International Journal of Contemporary Academic Research
*Volume 6 Number 2, April-June,. 2025. Doi:**10.5281/zenodo.15259604;** ISSN: 2782-8476*

Microbial Population Structure in the Rhizosphere of Maize (*Zea mays* L), and Okra [*Abelmoschus esculentus* (L.) Moench] at Various Stages of Plant Development.

Nengi-Benwari, A.O.[1] & Akpan, E.U[1].

[1]Department of Crop and Soil Science,
Faculty of Agriculture, University of Port Harcourt, Rivers State, Nigeria.
Corresponding Author's Email: anitabenwari@yahoo.com

Abstract

This study investigated microbial population structure in the rhizosphere of maize and okra at different stages of plant development. The study was conducted at faculty of Agriculture Teaching and Research Farm, University of Port Harcourt, Rivers State, Nigeria. Seeds of maize and okra were purchased and planted, soil samples were collected and analyzed before planting and at different stages of plant development, bacterial and fungal count and isolation, and extraction of plant parasitic nematodes were done using standard methods. Data generated was subjected to analysis of variance (ANOVA) and the mean difference was separated using least significant difference at 5%. Results showed highest occurrence as follows: *Bacillus spp* (54%) in the rhizosphere of maize and okra during seedling and maturity stages respectively, *Staphylococcus spp* (38%) in the rhizosphere of maize during flowering stage, *Streptococcus spp* (18%) in the rhizosphere of okra during flowering stage, Lactobacillus (12%) in the rhizosphere of maize during flowering stage; *Rhizopus spp* (63%) in the rhizosphere of okra during flowering stage, *Aspergillus spp* (41%) in the rhizosphere of maize during seedling stage, *Yeast spp* (15%) in the rhizosphere of maize during seedling stage, *Fusarium spp* (30%) in the rhizosphere of okra during maturity stage, and *Mucor spp* occurrence (7%) in the rhizosphere of maize during flowering stage; *Meloidogyne spp* (17%) in the rhizosphere of okra during flowering stage, *Pratylenchus spp* (41%) in the rhizosphere of maize during seedling stage, *Helicotylenchus spp* (67%) in the rhizosphere of maize during flowering stage, and *Tylenchus spp* (33%) in the rhizosphere of maize during maturity stage. The study concluded that there were variations in microbial communities in response to plant growth and development.

Keywords: Population Structure, Rhizosphere, Maize, Okra, Seedling Stage, Fruiting Stage

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important crops in the world (Hou *et al*., 2020), it is a major source of food, animal feed, and fuel and is grown in many nations worldwide (Chebotar *et al*., 2023). Maize yield is affected by applied hybrid and fertilization, and the rhizosphere of maize has been reported to harbor an array of microorganisms (Bojtor *et al*., 2021; Mousavi *et al*., 2021).

Okra (*Abelmoschus esculentus* [L.] Moench) is a common annual vegetable crop that is grown in tropical and subtropical regions worldwide (Meena *et al*., 2017). The fibrous fruits or pods that contain spherical white seeds are highly prized due to their frequent use in soups, salads, and as a spice when dried and ground into powder (Roslan *et al*., 2022). Also, because of its high vitamin, mineral, and antioxidant content, okra has been rated as a very nutritious vegetable, and it is commonly grown in economically disadvantaged areas of Asia and Africa and can promote food security during periods of environmental change (Perveen *et al*., 2023). In addition to vitamins, minerals, and plant proteins, fresh okra fruit is a good source of dietary fibre, and the mucilage of okra, which has a protein and edible oil content of around 20%, is used as medication (Agregán *et al*., 2022). Additionally, minerals including pyridoxine, folates, calcium, iron, and phosphorus, as well as vitamins C, B6, and K, support the maintenance of physiological bodily functions (Petropoulos *et al*., 2018). Abiotic stressors, environmental factors, infections, and nutrient losses all significantly reduce okra output (Saima *et al*., 2022). Poor okra growth and yield are made worse by low soil fertility or an improper fertilization approach (Roslan *et al*., 2022). For the top 10 okra-producing nations, such as Cameroon, Nigeria, and Iraq, which are considered low yielders (<6 t/ha) in comparison to India (12.3 t/ha), this is especially concerning (Food and Agriculture Organization [FAO], 2022).

The nutrient-rich, extremely malleable soil layer that envelops the plant root is called the rhizosphere, and a rich and varied fauna, including microorganisms (microbiomes), can be found in this microzone (Roslan *et al*., 2022). According to Singh and Godwin (2022), plant microbiomes are made up of a variety of microorganisms that can be friendly, neutral, or harmful, such as bacteria, fungi, oomycetes, algae, protozoa, nematodes, and viruses; these

beneficial microbial communities support the growth, health, and productivity of plants (Brader *et al*., 2017; Lemanceau *et al*., 2017). For example, root endophytic bacteria encourage maize development in cold environments (Beirinckx *et al*., 2020), while the root bacterial population improves the growth and health of *Arabidopsis thaliana* plants cultivated in greenhouses (Duran *et al*., 2018). Also, by altering the expression of defense genes, the endophyte *Metarhizium robertsii* suppresses insect proliferation and promotes plant growth, hence maintaining a favorable connection with maize (Niu *et al*., 2017; Ahmad *et al*., 2020). The microbiome is greatly impacted by abiotic factors, including soil pH, soil type, root exudates, soluble dissolved organic matter, temperature, UV radiation, moisture, field location, plant age, pathogens, agricultural methods, and plant genetics (Correa-Galeote *et al*., 2018; Singh and Godwin, 2022). All of the aforementioned factors have the potential to alter plant microbiome, which could affect plant productivity and health (Singh and Godwin, 2022).

