

Impact of floods and landslides on beneficial soil microbes and nutrients in selected high ranges of Kerala, India

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To ascertain the impacts of flood-affected and landslide-impacted soils on the microbial community and soil nutrient status, an assessment between disturbed and undisturbed soils was conducted. Without discernible differences between soils impacted by flooding and landslides, the total bacterial and fungal population had decreased in disturbed soils. The lack of organic carbon and copper in flood-affected soils profoundly impacted the bacterial population. The disturbed soils were found to have reduced organic carbon, nitrogen and micronutrients. The microbial isolates that persisted even in these degraded conditions may be considered potential bioagents for the restoration of disturbed soils.

Keywords: Floods, high-range areas, landslides, microbial community, soil nutrients.

CLIMATE change and climate-related disasters directly affect global food security, especially in developing countries¹. The structure of the soil is disturbed, and the availability of nutrients is diminished by floods and landslides². The restoration of vegetation and soil cover is directly influenced by the organic matter, nutrient content and physical properties of the soil³, which are the limiting factors in landslide areas⁴.

Microorganisms react to climatic disasters in different ways based on the type, number, length, severity of the disaster, as well as the functional and compositional features of the ecosystems and the degree of functional redundancy⁵. Microbial activities through nutrient cycling provide a supportive approach for pre- and post-disaster management strategies, such as increasing soil fertility, which is reduced during heavy rainfall. Hence, utilizing beneficial plant-microbe interactions might help in the survival of crops under extreme stress conditions¹.

Climatic changes disturb the microbial communities, and their interactions make certain populations adaptable to the conditions while others get suppressed⁶. Our knowledge of how climate change affects soil microbes and how the microbes control climate is limited, although soil microbes play a crucial role in controlling the dynamics of soil organic matter (SOM)⁷. The vast geographical variation of

terrestrial ecosystems in terms of climate, diversity of plants and structure, soil science, composition of soil microbial communities, and past evolution is expected to significantly impact soil microbes in different ecosystems⁸. According to Dutta⁹, microorganisms have been generally ignored in discussions regarding climate change, both in terms of their contribution and impact on microbial ecosystems. As ecosystems in natural settings are complex, their responses are unpredictable, and their processes are time-dependent, the effects of climate change on soil microbes will not exhibit a linear increase or decrease over longer ecological timeframes⁸. Plant ecosystem productivity can be restored by improving plant responses to the environment, for which rhizosphere understanding, prediction and control are fundamental. The resilience of the microbial community in comparison with unaffected areas is lacking. In this context, the analysis of soil microbiomes, SOM, along with soil nutritional status in the affected agricultural sites can shed light on the restoration of SOM and improve crop yield.

Since 2018, increased natural disasters have made a negative impact on the agricultural sector of Kerala, India, especially in the high-range areas. A study was undertaken on the impact of floods and landslides in the high ranges of Attapadi and Nelliampathy in Palakkad district, Kerala. The microbial population and nutrients in the disturbed and undisturbed soils of Attapadi and Nelliampathy were assessed. Soil samples from the flood-affected areas, landslide and undisturbed locations (locations which remained unaffected by floods and landslides) were analysed for their microbial population and compared with respect to major nutrients, micronutrients and heavy metals to determine the impact of climatic disasters on the microbial population and nutrient status, and to identify the predominant isolates that survived in disturbed soils to rejuvenate SOM.

Materials and methods

Location details

Flood-affected and landslide-impacted soil samples, along with those from undisturbed soils were collected from both Attapadi and Nelliampathy. The Attapadi block, located

