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Review Article

Organic amendments, soil microbial diversity and extracellular enzyme activity: a critical review with emphasis on tropical and Nigerian soils

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Abstract

Organic amendments are central to restoring degraded agricultural soils, yet their effects on soil microbial communities and the enzymes that drive nutrient cycling are often summarized too simply. This critical review synthesizes evidence from global meta-analyses and from field studies in sub-Saharan Africa, with emphasis on Nigeria, on how compost, animal manures, crop residues, green manures and biochar affect microbial biomass, diversity, community composition and extracellular enzyme activity. Across meta-analyses, organic amendments increased microbial biomass carbon by 36–63% relative to mineral fertilization or unfertilized controls, and increased C-, N- and P-acquiring enzyme activities by about 22–48%. Effects on α-diversity were smaller and less consistent than effects on biomass and community structure. Compositional shifts commonly favoured Bacteroidetes and Proteobacteria over Acidobacteria, but amendment-induced pH change was a major driver of these shifts. Biochar differed from labile amendments: it increased microbial biomass and some N- and P-cycling enzymes while sometimes suppressing C-cycling enzymes, mainly through pH, habitat and sorption effects that can also bias enzyme assays. Responses were moderated by amendment quality and rate, duration, soil pH, texture and initial organic carbon. African field studies, including long-term trials in Burkina Faso and Kenya, broadly support these patterns, but Nigerian evidence remains scarce, short-term and often culture-based. Priorities include long-term trials on Nigerian Alfisols and Ultisols, standardized enzyme assays, sequencing-based community analysis, explicit tests of diversity–function links, and assessment of trade-offs such as antibiotic-resistance genes, metals and nitrous oxide emissions.

1. Introduction

Soil degradation threatens agricultural sustainability across sub-Saharan Africa, where nutrient mining, continuous cultivation and climate stress accelerate the loss of soil organic matter (SOM) and increase risks to food security (IPCC, 2019; FAO, 2021). In West African agro-ecosystems outside the forest zone, soil organic carbon (SOC) is inherently low because of low biomass inputs, rapid turnover under high temperatures and low clay contents, and under continuous cultivation SOC can decline by up to 4.7% per year on sandy soils (Bationo *et al.,* 2007). Because the clay fraction of these soils is dominated by kaolinite, cation exchange capacity depends largely on SOC, so its loss directly reduces nutrient retention (Bationo *et al.,* 2007). Surveys of savanna soils in northern Nigeria similarly report low organic carbon and multiple nutrient deficiencies (Mustapha *et al.,* 2020, 2021).

Organic amendments, such as animal manures, compost, crop residues, green manures and biochar, are a principal means of replenishing SOM and are a core component of integrated soil fertility management in sub-Saharan Africa (Vanlauwe *et al.,* 2015; Lal, 2020). Many of their benefits are mediated by soil microorganisms, which drive biogeochemical cycling (Falkowski *et al.,* 2008; Bardgett and van der Putten, 2014) and produce the extracellular enzymes that depolymerize organic matter and release carbon (C), nitrogen (N) and phosphorus (P) in available forms (Burns *et al.,* 2013). High-throughput sequencing has greatly improved understanding of the composition and functions of soil microbial communities (Thompson *et al.,* 2017; Bahram *et al.,* 2018).

Global meta-analyses now show that organic amendments generally increase microbial biomass, alter community composition and stimulate enzyme activities (Lori *et al.,* 2017; Luo *et al.,* 2018; Shu *et al.,* 2022), and separate syntheses exist for biochar (Pokharel *et al.,* 2020; Deshoux *et al.,* 2023; Xu *et al.,* 2023). However, three limitations constrain how these findings can be applied to tropical smallholder systems. First, the evidence base is dominated by temperate and Chinese studies;

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for example, most observations in a recent biochar meta-analysis were from China and from experiments shorter than three months (Deshoux *et al.,* 2023). Second, effects on microbial diversity, community composition and enzyme activity are often discussed separately, and the extent to which compositional shifts explain changes in function is rarely examined. Third, methodological heterogeneity, particularly in enzyme assays and diversity metrics, is seldom considered when results are compared (Nannipieri *et al.,* 2018).

This review therefore aims to: (i) synthesize quantitative evidence on how different organic amendments affect soil microbial biomass, diversity, community composition and extracellular enzyme activity; (ii) examine the mechanisms and moderators of these responses, distinguishing biochar from labile amendments; (iii) evaluate how far diversity and enzyme responses are linked; (iv) assess the evidence from sub-Saharan Africa and Nigeria; and (v) identify trade-offs, methodological issues and research priorities for tropical soils.

