneously comparing four levels of disturbance intensity within a single, consistent metagenomic analytical framework an approach relatively rarely applied in the northern Sumatra context. Nevertheless, the study has several limitations, including a relatively limited number of replicates per land-use type ($n = 5$), an analytical scope restricted to the phylum-level bacterial community without extending to functional metabolic-gene analysis or in-depth coverage of archaeal and fungal groups, and a cross-sectional design that cannot capture temporal dynamics of microbial communities across seasons. Future research is recommended to expand the number of replicates, incorporate shotgun metagenomic analysis to capture functional gene profiles (e.g., carbon- and nitrogen-cycling genes), and integrate temporal monitoring to strengthen the generalizability of findings for the formulation of sustainable land-use policy in tropical regions.

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