Impacts of bioclimates, cropping systems, land use and management on the cultural microbial population in black soil regions of India

K. Velmourougane[1,*], M. V. Venugopalan[1], T. Bhattacharyya[2], D. Sarkar[2], S. K. Ray[2], P. Chandran[2], D. K. Pal[3], D. K. Mandal[2], J. Prasad[2], G. S. Sidhu[4], K. M. Nair[5], A. K. Sahoo[6], K. S. Anil Kumar[5], A. Srivastava[7], T. H. Das[6], R. S. Singh[8], C. Mandal[2], R. Srivastava[2], T. K. Sen[2], S. Chatterji[2], N. G. Patil[2], G. P. Obireddy[2], S. K. Mahapatra[4], K. Das[6], S. K. Singh[6], S. K. Reza[9], D. Dutta[6], S. Srinivas[5], P. Tiwary[2], K. Karthikeyan[2], Mausumi Raychaudhuri[10], D. K. Kundu[10], K. G. Mandal[10], G. Kar[10], S. L. Durge[2], G. K. Kamble[2], M. S. Gaikwad[2], A. M. Nimkar[2], S. V. Bobade[2], S. G. Anantwar[2], S. Patil[2], M. S. Gaikwad[2], V. T. Sahu[2], H. Bhondwe[2], S. S. Dohtre[2], S. Gharami[2], S. G. Khapekar[2], A. Koyal[5], Sujatha[5], B. M. N. Reddy[5], P. Sreekumar[5], D. P. Dutta[9], L. Gogoi[9], V. N. Parhad[2], A. S. Halder[6], R. Basu[6], R. Singh[8], B. L. Jat[8], D. L. Oad[8], N. R. Ola[8], A. Sahu[2], K. Wadhai[2], M. Lokhande[2], V. T. Dongare[2], A. Hukare[2], N. Bansod[2], A. Kolhe[2], J. Khuspure[2], H. Kuchankar[2], D. Balbuddhe[2], S. Sheikh[2], B. P. Sunitha[5], B. Mohanty[4], D. Hazarika[9], S. Majumdar[6], R. S. Garhwal[8], S. Mahapatra[10], S. Puspamitra[10], A. Kumar[7], N. Gautam[2], B. A. Telpande[2], A. M. Nimje[2], C. Likhar[2] and S. Thakre[2]

[1]Central Institute for Cotton Research, Nagpur 440 010, India
[2]Regional Centre, National Bureau of Soil Survey and Land Use Planning, Nagpur 440 033, India
[3]International Crops Research Institute for the Semi-Arid Tropics, Patancheru 502 324, India
[4]Regional Centre, National Bureau of Soil Survey and Land Use Planning, New Delhi 110 012, India
[5]Regional Centre, National Bureau of Soil Survey and Land Use Planning, Bangalore 560 024, India
[6]Regional Centre, National Bureau of Soil Survey and Land Use Planning, Kolkata 700 091, India
[7]National Bureau of Agriculturally Important Microorganisms, Mau 275 101, India
[8]Regional Centre, National Bureau of Soil Survey and Land Use Planning, Udaipur 313 001, India
[9]Regional Centre, National Bureau of Soil Survey and Land Use Planning, Jorhat 785 004, India
[10]Directorate of Water Management, Bhubaneswar 751 023, India

The present study documents the biological properties of the black soil region (BSR) of India in terms of culturable microbial population. Besides surface microbial population, subsurface population of individual soil horizons is described to improve the soil information system. An effort has been made to study the depth-wise distribution and factors (bioclimates, cropping systems, land use, management practices and soil properties) influencing the microbial population in the soils of the selected benchmark spots representing different agro-ecological sub-regions of BSR. The microbial population declined with depth and maximum activity was recorded within 0–30 cm soil depth. The average microbial population ($\log_{10}$ cfu g^{-1}) in different bioclimates is in decreasing order of SHm > SHd > SAd > arid. Within cropping systems, legume-based system recorded higher microbial population ($6.12 \log_{10}$ cfu g^{-1}) followed by cereal-based system ($6.09 \log_{10}$ cfu g^{-1}). The mean microbial population in different cropping systems in decreasing order is legume > cereal > sugarcane > cotton. Significantly higher ($P < 0.05$) microbial population has been recorded in high management ($6.20 \log_{10}$ cfu g^{-1}) and irrigated agrosystems ($6.33 \log_{10}$ cfu g^{-1}) compared to low management ($6.12 \log_{10}$ cfu g^{-1}) and rainfed agrosystems ($6.17 \log_{10}$ cfu g^{-1}). The pooled analysis of data inclusive of bioclimates, cropping systems, land use, management practices, and edaphic factors indicates that microbial population is positively influenced by clay, fine clay, water content, electrical conductivity, organic carbon, cation exchange capacity and base saturation, whereas bulk density, pH, calcium carbonate and exchangeable magnesium percentage have a negative effect on the microbial population.

Keywords: Agro-ecological sub-regions, benchmark spots, black soil regions, principal component analysis, soil microbial population.

*For correspondence. (e-mail: velicar@gmail.com)

Introduction

SOIL quality is one of the significant agro-ecosystem components for which management efforts must be intensified to achieve sustainability. In recent times there has been an increased interest in developing various techniques of evaluating soil health[1]. Among the soil components,

microorganisms play a key role in ecologically important bio-geochemical processes[2]. Furthermore, microbiological properties are the most sensitive and rapid indicators of perturbations and land-use changes, as they develop in response to constraints and selection pressures in their environment[3]. In this sense, quantitative description of microbial community structure and diversity has aroused great interest in soil quality evaluation[4,5]. Soil microbial diversity can directly influence plant productivity and diversity by influencing plant growth and development, plant competition, and nutrient and water uptake[6]. Thus, microbial diversity needs to be considered in soil quality studies[7].