Given the aforementioned findings, our aim was to investigate microbial population structure in the rhizosphere of maize and okra at different stages of plant development. This is to add to existing literature, and provide more basis for the use of maize and okra as intercrops to increase soil microbial biomass which aids in organic matter decomposition, thereby improving soil fertility.

Materials and Methods

Study Area

The study was conducted at faculty of Agriculture Teaching and Research Farm, University of Port Harcourt, Rivers State, Nigeria between May and September 2024. Port Harcourt is found in the subequatorial region of Nigeria. Port Harcourt lies between latitude 4^0,07" and 5^05^0N and longitude 60^0,56'04" and 7^03'20"E on an elevation of 18m above sea level. The mean annual rainfall ranges from about 3000-4500mm (FAO, 1984) with a bimodal pattern, starting in March and ending in November with peaks in June and September and short period of dry spell in August usually known as August break (Eludoyin et al., 2015).

Experimental Layout

An experimental area of 20m x 20m was used to carry out the study. The experimental area was manually cleared and the layout was marked using tape, pegs, and ropes. Beds of 4m x 4m were raised on each of the plot with a 1m allay way. Randomized Complete Block Design (RCBD) with five (5) replications was also adopted.

Source of Planting Materials and Planting

The seeds of maize, and okra, were purchased from Aluu community local market, Port Harcourt, Rivers State, Nigeria. Maize and okra seeds were planted directly on the Field at a depth of 0.5m.

Soil Sampling

Soil samples were collected using a soil auger at a depth of 0-20cm before planting. Rhizosphere soil samples were collected from two plant stands in each plot, by carefully uprooting and shaking the soil adhering to the roots into a labeled polybag at each growth stages. The collected soil samples from the two plant stands per plot were bulked into a composite sample for microbial analysis and physiochemical analysis. Samples were collected from each treatment with 3 replicates. A total of 12 samples were collected at each sampling interval. They were placed into well labeled poly bags and then transferred to laboratory for analysis. Cylindrical metal cores of 6cm were used to obtain undisturbed soil samples for physical analysis.

Sample Collection for Nematode

The roots and soil at the rhizosphere were randomly collected from two plants per plot and were bulked into a composite sample; this was repeated at the three (3) selected growth stages (seedling, flowering, and maturity).

Soil samples were collected from two plant stands in each plot using at a depth of 0-20cm with a hand trowel in the rhizosphere of each plant at the different growth stages. The collected soil samples from the two plant stands per plot were bulked into a composite sample. The samples were properly labeled in polythene bags with the crop type, replicate and the growth stage at which the sample was collected. A total of 25 soil samples were collected at each growth stage.

Roots of each crop were collected from the same plant stand from which the soils samples were collected. The roots of the plants were removed using knife after the soil had been removed to expose the roots. The roots were also bulked

into composite samples and were properly labeled in polythene bags as the soil samples, so as to prevent moisture loss and desiccation of roots prior to laboratory analysis.

Bacteria count and isolation

Bacteria communities in soils were determined using viable plate count for counting colony from bacterial and propagules. The bacteria count and isolation was determined using the serial dilution and spread plate techniques in nutrient agar as described by Fawole *et al.,* (2001). The samples were inoculated for 24 hours, and biochemical tests were carried out for identification of isolates.

Fungal count and isolation

Fungal count was determined using the spread plate method on potato dextrose agar (PDA) as described by Monica (2001). Soil samples were prepared by 10 fold serial dilution with 1 gram of soil sample. The samples were inoculated for 4 days and the isolated colonies were counted, identified using lacto-phenol and direct microscopic view as described by Monica (2001).

Extraction of Plant Parasitic Nematodes from Soil Samples

Plant parasitic nematodes were extracted from soil samples using extraction tray method as described by Coyne *et al.,* (2007). Each of the composite samples was mixed and 250ml of soil was measured using a 25oml beaker and was poured into lined plastic sieve with facial tissue which was placed on well labeled plastic flat plate. 200ml of water was poured into the side of the plastic sieve to gradually wet the soil. The set-up was left undisturbed in the laboratory for 48hours, after which the sieve was carefully lifted from the plastic plate while the nematode suspension in the plate was poured into well labeled small disposable cup, the plate was rinsed into the suspension in the cup and was allowed to settle. The nematode suspension was decanted and the supernatant was poured into a labeled 30ml vials and kept in the refrigerator at 4^0C prior to identification and counting of nematode species.