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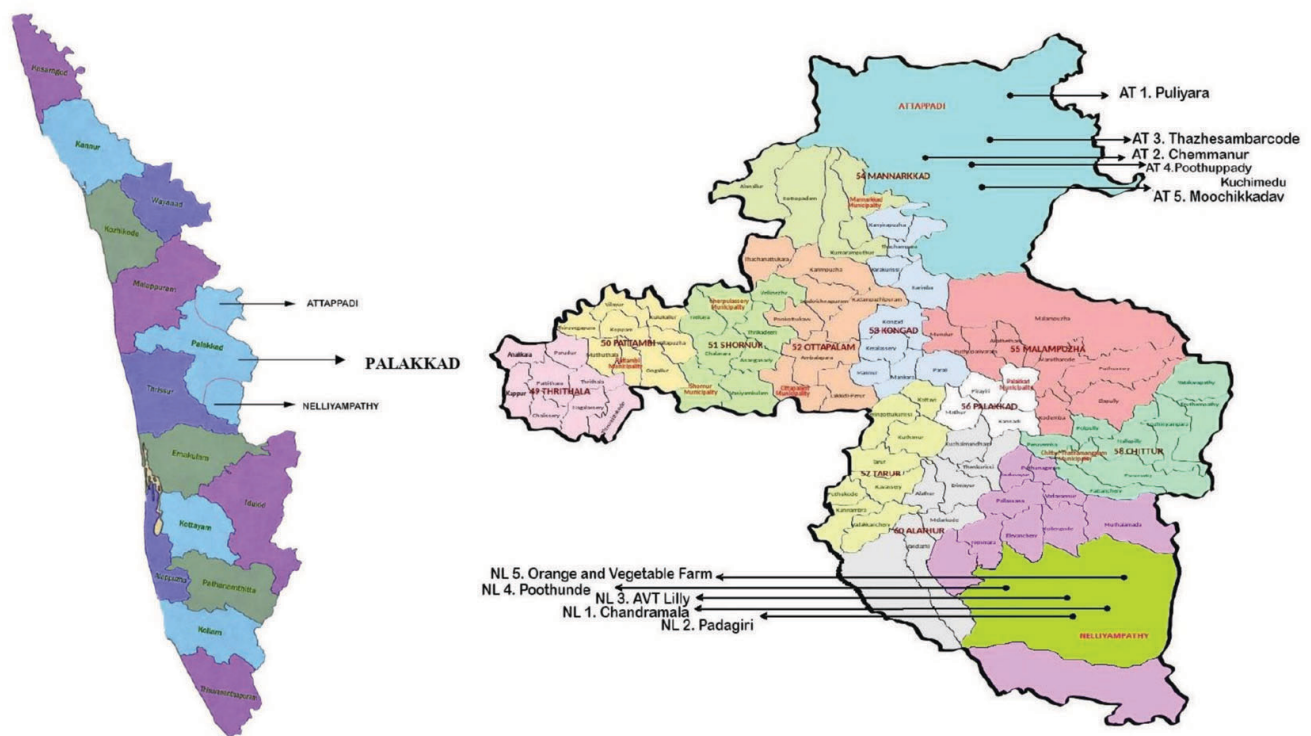


Figure 1. Map showing the locations of soil sample collection in Attappadi and Nellyampathy, Palakkad, Kerala, India.

in the Mannarkkad taluk of Palakkad district, Kerala, lies between the Nilgiri hill ranges in the north and Vellinkiri hill ranges in the south (1200 m amsl) (Figure 1). In Attappadi, 51,194 ha of agricultural land was damaged due to silting or washing out of top fertile soil due to water erosion, and 236,650 ha of crops was damaged, with maximum loss in pepper, cardamom, tea, coffee, coconut, arecanut, rubber, banana and paddy¹⁰. To evaluate and compare the flood-affected (FA) and landslide-impacted (LS) soils of Attappadi (11.071808, 76.571502), rhizosphere soil samples were collected in August 2020 (1–2 years after the disaster) from five different locations, viz. Attappadi Puliyara landslide (AT-1 LS and FA), Chemmanur (AT-2 FA), Thazhesambarcode (AT-3 FA), Pothumpady kuchimedu (AT-4 LS) and Muchikadavu (AT-5 FA) (Figure 1). Two landslide-impacted soil samples and four flood-affected soil samples were collected.

Nellyampathy is 56 km from Palakkad (467 m amsl) (Figure 1) which is famous for tea, coffee, cardamom and orange plantations. To assess the microbial population of disturbed and undisturbed soils of Nellyampathy (10.533180, 76.691730), rhizosphere soil samples were collected in October 2020 (1–2 years after the disaster) from five different locations, Chandramala (NL-1 LS), Padagiri (NL-2 LS), AVT Lilly (NL-3 LS), Poothunde (NL-4 LS) and Orange and Vegetable farm (NL-5 FA) (Figure 1). One soil sample from a flood-affected area and four samples from landslide-impacted areas were collected. Tea, pepper, orange and cardamon are the major cultivated crops in Nellyampathy.

There were five flood-affected soil samples, six landslide-impacted samples, and ten undisturbed (UD) samples for comparison.

Isolation of soil microflora

Bacteria were isolated on soil extract agar and fungi on Rose Bengal agar medium by serial dilution plate count method¹¹. The populations of bacteria and fungi were recorded, and the isolates with different morphotypes were purified and preserved for further studies.