2. Scope and approach

This is a critical narrative review. Literature was identified through searches of Web of Science, Scopus and Google Scholar using combinations of the terms "organic amendment", "compost", "manure", "crop residue", "green manure", "biochar", "microbial biomass", "microbial diversity", "community composition", "enzyme activity", "tropical", "Africa" and "Nigeria", supplemented by citation tracking from key reviews. Priority was given to (i) meta-analyses, because they provide the most reliable estimates of average effects and their moderators, and (ii) field studies from sub-Saharan Africa, which were sought specifically to assess the regional evidence base. Foundational studies were retained where they define concepts or methods. A formal quantitative synthesis was not attempted; effect sizes are quoted as reported by the original meta-analyses, together with their comparison (organic amendment vs mineral fertilizer, vs unfertilized control, or organic vs conventional farming), because the choice of comparator strongly affects the magnitude of reported effects.

3. Organic amendments: types and quality

Organic amendments differ widely in the amount and form of C and nutrients they supply, and therefore in how quickly and how strongly they stimulate soil microorganisms (Table 1). Resource quality, defined mainly by N, lignin and polyphenol contents, governs decomposition and nutrient release in tropical soils, and decision frameworks based on these properties have been developed to guide the use of organic resources in smallholder systems (Palm *et al.,* 2001). High-quality materials such as fresh leaves of *Tithonia diversifolia* decompose and release nutrients rapidly. *Tithonia* leaves contain about 3.5% N, 0.37% P and 4.1% K on a dry-matter basis (Jama *et al.,* 2000). In a Ghanaian incubation, *Tithonia* leaves had a C:N ratio of 13.8, 5.0% lignin and 1.7% polyphenols, lost about 80% of their mass within 7 days of burial in litterbags and, in an 84-day laboratory incubation, and produced the highest microbial biomass C and β-glucosidase activity among nine residues tested (Partey *et al.,* 2019). In contrast, low-quality residues such as cereal straw (high C:N and lignin) can cause net N immobilization, although residue C:N alone does not always predict this outcome (Chen *et al.,* 2014).

Manures and composts supply both labile C and nutrients, and they also introduce microorganisms. Composts are more stabilized than fresh manures, so their effects tend to be smaller in the short term but longer-lasting. Biochar differs fundamentally from these materials: it is produced by pyrolysis, consists largely of condensed aromatic C, and acts on soil biota mainly through changes in pH, pore habitat and sorption rather than through substrate supply (Lehmann *et al.,* 2011). It should therefore be analysed separately from labile organic amendments (Section 6). Locally available organic materials in northern Nigeria, including animal manures and plant residues, vary considerably in their chemical composition and hence in their suitability as amendments (Abdulrahman and Mustapha, 2021).

4. Effects on microbial biomass, diversity and community composition

4.1. Microbial biomass

Microbial biomass is the most consistent and largest microbial response to organic amendments (Table 2). Relative to inorganic fertilization, manure-based amendments increased microbial biomass C by 36% and microbial biomass N by 27%, with amendment chemistry and application rate as the strongest controls (Kallenbach and Grandy, 2011). Across 690 experiments, organic amendments increased microbial biomass C by 51% and microbial biomass N by 24% relative to mineral fertilization alone (Luo *et al.,* 2018). Organic farming systems had 41% higher microbial biomass C, 51% higher microbial biomass N and 59% higher total phospholipid fatty acids than conventional systems (Lori *et al.,* 2017), and organic fertilization increased microbial biomass C by 62.6% relative to unfertilized controls (Shu *et al.,* 2023). Straw return increased microbial biomass C by 31% across 68 field studies (Somchanh *et al.,* 2026), and cover crops increased microbial abundance by 27% relative to bare fallow (Kim *et al.,* 2020).

4.2. Microbial diversity

Responses of microbial diversity are smaller and less consistent than those of biomass. A meta-analysis of 219 studies found that organic amendments significantly increased microbial Shannon diversity, richness and phylogenetic diversity relative to mineral fertilization, and that diversity was positively related to microbial functionality and crop yield (Shu *et al.,* 2022). However, in a meta-analysis of 86 field studies, organic fertilization had no significant overall effect on bacterial Shannon diversity or richness relative to unfertilized controls, although compost increased richness by 9.3% and NPK combined with crop residue decreased it by 11.3% (Shu *et al.,* 2023). Cover crops increased

Table 1. Main classes of organic amendments, their dominant modes of action on soil microorganisms and typical responses