Black soils, popularly known as black cotton soils, are usually deep to very deep and dominated by highly expansive smectitic clays. They are characterized by the presence of either slickensides or wedge-shaped peds, ≥ 30% clay and cracks that open and close periodically. These soils are grouped as Vertisols. Revised estimation indicates that black soils occupy nearly 76.4 m ha area in the country. Maharashtra, Madhya Pradesh and Gujarat have the major share of black soils in India. Black soils are also reported from Kerala, Jammu and Kashmir and Andaman and Nicobar Islands. In spite of the fact that some studies have reported about the soil microbial activities in Indian soils[8–10], comparatively little information is available on the impact of climatic, cropping and land use systems on soil microbial population in different agro-ecological sub-regions (AESRs) of the black soil regions (BSR) in India. To improve our understanding of microbial populations and their diversity in BSR, a survey has been undertaken in the established benchmark (BM) soil series of BSR of India with the objective to study the impact of bioclimates, cropping systems, land use system and management practices on the distribution of microbial population at different soil depths. The information generated on soil microbial attributes through this study, will improve the Indian soil information system, which will be useful for the assessment of soil/land quality and changes in the soil quality indicators for sustainable land resource management in the BSR of India.

Materials and methods

Site description and sampling

Soils for the present study were chosen from the established BM sites, the reason being that each soil would cover an extensive area in the landscape and monitoring these BM sites would be easy. Though a few selected soils do not belong to the BM sites, it has been ascertained that each of these soil series covers an area much larger than 20,000 ha (area required for any soil series to have BM status). Based on variations in mean annual rainfall (mm), the BSR was grouped as under arid A: <550 mm, semi-arid (dry) SAd: 550–850 mm, semi-arid (moist) SAm: 1000–850 mm, sub-humid (dry) SHd: 1100–1000 mm and sub-humid (moist) SHm: > 1100 mm in 6 AERs (agro-ecological regions) and 17 AESRs (3.0, 5.1, 5.2, 6.1, 6.2, 6.3, 6.4, 7.1, 7.2, 7.3, 8.1, 8.2, 8.3, 10.1, 10.2, 10.3 and 5.1)[11] accounting for 19% (76.4 m ha)[12] of the total geographical area of the country. The soil series were selected in such a way that in any agricultural system under a particular cropping pattern, two representative soil profiles (under the same soil series) were included (Table 1). The soil series under low management (LM) were characterized by application of low NPK, organic manure rarely applied, removal of residues and biomass and no soil moisture conservation practices followed. The soil series under high management (HM) were characterized by application of recommended levels of NPK, regular application of organic manure, incorporation of residues and adoption of soil moisture conservation techniques (ridge furrows, bunding, broad bed and furrow).

Soil physical and chemical characteristics

The soil samples collected from different BM spots were air-dried and ground to pass through a 2 mm sieve before analysis. The international pipette method was used for particle-size analysis for quantifying the sand (2000–50 μm), silt (50–2 μm) and clay (< 2 μm) fractions, according to the size segregation procedure of Jackson[13]. The $CaCO_3$, pH (1 : 2), cation exchange capacity (CEC) and exchangeable sodium percentage (ESP) were determined on the total fine earth (< 2 mm) by standard methods[14]. Exchangeable magnesium percentage (EMP) was determined following the 1 N NaCl solution extraction method[15]. Carbonate clay was determined on the basis of the gravimetric loss of carbon dioxide using Collin's calcimeter[16]. The saturated hydraulic conductivity (sHC; cm/h) was measured by taking 200 g of soil, uniformly tapped and saturated overnight. It was measured by taking an hourly observation until three constant observations were obtained in the permeameter[14]. Available water content (AWC) was calculated using the water retained between 33 and 1500 kPa of less than 2 mm size soil samples[14]. The bulk density (BD) was determined by a field-moist method using core samples (diameter 50 mm) of known volume (100 cm^3)[17].

Soil microbiological characteristics

Soil samples collected at different soil depths from BM spots were passed through a 2 mm sieve and stored at 4°C for subsequent analyses. For microbial analysis, samples were serially diluted up to 10^{-4} dilution and 1 ml of aliquot was pour-plated in enumeration media (nutrient agar for

Table 1. Characteristics of selected benchmark spots in black soil regions of India