Identification of predominant microflora

By employing Illumina 16SrRNA/ITS sequencing, the morphologically dominant isolate was identified. Using a sequencer kit (NucleoSpin Tissue Kit) and following the manufacturer's instructions, the genomic DNA of the most prevalent bacteria and fungus from FA and LS regions was isolated. Using 16SrRNA primers, the extracted bacterial DNA was amplified (16S-RS-F, forward primer CAGGCCTAACACATGCAAGTC and 16S-RS-R reverse primer GGGCGWGTGTACAAGGC). Using ITS primers (ITS-1F forward primer TCCGTAGGTGAACCTGCGG and ITS-4R reverse primer TCCTCCGCTTATTGATATGC), fungal DNA was amplified. A PCR thermal cycler was used to perform the PCR amplification (GeneAmp PCR System 9700, Applied Biosystems, USA). ExoSAP-IT-treated PCR

Table 1. Microbial population in the flood-affected and landslide-impacted soils of Attapadi and Nelliampathy, Palakkad, Kerala, India

Sample	Landslide-impacted soil				Sample	Flood-affected soil			
	Bacteria		Fungi			Bacteria		Fungi	
	UD	LS	UD	LS		UD	FA	UD	FA
AT-1	40.33×10^4	9×10^4	0.33×10^3	0.57×10^3	AT-1	40.33×10^4	5.37×10^4	0.33×10^3	0.43×10^3
AT-4	156.7×10^4	36.7×10^4	11×10^3	1.33×10^3	AT-2	47.33×10^4	10.67×10^4	0.16×10^3	1.37×10^3
NL-1	110×10^4	13.3×10^4	5×10^3	6.33×10^3	AT-3	160×10^4	90×10^4	13×10^3	11×10^3
NL-2	106.7×10^4	53.3×10^4	16×10^3	15.67×10^3	AT-5	176.7×10^4	70×10^4	8.33×10^3	5×10^3
NL-3	100×10^4	40×10^4	16.33×10^3	10.33×10^3	NL-5	76.7×10^4	430×10^4	19×10^3	18×10^3
NL-4	256.7×10^4	96.7×10^4	6×10^3	5.67×10^3					
Microbial isolates	19	14	29	23		20	22	21	22
<i>F</i> -value	7.791	14.718	13.959	13.572	<i>F</i> -value	29.286	516.148	45.055	53.622

UD, Undisturbed; LS, Landslide-impacted; FA, Flood-affected; AT, Attapadi; NL, Nelliampathy. *F*-values at $\alpha = 0.005$.

products were sequenced using the BigDye Terminator v3.1 Cycle sequencing kit (Applied Biosystems, USA) in a PCR thermal cycler (GeneAmp PCR System 9700, Applied Biosystems), in accordance with the manufacturer's instructions. Sequence Scanner Software v1 was used to evaluate the sequence quality (Applied Biosystems). Using Geneious Pro v5.1, the obtained sequences were edited and sequence alignment was done¹².

Physico-chemical analysis of soil parameters

All 21 soil samples (five FA, six LS and ten UD) were air-dried and sieved (2 mm sieve) for physical and chemical analysis. pH was determined using a pH meter¹³; moisture content in the soil samples was analysed using a moisture analyser, and organic carbon was determined by the modified Walkley and Black¹⁴ digestion method. Kjeldahl digestion method was used to assess nitrogen content in the soil. Phosphorus was estimated by the Bray and Kurtz¹⁵ method for acidic soils and the Olsen *et al.*¹⁶ method for neutral to alkaline soils, followed by the reduced molybdenum-blue colour method. Available sulphur was estimated using the CaCl₂-extractable method of Williams and Steinbergs¹⁷, and boron was estimated using the azomethine-H method¹⁸. Soil texture was determined by the hydrometer method¹⁹. Potassium and sodium were analysed using the ammonium acetate method in a flame photometer (ELICO CL378, India). Neutral normal ammonium acetate extractable calcium and magnesium and diethylenetriamine pentaacetate extractable micronutrients such as copper, zinc and manganese were analysed using an atomic absorption spectrophotometer (VARIAN AA 240, USA).

Results and discussion

Microbial populations in disturbed and undisturbed soils

A total of 11 rhizosphere soils, which included six landslide-impacted locations (AT-1, AT-4, NL-1, NL-2, NL-3, NL-4)

and five flood-affected locations (AT-1, AT-2, AT-3, AT-5, NL-5) from Attapadi and Nelliampathy were analysed separately in comparison with the ten undisturbed soil samples.

Among the 11 locations tested, fewer bacteria were detected in ten places (five FA and five LS), while fewer fungi were found in five locations (three FA and two LS) (Table 1). In flood-affected areas, the bacteria : fungi ratio had reduced²⁰, but specific studies on the individual impacts of floods and landslides on the microbial population are lacking. It is widely known that soil microorganisms play an important role in the productivity and health of their hosts²¹. A low microbial population combined with other factors could reduce the yield and render the soil unfit for cultivation. It is evident from the present study that floods, landslides and other climatic disasters disturb the microbial population. No significant differences were noted between the flood-affected and landslide-impacted soil samples with regard to bacterial and fungal populations.