Amendment	Key properties	Dominant mechanisms	Typical microbial and enzyme responses	Key sources
Animal manure (cattle, poultry, swine)	Labile C, N and P; raises pH; contains microorganisms; may contain antibiotic residues and metals	Substrate and nutrient supply; pH change; microbial inoculation	Large increase in microbial biomass; increased hydrolase and dehydrogenase activities; compositional shifts	Kallenbach and Grandy (2011); Shu *et al.* (2023); Zhu *et al.* (2013)
Compost	Partly stabilized organic matter; lower labile C than fresh manure	Gradual substrate supply; habitat improvement; inoculation	Increased biomass and richness; sustained enzyme stimulation	Shu *et al.* (2023); Bonanomi *et al.* (2018)
High-quality green manures (e.g., *Tithonia diversifolia*, legume leaves)	High N (≈3–3.5%), low lignin and polyphenols; rapid decomposition	Rapid release of labile C and N	Rapid increase in microbial biomass and β-glucosidase; short-lived pulse	Jama *et al.* (2000); Partey *et al.* (2019)
Low-quality crop residues (e.g., cereal straw)	High C:N and lignin; slow decomposition	Slow C supply; possible N immobilization	Moderate increases in biomass and C-degrading enzymes; effects weaken in long-term trials	Chen *et al.* (2014); Somchanh *et al.* (2026)
Biochar	Condensed aromatic C; alkaline; porous; high sorption capacity	pH change; habitat provision; sorption of nutrients, enzymes and substrates	Increased biomass and N- and P-cycling enzymes; C-cycling enzymes variable or reduced; diversity variable	Lehmann *et al.* (2011); Pokharel *et al.* (2020); Zhang *et al.* (2019)

Note: Dehydrogenase (animal manure row) is an intracellular enzyme and indicates overall microbial metabolic activity rather than extracellular nutrient acquisition; the other enzymes listed act mainly extracellularly

microbial diversity by only 2.5% (Kim *et al.*, 2020). In the 32-year Kabete trial in Kenya, farmyard manure and maize stover increased bacterial and fungal diversity assessed by denaturing gradient gel electrophoresis, whereas mineral fertilizer alone depressed bacterial diversity (Kamaa *et al.*, 2011).

These differences partly reflect the comparator (mineral fertilizer vs unfertilized control), but they also show that α-diversity is a coarse indicator: organic amendments can reorganize community composition (β-diversity) substantially without changing the number of taxa (Shu *et al.*, 2023). Studies that report culture-based diversity indices are not comparable with sequencing-based studies, because culture-dependent methods recover only a small fraction of soil microorganisms. This limitation applies to the only Nigerian field study that reported microbial diversity after compost, poultry manure and *Tithonia* application, which used plate counts on two Alfisols (Alori *et al.*, 2023).

4.3. Community composition: copiotrophs, oligotrophs and soil pH

The copiotroph–oligotroph framework provides a useful lens for interpreting compositional shifts. Across 71 soils, the relative abundance of Acidobacteria decreased and that of β-Proteobacteria and Bacteroidetes increased with C mineralization rate, and these trends were confirmed by experimental sucrose additions (Fierer *et al.*, 2007). Consistent with this framework, organic fertilization increased Bacteroidetes by 49.4% and Proteobacteria by 6.5%, while combined organic and chemical fertilization reduced Acidobacteria by 11.1% (Shu *et al.*, 2023). During crop-residue decomposition, changes in bacterial and fungal community composition are closely linked to C and N dynamics (Rezgui *et al.*, 2021).

Two caveats are important. First, soil pH is the strongest single predictor of bacterial community composition across soils (Lauber *et al.*, 2009), and bacterial diversity almost doubled from pH 4 to pH 8 along a liming gradient (Rousk *et al.*, 2010). Because manures raise soil pH, whereas combined NPK and residue or manure applications lowered it (Shu *et al.*, 2023), part of the apparent "copiotroph" response to amendments is a pH effect, and pH change was the main predictor of community structure in organically fertilized soils (Shu *et al.*, 2023). Second, phyla proposed as copiotrophic or oligotrophic do not respond consistently across conditions, so life-strategy inferences should be made at family or finer taxonomic resolution (Ho *et al.*, 2017). Acidobacteria are physiologically diverse, although many members are adapted to low-nutrient, acidic conditions (Kielak *et al.*, 2016). Gemmatimonadetes should not be grouped with copiotrophs without evidence; in a biochar meta-analysis their relative abundance increased by 19.8% while Acidobacteria decreased by 14.6%, a pattern consistent with the pH and habitat effects of biochar (Xu *et al.*, 2023).

Fungi respond to amendments differently from bacteria. Their filamentous growth and production of lignocellulolytic

Table 2. Selected meta-analyses of organic amendment effects on soil microbial biomass, diversity and enzyme activities