AESR	Bio-climate	MAR (mm)	Soil series	Soil subgroup classification	MSL (m)	District	State	Cropping systems and land use (HM)	Cropping systems and land use (LM)
6.1	Arid	520	Nimone	Sodic Haplusterts	517	Ahmednagar	Maharashtra	Soybean–wheat/chick pea[I]	Soybean/pearl millet/chickpea[I]
5.1	Arid	533	Sokdha	Leptic Haplusterts	25	Rajkot	Gujarat	Cotton + green gram/pearl millet[R]	cotton + green gram/ pearl millet/sorghum[R]
8.1	SAd	612	Coimbatore	Typic Haplustepts	421	Coimbatore	Tamil Nadu	Maize–chick pea[I]	Chick pea[R]
3.0	SAd	632	Teligi	Sodic Haplusterts	379	Bellary	Karnataka	Triple cropping of rice[I]	Maize/sorghum–chick pea[R]
6.4	SAd	638	Achamatti	Sodic Haplusterts	573	Dharwad	Karnataka	Cotton–wheat/safflower/sorghum[I]	Maize–chick pea[R]
7.1	SAd	650	Nandyal	Sodic Haplusterts	212	Kurnool	Andhra Pradesh	Rice–rice[I]	Cotton/sunflower[R]
5.1	SAd	650	Bhola	Vertic Haplustepts	76	Rajkot	Gujarat	Cotton–wheat[I]	Cotton–wheat[I]
8.3	SAd	660	Kovilpatti	Gypsic Haplusterts	81	Tuticorin	Tamil Nadu	Sorghum[R]	Single cropping of cotton/ sunflower/chick pea[R]
8.2	SAd	661	Siddalaghatta	Vertic Haplustepts	717	Kolar	Karnataka	Fruits crops + sunflower/Sorghum	Rice–maize–tomato[I]
7.2	SAd	764	Kasireddipalli	Typic Haplusterts	538	Medak	Andhra Pradesh	Soybean + pigeon pea/maize–sunflower[R]	Chickpea/sorghum[R]
6.2	SAd	789	Vasmat	Typic Haplusterts	372	Hingoli	Maharashtra	Sugarcane[I]	Rice–fallow[I]
6.3	SAd	794	Paral	Sodic Haplusterts	267	Akola	Maharashtra	Cotton + soybean/green gram + sorghum[I]	Cotton + black gram/chickpea + sorghum[I]
5.2	SHd	1053	Sarol	Typic Haplusterts	564	Indore	Madhya Pradesh	Soybean–wheat[I]	Soybean–chick pea[I]
10.3	SHd	1100	Ghulguli	Typic Haplusterts	509	Shahdol	Madhya Pradesh	Pigeon pea/mustard/green gram[R]	Rice–wheat/chick pea[I]
10.2	SHm	1127	Panjri	Typic Haplusterts	309	Nagpur	Maharashtra	Single crop of cotton/soybean[R]	Soybean–wheat/soybean–chick pea[R]
10.1	SHm	1209	Nabibagh	Typic Haplusterts	501	Bhopal	Madhya Pradesh	Soybean–wheat/soybean–chick pea[I]	Soybean–wheat/soybean–chick pea[I]
7.3	SHm	1250	Tenali	Sodic Haplusterts	15	East Godavari	Andhra Pradesh	Rice–rice[I]	Rice–rice[I]

AESR, Agro-ecological sub-regions; MAR, Mean annual rainfall (mm); Arid (< 550 mm); SAd, Semi-arid dry (850–550 mm); SHd, Sub-humid dry (1100–1000 mm); SHm, Sub-humid moist (> 1100 mm); MSL, Elevation above mean sea level; I, Irrigated agrosystem; R, Rainfed agrosystem; HM, High management; LM, Low management.

bacteria, Martin's rose Bengal agar for fungi, Ken Knights and Munaier's agar for actinomycetes and buffered yeast agar for yeast). The plates were incubated at optimum temperature (28 ± 1°C for bacteria and yeast; 30 ± 1°C for fungi and actinomycetes) in triplicate. The microbial colonies appearing after the stipulated time of incubation (3 days for bacteria and yeast; 5 days for fungi; 7 days for actinomycetes) were counted as total culturable colony forming units (cfu) and expressed in $\log_{10}$ cfu g^{-1} of the sample.

The weighted mean averages of total culturable microbial population at different soil depths (cm) were derived as follows:

[(First soil core length × culturable microbial population) + (second soil core length × culturable microbial population) ··· (*n*th soil core length × culturable microbial population)]/total sampling depth (cm).

Statistical analyses

To study the impact of different factors on the microbial population, data pertaining to BSR under different bioclimates, cropping systems, land use and management practices were pooled and analysed using ANOVA for a two factorial design (soil depth × bioclimate/cropping system/land use/management). Tukey's honest significant difference (HSD) test was used (if ANOVA indicated significant differences) as a post hoc mean separation test ($P < 0.05$) using SAS 9.1 (SAS Institute, Cary, NC). Principal component analysis (PCA) was performed using XLSTAT 2013 software.

Results and discussion

Variability of culturable microbial population with soil depth

The culturable microbial population declined in all the BM spots with soil depth (Table 2). Surface soil horizon (0–15 cm) recorded maximum population and almost 50% of microbial population was restricted within 0–30 cm soil depth. Microbial population differed significantly ($P < 0.01$) from one BM spot to another. HM spots showed higher microbial population compared to LM spots. Among the BM spots in HM, Coimbatore soil series of Tamil Nadu recorded the highest microbial population (6.40 $\log_{10}$ cfu g^{-1}), and Bhola soils of Gujarat showed the lowest microbial count (5.68 $\log_{10}$ cfu g^{-1}) at 15 cm soil depth. In LM, Teligi soils of Karnataka recorded highest population (6.35 $\log_{10}$ cfu g^{-1}), and Sidalghatta soils of Karnataka showed lowest population (5.77 $\log_{10}$ cfu g^{-1}). The increased microbial population in the surface soil compared to subsurface soil is attributed to the greater availability of organic carbon, nutrients, moisture and aeration. Depth of root penetration and nutrient exhaustive characteristics of crops also may be an additional reason for the decline of culturable microbial population in deeper layers. Impact of soil depth on proportion of microbial activity has already been reported[4,18].