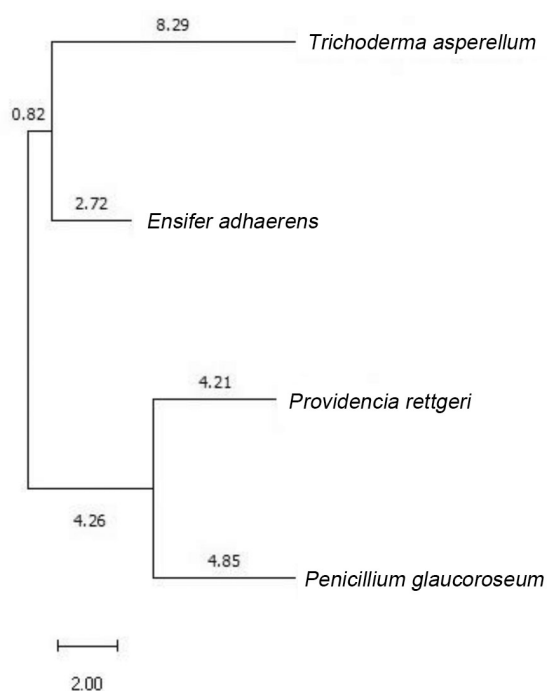
The microorganisms showed variation in their morphotypes. A total of 164 microbial isolates were obtained (Table 1). The highest number of morphotypes was obtained in the case of fungi (94), followed by bacteria (70). Data showed that the population of microbes in flood-affected, landslide-impacted and undisturbed soils of Attapadi and Nelliampathy were significantly different (Table 1).

Identification of predominant microflora and phylogenetic tree based on distance between species

The predominant bacterial and fungal isolates from the flood-affected and landslide-impacted soils were identified based on 16SrRNA/ITS sequencing. The most common bacterial strain found in samples from flood-affected areas was *Providencia rettgeri* (accession number: OP435589), while *Ensifer adhaerens* (accession number: OP435587), was found in landslide-impacted soils. Both isolates are known to benefit plants. Jiang *et al.*²² reported that the halotolerant bacteria, *P. rettgeri* increases the availability of nutrients (specifically phosphorus) to the plants. *E. adhaerens* is a

Table 2. Moisture, pH and organic carbon in the flood-affected and landslide-impacted soils of Attapadi and Nelliampathy

Sample	Landslide-impacted soil					
	Moisture content (%)		pH		Organic carbon (%)	
	UD	LS	UD	LS	UD	LS
AT-1	22.4	19.6	6.05 (moderately acidic)	6.39 (slightly acidic)	1.09 (moderate)	1.09 (moderate)
AT-4	22.2	23.2	6.81 (neutral)	6.57 (slightly acidic)	1.61 (high)	0.98 (moderate)
NL-1	24.4	26.8	5.62 (moderately acidic)	5.85 (moderately acidic)	1.64 (high)	0.41 (low)
NL-2	19.4	26	5.67 (moderately acidic)	5.44 (strongly acidic)	1.77 (high)	1.23 (moderate)
NL-3	17.8	14.8	6.7 (neutral)	6.01 (moderately acidic)	1.77 (high)	0.41 (low)
NL-4	20.4	23.2	5.87 (moderately acidic)	5.98 (moderately acidic)	2.67 (high)	0.55 (low)
	Flood-affected soil					
	UD	FA	UD	FA	UD	FA
	AT-1	22.4	25.4	6.05 (moderately acidic)	6 (moderately acidic)	1.09 (moderate)
AT-2	20.2	19	6.55 (slightly acidic)	6.12 (slightly acidic)	1.36 (moderate)	0.55 (low)
AT-3	11.4	12.4	7.81 (slightly alkaline)	6.82 (neutral)	0.27 (low)	0.08 (low)
AT-5	10.8	14.4	6.75 (neutral)	6.83 (neutral)	0.95 (moderate)	0.76 (moderate)
NL-5	15.6	13.8	6.66 (neutral)	6.4 (slightly acidic)	1.91 (high)	2.18 (high)

**Figure 2.** Evolution history of the four isolates based on neighbor-joining method.

soil-dwelling bacteria belonging to Alphaproteobacteria in the Rhizobiales family²³. The predominant fungal isolate obtained from flood-affected soils was *Penicillium glaucoroseum* (accession number: OP459183) and from landslide-impacted soils it was *Trichoderma asperellum* (accession number: OP459182). *Trichoderma* spp. has demonstrated effectiveness in plant disease, plant development, decomposition and bioremediation. Additionally, synthesising secondary metabolites in agroecosystems enables them to be used in environmental-friendly agricultural techniques²⁴. The genus *Penicillium* is found worldwide,

and many species are significant organic material decomposers²⁵.

