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Framework for developing the Chhattisgarh soil microbiome and functional ecology atlas

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Abstract

Chhattisgarh, with about 4.78 million hectares cultivated over three agro-climatic regions, and still remains one of India's least characterized agricultural regions concerning the soil microbiome ecology. The predominant soil series, Vertisols, Alfisols, Inceptisols, and Entisols cover significant portions, but vary remarkably concerning the pH, texture, and organically, mineralogically; however no environmental genomic reference has ever been explored from the Chhattisgarh region. The present Chhattisgarh Soil Microbiome and Functional Ecology Atlas strives to address this using a stratified approach during sampling across the major series found (Kanhra/Arang II Vertisol, Matasi Inceptisol, Bhata Entisol and Dorsa Alfisol), different seasons, management strategies, and within distinct microclimatic conditions of these soils, which profoundly influence the microbial processes in soil. The shotgun metagenomics at intermediate sequencing depths will likely underestimate the low abundance taxa and gene pathways and might further preclude specific ecological interpretation. The abundance of functional gene markers for nutrient cycling (*nifH*, *phoD*, *phoC*, *amoA*, *nirS/nirK*, *nosZ*, *mcrA*, *pmoA*) could serve as proxies for functional potential of these processes, would be best integrated with either a transcriptomic or metabolomic study. Multivariate analyses will be used to evaluate whether soil series represents the primary determinant of soil microbial community structure and functional ecology relative to geographic distance, management, and seasonal variation. The Chhattisgarh Soil Microbiome and Functional Ecology Atlas is the first environmental genomics initiative to characterize soil microbial communities across the state's major soil types using shotgun metagenomics, establishing a baseline framework for soil-specific microbial assessment and sustainable agricultural management.

Keywords: Soil microbiome ecology, Shotgun metagenomics, functional gene abundance, nutrient cycling, precision agriculture, agro-climatic zones, keystone taxa, arbuscular mycorrhizal fungi

1. Introduction

Soil health assessment under India's National Soil Health Card Scheme, the most common measures of soil quality primarily rely on conventional physicochemical extraction techniques-pH, electric conductivity, and the content of soil organic matter, nitrogen, phosphorus, and potassium (N, P, K)-used to assess some 20 million soil samples annually [1]. Although the use of such parameters increases fertilizer and overall input use efficiencies and crop productivity, their continued reliance on NPK as defining indices of soil quality fails to incorporate biological mechanisms controlling nutrient cycling, pathogen suppression and the long-term stability of soils, which leads to an incomplete appraisal of the agronomic relevance of these measures [2, 3]. A fundamental limitation of such chemically oriented approaches to soil testing is their inability to resolve processes where soil biology governs major soil functions. For example, an estimated 10 to 30 kg N/ha/year, from biological N-fixation in Indian soils under suitable conditions, remain invisible to chemically-oriented measurements of the N pool [4, 5]. Important reserves of calcium-bound phosphorus in the profile of Vertisols are unavailable to crop plants unless phosphate solubilizing communities are active, but their contributions are ignored in Olsen extract tests [6]. Importantly, soil inhabitants that cause millions of dollars in crop damage each year-plant pathogens such as *Fusarium oxysporum*, *Ralstonia solanacearum*, and *Meloidogyne* spp.-are never addressed in standard soil health card analysis. By taking a different approach that moved beyond measuring soil physical and chemical properties, to characterizing the microbial diversity, genetic potential, and metabolic activity in soils, the research conducted through