Impact of bioclimates on cultural microbial population

Culturable microbial population declined in all bioclimates with soil depth (Figure 1). In the surface horizon (0–15 cm), SHm recorded higher culturable microbial population (6.26 $\log_{10}$ cfu g^{-1}) and the arid regions showed least population (6.14 $\log_{10}$ cfu g^{-1}). The average culturable microbial population in different bioclimates was in decreasing order of SHm > SHd > SAd > arid. The higher microbial population in SHm and lower microbial population in arid regions, reflect the contrasting moisture and nutrient availability in these bioclimates. The variations in microbial populations among the bioclimates may also be attributed to the differences in soil physical and chemical properties. Soil moisture may differentially influence bacteria and fungi, either by directly affecting survival and growth or indirectly by shifting substrate availability[19]. Changes in soil microbial community composition due to flooding has also been reported[20]. Soil type has been reported as the principal factor determining soil microbial communities and their structure[21]. Studies of bacterial communities in soils and sediments[22] and in microcosms[23] indicated that hydraulically induced spatial isolation in drier soils leads to higher diversity (richness and evenness) relative to wetter, more hydraulically connected soil or sediment environments. Soil pH is also reported as the main factor that affects microbial population and structure[24]. Soil pH has been reported to be the best predictor of bacterial community composition across this landscape. Fungal community composition is most closely associated with changes in soil nutrient status[25]. Rietz and Haynes[26] conclude that agriculture-induced salinity and sodicity not only influence the chemical and physical characteristics of soils, but also greatly affect soil microbial and biochemical properties. In general, soil moisture is reported to influence the microbial activity in soils[27]. Variations in the frequencies and intensity of precipitation influence the spatio-temporal extent of fungal and bacterial activities[28]. Soil microbial functional diversity is found to decrease with increasing latitude and is positively correlated with measures of atmospheric temperature and higher acidity[29]. Low organic matter content and poor moisture availability of soils are the major factors limiting optimum microbial activity[8].

Impact of cropping systems on cultural microbial population

Significant difference in microbial population ($P < 0.05$) has been observed in different cropping systems and soil

Table 2. Weighted mean average of total culturable microbial population ($\log_{10}$ cfu g^{-1}) at different soil depths

	Soil depth (cm)									
	0–15		15–30		30–50		50–100		100–150	
Soil series	HM	LM	HM	LM	HM	LM	HM	LM	HM	LM
Nimone	6.27	6.22	6.22	6.21	6.19	6.17	6.12	6.06	6.04	5.96
Sokdha	6.03	6.07	6.01	6.07	5.95	6.07	5.87	6.05	–	–
Coimbatore	6.40	6.32	6.37	6.29	6.36	6.28	6.31	6.21	6.27	6.12
Teligi	6.26	6.35	6.23	6.31	6.20	6.27	6.14	6.20	6.08	6.12
Achhamatti	6.27	6.20	6.25	6.17	6.24	6.15	6.20	6.07	6.14	6.00
Nandyal	6.25	6.18	6.23	6.16	6.20	6.14	6.13	6.06	6.07	5.97
Bhola	5.68	ND	5.57	ND	5.53	ND	5.44	ND	–	ND
Kovilpatti	6.28	6.20	6.27	6.15	6.24	6.10	6.18	6.00	6.08	5.89
Sidalghatta	5.87	5.77	5.86	5.74	5.83	5.69	5.74	5.56	5.67	5.48
Kasireddipalli	6.37	6.16	6.15	5.99	6.09	5.88	5.94	5.74	–	–
Vasmat	6.17	6.19	6.12	6.15	6.08	6.13	6.02	6.08	5.97	6.04
Paral	6.25	6.13	6.16	5.98	6.13	5.95	6.06	5.84	5.96	5.74
Sarol	6.26	6.24	6.18	6.14	6.16	6.09	6.10	5.98	6.02	5.88
Ghulghuli	6.25	6.12	6.23	6.08	6.20	6.04	6.09	–	6.00	–
Panjari	6.10	5.99	6.06	5.94	5.99	5.88	5.89	5.80	5.79	5.73
Nabibagh	5.97	5.83	5.97	5.72	5.92	5.64	5.87	5.49	5.82	5.39
Tenali	6.27	6.23	6.25	6.22	6.23	6.19	6.18	6.11	6.12	5.99
($P < 0.01$)	*	*	*	*	*	*	*	*	*	*

ND, Not determined; *, Significant at 1% probability level.