Source	Scope	Comparison	Main findings
Kallenbach and Grandy (2011)	Agricultural systems	Manure-based amendments vs inorganic fertilizer	Microbial biomass C +36%, N +27%; amendment chemistry and rate were the strongest controls
Lori *et al.* (2017)	56 papers, 149 comparisons	Organic vs conventional farming	Microbial biomass C +41%, N +51%; total PLFA +59%; dehydrogenase +74%, protease +84%, urease +32%
Luo *et al.* (2018)	690 experiments	Organic amendment vs mineral fertilizer alone	Microbial biomass C +51%, N +24%; C-, N- and P-acquiring enzymes +39%, +22%, +48%; oxidative enzymes +58%
Miao *et al.* (2019)	85 articles, Chinese croplands	Manure + chemical fertilizer vs unfertilized	Urease +86%, phosphatase +34%, invertase +37%
Kim *et al.* (2020)	60 studies	Cover crops vs bare fallow	Microbial abundance +27%, activity +22%, diversity +2.5%
Shu *et al.* (2022)	219 studies	Organic amendment vs mineral fertilization	Shannon diversity, richness and phylogenetic diversity increased; diversity related to functionality and yield
Shu *et al.* (2023)	86 papers, 183 observations	Organic fertilization vs unfertilized	Microbial biomass C +62.6%; no overall change in Shannon diversity or richness; Bacteroidetes +49.4%; pH change the main predictor of community structure
Somchanh *et al.* (2026)	68 field studies	Straw return vs removal	Hydrolytic C-degrading enzymes +25%, microbial biomass C +31%; enzyme effect weaker after ≥10 years
Pokharel *et al.* (2020)	72 papers	Biochar vs no biochar	Microbial biomass C +21.7%; urease +23.1%; alkaline phosphatase +25.4%; dehydrogenase +19.8%; larger effects at pH < 6.5
Zhang *et al.* (2019)	43 studies	Biochar vs no biochar	N-cycling enzymes +14%, P-cycling +11%, C-cycling −6.3%
Xu *et al.* (2023)	Global	Biochar vs no biochar	Bacterial richness and diversity increased; Acidobacteria −14.6%, Gemmatimonadetes +19.8%
Deshoux *et al.* (2023)	181 publications	Biochar vs no biochar	Prokaryotic responses controlled by biochar properties; fungal diversity controlled by soil properties

Note: PLFA, phospholipid fatty acids. Percentages are mean changes as reported by each study for the stated comparison. Dehydrogenase (Lori *et al.*, 2017; Pokharel *et al.*, 2020) is an intracellular enzyme and indicates overall microbial metabolic activity rather than extracellular nutrient acquisition; the other enzymes listed act mainly extracellularly.

enzymes make them important decomposers of complex organic matter (Boer *et al.,* 2005), and fungal diversity was more strongly controlled by soil properties than by amendment properties in biochar-amended soils (Deshoux *et al.,* 2023). Fungal responses remain under-studied: of 181 publications in one meta-analysis, only 30 reported fungal data (Deshoux *et al.,* 2023).

5. Extracellular enzyme activity

5.1. Magnitude of enzyme responses

Organic amendments generally increase the activity of C-, N- and P-acquiring enzymes, but the magnitude depends on the enzyme, amendment and comparison (Table 2). Relative to mineral fertilization alone, organic amendments increased C-acquiring hydrolase activities by 39%, N-acquiring by 22%, P-acquiring by 48% and oxidative enzyme activities by 58% (Luo *et al.,* 2018). Organic farming systems had higher dehydrogenase (+74%), protease (+84%) and urease (+32%) activities than conventional systems (Lori *et al.,* 2017). In long-term Chinese cropland trials, manure combined with chemical fertilizer increased urease by 86%, phosphatase by 34% and invertase by 37% relative to unfertilized controls (Miao *et al.,* 2019). Straw return increased hydrolytic C-degrading enzyme activities by 25%, but this effect weakened in trials lasting 10 years or more (Somchanh *et al.,* 2026). Enzyme activity also

increased during the transition from conventional to organic farming (Serrano-Grijalva *et al.,* 2024).

African studies support these patterns (Table 3). In a 26-year trial at Saria, Burkina Faso, annual manure application produced the highest microbial biomass and β-glucosidase and acid phosphatase activities (Diallo-Diagne *et al.,* 2016). In the Central Highlands of Kenya, organic inputs increased acid phosphomonoesterase activity by 17–26% (Kiboi *et al.,* 2018). In Ghana, β-glucosidase activity after incorporation of *Tithonia* leaves (519.8 mg p-nitrophenol kg^{-1} h^{-1}) was about six times that after maize stover (84.5 mg p-nitrophenol kg^{-1} h^{-1}) (Partey *et al.,* 2019). In a degraded Ultisol in south-eastern Nigeria, poultry and swine manure (30 t ha^{-1}) increased alkaline phosphatase activity about four- to thirteen-fold over 84 days (Afangide *et al.,* 2020).

Dehydrogenase is frequently reported alongside hydrolases but is an intracellular enzyme, so it indicates overall microbial metabolic activity rather than extracellular nutrient acquisition (see notes to Tables 1 and 2). Oxidative enzymes such as phenol oxidase and peroxidase, which act on lignin and other recalcitrant compounds, showed the largest mean increase in one meta-analysis (+58%; Luo *et al*., 2018), but their activities vary more widely among soils and studies than those of hydrolases and are strongly influenced by soil pH (Sinsabaugh *et al.,* 2008; Sinsabaugh, 2010;).