environmental genomics and metagenomics offered an “expanded vision” of the functioning of soil ecosystem including how it cycles nutrients and supports its long-term health. This, nevertheless, requires suitable reference baselines to be established because functional gene abundances, by themselves, may not distinguish typical variations in ecosystem function from environmentally triggered responses. Metagenomic dataset cannot be interpreted into actionable decision-making information regarding soil management without well calibrated, soil specific benchmarks. Chhattisgarh state provides an ideal research site for understanding the impact of spatial environmental variability and the corresponding response in soils across a broad array of contexts. We examined the microbial properties of four major soil types in ~ 5 million ha Chhattisgarh that fall within three agro-climatic zones: Kanhar/Arang II (heavy clay Vertisol with pH 7.5-8.7, showing an enrichment in anaerobic, Clostridium based, methanogens driving methane production from and increase of methanogens that also carry a gene, *nifH* involved in biological Nitrogen Fixation [BNF]) when influenced by water logging [7]; Dorsa (clay loam Alfisol with a high range of pH 4.4-7.7, containing diverse microbial communities but with an array of complementary phosphatase genes; Matasi (sandy loam Inceptisol with pH 4.7-7.9 that, owing to the influence of repeat intensive tilling and recurrent drying events, results in reduced abundance of AMF and the suppression of effective nutrient uptake; Bhata (lateritic gravel Entisol, pH 4.5-6.0) where we detected reduced *nifH* abundance and increased P fixation rates under frequent cycles of drought that again impact nutrient Availability. The lack of sufficient soil micro biome sampling from these environments has to be accounted for by well defined, robust, statistically validated reference datasets. This problem will be resolved by the establishment of the Chhattisgarh Soil Microbiome Atlas that represents a new framework for assessing soil biological function.

Characterization of prokaryotic (16S rRNA) and fungal (ITS) alpha and beta diversity across the four major soil series and three agro-climatic zones of Chhattisgarh. During the study, the influence of soil series on microbial community variation was evaluated using PERMANOVA to determine whether soil series explained a statistically significant proportion of community variance [8]. Reference intervals for key functional gene pools, including *nifH*, *phoD*, *phoC*, *amoA*, *nirS/nirK*, *nosZ*, *mcrA*, and *pmoA*, were quantified for each soil series [9]. Keystone taxa and ecological network hubs were identified for each soil series using Consensus Mutual Information-based Microbiome Network (CMIMN) analysis [10]. Taxa associated with disease-suppressive and disease-conducive soil states were identified, and pathogen background loads were established across the studied soil series and analysis is done as shown in Figure 2. Establish pathogen background loads (*Fusarium* species, *Ralstonia solanacearum*, *Rhizoctonia solani*, *Pythium* species, *Meloidogyne* species) per soil series; define the baseline against which field alerts are assessed [11].

2. Comparative Characterization of Major Soil Series in Chhattisgarh

Four-soil series were studied representing a range of environments differing by their composition, physicochemical traits and land use history. The differences would affect microbiome community structure and

distribution of functional genes, and the soil biological limitations. These comparative characteristics thus lay an ecological foundation for establishing microbiome reference frames specific to soil series as shown in Table 1.

Kanhar/Arang II Series (Vertisol): It is a heavy clay soil having predominantly smectitic mineralogy, pH 7.5-8.7, high CEC and SOC 0.35-0.80%, and prone to seasonal water logging. It harbors high bacterial biomass having dominantly Firmicutes, Proteobacteria and Actinobacteria while in flood scenario microbial biomass, especially the fungi, is suppressed. Features of functional genes having increased abundances are *nifH* and *phoD* while *mcrA* being seasonally induced due to anaerobic condition and is associated with the bio-constraints of phosphorus fixation, Zn/B deficiency and microbial response (flooding-induced effects) along with the threat from soil borne disease pathogens like *Rhizoctonia*, *Pythium* [13-15].

Dorsa Series (Alfisol) Alfisol considered by the studied researchers as clay loam soil and mineral composition consisted of kaolinite-illite-smectite (mixed types). The soil pH varies from 4.4-7.7 and the SOC varying from 0.20-0.70%. The moderate C.E.C. and highest richness of microorganism communities and the ratio moderate bacterial to fungal ratio as well as good *Pseudomonas*, *Bacillus* and AMF community were emphasized. Functional genes reveal relatively abundant *nifH*, *phoD* and *phoC*, indicating capacity for robust phosphorus cycle. Primary biological constraints in this soil type include Fe/Al fixation for phosphorus, Zn-deficiency, and risk of bacterial wilt (*Ralstonia*) [13-15].

Matasi Series (Inceptisol): Matasi Series (Inceptisol) is a sandy loam soil low in clay content and with kaolinitic mineralogy, pH 4.7-7.9, low CEC, and variable SOC. Microbial biomass are depressed, with stress adapted Actinobacteria and Acidobacteria dominating and with lower levels of AMF. Functional genes show under-representation of *nifH* and nutrient cycling potential is low. K-mobilising bacteria activity is moderate. AMF depletion and nutrient leaching, drought sensitivity, and presence of nematodes are the primary biological constraints [13-15].