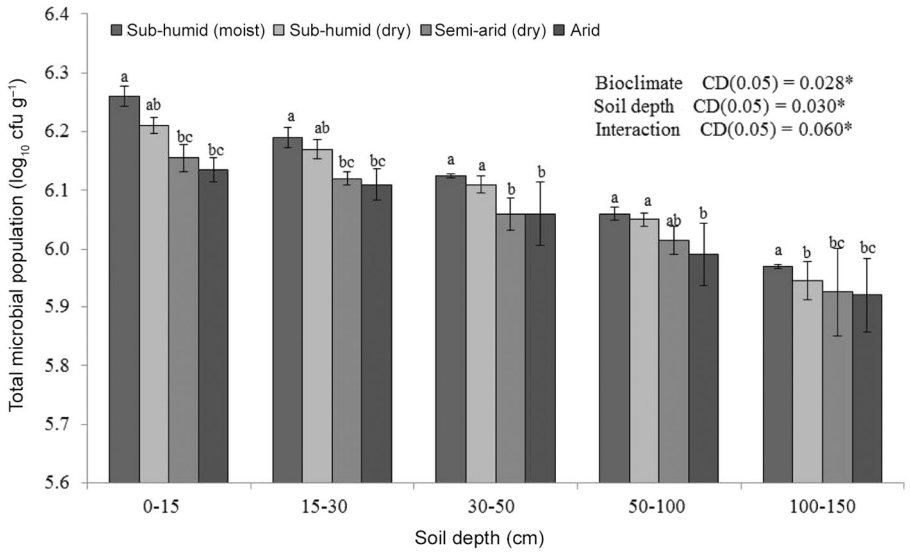

Figure 1. Impact of bioclimate on total culturable microbial population in BSR. *Critical difference value significant at alpha = 0.05 probability level. Error bars (± SD) with the same letter are not significantly different ($\alpha = 0.05$) following Tukey's HSD.

depths in all BM spots studied. Soils with legume-based cropping system (chickpea/soybean/pigeon pea) recorded higher culturable microbial population followed by soils with cereal-based cropping system (Figure 2). In legume-based system, pigeon pea (6.26 $\log_{10}$ cfu g^{-1}) followed by chick pea (6.25 $\log_{10}$ cfu g^{-1}) recorded higher culturable microbial population. In cereal-based system, maize (6.33 $\log_{10}$ cfu g^{-1}) followed by rice (6.15 $\log_{10}$ cfu g^{-1}) recorded higher culturable microbial population. Soils with cotton-based cropping system recorded the lowest microbial population (6.07 $\log_{10}$ cfu g^{-1}). The mean culturable microbial population in soils with different cropping systems was in decreasing order of legume > cereal > sugarcane > cotton. The higher microbial activity in the legume-based system showed the contribution of legumes towards the greater availability of organic carbon and subsequent microbial activity. Higher microbial population in legume-based system is also attributed to crop growth characteristics, such as root growth, and nitrogen fixation and utilization pattern. The lesser microbial

Table 3. Correlation matrix (Pearson) for soil variables and culturable microbial population at different soil depths

					Moisture retention												
Soil depth (cm)	Silt	Clay	Fine clay	BD	1/3 bar	15 bar	sHC	pH	EC	OC	$CaCO_3$	CEC	BS	ESP	EMP	N	P	K
0–15	–0.217	**0.468**	0.276	–0.213	0.233	0.289	0.078	–0.005	0.250	0.293	–0.024	0.303	**0.349**	–0.197	–0.221	–0.004	–0.271	0.285
15–30	–0.256	0.275	0.196	0.047	0.178	0.308	–0.079	0.036	**0.469**	**0.499**	–0.001	0.260	0.220	0.110	–0.306	0.029	0.105	0.313
30–50	**–0.460**	**0.388**	**0.434**	–0.111	0.272	0.245	–0.078	0.011	**0.493**	0.131	–0.007	0.285	**0.513**	0.105	**–0.444**	–0.225	0.086	0.138
50–100	–0.090	0.171	0.124	0.041	**0.419**	**0.403**	–0.346	–0.001	**0.666**	0.157	–0.014	0.279	**0.529**	**0.371**	–0.218	0.245	0.083	–0.067
100–150	–0.105	0.143	0.164	0.046	0.217	0.181	–0.163	–0.118	**0.505**	0.363	0.216	0.151	0.356	0.285	–0.296	0.069	–0.071	–0.058

Values in bold are significant at alpha 0.05. BD, Bulk density; sHC, Saturated hydraulic conductivity; EC, Electrical conductivity; OC, Organic carbon; CEC, Cation exchange capacity; BS, Base saturation; ESP, Exchangeable sodium percentage; EMP, Exchangeable magnesium percentage.

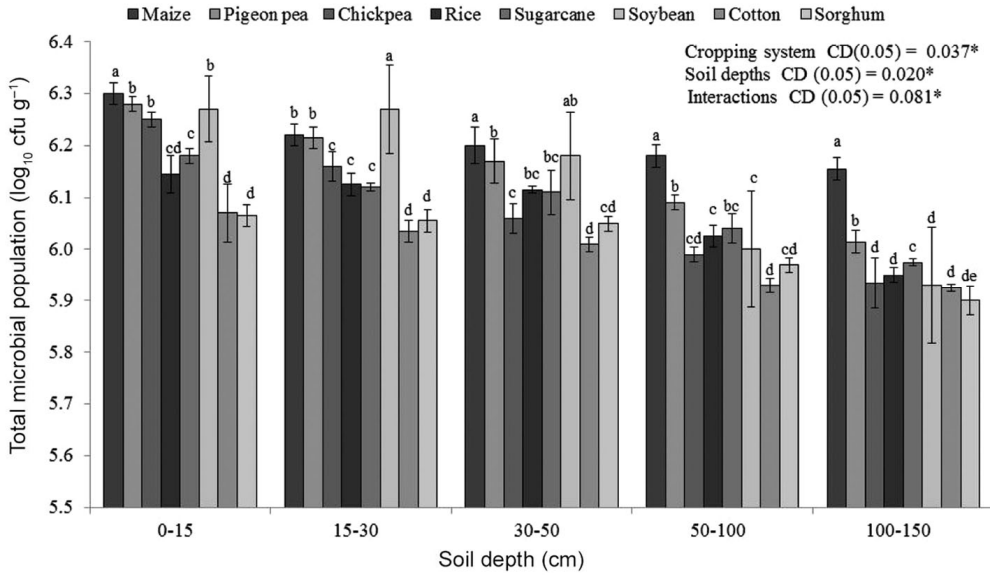

Figure 2. Impact of cropping systems on total culturable microbial population in BSR. *Critical difference value significant at alpha = 0.05 probability level. Error bars (± SD) with the same letter are not significantly different ($\alpha = 0.05$) following Tukey's HSD.

population in soils with cotton-based cropping systems is mainly because of the crop characteristics (deep-rooted and nutrient-exhaustiveness) and management levels (mostly rainfed with low inputs). Cropping systems that include legumes are reported to be more productive than systems without legumes in hot, dry climates[30].