Extraction of Plant Parasitic Nematodes from Root Samples

Plant parasitic nematodes were extracted from root samples using extraction tray method as described by Coyne *et al.,* (2007). Each of the composite samples was rinsed with distilled water in to remove soil particles. The roots were finely chopped into small pieces of 1-2cm with a sharp knife. 10g was weighed using a sensitive balance and was poured into lined plastic sieve with facial tissue which was placed on well labeled plastic flat plate. 200ml of water was poured into the side of the plastic sieve to gradually wet the root. The set-up was left undisturbed in the laboratory for 48hours, after which the sieve was carefully lifted from the plastic plate while the nematode suspension in the plate was poured into well labeled small disposable cup, the plate was rinsed into the suspension in the cup and was allowed to settle. The nematode suspension was decanted and the supernatant was poured into a labeled 30ml vials and kept in the refrigerator at 4^0C prior to identification and counting of nematode species.

Nematode Identification and Counting

Aliquot of 2ml nematode suspension was pipette into a Doncaster counting dish as described by Doncaster (1962). The Doncaster counting dish was placed under a dissecting microscope and compound microscope alternately for identification and counting of plant parasitic nematodes using Bell's Key (Bell, 2004). The mean number of nematodes calculated from the suspension was multiplied by the total volume of the suspension to get the total number of plant parasitic nematodes in each sample.

Statistical Analysis

Data generated was subjected to analysis of variance (ANOVA) and the mean difference was separated using least significant difference at 5%. Analytical software used was Genstart Discovery 3rd edition, 2009.

RESULT

Soil Microbial Count and Population Structure before Planting

The result for soil microbial counts and soil microbial population structure before planting is shown in Table 1. Nematode count was the same (600) in both maize and okra plots, bacteria count was higher in maize plot (100) compared with okra plot (85), while fungi count was higher in okra plot (8) compared with maize plot (4). Bacteria species include: *Staphylococcus spp, Bacillus spp, streptococcus spp*, Fungi species include: *Aspergillus spp, Rhizopus, Yeast*, while nematode species include: *Pratylenchus spp*.

Table 1: Soil Microbial Count and Population Structure before Planting

Microbial Count	Maize Plot	Okra Plot	Microbial Species
Bacteria ($x10^3$Cfu/g of soil)	100	85	*Staphylococcus spp, Bacillus spp, streptococcus spp*
Fungi ($x10^3$Cfu/g of soil)	4	8	*Aspergillus spp, Rhizopus, Yeast.*
Nematode	600	600	*Pratylenchus spp.*

Soil Microbial Population Structure at Seedling Stage

The result of microbial population structure at seedling stage is shown in Table 2. Bacteria species were the same in the rhizosphere of maize and okra and include: *Staphylococcus spp, streptococcus spp,* and *Bacillus spp.* For fungi species, *Aspergillus, Rhizopus,* and *Yeast* were isolated in the rhizosphere of maize while *Aspergillus, Rhizopus,* and *Fusarium* were isolated in the rhizosphere of okra. For nematode, *Helicotylenchus spp* was isolated in the rhizosphere of okra while *Helicotylenchus spp,* and *Pratylenchus spp* were isolated in the rhizosphere of okra.

Table 2: Soil Microbial Population Structure at Seedling Stage

	Seedling Stage		
Crops	**Bacteria Isolates**	**Fungi Isolates**	**Nematode Isolates**
Maize	*Staphylococcus spp, streptococcus spp, Bacillus spp.*	*Aspergillus, Rhizopus, Yeast.*	*Helicotylenchus spp.*
Okra	*Staphylococcus spp, streptococcus spp, Bacillus spp.*	*Aspergillus, Rhizopus, Fusarium.*	*Helicotylenchus spp, Pratylenchus spp.*

Soil Microbial Population Structure at Flowering Stage

The result of soil microbial population structure at flowering stage is shown in Table 3.

Bacteria species in the rhizosphere of maize include: *Staphylococcus spp, streptococcus spp, Lactobacillus,* and *Bacillus spp,* while those in the rhizosphere of okra include: *Staphylococcus spp, streptococcus spp, Corynebacterium,* and *Bacillus spp.* For fungi species, *Aspergillus, Rhizopus,* and *Yeast* were isolated in the rhizosphere of maize while *Aspergillus, Rhizopus,* and *Mucor* were isolated in the rhizosphere of okra. For nematode, *Helicotylenchus spp* and *Pratylenchus spp* were isolated in the rhizosphere of okra while *Meloidogyne spp, Helicotylenchus spp,* and *Pratylenchus spp* were isolated in the rhizosphere of okra.

Table 3: Soil Microbial Population Structure at Flowering Stage

Crops	Bacteria Isolates	Fungi Isolates	Nematode Isolates
Maize	*Staphylococcus spp, streptococcus spp, Lactobacillus, Bacillus spp.*	*Aspergillus, Rhizopus, Yeast.*	*Helicotylenchus spp, Pratylenchus spp.*
Okra	*Staphylococcus spp, streptococcus spp, Corynebacterium, Bacillus spp.*	*Aspergillus, Rhizopus, Mucor.*	*Meloidogyne spp, Helicotylenchus spp, Pratylenchus spp.*

Soil Microbial Population Structure at Maturity Stage

The result of soil microbial population structure at maturity stage is shown in Table 4. Bacteria species in the rhizosphere of maize include: *Staphylococcus spp, streptococcus spp,* and *Bacillus spp,* while those in the rhizosphere of okra include: *Staphylococcus spp, streptococcus spp,* and *Pseudomonas.* For fungi species, *Aspergillus,* and *Rhizopus* were isolated in the rhizosphere of maize while *Aspergillus, Rhizopus,* and *Fusarium* were isolated in the rhizosphere of okra. For nematode, *Tylenchus spp* was isolated in the rhizosphere of okra while *Tylenchus spp, Helicotylenchus spp, Pratylenchus spp* were isolated in the rhizosphere of okra.