Bhata Series (Entisol): Bhata Series (Entisol) is a lateritic gravelly soil and is a typically acidic soil, with a low pH 4.5-6.0, very low SOC and CEC, dominated by the characteristics of Fe/Al oxide minerals. The microbial biomass in the Bhata series is very low and Acidobacteria and Planctomycetes that are able to thrive under acidic and Fe/Al oxide environments are dominated. Functional gene shows suppressed *nifH*, *phoD* and *amoA* as mentioned in Table 2, which could attribute the low capacity for nutrient (N and P) cycling in such soil. Primary constraints is the extreme erosion rate with the subsequent development of aluminum toxicity, phosphorus fixation capacity of the soil, and reduced crop yield due to limited nutrient availability [13-15].

3. Analytical Framework

3.1. Multivariate Community Analysis

Previous soil metagenomic studies have reported that environmental variables such as soil type, pH, and organic carbon can explain substantial proportions of microbial community variation. The contribution of soil series in Chhattisgarh soils will be evaluated using PERMANOVA [10]. Co-variables include: agro-climatic region, cropping system, sampling season (Kharif/Rabi/pre-sowing), and

land-use history. Variance accounted for (R²) by soil series was 25–45% across published soil metagenomics work. The main soil physiochemical characteristics influencing results are soil pH and SOC level [23, 24]. Soil series variance explained <15%: calibration-first architecture lacks statistical support; analytical strategy revision required. NMDS (Non-Metric Multidimensional Scaling) will quantify community separation by soil series and agro-climatic zone, with convex hull delineation. PCoA (Principal Coordinates Analysis) using UniFrac distances will quantify phylogenetic differentiation across soil series independent of abundance. N-cycling functional balance index.

$$\text{N-cycling balance} = (\text{nifH_PGPR-filtered} + \text{nosZ})/(\text{amoA_AOB} + \text{nirS} + \text{nirK})$$

3.2 Alpha Diversity Analysis

Microbial diversity will be assessed to understand the influence of soil conditions overall complexity and stability of microbial communities across different soil series. All samples will be assessed by the Alpha diversity indices Shannon diversity, Simpson diversity, Chao1 richness to compare the variations in microbial richness and evenness. It is understood that microbial diversity does not give a good measure of soil health [25, 26]. High microbial diversity alone does not necessarily translate into improved soil fertility, enhanced nutrient cycling, or greater plant productivity, as ecosystem functions are largely determined by the functional capabilities and activities of specific microbial groups, the enhanced nutrient supply or greater plant growth will not be observed. It does not imply an enhancement in nutrient supply and growth of the plants. Therefore, diversity results will be interpreted together with functional gene abundance, soil chemical properties, and microbial interaction patterns. Based on differences in soil texture, mineral composition, organic carbon status, and moisture conditions, Dorsa Alfisol is expected to support comparatively higher microbial diversity, followed by Kanhar Vertisol, Matasi Inceptisol, and Bhata Entisol. This is the working hypothesis resulting from ecological data and it will be validated by experimental observations

3.3 Ecological Network Analysis

Soil microorganisms do not exist as individuals but as a group of interconnected units where individuals or groups could serve most important position on the overall functioning of ecosystem processes. Thus we will explore interactions between different groups of soil microbes, and the Taxonomic groups possibly serving as central organizing hub on the microbial communities with microbial networks analysis. Microbial networks with microbial abundance data, Highly connected taxa such as key-role group of organisms will be characterized through common network measures, such as degree, betweenness, closeness, centrality, centrality [27]. These highly connected taxa were named 'putative keystone' group or 'hub' taxa. Although, network analysis describes the statistical associations not the cause effect relationship, the hub genera will be selected as putative biomarkers for disease management which necessitates experimental validation. Microbial communities in diseased soil will be correlated with corresponding soils obtained from diseased free soil in similar fields for identifying networks associated with take-

all and suppression mechanisms, not a single causative microorganism [28].

3.4 Development of Functional Gene Reference Ranges

Functional genes provide valuable information about the potential biological capacity of soil microbial communities. However, gene abundance should not be directly interpreted as actual nutrient availability because gene expression depends on environmental conditions and microbial activity [29]. Therefore, functional gene thresholds in this study will be developed from the Phase 0 calibration dataset rather than adopting fixed values from literature. Soil-series-specific ranges will be established based on the observed distribution of functional gene abundance. Samples will be categorized as: High: all values exceeding the 75th percentile; Low: all values less than the 25th percentile; Middle: all values within the 25th–75th percentile. This interpretation considers that soil microbial communities are inherently different among soil types, and different universal standards cannot be used with biologically different soils.