Microbial communities associated with different crop types and varieties differ in terms of composition, activity and their nutrient content[31]. Lupwayi *et al.*[32] reported higher diversity of soil microbial communities under legume-based crop rotations[33]. Multi-cropping systems have been reported to increase microbial activity and diversity compared to mono-cropping systems[34]. Crop rotation as a management practice is reported to increase soil carbon sequestration in comparison with continuous crop; and more intensive cropping rotations are also reported to increase microbial activity[35]. Soil biota is also directly affected by cropping systems, crop rotation and crop types[36]. Application of organic manure in the form of leguminous green manure crops also encourages soil microflora than farming systems which receive applications of chemical fertilizers[37]. Major difference in microbial activity and community composition between different cropping systems is mainly attributed to the carbon sources utilized by microbial communities from different plant rhizospheres and carbohydrates, carboxylic acids and amino acids, which are the substrates[38,39].

Impact of land use and management practices on cultural microbial population

The pooled analysis of culturable microbial population data indicated significant differences ($P < 0.05$) between the land use types (irrigated and rainfed agro-ecosystems) at all the soil depths (Figure 3). The average culturable microbial population in surface soil (0–15 cm) in irrigated system was 6.33 $\log_{10}$ cfu g^{-1}, and rainfed systems recorded 6.17 $\log_{10}$ cfu g^{-1}. At deeper horizon (100–150 cm), values of 5.96 and 5.30 $\log_{10}$ cfu g^{-1} were observed in irrigated and rainfed agro-ecosystems respectively. The pooled data on management practices indicated significant differences ($P < 0.05$) between the management level and soil depth (Figure 4). HM recorded higher microbial population (6.20 $\log_{10}$ cfu g^{-1}) compared to LM (6.12 $\log_{10}$ cfu g^{-1}) at the surface horizon (0–15 cm). Cultivation of soils represents a type of land use with important effects on soil characteristics and microbiology. Various soil management and cultural practices influence soil microbial populations and their activities[40]. Management practice and type of cultivation have more influence on soil biota than different soil types[41,42]. Differences in tillage intensity have an impact on microbial community composition[43]. Compared with conventional practices, organic farming practices promote higher microbial biomass[44,45]. Bossio *et al.*[46] observed that conventionally managed, organic and low-input management systems had significantly different microbial communities and that organic soils had higher fungal : bacterial biomass ratios than conventionally managed soils. Organic practices rapidly improve soil microbial characteristics and slowly increase soil organic carbon[47]. Organic manuring with plant residues has a stronger impact on soil microbial activity compared to other fertilization methods[48]. Application of half organic manure with mineral fertilizer NPK produced higher culturable microbial counts than application of mineral fertilizers alone[49]. Chemical fertilization,

though reported to have a greater impact on the growth and activity of microorganisms[50], is often highly species-specific[51]. In India, integrated use of optimal NPK fertilizers and farmyard manure (FYM), stimulates the growth of bacteria, fungi and actinomycetes compared with only optimal NPK fertilizers[9]. Based on fatty acid methylester (FAME) and terminal restriction fragment length polymorphisms (T-RFLP) analyses, Suzuki *et al.*[52] reported that chemical fertilizer application, especially ammonium–nitrogen fertilizer, had a greater impact on microbial community compared to organic fertilizers. Ye and Wright[53], based on cluster and discriminate analyses, reported that agricultural management, especially historic phosphorus fertilization, altered soil nutrient availability and consequently modified the microbial community composition and function. Jesus *et al.*[54] reported that the main differences in bacterial community structure were related to changes in the soil attributes (base saturation and pH) that, in turn, were correlated with land use.

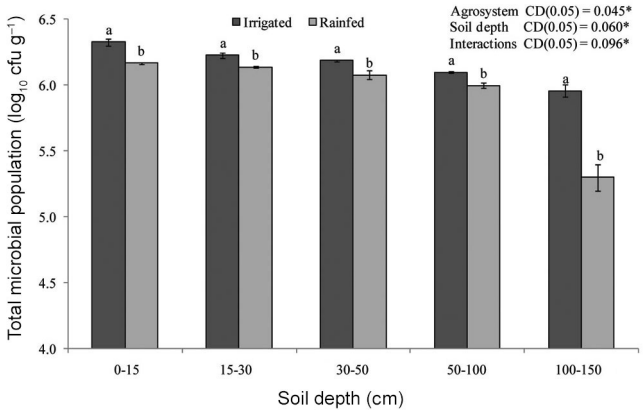

Figure 3. Impact of land use systems on total culturable microbial population in BSR. *Critical difference value significant at alpha = 0.05 probability level. Error bars (± SD) with the same letter are not significantly different ($\alpha = 0.05$) following Tukey's HSD.