5.2. Enzyme stoichiometry and nutrient limitation

Across ecosystems, the ratio of C-, N- and P-acquiring hydrolase activities converges on approximately 1:1:1 (Sinsabaugh *et al.,* 2008), and deviations from this ratio indicate relative resource limitation of microbial communities. A decrease in the C:P enzyme ratio (e.g., β-glucosidase:phosphatase) indicates greater relative investment in P acquisition and hence greater microbial P demand relative to C, whereas an increase indicates relatively greater C limitation. Vector analysis provides a more robust approach: vector length expresses relative C versus nutrient limitation and vector angle expresses relative P versus N limitation (Moorhead *et al.,* 2016). Using this approach, a meta-analysis of biochar studies reported increased vector length, indicating stronger microbial C limitation (Chen *et al.,* 2022). This inference does not agree with the decrease in C-cycling relative to N- and P-cycling enzyme activities reported by Zhang *et al.* (2019) (Section 6), which would shorten rather than lengthen the vector. The discrepancy may reflect differences between the two syntheses in the studies, enzymes and biochars included, as well as sorption of enzymes and substrates by biochar during assays (Section 5.3), so enzyme-based inferences of microbial C limitation under biochar should be treated with caution. Stoichiometric analyses have rarely been applied to labile amendments in tropical soils, where P limitation is common, and represent an important opportunity.

5.3. Methodological considerations

Enzyme assays measure potential activity under laboratory conditions, and differences in pH, temperature, substrate concentration, incubation time and detection (colorimetric p-nitrophenol vs fluorometric methylumbelliferone substrates) strongly affect results (German *et al.,* 2011). Many studies use protocols that are not optimized for these factors, and a large part of hydrolytic activity derives from enzymes stabilized on clays and organic matter rather than from current microbial activity; both issues confound comparisons across studies and meta-analyses (Nannipieri *et al.,* 2018). Biochar creates additional artefacts: it can adsorb enzymes and substrates, reducing apparent activity, and fluorometric assays were more robust than colorimetric assays in biochar-amended soils (Bailey *et al.,* 2011; Lammirato *et al.,* 2011). Studies should therefore report assay conditions in full, express activities per unit soil mass and per unit microbial biomass, and avoid comparing absolute values across studies that used different methods.

6. Biochar: a distinct case

Biochar effects on soil biota depend on its sorption properties, pH and physical structure (Lehmann *et al.,* 2011). Across 72 studies, biochar increased microbial biomass C by 21.7%, urease by 23.1%, alkaline phosphatase by 25.4% and dehydrogenase by 19.8%, with no significant negative effect on any enzyme; effects were larger in soils with pH below 6.5, low total C and N, and fine texture, and with biochars produced at 350–550 °C (Pokharel *et al.,* 2020). Another meta-analysis found that biochar increased N-cycling (+14%) and P-cycling (+11%) enzyme activities but decreased C-cycling enzyme activities (−6.3%), particularly with high-temperature or lignocellulosic biochars (Zhang *et al.,* 2019). Biochar increased microbial biomass C and N by 25% and reduced the metabolic quotient by 13% (Zhou *et al.,* 2017), but its effects on diversity were variable and were most positive in acidic, sandy, low-SOC soils (Li *et al.,* 2020). Biochar increased bacterial richness and diversity in a global meta-analysis, with responses moderated by biochar load, C/N, pyrolysis temperature and pH, and by soil C/N and pH (Xu *et al.,* 2023).

In the West African savanna, rice-husk biochar (20 t ha^{-1}) increased SOC by up to 123% and microbial biomass C by 34% after about one year in wastewater-irrigated urban soils in Tamale, Ghana (Asirifi *et al.,* 2021). On an Alfisol under rain-fed rice in Nigeria, the effects of rice-husk biochar on microbial biomass pools depended on biochar dose, N rate and soil depth, and biochar combined with N increased the fungal: bacterial ratio (Oladele *et al.,* 2019). These results suggest that biochar may be particularly beneficial on the acidic, low-SOC soils common in the region (Li *et al*., 2020; Pokharel *et al*., 2020), although the effect of texture is inconsistent between meta-analyses and but long-term field evidence is lacking. Biochar also has implications for climate change mitigation that extend beyond its effects on soil biota (Lehmann *et al.,* 2021).

7. Linking microbial diversity and enzyme function

Although the titles of many studies refer to diversity–function relationships, few test them directly. Evidence from other contexts suggests that such links exist: soil microbial diversity was positively related to ecosystem multifunctionality across global drylands and Scottish sites (Delgado-Baquerizo *et al.,* 2016), experimental reduction of soil biodiversity impaired nutrient cycling and other functions (Wagg *et al.,* 2014), and changes in microbial composition after disturbance are often associated with changes in process rates, which argues against assuming complete functional redundancy (Allison and Martiny, 2008). In organically amended soils, diversity and community structure were positively related to microbial functionality (Shu *et al.,* 2022). By contrast, Ghana microbial biomass C was closely related to mineral N after residue incorporation (r^2 = 0.96) (Partey *et al.,* 2019) which links biomass, rather than diversity, to nutrient supply.