3.5 Soil Pathogen Assessment

The presence of pathogen DNA in soil does not always indicate disease occurrence because many soil-borne pathogens can survive at background levels without causing visible symptoms. Therefore, pathogen interpretation in this framework will focus on comparing observed pathogen abundance with the normal background level of each soil series. A two-level pathogen monitoring approach will be followed. Major soil-borne pathogens that affect multiple crops will be included in the general screening panel, whereas additional pathogens will be included depending on crop requirements [30]. The framework will consider pathogen abundance, crop susceptibility, and environmental conditions together before assigning disease risk. This approach reduces the possibility of unnecessary recommendations based only on pathogen detection.

3.6 AMF Community Assessment

Arbuscular Mycorrhizal Fungi, as an essential link in the function of the biological processes of soil, aid in phosphorus acquisition, as well as root formation, and improve plants' tolerance to adversity. Therefore, AMF community profiling will be included as an indicator of biological nutrient acquisition potential. ITS2-based sequencing will be used to evaluate AMF composition and identify dominant genera associated with different soil series. However, AMF abundance will not be interpreted independently because successful plant-fungus interactions depend on crop type, nutrient availability, and environmental conditions. Therefore, AMF indicators will be integrated with soil phosphorus status and crop response information before making biological recommendations [31].

4. Role of Soil Chemical Measurements

Molecular techniques provide detailed information regarding the functioning of microbial communities in the soil. Direct measurement of traditional soil parameters will continue to provide relevant evaluation regarding the fertility of the soil. Factors like pH, EC and K availability reflect inherent physical characteristics, of which the development of microbial indicators substitute is not possible as of now. Therefore, we still rely solely on direct laboratory methods for physical-chemical parameters. Soil

electrical conductivity, potassium, soil nitrogen, soil phosphorus, organic carbon, and soil textural profile will be evaluated. Molecular predictions for some parameters, including soil phosphorus, soil nitrogen, soil organic carbon, and microbial biomass carbon, will not be considered until adequate comparison with laboratory-measured values is achieved [32].

Molecular methods are extremely useful for understanding the community structure and functional potential of soil microbes. They cannot replace conventional laboratory analyses for assessing soil fertility status. Soil pH, Electrical Conductivity (EC), Available Potassium and Texture are intrinsic physicochemical characteristics which must be measured in the lab as shown in Figure 3. So, these become the standard which molecular information will be calibrating and validating. Thus, all Phase 0 samples will be examined for these characteristics in the laboratory, as will be soil pH (1:2.5 soil: water extraction), Electrical Conductivity (1:2.5 solution), Available Nitrogen, Available Phosphorus, Available Potassium, Soil Organic Carbon, Sand, Silt, and Clay as per conventional analytical methods [33].

Available Sulphur, available micronutrients (Zn, Fe, Cu, and Mn) and B will be included where resource availabilities permit as further nutrient characterization. Site specific analysis will also include investigation of CaCO₃ in the Kanhar Vertisol (for potential to fix P) and exchangeable Aluminium in Bhata Entisol (for potential aluminium toxicity) [34]. Prediction methods based on molecular parameters will be investigated for such properties as available Nitrogen and Phosphorus, total Organic Carbon and Microbial Biomass Carbon, but these will only be utilised once they have been demonstrated to be predictable from physical properties.

5. Delta Index — The Gradient Principle

The amount of organisms in the soil is not always a good indicator of whether the biological soil processes are taking place efficiently. In agricultural soil, there is interaction between plant and soil organisms, and especially around the root system where biological activity may vary from soil as a whole there are differences in microbiology. Therefore, this study will use the Tri-Zone Ecological Model (BLK, RZS, and RHZ) to measure the strength of biological enrichment between bulk soil and the rhizosphere through the Delta Index [35].