Table 4: Soil Microbial Population Structure at Maturity Stage

Crops	Bacteria Isolates	Fungi Isolates	Nematode Isolates

Maize	*Staphylococcus spp, streptococcus spp, Bacillus spp.*	*Aspergillus, Rhizopus.*	*Tylenchus spp.*
Okra	*Staphylococcus spp, streptococcus spp, Pseudomonas spp.*	*Aspergillus, Rhizopus, Fusarium*	*Tylenchus spp, Helicotylenchus spp, Pratylenchus spp.*

Percentage Occurrence of Bacteria Species at Different Stages of Growth

The result of percentage occurrence of bacteria species at different stages of growth is shown in Table 5. *Bacillus spp* occurrence was highest (54%) in the rhizosphere of maize and okra during seedling and maturity stages respectively, *Staphylococcus spp* occurrence was highest (38%) in the rhizosphere of maize during flowering stage, *Streptococcus spp* occurrence was highest (18%) in the rhizosphere of okra during flowering stage, Lactobacillus was highest (12%) in the rhizosphere of maize during flowering stage, among others.

Table 5: Percentage Occurrence of Bacteria Species at Different Stages of Growth

Crops	*Bacillus spp*	*Staphylococcus spp*	*Streptococcus spp*	*Lactobacillus*	*Pseudomonas spp*	*Cyanobacterium*	*E. coli*
			Seedling Stage				
Maize	54	32	13	0	0	0	0
Okra	50	36	14	0	0	0	0
			Flowering Stage				
Maize	27	38	22	12	0	0	0
Okra	47	28	18	4	0	2	0
			Maturity Stage				
Maize	52	18	15	0	0	0	0
Okra	54	35	13	0	5.7	0	0

Percentage Occurrence of Fungi Species at Different Stages of Growth

The result of percentage occurrence of fungi species at different stages of growth is shown in Table 6. *Rhizopus spp* occurrence was highest (63%) in the rhizosphere of okra during flowering stage, *Aspergillus spp* occurrence was highest (41%) in the rhizosphere of maize during seedling stage, *Yeast spp* occurrence was highest (15%) in the rhizosphere of maize during seedling stage, *Fusarium spp* occurrence was highest (30%) in the rhizosphere of okra during maturity stage, and *Mucor spp* occurrence was highest (7%) in the rhizosphere of maize during flowering stage.

Table 6: Percentage Occurrence of Fungi Species at Different Stages of Growth

Crops	*Rhizopus spp*	*Aspergillus spp*	*Yeast spp*	*Fusarium spp*	*Mucor spp*
		Seedling Stage			
Maize	44	41	15	0	0
Okra	53	39	0	8	0
		Flowering Stage			
Maize	49	38	5	0	7
Okro	63	31	0	0	6
		Maturity Stage			
Maize	55	37	6	0	0
Okro	41	29	0	30	0

Percentage Occurrence of Nematode Species at Different Stages of Growth

The result of percentage occurrence of nematode species at different stages of growth is shown in Table 7. *Meloidogyne spp* occurrence was highest (17%) in the rhizosphere of okra during flowering stage, *Pratylenchus spp* occurrence was highest (41%) in the rhizosphere of maize during seedling stage, *Helicotylenchus spp* occurrence was highest (67%) in the rhizosphere of maize during flowering stage, and *Tylenchus spp* occurrence was highest (33%) in the rhizosphere of maize during maturity stage.

Table 7: Percentage Occurrence of Nematode Species at Different Stages of Growth

Crops	***Meloidogyne spp***	***Pratylenchus spp***	***Helicotylenchus spp***	***Tylenchus spp***
		Seedling Stage		
Maize	0	0	33	0
Okra	0	50	50	0

Flowering Stage				
Maize	0	33	67	0
Okra	17	33	50	0
Maturity Stage				
Maize	0	0	0	33
Okra	0	50	25	25

DISCUSSION

Soil microorganisms despite making up less than 0.5% (w/w) of the soil mass, are essential to its characteristics and functions (Yan *et al*., 2015). By converting organic debris into plant nutrients, they play a crucial part in soils. Nonetheless, a number of biotic and abiotic variables influence the microbial characteristics, community structure, and functions of soil microorganisms (Szoboszlay *et al*., 2019; Kumar *et al*., 2020; Wang *et al*., 2021).