The evolution history of the four isolates was constructed using the neighbour-joining method (Figure 2)²⁶. The branch lengths (next to the branches) on the tree are shown to scale in the figure and have the same units as the evolutionary distances used to estimate the phylogenetic tree. The evolutionary distances, which are measured as base substitutions per site, were calculated using the maximum composite likelihood method²⁷. For each sequence pair, all the unclear locations were eliminated (pairwise deletion option). The final dataset contained 851 locations in total. Evolutionary analyses were conducted using MEGA11 (ref. 28). The two isolates *P. glaucoroseum* and *P. rettgeri* from the flood-affected locations showed maximum similarity, while *T. asperellum* and *E. adhaerens* obtained from the landslide-impacted locations also showed similarity.

Correlation between microbial population and soil physico-chemical parameters in the flood affected and landslide-impacted soils

Soil parameters, viz. pH, moisture content, major and micro-nutrients, and soil texture were assessed. The populations of bacteria and fungi in the flood-affected and landslide-impacted soils were correlated separately with the soil nutritional parameters using the Pearson correlation matrix and OPSTAT software.

The same pH range was found in five locations, which included three flood-affected (AT-1: moderately acidic, AT-2: slightly acidic and AT-5: neutral) and two landslide-impacted locations (NL-1: moderately acidic and NL-4: moderately acidic), whereas the other six locations had a different pH range (Table 2). The microbial population is affected by soil pH, which is an important soil property like organic carbon. In the present study, pH negatively influenced

Table 3. Major nutrients in the flood-affected and landslide-impacted soils of Attapadi and Nelliampathy

Sample	Landslide-impacted soil											
	Nitrogen (kg/h)		Sulphur (kg/h)		Phosphorus (kg/h)		Magnesium (kg/h)		Calcium (kg/h)		Potassium (kg/h)	
	UD	LS	UD	LS	UD	LS	UD	LS	UD	LS	UD	LS
AT-1	313.6 (moderate)	313.6 (moderate)	38.93 (high)	24.46 (high)	8.67 (low)	14.9 (moderate)	343.84 (high)	207.73 (high)	782.04 (high)	698.04 (high)	239.68 (moderate)	443.52 (high)
AT-4	313.6 (moderate)	250.88 (low)	11.63 (high)	6.61 (moderate)	132.99 (high)	32.93 (high)	662.37 (high)	768.85 (high)	1907.64 (high)	1839.04 (high)	568.96 (high)	529.76 (high)
NL-1	188.16 (low)	137.98 (low)	19.5 (high)	13.2 (high)	231 (high)	154.6 (high)	159.99 (high)	63.28 (low)	839.72 (high)	102.2 (low)	498.4 (high)	87.36 (low)
NL-2	313.6 (moderate)	326.14 (moderate)	52.2 (high)	15.9 (high)	144.6 (high)	24.37 (moderate)	254.8 (high)	88.23 (low)	566.44 (high)	123.2 (low)	499.52 (high)	362.88 (high)
NL-3	351.23 (moderate)	263.42 (low)	18.1 (high)	7.41 (moderate)	62.34 (high)	119.4 (high)	221.59 (high)	46.15 (low)	1156.12 (high)	122.92 (low)	740.32 (high)	109.76 (low)
NL-4	288.51 (moderate)	250.88 (low)	7.68 (moderate)	4.61 (low)	194.1 (high)	75.24 (high)	287.98 (high)	186.62 (high)	1163.96 (high)	479.36 (high)	393.12 (high)	228.48 (moderate)
Sample	Flood-affected soil											
	UD		FA		UD		FA		UD		FA	
	UD	FA	UD	FA	UD	FA	UD	FA	UD	FA	UD	FA
AT-1	313.6 (moderate)	250.88 (low)	38.93 (high)	37.09 (high)	8.67 (low)	19.06 (moderate)	343.84 (high)	264.07 (high)	782.04 (high)	729.4 (high)	239.68 (moderate)	215.04 (moderate)
AT-2	313.6 (moderate)	313.6 (moderate)	41.6 (high)	30.37 (high)	112.2 (high)	202.09 (high)	325.39 (high)	315.17 (high)	1216.04 (high)	983.92 (high)	678.72 (high)	375.2 (high)
AT-3	188.16 (low)	188.16 (low)	10.08 (moderate)	8.04 (moderate)	231.39 (high)	95.45 (high)	203.48 (high)	263.4 (high)	3332.84 (high)	1424.36 (high)	313.6 (high)	127.68 (moderate)
AT-5	250.88 (low)	213.25 (moderate)	8.04 (moderate)	7.86 (moderate)	175.03 (high)	105.71 (high)	640.7 (high)	474.07 (high)	1741.04 (high)	1658.72 (high)	769.44 (high)	776.16 (high)
NL-5	326.14 (moderate)	275.97 (low)	13 (high)	2.93 (low)	308.3 (high)	271.5 (high)	152.91 (high)	111.5 (moderate)	758.24 (high)	459.76 (high)	684.32 (high)	428.96 (high)