Based on the existing calculations like relative change across environment formula, we can calculate the delta index in such a way like:

The Delta Index will be calculated as:

$$\text{Delta Index (\%)} = [(\text{RHZ score} - \text{BLK score}) / \text{BLK score}] \times 100$$

This index represents the relative increase or decreases in biological activity at the plant-soil interface compared with background soil conditions. A higher positive Delta Index indicates stronger rhizosphere enrichment, suggesting active plant-microbe interactions and improved biological functioning. A moderate gradient indicates normal biological differentiation, whereas a weak or absent gradient suggests limited rhizosphere stimulation and the need to investigate possible factors such as nutrient imbalance, chemical stress, or poor microbial establishment. A negative Delta Index indicates an inverted gradient, where

rhizosphere activity is lower than bulk soil activity, suggesting possible suppression of beneficial biological processes [36].

6. Expected Results and Hypotheses

This study aims to provide an overall landscape in understanding the impacts of soil series, environmental controls, and management strategies on microbial community structure, potential functioning and soil biological health. We expect that this study will uncover the soil-specific microbial markers, microbial functional groups, ecological drivers related to the nutrient cycling process, plant-microbes interactions and pathogen-inhabiting in contrasting soil environments. The following are the hypothesis based on published soil metagenomics literature and the ecological characterization.

6.1. Soil Series-Specific Variation in Prokaryotic and Fungal Microbiomes

Soil Series shows the Variance of Prokaryotic and Fungal Microbiomes. The framework outlines testing to evaluate whether soil series account for a considerable part of prokaryotic (16S rRNA) and fungal (ITS) community variance after accounting for space, seasons and other environmental variation. Soil microbiome research has highlighted soil pH and soil organic carbon will be major driver for soil communities in this work. [37, 8].

6.2. Functional gene gradient by soil series

The abundance of *nifH* will rank as Kanhar Vertisol > Dorsa Alfisol > Matasi Inceptisol > Bhata Entisol, consistent with the SOC gradient. *phoD* will show the opposite pattern to *phoC* across the pH gradient (Kanhar high *phoD*/low *phoC*; Bhata low *phoD*/high *phoC*) [13].

6.3. Keystone taxa stability

Gaiella may emerge as a candidate for keystone taxon in Vertisols network analysis; *Pseudomonas* and *Bacillus* will emerge as hubs in Alfisol networks. These taxa serve as ecological stability indicators [28].

6.4. AMF depletion in Inceptisols

Based on reported effects of soil disturbance, tillage intensity, and resource limitation on arbuscular mycorrhizal fungal communities, the framework predicts that Matasi Inceptisol soils may exhibit reduced *Glomeromycota* abundance compared with more favorable soil environments such as Dorsa Alfisols. This prediction will be evaluated using empirical community profiling [38].

6.5. Pathogen background by land use

Fields with paddy monoculture history (> 5 seasons) will show significantly higher *Rhizoctonia solani* and *Pythium* background loads than fields under diverse crop rotation [39].

7. Scientific Contribution and Significance

The Chhattisgarh Soil Microbiome Atlas makes four distinct scientific contributions. It is the first large-scale, statistically powered environmental genomics baseline for any agricultural zone in Madhya Pradesh/Chhattisgarh. No comparable dataset exists for these soil orders in central India. The functional gene reference intervals per soil series provide the calibration data without which metagenomic advisory systems cannot operate. These intervals will be

cited by every subsequent study that deploys this framework in Chhattisgarh. The keystone taxa identification and network analysis contribute to the ecological literature on tropical agricultural soil microbiome stability—a field dominated by temperate-zone studies ^[40]. The Delta Index distributions per soil series provides a novel gradient-based ecological baseline that extends the single-point measurement paradigm of existing soil health card assessments ^[41].

Table 1: Comprehensive Overview of the Agro-Climatic Zone and Associated Agricultural Features

Agro-climatic Zone	Representative Districts	Rainfall Range (mm year ⁻¹)	Major Soil Orders/Series	Predominant Cropping Systems	Citations
Chhattisgarh Plains	Raipur, Durg, Rajnandgaon, Bilaspur, Raigarh	1,200-1,400	Vertisols (Kanhra/Arang II), Inceptisols (Matasi)	Paddy-based systems, soybean–chickpea, paddy–wheat, paddy–linseed	[12]
Bastar Plateau	Bastar, Kondagaon, Sukma, Dantewada, Bijapur	1,300–1,600	Alfisols (Dorsa), Entisols (Bhata)	Paddy–fallow, millets, forest-edge agriculture, shifting cultivation	
Northern Hills	Surguja, Koriya, Surajpur, Balrampur	1,100–1,400	Inceptisols, Entisols, upland Alfisols	Rice–fallow, maize, upland pulses, shifting cultivation	

The major agro-climatic zones, representative districts, rainfall patterns, soil orders, and cropping systems are summarized (Table 1).