In this study, before planting, three bacterial species (*Staphylococcus spp, Bacillus spp, streptococcus spp*) were isolated from the soil in the study area (Table 1), these species were also isolated during seedling stage (Table 2), and at the flowering stage, *Lactobacillus,* and *Corynebacterium* were isolated from the rhizosphere of maize and okra respectively increasing the number of bacterial isolates to five (Table 3). At the maturity stage, *Lactobacillus,* and *Corynebacterium* were absent but *Pseudomonas spp* was isolated in the rhizosphere of okra in addition to the bacterial isolates recorded during the seedling stage thereby bringing the total number of bacterial isolates to four (Table 4). These bacterial species are among the 20 species that were isolated in the rhizosphere and rhizoplane of okra in the study by Pandey *et al*. (2020). The current results concur with those of Nidhi *et al*. (2016) and Pandey *et al*. (2018), who observed a comparatively similar bacterial diversity and physical traits in the wheat rhizosphere. More or less comparable rhizobacteria have been found in the rhizosphere and rhizoplane of *Brassica oleracea* by Fazal Mahmood *et al*. (2018). In agreement with these findings, Navarro-Noya *et al*. (2022) reported that the degree to which the maize rhizosphere impacted the soil bacterial community varied according to the community trait and the stage of development of the maize plant. Arguably, the increase in the species of bacteria during flowing could be due to fact that the rhizosphere began to enrich specific bacteria and functions related to cofactors and vitamin synthesis during flowering, but functions related to biosynthesis decreased. This position is supported by Navarro-Noya *et al*. (2022) who posited that the bacterial community structure, taxonomic diversity, and functional diversity of the soil bacteria in the maize rhizosphere were different during maize development, and bacterial functions favored in the rhizosphere during plant growth showed that at the early stages of maize development root exudates stimulated bacterial growth. Also, a number of studies have documented that the composition of the bacterial community in the rhizosphere varies throughout plant development, suggesting that roots choose for distinct microorganisms at different times, most likely due to variations in the composition of the root-exudates (Qiao *et al*., 2017; Yin *et al*., 2017; Wattenburger *et al*., 2019).

Furthermore, in this study, fungi and nematode species isolated before planting are *Aspergillus spp, Rhizopus, Yeast,* and *Pratylenchus spp* (Table 1), during seedling stage, *Aspergillus, Rhizopus, Yeast, Fusarium, Helicotylenchus spp*, and *Pratylenchus spp* were isolated (Table 2), during flowering stage, *Aspergillus, Rhizopus, Yeast, Mucor, Meloidogyne spp, Helicotylenchus spp,* and *Pratylenchus spp* were isolated (Table 3), and during maturity stage, *Aspergillus, Rhizopus, Fusarium, Tylenchus spp, Helicotylenchus spp,* and *Pratylenchus spp* were isolated (Table 4). At various phases of maize and okra growth, notable variations in fungal and nematode populations were observed. These variations in terms of richness, diversity, and relative abundances of taxa and metabolic processes have been reported in studies by Vital-Lopez *et al*. (2016), Szoboszlay *et al*. (2019), and Singh and Godwin (2022). Curiously, in addition to variations due to growth phases, other research have demonstrated variations in bacterial and fungal communities among cultivars, transgenic and non-transgenic lines, and soil types (van Wyk *et al*., 2017). As opined by Singh and Godwin (2022), the rhizosphere of maize had a stronger effect on bacterial communities than on fungal communities due to the ecological and environmental filtering action of the root.

Furthermore, the rhizobiome community structure in the carbon-rich area surrounding the plant root differs between plant species and genotypes (Semchenko *et al*., 2021), because of the influence of the plant, including differences in root exudate patterns (Lopez-Guerrero *et al*., 2022). Differential generation of root exudates and community utilization are the basis for the host genotype-dependent variation in the root exudate profile and the ensuing substrate-driven or bottom-up changes in the microbial community structure (Yadav *et al*., 2023). Maize and Okra rhizosphere microbiome has been found to be shaped in part by soil characteristics as pH, nitrogen and potassium availability, phosphate fertilization, and root exudates (Tao *et al*., 2017; Emmett *et al*., 2020). These factors might have contributed to the variations in microbial population structure in this study. Furthermore, the composition of maize endophytes was impacted by the combined application of heavy metals and chelants in the soil, indicating their potential to

enhance maize's phytoremediation ability (Islam *et al*., 2016; Vigliotta *et al*., 2016; Chen *et al*., 2017; Wu *et al*., 2017; Panitlertumpai *et al*., 2018; Sun *et al*., 2018).

The kind of soil and the stage of development of maize growth and okra had have a substantial impact on the rhizosphere microbiome and percentage occurrence of microorganisms also showed significant variations in this study (Tables 5, 6, and 7). Similarly, Wolters *et al*. (2018) reported that the rhizosphere effect was stronger for young roots than for mature maize plants. In addition to the impacts of different stages of plant development, the long-term use of organic fertilizers such chicken manure and sewage sludge have been reported to have a major impact on microbial communities in the soil and the phyllosphere (Chen *et al*., 2018). According to Correa-Galeote *et al*. (2018), another element that shapes maize endophytes is the history of soil cultivation, which increases the richness of bacterial communities over a prolonged period of soil cultivation as opposed to fallow soil. Both healthy and asymptomatic plants are colonized by a wide variety of microorganisms in nature (Roslan *et al*., 2022). The intricate plant-associated microbial community is known as the second genome of plants because of its impact on plant growth and production (Hacquard, 2016). Notably, nutrient activation, stress tolerance, defense against soil-borne illnesses, and resilience to climate change-related environmental changes like drought, salt, and fluctuating temperatures are just a few of the ways the microbes help the host plants (Canarini *et al*., 2019; Hassan *et al*., 2019; Khan *et al*., 2021; Lazcano *et al*., 2021; Xiong *et al*., 2021). This study found that the bacterial rhizosphere microbiome of okra showed a complex soil microbial community structure. This suggests that the rhizosphere soil microbial populations may be influenced by the various stages of plant development, which could be a crucial step in increasing maize and okra output and growth.