However, enzyme responses to amendments are not necessarily a consequence of changes in diversity. Increases in enzyme activity may result from greater microbial biomass, from induction of enzyme synthesis by new substrates, from changes in soil pH, or from stabilization of enzymes on organic matter and clays (Burns *et al.,* 2013; Nannipieri *et al.,* 2018). Distinguishing these pathways requires studies that measure biomass, composition, functional genes and enzyme activities together, and that analyse their relationships explicitly, for example with structural equation models. Such links also matter for SOM formation: microbial products and necromass contribute substantially to stable SOM, and their accumulation depends on community composition and growth efficiency (Kallenbach *et al.,* 2016; Liang *et al.,* 2017). The main pathways and moderators are summarized in Fig. 1.

8. Moderators of microbial and enzyme responses

Five groups of moderators emerge from the meta-analyses. (i) Amendment chemistry and rate: amendment chemistry and application rate were the strongest controls on microbial biomass responses (Kallenbach and Grandy, 2011), and Bacteroidetes responses were correlated with application rate (Shu *et al.,* 2023). (ii) Soil pH change: pH change was the main predictor of community structure under organic fertilization (Shu *et al.,* 2023), and biochar effects were larger in acidic soils (Pokharel *et al.,* 2020). (iii) Soil texture and initial C: biochar effects on biomass and diversity were greater in sandy or low-SOC soils (Li *et al.,* 2020), and fungal diversity responded more strongly in medium-textured, low-pH, high-SOC soils (Deshoux *et al.,* 2023). (iv) Duration: urease responded within 100 days of biochar application, whereas alkaline phosphatase responded only after more than one year (Pokharel *et al.,* 2020), and straw effects on C-degrading enzymes weakened after 10 years (Somchanh *et al.,* 2026). (v) Climate, land use and experimental setting: effects differed among climatic zones and land uses (Kim *et al.,* 2020; Lori *et al.,* 2017), and microbial biomass and N-acquiring enzymes increased in field studies but not in laboratory incubations (Pokharel *et al.,* 2020). Because tropical soils are typically acidic, coarse-textured, low in SOC and exposed to high temperatures, these moderators

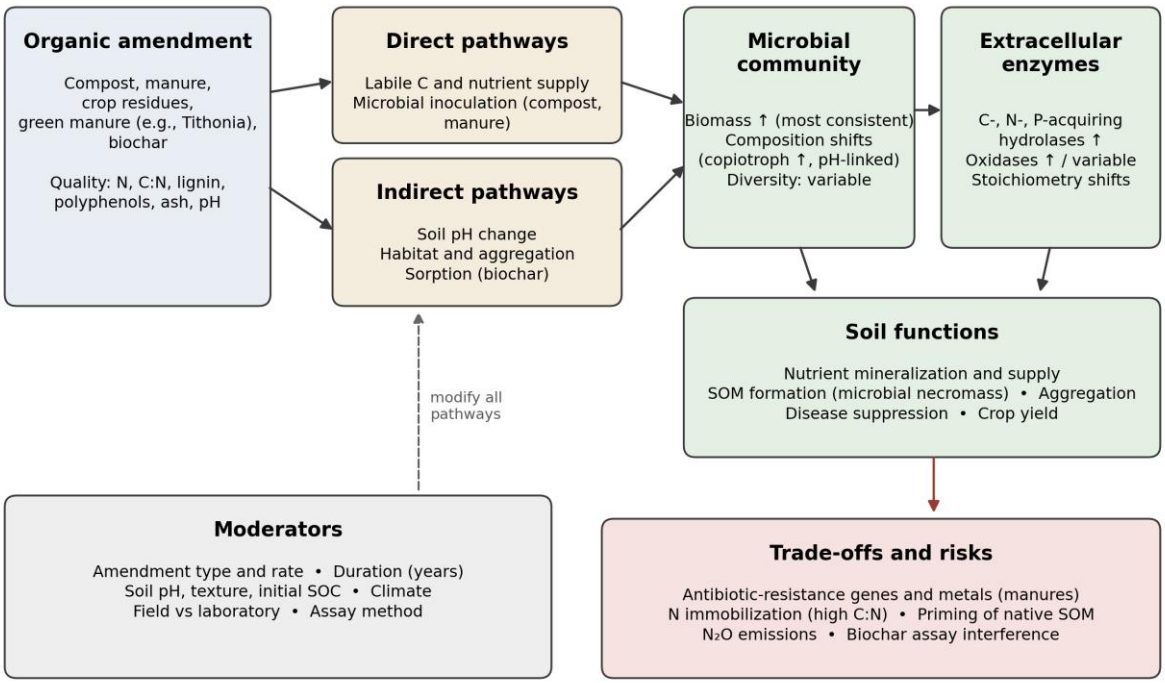


Figure 1. Conceptual framework of the pathways through which organic amendments affect soil microbial communities, extracellular enzyme activity and soil functions, with the main moderators and trade-offs identified in this review.

suggest that responses in Nigeria may differ in magnitude from the global averages, which underlines the need for local evidence.