the fungal population in the landslide-impacted soil samples ($r = -0.909^*$ at $P < 0.05$). The landslide-impacted soil samples had a pH range from 5.44 to 6.57 (Table 2), which is considered suitable for fungi. Considering a pH range 4–8.3, Rousk *et al.*²⁹ concluded that fungi are less affected by the variation in soil pH because of wider optimal pH ranges. However, the present study gives contradictory results for landslide-impacted soil samples, with pH range above 6.0 resulting in a reduced fungal population. However, the results from the present study that $\text{pH} > 6$ is unsuitable for fungi cannot be considered conclusive as other samples with higher pH showed higher fungal population.

Moisture percentage ranged between 10.8 and 26.8, which showed variations in the disturbed soil samples when compared with undisturbed soil samples of Attapadi and Nelliampathy (Table 2). Correlation studies showed that moisture negatively affected bacterial growth in undisturbed soils ($r = -0.959^{**}$ at $P < 0.05$). Moisture percentage in these locations varied from 10.8 to 22.4. Excessive moisture is known to reduce the microbial biomass²⁰. However, this correlation was contradicted by higher bacterial population in other soils with moisture contents greater than 22.4%.

Organic carbon percentage was lower in six disturbed samples (three landslide-impacted samples: NL-1, NL-3 and NL-4 and three flood-affected samples: AT-1, AT-2 and AT-3), whereas only one undisturbed soil sample (AT-3) showed low organic carbon content (Table 2). The correlation data showed that organic carbon contents had a pos-

itive impact on the bacterial population ($r = 0.926^{**}$ at $P < 0.05$ for the undisturbed soils). Though there was a positive effect of flood on the bacterial population ($r = 0.884^*$ at $P < 0.05$), landslides were found to not elucidate such an impact on the studied microbial population. The flood-affected soil in Nelliampathy (NL-5) was the only location which had higher bacterial population than the undisturbed soil samples and this can be attributed to the comparatively higher organic carbon content in the former soil (2.18%) than the latter, which in turn justifies the correlation between the soil parameter and bacterial population. The abundance of soil bacterial phyla was positively correlated with the soil organic content³⁰.

The macronutrients in the soil were assessed for nitrogen, sulphur, phosphorus, magnesium, calcium and potassium (Table 3). Four landslide-impacted soil samples (AT-4, NL-1, NL-3 and NL-4) and four flood-affected samples (AT-1, AT-3, AT-5 and NL-5) had low nitrogen content. Whereas one landslide-impacted (NL-4) and one flood-affected sample (NL-5) had low sulphur content. All the other disturbed soils had medium to high sulphur. No significant correlation was observed for both the nutrients and the microbial population.

Phosphorus content was moderate to high for all the disturbed soil samples. The fungal population from the undisturbed soils which was compared with flood affected soils showed a positive correlation ($r = 0.944^*$ at $P < 0.05$) with phosphorus. Undisturbed soils which was compared

Table 4. Micronutrients and texture of flood-affected and landslide-impacted soils of Attapadi and Nelliampathy