Table 2: Ecological Functions and Environmental Determinants of Key Soil Microbial Functional Marker Genes

Functional marker	Function	Major environmental controls	Key evidence	Citations
<i>nifH</i>	Biological nitrogen fixation	Soil organic carbon, pH, moisture, oxygen availability	Diazotrophic communities are strongly influenced by carbon availability, soil pH, and moisture conditions.	[16]
<i>phoD</i>	Alkaline phosphatase-mediated organic P mineralization	Alkaline pH, organic P availability, microbial biomass	<i>phoD</i> abundance is associated with alkaline soils and microbial phosphorus cycling.	[17]
<i>phoC</i>	Acid phosphatase-mediated organic P mineralization	Acidic pH, organic matter, Fe/Al-associated P	Acid phosphatase activity generally increases under acidic soil conditions.	[18]
<i>amoA</i>	Ammonia oxidation (nitrification)	Oxygen, ammonium availability, pH	Ammonia-oxidizing microorganisms are regulated by soil pH and oxygen availability.	[19]
<i>nosZ</i>	Nitrous oxide reduction	Carbon availability, anaerobic microsites	Denitrification and N ₂ O reduction depends on oxygen limitation and organic carbon availability.	[20]
<i>mcrA</i>	Methanogenesis	Anaerobic conditions, waterlogging, organic substrates	Methanogens proliferate in waterlogged, anaerobic soils.	[21]
<i>pmoA</i>	Methane oxidation	Methane availability, oxygen diffusion	Methanotrophs oxidize methane in aerobic soil zones where methane is available.	[22]

The literature-based evidence on key microbial functional marker genes and the environmental factors governing their occurrence in agricultural soils in Table 2.

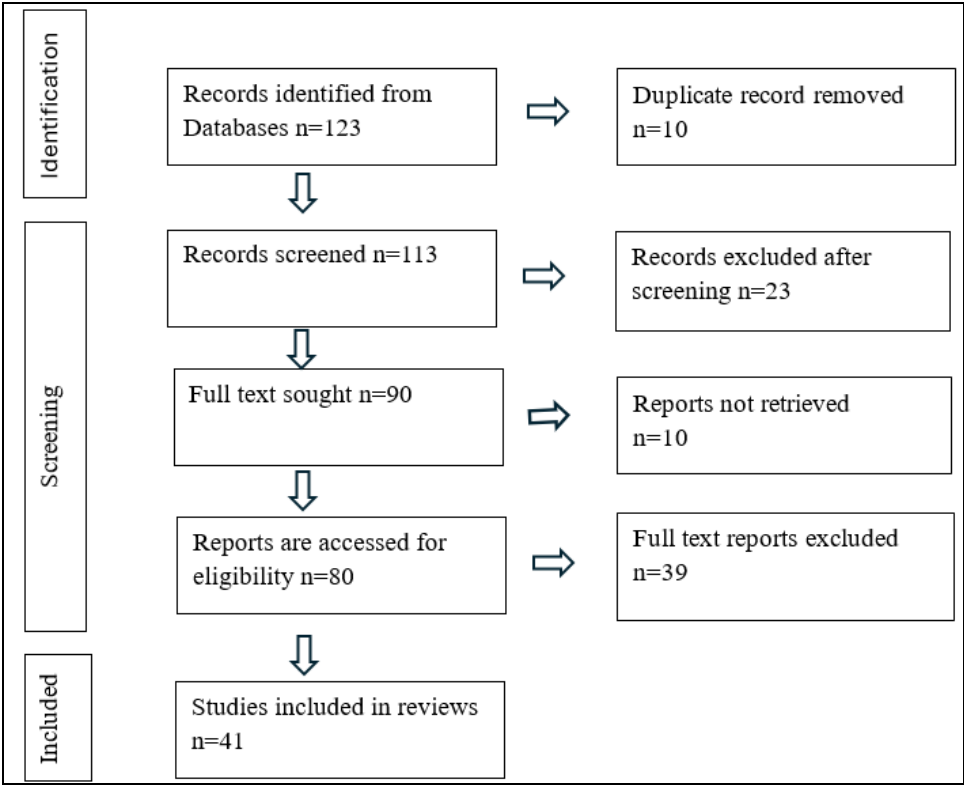


Fig 1: PRISMA flow diagram showing the identification, screening, eligibility, and inclusion of studies from databases and registers