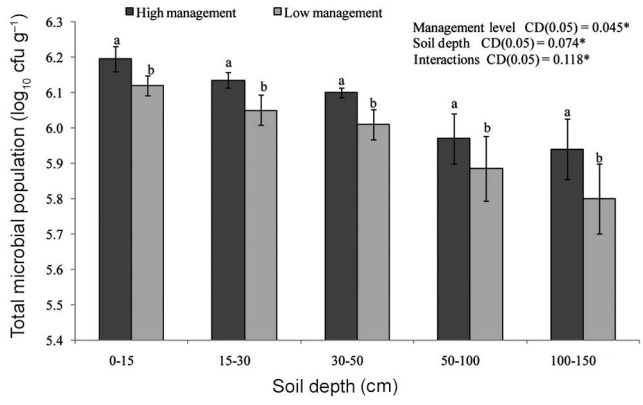

Figure 4. Impact of management levels on total culturable microbial population in the BSR. *Critical difference value significant at alpha = 0.05 probability level. Error bars (± SD) with the same letter are not significantly different ($\alpha = 0.05$) following Tukey's HSD.

Impact of soil properties on culturable microbial population – PCA

The data on correlation between soil properties and microbial population are presented in Table 3 and PCA of soil properties as loading plots from the surface (0–15 cm) to subsurface (100–150 cm) soil horizons is presented in Figures 5. Eigen values from the PCA indicate that the first seven principal components (PC) accounted for 80% of the variance in the microbial population at the surface horizon (0–15 cm). Clay, fine clay, AWC, EC, OC, BS, CEC and K are positively correlated with microbial population in the 0–15 cm depth, and clay and BS are significantly correlated with microbial population (Figure 5 *a*). Though BD, pH, $CaCO_3$, ESP and EMP show negative correlation with microbial population, significance is not established. At soil depth of 15–30 cm, eigen values from the PCA indicate that the first eight PCs account for 84% of the variance in the microbial population. Clay, fine clay, AWC, EC, OC, BS, CEC and K are positively correlated with the microbial population, and EC and OC are significantly correlated with the microbial population (Figure 5 *b*). Although EMP and $CaCO_3$ exhibit negative effect on microbial population, significance is not observed. At soil depth of 30–50 cm, the first seven PCs account for 82% of the variance in the microbial population. Clay, fine clay, AWC, EC, OC, BS and CEC are positively correlated with microbial population; clay, fine clay, EC and BS are significantly correlated (Figure 5 *c*). EMP exhibits negative effect on microbial population at 30–50 cm depth. At the subsurface (50–100 cm), the first seven PCs account for 83% of the variance in the microbial population. Clay, fine clay, AWC, EC, OC, BS, CEC, ESP and N are positively correlated with microbial population, while EC, BS and ESP are significantly correlated (Figure 5 *d*). Though pH, EMP and HC exhibit negative effect on microbial population at 50–100 cm soil depth, significance is not observed. In subsurface soil (100–150 cm), eigen values from the PCA indicate that the first seven PCs account for 81% of the variance in the microbial population. Clay, fine clay, AWC, EC, OC, BS, CEC, $CaCO_3$ and ESP are positively correlated with microbial population, and only EC is significantly correlated with microbial population (Figure 5 *e*). Though EMP, sHC and pH exhibit negative effect on microbial population, significance is not observed.

The importance of edaphic factors on microbial population has been established by several studies[55–57]. Researchers have studied the relationship between microbial biomass and soil properties like moisture[58], temperature[59], soil organic matter content[60] and texture[61]. Soil moisture as an abiotic driver of soil organic matter dynamics[62] and as an important factor related to the soil microbial activity[63] is well studied. The positive correlation of microbial biomass with soil moisture has been reported[64–66]. Long-term application of organic and inorganic