9. Trade-offs and risks

The benefits of organic amendments must be weighed against potential risks. Manures are reservoirs of antibiotic-resistant bacteria and resistance genes, and their application can spread these genes into agricultural soils, often on mobile genetic elements (Heuer *et al.,* 2011). On Chinese swine farms, 63 antibiotic-resistance genes were enriched by a median of 192-fold in manure and manure-amended soils relative to antibiotic-free controls, and their abundance was correlated with antibiotic and heavy-metal concentrations (Zhu *et al.,* 2013). Livestock manures can also be a major source of Zn and Cu inputs to agricultural soils (Nicholson *et al.,* 2003). Low-quality residues with high C:N ratios can immobilize soil N, with consequences that depend on synchrony with crop demand (Chen *et al.,* 2014). Fresh organic inputs can accelerate the decomposition of native SOM through priming (Kuzyakov *et al.,* 2000), and organic amendments emit nitrous oxide, with residues to 1.21% for slurries and biosolids (Charles *et al.,* 2017). On the positive side, organic amendments can enhance emission factors ranging from 0.02% for composts and the suppression of soil-borne diseases through effects on the soil microbiota (Bonanomi *et al.,* 2018). These trade-offs are rarely measured in tropical amendment trials, and the antibiotic and metal loads of manures used in Nigeria are largely unknown.

10. The Nigerian and West African context

The soils that dominate Nigerian agriculture are highly weathered, kaolinitic and low in SOC, so their nutrient-holding capacity and biological activity depend strongly on organic inputs (Bationo *et al.,* 2007; Mustapha *et al.,* 2020, 2021). Field studies of amendment effects on soil biology in Nigeria have been conducted mainly on Alfisols (Oladele *et al.,* 2019; Alori *et al.,* 2023) and on Ultisols in the south-east (Afangide *et al.,* 2020). Collectively, these studies show that compost, poultry and swine manures, *Tithonia* and biochar can increase culturable microbial populations, microbial biomass and phosphatase activity (Table 3). However, they are few, short-term (84 days to two years) and mostly culture-based; we

Table 3. Field and incubation studies from sub-Saharan Africa on organic amendment effects on soil microbial properties and enzyme activities.

Country and soil	Amendment and duration	Methods	Main findings	Source
Nigeria (Kwara State); Alfisols, sandy loam and sand	Compost 3.4, poultry manure 4.2, *Tithonia* 4.8 t ha^{-1}; one season	Plate counts; Shannon index	Compost increased fungal counts by 12–178%; *Tithonia* increased bacterial diversity by about 11–75% (culturable organisms only)	Alori *et al.* (2023)
Nigeria; Alfisol under rain-fed rice	Rice-husk biochar 0–12 t ha^{-1} × urea 0–90 kg N ha^{-1}; 2 years	Microbial biomass C, N, P; CO_2 flux	Effects depended on biochar dose, N rate and depth; biochar + N increased the fungal:bacterial ratio	Oladele *et al.* (2019)
Nigeria (south-east); degraded Ultisol	Poultry and swine manure 30 t ha^{-1}; 84 days	Phosphatase activity; plate counts	Alkaline phosphatase increased about four- to thirteen-fold; heterotrophic bacterial counts increased	Afangide *et al.* (2020)
Ghana (Kumasi); Ferric Acrisol, sandy loam	Nine plant residues incl. *Tithonia* and maize stover (5 t ha^{-1} equivalent); 84 days	Microbial biomass C; β-glucosidase	Microbial biomass C 24.9 (control) to 298.2 mg kg^{-1} (*Tithonia*); β-glucosidase highest with *Tithonia*, lowest with maize stover	Partey *et al.* (2019)
Ghana (Tamale); Petroplinthic Cambisol	Rice-husk biochar 20 t ha^{-1} ± NPK; about 1 year	Microbial biomass C; respiration; enzyme activities	SOC up to +123%; microbial biomass C +34%; more diverse C-cycling enzyme profile	Asirifi *et al.* (2021)
Burkina Faso (Saria)	Manure, straw and urea; 26-year trial	Microbial biomass C; β-glucosidase; acid phosphatase; DGGE	Annual manure gave the highest biomass and enzyme activities; communities under manure distinct from mineral and straw plots	Diallo-Diagne *et al.* (2016)
Kenya (Kabete)	Farmyard manure and maize stover ± NPK; 32-year trial	DGGE (bacteria and fungi)	Organic inputs increased bacterial and fungal diversity; mineral fertilizer alone depressed bacterial diversity	Kamaa *et al.* (2011)
Kenya (Central Highlands)	Crop residues, manure, *Tithonia*, legumes; 3 seasons	Microbial biomass C, N; acid phosphatase	Microbial biomass C +19–51%; acid phosphatase +17–26%	Kiboi *et al.* (2018)

Note: DGGE, denaturing gradient gel electrophoresis.