Sample	Landslide-impacted soil											
	Copper (kg/h)		Boron (kg/h)		Manganese (kg/h)		Zinc (kg/h)		USDA texture			
	UD	LS	UD	LS	UD	LS	UD	LS	UD	LS		
AT-1	14.34 (moderate)	2.73 (moderate)	1.32 (moderate)	1.28 (moderate)	10.37 (moderate)	10.04 (moderate)	2.05 (moderate)	4.77 (moderate)	Sandy clay loam	Sandy clay loam		
AT-4	49.19 (high)	2.912 (moderate)	0.99 (moderate)	0.76 (moderate)	11.76 (moderate)	16.64 (moderate)	20.04 (moderate)	4.52 (moderate)	Sandy loam	Sandy loam		
NL-1	20.36 (high)	0.96 (low)	0.58 (moderate)	0.58 (moderate)	13.96 (moderate)	4.32 (moderate)	10.45 (moderate)	2.17 (moderate)	Sandy loam	Sandy loam		
NL-2	43.82 (high)	11.31 (moderate)	0.65 (moderate)	0.72 (moderate)	14.67 (moderate)	16.76 (moderate)	24.16 (moderate)	3.52 (moderate)	Sandy loam	Sandy clay loam		
NL-3	32.79 (high)	1.05 (low)	0.67 (moderate)	0.56 (moderate)	12.54 (moderate)	5.13 (moderate)	25.19 (moderate)	0.95 (low)	Sandy loam	Sandy loam		
NL-4	5.06 (moderate)	0.99 (low)	0.69 (moderate)	0.6 (moderate)	21.12 (moderate)	4.15 (moderate)	17.45 (moderate)	1.61 (moderate)	Sandy loam	Sandy loam		
Sample	Flood-affected soil											
	UD		FA		UD		FA		UD		FA	
	UD	FA	UD	FA	UD	FA	UD	FA	UD	FA	UD	FA
AT-1	14.34 (moderate)	25.6 (high)	1.32 (moderate)	1.32 (moderate)	10.37 (moderate)	13.19 (moderate)	2.05 (moderate)	3.26 (moderate)	Sandy clay loam	Sandy clay loam		
AT-2	11.38 (moderate)	18.95 (moderate)	1.46 (moderate)	1.25 (moderate)	11.18 (moderate)	10.22 (moderate)	12.93 (moderate)	3.95 (moderate)	Sandy clay loam	Sandy clay loam		
AT-3	2.94 (moderate)	7.19 (moderate)	0.58 (moderate)	0.58 (moderate)	0.76 (low)	9.32 (moderate)	3.21 (moderate)	3.84 (moderate)	Sandy loam	Sandy clay loam		
AT-5	6.79 (moderate)	7.01 (moderate)	0.63 (moderate)	0.83 (moderate)	16.8 (moderate)	13.28 (moderate)	5.89 (moderate)	19.03 (moderate)	Sandy clay loam	Sandy clay loam		
NL-5	15.21 (moderate)	108.82 (high)	0.67 (moderate)	0.72 (moderate)	10.08 (moderate)	7.19 (moderate)	4.44 (moderate)	4.77 (moderate)	Sandy clay loam	Sandy clay loam		

with flood affected soils (four out of five) had high phosphorus and substantial fungal count. The result indicates that the fungi obtained might be efficient P-solubilizers. The population and phosphate-solubilizing fungi, and the levels of total phosphorus in the soil were significantly correlated. Kucey³¹ also noted that fungi outperformed bacteria as P-solubilizers.

Magnesium and calcium were almost similar in all the disturbed and undisturbed soil samples. Both the nutrients were higher in the flood-affected soils, whereas three landslide-impacted soils (NL-1, NL-2 and NL-3) had low magnesium and calcium contents. Potassium was low in two landslide samples (NL-1 and NL-3), whereas all other samples had moderate to high potassium content. The microbial population affected by floods and landslides did not significantly correlate with these nutrients. The micronutrients analysed included copper, boron, manganese and zinc (Table 4). Three landslide samples (NL-1, NL-3 and NL-4) had a low copper content, whereas the others had moderate to high copper content. Copper and the bacterial population affected by floods had a positive correlation ($r = 0.925^*$ at $P < 0.05$). As copper functions as an electron transporter and redox catalyst in a variety of cuproenzymes, it is a crucial micronutrient for bacterial growth³². All the landslide-impacted and flood-affected soil samples showed moderate boron content (above 0.5 kg/ha).

Manganese was deficient (0.76 kg/ha) only in one undisturbed location (AT-3), and all other soil samples had ade-

quate manganese content. The correlation of the nutrient with the undisturbed bacterial population ($r = 0.868^*$ at $P < 0.05$) is thus justified. Except for one landslide-impacted soil sample (NL-3; low), all other samples showed optimum zinc content. Zinc served as a positively influencing nutrient for fungal population in undisturbed soils (Table 5). Zinc was moderately higher (relative to the flood-affected and landslide-impacted soils) in the undisturbed soils. Thus, the correlation for the undisturbed population indicates that small amounts of the element stimulate fungus development.

Sand clay loam and sandy loam were identified as the soil types at all the studied sites – flood-affected, landslide-impacted and undisturbed areas (Table 4). The two soil forms (sandy clay loam and sandy loam) did not affect the microbial community in this study as both are generally considered suitable for cultivation. Loam-textured soils are often considered ideal for agriculture because they include practically equal amounts of sand, silt and clay, which the farmers may use to grow crops³³.