CONCLUSION

In conclusion, field crops promoted bacterial, fungal and nematode population and diversity**;** there were variations in these microbial communities in response to plant growth and development**.** Measures of bacterial and fungal activity revealed that crop growth stage influences rhizodeposition. These communities response was obvious between seedling and matured crops and may reflect changes in the root exudates pattern of young crops to that of matured crops. It was observed in this study that Okra promoted the highest bacterial and fungal growth thus can be used as an intercrop to increase soil microbial biomass which aids in organic matter decomposition, thereby improving soil fertility.

REFERENCES

Agregán, R., Pateiro, M., Bohrer, B.M., Shariati, M.A., Nawaz, A., Gohari, G. & Lorenzo, J.M. (2022). Biological activity and development of functional foods fortified with okra (*Abelmoschus esculentus*). *Crit. Rev. Food Sci. Nutr*., 1–16.

Ahmad, I., Jiménez-Gasco, M. D. M., Luthe, D. S., Shakeel, S. N. & Barbercheck, M. E. (2020). Endophytic Metarhizium robertsii promotes maize growth, suppresses insect growth, and alters plant defense gene expression. *Biol. Control*., 144:104167.

Beirinckx, S., Viaene, T., Haegeman, A., Debode, J., Amery, F., Vandenabeele, S., Nelissen, H., Inzé, D., Tito, R., Raes, J., Tender, C. D. & Goormachtig, S. (2020). Tapping into the maize root microbiome to identify bacteria that promote growth under chilling conditions. *Microbiome*, 8:54.

Bell M. (2004) Plant Parasitic Nematodes: Lucid Key to 30 Genera of Plant Parasitic Nematode: http//www.lucicentral.com/keys/nematodes

Bojtor, C., Mousavi, S.M.N., Illés, Á., Széles, A., Nagy, J. & Marton, C.L. (2021). Stability and adaptability of maize hybrids for precision crop production in a long-term field experiment in Hungary. *Agronomy*, *11*, 2167

Brader, G., Compant, S., Vescio, K., Mitter, B., Trognitz, F., Ma, L. J. & Sessitsch, A. (2017). Ecology and genomic insights into plant-pathogenic and plant-nonpathogenic endophytes. *Annu. Rev. Phytopathol*., 55:61-83.

Canarini, A., Kaiser, C., Merchant, A., Richter, A. and Wanek, W. (2019). Root exudation of primary metabolites: Mechanisms and their roles in plant responses to environmental stimuli. *Front. Plant Sci*., 10, 157.

Chebotar, V. K., Chizhevskaya, E. P., Andronov, E. E., Vorobyov, N. I., Keleinikova, O. V., Baganova, M. E., Konovalov, S. N., Filippova, P. S., & Pishchik, V. N. (2023). Assessment of the Rhizosphere Bacterial Community under Maize Growth Using Various Agricultural Technologies with Biomodified Mineral Fertilizers. *Agronomy*, *13* (7), 1855. https://doi.org/10.3390/agronomy13071855

Chen, Y., Wang, J., Yang, N., Wen Z., Sun, X., Chai, Y. & Ma, Z. (2018). Wheat microbiome bacteria can reduce virulence of a plant pathogenic fungus by altering histone acetylation. *Nat. Commun*., 9:3429.

Chen, Z., Zheng, Y., Ding, C., Ren, X., Yuan, J., Sun, F. & Li, Y. (2017). Integrated metagenomics and molecular ecological network analysis of bacterial community composition during the phytoremediation of cadmium contaminated soils by bioenergy crops. *Ecotoxicol. Environ. Saf*., 145:111- 118.

Correa-Galeote, D., Bedmar, E. J. & Arone, G. J. (2018). Maize endophytic bacterial diversity as affected by soil cultivation history. *Front. Microbiol*., 9:484.

Coyne D. L., Nicol J. M. & Claudius-Cole B. (2007) Practical Plant Nematology: A Field and Laboratory Guide. SP. IPM Secretariat, International Institute of Tropical Agriculture (IITA), Cottonou, Benin.

Doncaster C. C. (1962) A Counting Dish for Nematodes. *Nematologica* 7:33-36

Durán, P., Thiergart, T., Garrido-Oter, R., Agler, M., Kemen, E., SchulzeLefert, P. & Hacquard, S. (2018). Microbial interkingdom interactions in roots promote Arabidopsis survival. *Cell*, 175:973-983.e14.

Eludoyin O. S., Oladele A. T., & Iyanda O. M. (2015) Mapping and Assessment of Ethno-Medicinal Trees in Built Up Areas -University of Port Harcourt, Nigeria. *South-east Eur* 6 (1):129-140.