Table 4. Knowledge gaps and research priorities for organic amendment–microbe–enzyme research in tropical and Nigerian soils

Knowledge gap	Why it matters	Recommended approach
Few long-term field trials in Nigeria	Short-term pulses may not reflect lasting change; enzyme and community responses change with time	Replicated trials of ≥5 years on Alfisols and Ultisols comparing amendment types and rates
Reliance on culture-based methods	Plate counts capture a small fraction of soil microorganisms and are not comparable with sequencing data	16S rRNA and ITS amplicon sequencing; qPCR of functional genes; shotgun metagenomics where feasible
Unstandardized enzyme assays	Assay conditions strongly affect values and prevent comparison	Assays at soil pH and field-relevant temperature; fluorometric methods; full reporting; expression per unit biomass
Diversity–function links rarely tested	Enzyme changes may reflect biomass, pH or substrate induction rather than diversity	Concurrent measurement of biomass, composition, functional genes and enzymes; structural equation modelling
Little stoichiometric analysis	Nutrient limitation (especially P) is common in tropical soils	Enzyme stoichiometry and vector analysis alongside soil and microbial C:N:P
Fungi under-studied	Fungi drive decomposition of complex residues and SOM formation	ITS sequencing and fungal biomass measures
Trade-offs unquantified	Antibiotic-resistance genes, metals and N_2O may offset benefits	Screen manures for antibiotics, resistance genes and metals; measure N_2O and priming
Biochar evidence mostly from outside Africa	Effects depend on soil pH, texture and biochar properties	Field trials with locally produced biochars, fully characterized

Note: DGGE, denaturing gradient gel electrophoresis.

found no Nigerian study that combined sequencing-based community analysis with enzyme measurements under organic amendments.

Longer-term evidence from elsewhere in sub-Saharan Africa is more robust. The 26-year Saria trial in Burkina Faso (Diallo-Diagne *et al.,* 2016) and the 32-year Kabete trial in Kenya (Kamaa *et al.,* 2011) show that sustained manure inputs gave the highest microbial biomass and enzyme activities at Saria and that manure and maize stover increased microbial diversity relative to mineral fertilizer alone at Kabete. In Kenya, *Tithonia* produced the highest microbial biomass among several organic inputs (Mugendi *et al.,* 2007), and organic inputs increased microbial biomass C by 19–51% across two sites (Kiboi *et al.,* 2018).

Locally available biomass offers practical opportunities. *Tithonia diversifolia* is widespread, nutrient-rich and decomposes rapidly, and green manuring with *Tithonia* improved soil properties and tomato yield in Nigeria (Adekiya, 2019). However, cutting and carrying *Tithonia* biomass is labour-intensive, and it has been more profitable on high-value vegetables than on maize (Jama *et al.,* 2000). The chemical composition of manures and plant materials available in Kano State varies considerably (Abdulrahman and Mustapha, 2021), so amendment selection should be guided by resource quality (Palm *et al.,* 2001) and combined with mineral fertilizers within an integrated soil fertility management approach (Vanlauwe *et al.,* 2015).

11. Knowledge gaps and research priorities

The evidence reviewed above points to several priorities for research in Nigeria and other tropical regions (Table 4). The most important are long-term, replicated field trials on the dominant Alfisols and Ultisols that compare amendment types and rates; standardized enzyme assays with full reporting of conditions; sequencing-based analysis of bacterial and fungal communities; explicit tests of diversity–function relationships; and measurement of trade-offs, including antibiotic-resistance genes, metals and greenhouse-gas emissions.

12. Conclusions

Organic amendments increase soil microbial biomass and the activity of C-, N- and P-acquiring enzymes, typically by about 20–60% depending on the amendment, enzyme and comparison. Effects on microbial diversity are smaller and less consistent than effects on biomass, while shifts in community composition towards fast-growing taxa are common but are partly driven by changes in soil pH. Biochar behaves

differently from labile amendments and requires separate assessment and appropriate assay methods. Responses depend on amendment quality and rate, duration, soil pH, texture and initial SOC, so global averages cannot be transferred directly to tropical soils. For Nigeria, organic amendments such as manures, compost and *Tithonia* are promising for restoring the biological functioning of degraded soils, but the local evidence base is thin, short-term and mostly culture-based. Long-term trials that combine sequencing, standardized enzyme assays, nutrient-cycling measurements and assessment of risks are needed to guide amendment selection and rates for Nigerian farming systems.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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