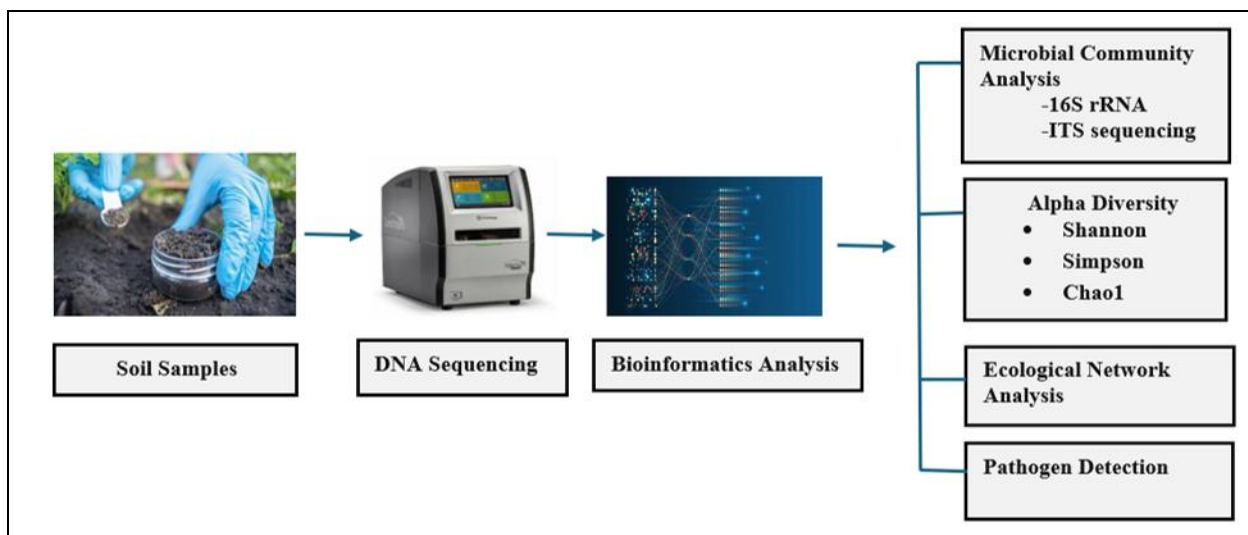


Fig 2: Workflow flow for soil microbial analysis

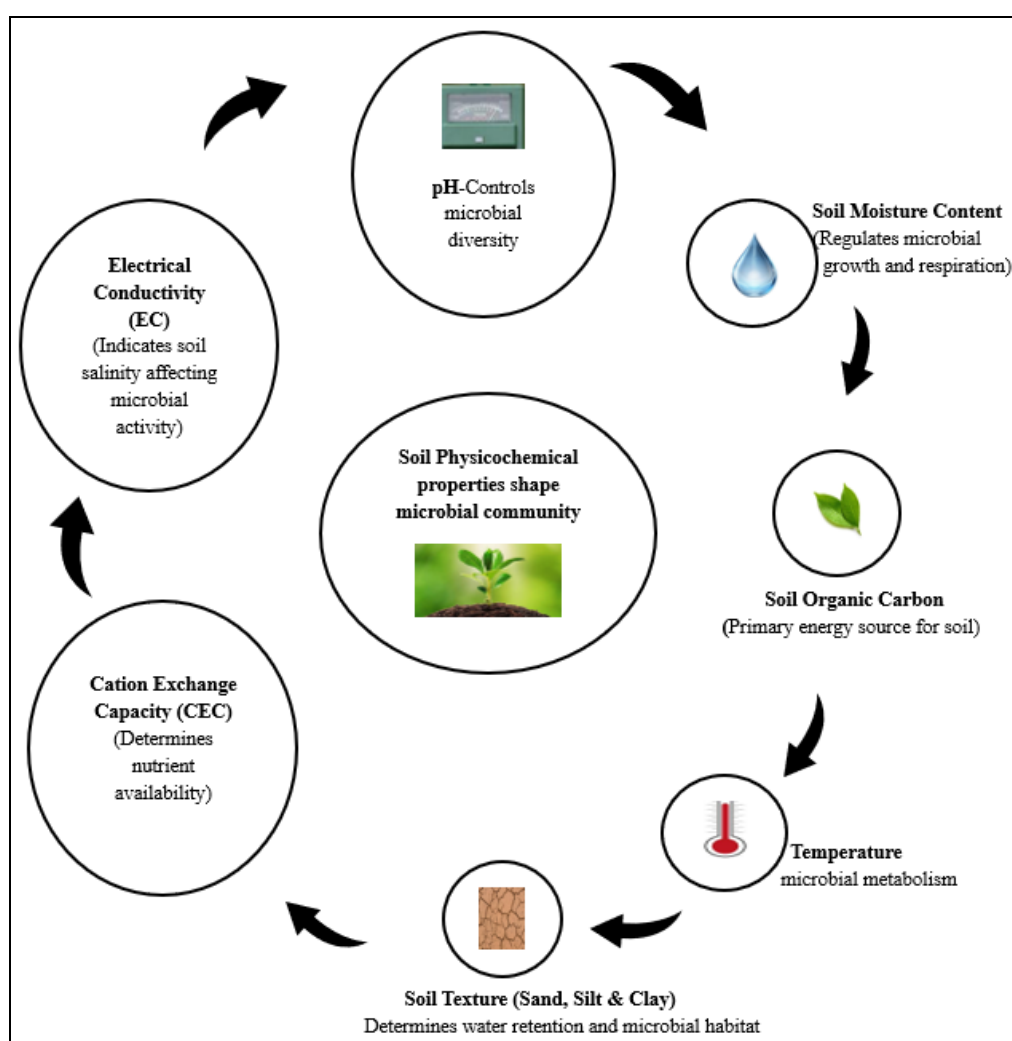


Fig 3: Major Soil Physicochemical Indicators Influencing Soil Health

8. Limitations

This study presents a proposed study design and analytical framework prior to empirical data generation. Consequently, the reference intervals presented are derived from published characterization literature and should be regarded as provisional calibration targets rather than validated biological thresholds. Absolute threshold and class value should be finalized only when the analysis of a suitable set of actual empirical data takes place. Higher sampling

densities would be required to develop reliable biological reference maps at finer spatial resolutions. The pathogen detection thresholds presented are technically derived from published evidence and have not been validated against local disease incidence data from Chhattisgarh. Their diagnostic and predictive performance under regional agroecological conditions therefore remains to be established through independent field validation.

9. Conclusions

The framework allows building of region-specific environmentally defined genomic profiles of central Indian agricultural soils integrating information from shotgun metagenomics, gene-functional analyses, diversity indices, ecological network analyses, AMF estimations, pathogen scouting, and traditional physical and chemical characterizations of soil. Recognizing that soil ecosystem function and health depends on specific interplay of factors as soil series, agro-climatic conditions, cropping system, management, seasonality, and land-use history, it places a strong emphasis on the development of soil-specific microbial reference standards rather than generic standards. The proposed method will produce a comprehensive information regarding the structure of soil microbial communities, their capacity of Nutrient Cycling, presence of key ecological indicators, levels of common soil pathogens and patterns of rhizosphere enrichment as a function of different environments of study. Moreover, molecular metrics do provide information on the intrinsic functional capacities of microorganisms, but require proper interpretation considering chemical characteristics of soil, yields, and future studies integrates omics technologies like transcriptomic or metabolomic analysis in real time of functional processes within the soils. The biological and ecosystem benchmark described can augment current approaches to assessing soil health. They do provide a tool that can help us move beyond a static concept of soil health to more dynamic functional properties, including sustainable management of nutrients, development of microbiome agriculture and enhancing the knowledge of soils being active and biologically active organisms. Incorporation into standard health assessments of soil to better manage can result from understanding and incorporating such principles. They will need field demonstrations and practical assessment in as many varying agroecological conditions as possible to make adoption achievable.

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11. Author contributions

BD contributed to the study of conception and design. Material Preparation were performed by MR, CA, AG, SP. BD and PM read and approved the final manuscript.

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13. Conflict of Interest

The authors declare no conflict of interest.

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