Emmett, B. D., Buckley, D. H. & Drinkwater, L. E. (2020). Plant growth rate and nitrogen uptake shape rhizosphere bacterial community composition and activity in an agricultural field. *New Phytol*., 225:960-973.

Fawole M. O. and Oso B. A. (2001) Laboratory Manual for Microbiology 10:0946480311

Fazal Mehmood, K., Inamul, H., Nimatullah, T. S., Muhammad, F., Ohia, C. & Tauseef, A. (2018). Isolation, Characterisation and Identification of Plant Growth Promoting Rhizobacteria from Cauliflower (*Brassica oleracea*). *Arch. Bas. App. Med*., 6:55 – 60

Hacquard, S. (2016). Disentangling the factors shaping microbiota composition across the plant holobiont. *New Phytol*., 209, 454–457.

Hassan, M., McInroy, J. & Kloepper, J. (2019). The interactions of rhizodeposits with plant growth-promoting rhizobacteria in the rhizosphere: A review. *Agriculture*, 9, 142

Hou, P., Liu, Y., Liu, W., Liu, G., Xie, R., Wang, K., Ming, B., Wang, Y., Zhao, R. & Zhang, W. (2020). How to increase maize production without extra nitrogen input. *Resour. Conserv. Recycl. 160*, 104913.

Islam, F., Yasmeen, T., Arif, M. S., Riaz, M., Shahzad, S. M., Imran, Q. & Ali, I. (2016). Combined ability of chromium (Cr) tolerant plant growth promoting bacteria (PGPB) and salicylic acid (SA) in attenuation of chromium stress in maize plants. *Plant Physiol. Biochem*., 108:456-467.

Khan, N., Ali, S., Shahid, M.A., Mustafa, A., Sayyed, R.Z. & Curá, J.A. (2021). Insights into the interactions among roots, rhizosphere, and rhizobacteria for improving plant growth and tolerance to abiotic stresses: A review. *Cells*, 10, 1551.

Kumar, A., Singh, S., Gaurav, A. K., Srivastava, S., & Verma, J. P. (2020). Plant growth-promoting bacteria: biological tools for the mitigation of salinity stress in plants. *Front. Microbiol.* 11:1216. DOI: 10.3389/fmicb.2020.01216

Lazcano, C., Boyd, E., Holmes, G., Hewavitharana, S., Pasulka, A. & Ivors, K. (2021). The rhizosphere microbiome plays a role in the resistance to soil-borne pathogens and nutrient uptake of strawberry cultivars under field conditions. *Sci. Rep*., 11, 3188.

Lemanceau, P., Blouin, M., Muller, D. & Moenne-Loccoz, Y. (2017). Let the core microbiota be functional. *Trends Plant Sci*., 22:583-595.

Lopez-Guerrero, M.G., Wang, P., Phares, F., Schachtman, D.P., Alvarez, S. & van Dijk, K. A. (2022). Glass bead semi-hydroponic system for intact maize root exudate analysis and phenotyping. *Plant methods*, 18:1–21.

Meena, V.K., Dubey, A.K., Jain, V.K., Tiwari, A. & Negi, P. (2017). Effect of plant growth promoters on flowering and fruiting attributes of okra [*Abelmoschus esculentus* (L.) Moench]. *Crop Res*., 52, 37–40

Monica Cheesbrough (2001) District Laboratory Practice in Tropical Countries Pt 2-97805211676311

Mousavi, S.M.N., Bojtor, C., Illés, Á. & Nagy, J. (2021). Genotype by trait interaction (GT) in maize hybrids on complete fertilizer. *Plants*, *10*, 2388.

Navarro-Noya, Y.E., Chávez-Romero, Y., Hereira-Pacheco, S., de León Lorenzana, A.S., Govaerts, B., Verhulst, N. & Dendooven, L. (2022). Bacterial Communities in the Rhizosphere at Different Growth Stages of Maize Cultivated in Soil Under Conventional and Conservation Agricultural Practices. Microbiology Spectrum, 10 (2). DOI: 10.1128/spectrum.01834-21

Nidhi, S., Sunil, P., Vikram, S., Shreyas, B. & Anasuya, B. (2016). Study of Bacterial Diversity of Mangroves Rhizosphere. *Open Journal of Marine Science*, 6, 23-31.

Niu, B., Paulson, J. N., Zheng, X. & Kolter, R. (2017). Simplified and representative bacterial community of maize roots. Proc. Natl. Acad. Sci. U. S. A. 114:E2450-E2459.

Pandey, R., Kumar, B., Rani, S. & Kumari, P. (2018). Biodiversity of Bacteria in the Rhizosphere of *Solanum melongena* L. (Brinjal) and their characterization. *Int. J. Microbiol. App. Sci*, 7(3): 3252-3267

Pandey, R., Rani, S. & Kumar, B. (2020). Rhizosphere and Rhizoplane bacteria of Okra (*Abelmuscus esculentus* Linn.Moench) and Cauliflower (*Brassica oleracea* Linn. Var. Botrytis) and their characterization. IOSR *Journal of Biotechnology and Biochemistry*, 6 (3). DOI: 10.9790/264X-0603011731.