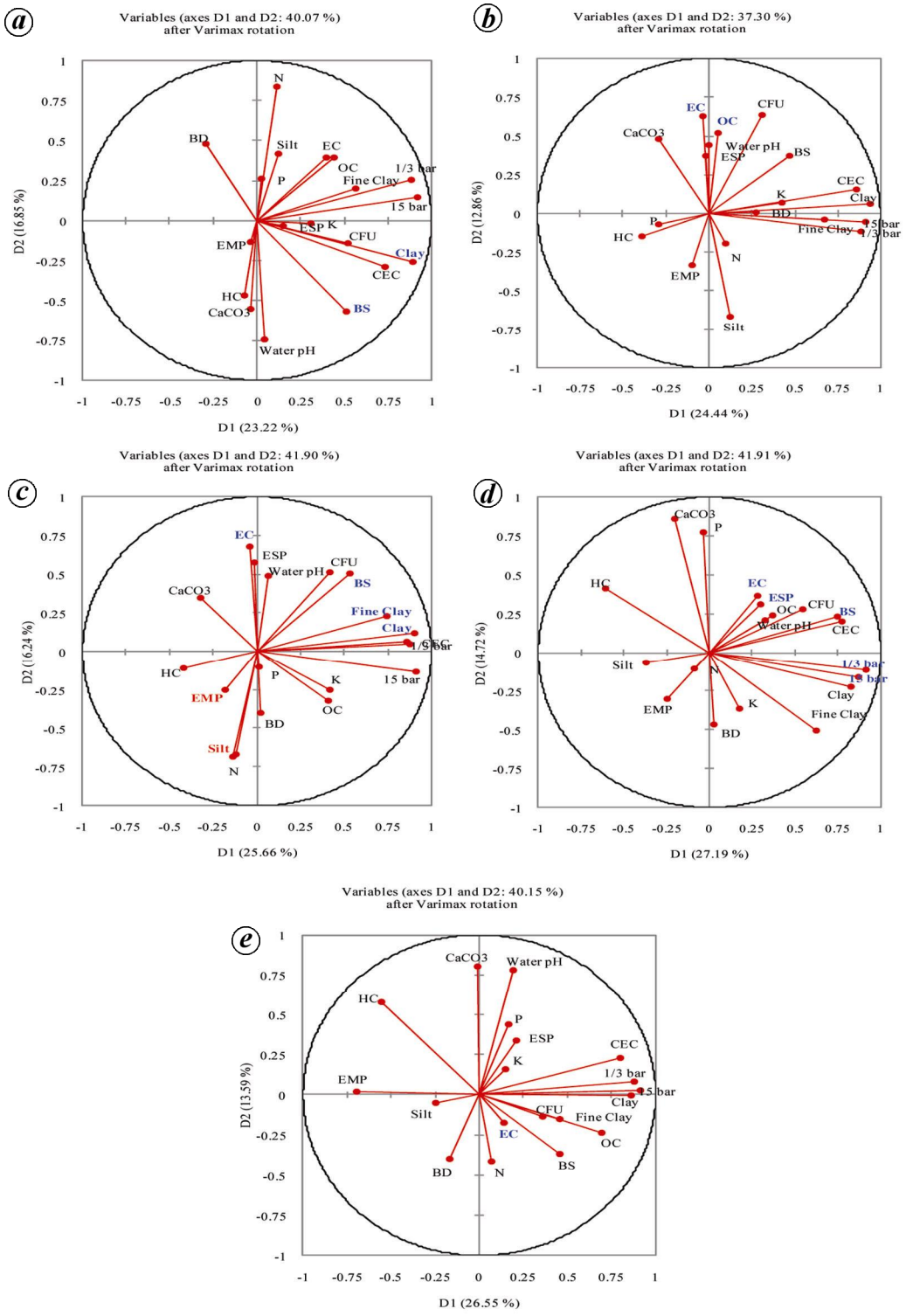

Figure 5. Principal component analysis: impact of physical and chemical variables on culturable microbial population at different soil depths. (***a***) 0–15 cm, (***b***) 15–30 cm, (***c***) 30–50 cm, (***d***) 50–100 cm, (***e***) 100–150 cm. Variables in blue and red colour indicate a significant ($P < 0.05$) positive and negative correlation respectively, with respect to the microbial population.

supplements helps in the accumulation of organic matter, which in turn has substantial incremental effect on the soil microbial biomass and its activities[10,67]. Positive correlation between biomass carbon and microbial population[66,68], and CEC[69] is also reported. Higher clay and silt content of the soil plays a major role in determining microbial biomass and promotes soil organic matter accumulation by aggregate formation and adsorption on

mineral surfaces[70,71], and greater soil extractable carbon, thus providing more carbon and nitrogen substrates for soil microbes[72]. Soil texture is also correlated with bacterial community composition[21,73]. Soils with high clay content are reported to stabilize soil organic carbon[74]. Hassink[75] has shown that the proportions of soil carbon and nitrogen in the biomass are higher in fine- than in coarse-textured soils. Soils containing more than 15% clay form aggregates along with the mineral particles (sand, silt and clay)[76]. Aggregate stabilization by extracellular metabolic products of colonies of bacteria and by root exudates has been demonstrated[77].

In our study, though microbial population has shown negative correlation with pH, significance could not be established. However, pH may represent the cumulative effects of many chemical attributes, including soil texture, hydraulic conductivity and nutrient status, which may have a significant impact on microbial communities. Soil pH is often correlated with bacterial community composition at multiple scales of geographic resolution[78,79]. Soil pH may impose a direct stress on bacterial cells, with certain pH levels selecting certain bacterial taxa over others[80,81]. Differences in soil pH can arise from many factors, including vegetation type, soil type and management regime[25]. Though BD shows negative correlation with microbial population in our study, significance could not be established. However, soil compaction reduces macroporosity[82] and total porosity, resulting in an increase of soil density and making root penetration more difficult. Since the restriction of the microbial community depends on the exudates for growth, the transformations of soil nutrients required by the crops would also be limited. Populations of bacteria, total fungi and biomass are significantly larger in uncompacted soil than in compacted soil[83,84]. Soils with excess magnesium are reported to cause loss of soil structure, resulting in reduced root respiration and production of toxic compounds in plants. Reduced soil air and insufficient calcium also result in the reduction of soil microbes and corresponding reduced breakdown of organic matter/nutrient availability to plants.

Conclusions

Many studies in the past have reported the distribution of microbial population in the soil, but the analyses do not directly associate microbial information with soil properties, even though such properties are being shown to have a greater influence on the bio-geographical patterns exhibited by soil microorganisms. In our study, we have shown that variability in edaphic factors across different bioclimates, cropping systems, land use and management practices along with soil depth can have a significant effect on culturable microbial population in different AESRs of BSR in India. The pooled analysis of data inclusive of bioclimates, cropping systems, land use, management practices, soil depth and edaphic factors has indicated that the microbial population is significantly and positively influenced by clay, fine clay, water content, electrical conductivity, organic carbon, cation exchange capacity and base saturation, whereas bulk density, hydraulic conductivity, pH, calcium carbonate and exchangeable magnesium percentage have a negative effect on microbial population. Our findings suggest that more detailed analyses of soil properties along with molecular-based studies will enable identification of microbial distribution in soils to reveal their community structure.

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