Soil nutritional aspects control microbial distribution in an environment. Soil physical analysis and individual nutrient parameters analysed in the present study show a valid correlation only for a few nutrients, such as organic carbon percentage and copper on bacteria. Even though a collective correlation of the major and minor nutrients may be the rationale for the variation of microbial distribution in the disturbed and undisturbed samples, identifying such a

Table 5. Pearson correlation matrix—correlation of soil nutrients with the microbial population

Parameter	Bacteria				Fungi			
	Landslide-impacted soil		Flood-affected soil		Landslide-impacted soil		Flood-affected soil	
	UD	LS	UD	FA	UD	LS	UD	FA
Moisture	-0.119 ^{NS}	0.086 ^{NS}	-0.959*	-0.508 ^{NS}	-0.739 ^{NS}	0.119 ^{NS}	-0.659 ^{NS}	-0.736 ^{NS}
pH	-0.021 ^{NS}	-0.296 ^{NS}	0.716 ^{NS}	0.155 ^{NS}	0.352 ^{NS}	-0.909*	0.534 ^{NS}	0.441 ^{NS}
Organic carbon (%)	0.926*	-0.128 ^{NS}	-0.609 ^{NS}	0.884*	0.206 ^{NS}	0.009 ^{NS}	0.140 ^{NS}	0.627 ^{NS}
Nitrogen	-0.097 ^{NS}	0.190 ^{NS}	-0.842 ^{NS}	0.134 ^{NS}	0.481 ^{NS}	0.200 ^{NS}	-0.252 ^{NS}	-0.172 ^{NS}
Sulphur	-0.654 ^{NS}	-0.649 ^{NS}	-0.858 ^{NS}	-0.682 ^{NS}	0.119 ^{NS}	-0.106 ^{NS}	-0.830 ^{NS}	-0.842 ^{NS}
Phosphorus	0.624 ^{NS}	-0.082 ^{NS}	0.462 ^{NS}	0.731 ^{NS}	0.026 ^{NS}	0.168 ^{NS}	0.944*	0.615 ^{NS}
Magnesium	0.164 ^{NS}	-0.022 ^{NS}	0.407 ^{NS}	-0.692 ^{NS}	0.006 ^{NS}	-0.591 ^{NS}	-0.412 ^{NS}	-0.630 ^{NS}
Calcium	0.430 ^{NS}	-0.062 ^{NS}	0.746 ^{NS}	-0.521 ^{NS}	0.127 ^{NS}	-0.680 ^{NS}	0.252 ^{NS}	-0.259 ^{NS}
Potassium	0.071 ^{NS}	-0.094 ^{NS}	0.182 ^{NS}	0.126 ^{NS}	0.831*	-0.407 ^{NS}	0.221 ^{NS}	-0.021 ^{NS}
Copper	-0.235 ^{NS}	0.089 ^{NS}	-0.845 ^{NS}	0.925*	0.731 ^{NS}	0.636 ^{NS}	-0.137 ^{NS}	0.723 ^{NS}
Boron	-0.419 ^{NS}	-0.482 ^{NS}	-0.825 ^{NS}	-0.558 ^{NS}	-0.539 ^{NS}	-0.524 ^{NS}	-0.860 ^{NS}	-0.818 ^{NS}
Manganese	0.868*	-0.114 ^{NS}	-0.081 ^{NS}	-0.764 ^{NS}	-0.002 ^{NS}	0.089 ^{NS}	-0.292 ^{NS}	-0.820 ^{NS}
Zinc	0.369 ^{NS}	-0.433 ^{NS}	-0.245 ^{NS}	-0.092 ^{NS}	0.950*	-0.447 ^{NS}	-0.393 ^{NS}	-0.098 ^{NS}

NS, Not significant. All values at $P < 0.05$. *Level of significance.

specific correlation is essential to finding solutions for soil microbial deficiencies. Xue *et al.*³⁴ reported that microbial distribution in the soil is contributed mostly by the soil properties rather than any other environmental factors. The variation in population signals the compliance of certain microbes to such environmental disturbances. Shade *et al.*⁵ reported that the microbiomes in some systems may not be resilient to stress and that they may not adapt to the new environment even after years of the stress event. The present study also classifies that there are factors which limit the ability of microbial populations to adapt to their surroundings.

Conclusion

By comparing the microbiological and nutritional components of the flood-affected and landslide-impacted soils with the undisturbed soils, which are essential for recovering agricultural productivity, the impacts of floods and landslides have been identified. Significant nutrients that contribute to soil fertility were found to be diminished in the affected soils, although the texture of the soil had not changed. The predominant bacteria (*P. rettgeri* and *E. adhaerens*) and fungi (*T. asperellum* and *P. glaucoroseum*) that proliferated and survived in the soils in spite of floods and landslides could be potential bioagents to rejuvenate SOM and can be used as a consortium to rejuvenate soil fertility.

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