Panitlertumpai, N., Nakbanpote, W., Sangdee A., Boonapatcharoen, N. & Prasad, M. N. V. (2018). Potentially toxic elements to maize in agricultural soils—microbial approach of rhizospheric and bulk soils and phytoaccumulation. *Environ. Sci. Pollut. Res*., 25:23954-23972

Perveen, R., Hussain, A., Ditta, A., Dar, A., Aimen, A., Ahmad, M., Alataway, A., Dewidar, A.Z. & Mattar, M.A. (2023). Growth and Yield of Okra Exposed to a Consortium of Rhizobacteria with Different Organic Carriers under Controlled and Natural Field Conditions. *Horticulturae*, 9, 8. https://doi.org/10.3390/horticulturae9010008

Petropoulos, S., Fernandes, Â., Barros, L. & Ferreira, I.C. (2018). Chemical composition, nutritional value and antioxidant properties of Mediterranean okra genotypes in relation to harvest stage. *Food Chem*., 242, 466–474.

Qiao, Q., Wang, F., Zhang, J., Chen, Y., Zhang, C., Liu, G., Zhang, H., Ma, C. & Zhang, J. (2017). The Variation in the rhizosphere microbiome of cotton with soil type, genotype and developmental stage. *Sci. Rep*., 7:3940. https://doi.org/10.1038/s41598-017-04213-7.

Saima, S., Ghaffar, F., Yasin, G., Nawaz, M. & Ahmad, K.M. (2022). Effect of salt stress on germination and early seedling growth in Okra (*Abelmoschus esculentus*). *Sarhad J. Agric*., 38, 388–397.

Singh, R. & Goodwin, S.B. (2022). Exploring the Corn Microbiome: A Detailed Review on Current Knowledge, Techniques, and Future Directions. *PhytoFrontiers*, 2:158-175 https://doi.org/10.1094/PHYTOFR-04-21-0026-RVW

Sun, W., Xiao, E., Krumins, V., Häggblom, M. M., Dong, Y., Pu, Z., Li, B., Wang, Q., Xiao, T. & Li, F. (2018). Rhizosphere microbial response to multiple metal (loid)s in different contaminated arable soils indicates cropspecific metal-microbe interactions. *Appl. Environ. Microbiol*., 84:e00701- 18.

Szoboszlay, M., Nather, A., Mullins, E. and Tebbe, C. C. (2019). Annual replication is essential in evaluating the response of the soil microbiome to the genetic modification of maize in different biogeographical regions. *PLoS One*, 14:e0222737.

Tao, J., Liu, X., Liang, Y., Niu, J., Xiao, Y., Gu, Y., Ma, L., Meng, D., Zhang, Y., Huang, W., Peng, D. & Yin, H. (2017). Maize growth responses to soil microbes and soil properties after fertilization with different green manures. *Appl. Microbiol. Biotechnol*., 101:1289-1299.

van Wyk, D. A. B., Adeleke, R., Rhode, O. H. J., Bezuidenhout, C. C. & Mienie, C. (2017). Ecological guild and enzyme activities of rhizosphere soil microbial communities associated with Bt-maize cultivation under field conditions in North West Province of South Africa. *J. Basic Microbiol*., 57:781-792.

Vigliotta, G., Matrella, S., Cicatelli, A., Guarino, F. & Castiglione, S. (2016). Effects of heavy metals and chelants on phytoremediation capacity and on rhizobacterial communities of maize. *J. Environ. Manage*., 179: 93-102.

Vital-López, L., Cruz-Hernández, M. A., Fernández-Dávila, S. & Mendoza-Herrera, A. (2016). Bacterial diversity in the rhizosphere of a transgenic versus a conventional maize (*Zea mays*). *Phyton* (Buenos Aires, Argent.), 85:210-217.

Wang, C.-Y., Zhou, X., Guo, D., Zhao, J.-H., Yan, L. & Feng, G.-Z. (2019). Soil pH is the primary factor driving the distribution and function of microorganisms in farmland soils in northeastern China. *Ann. Microbiol*. 69, 1461–1473. DOI: 10.1007/s13213-019-01529-9

Wattenburger, C.J., Halverson, L.J. & Hofmockel, K.S. (2019). Agricultural management affects root-associated microbiome recruitment over maize development. *Phytobiomes J*., 3:260–272. https://doi.org/10.1094/PBIOMES-03-19-0016-R

Wolters, B., Jacquiod, S., Sørensen, S. J., Widyasari-Mehta, A., Bech, T. B., Kreuzig, R. & Smalla, K. (2018). Bulk soil and maize rhizosphere resistance genes, mobile genetic elements and microbial communities are differently impacted by organic and inorganic fertilization. *FEMS Microbiol. Ecol*., 94. doi: 10.1093/femsec/fiy027

Wu,W.,Wu, J., Liu, X., Chen, X.,Wu, Y. & Yu, S. (2017). Inorganic phosphorus fertilizer ameliorates maize growth by reducing metal uptake, improving soil enzyme activity and microbial community structure. *Ecotoxicol. Environ. Saf*., 143:322-329.

Xiong, Q., Hu, J., Wei, H., Zhang, H. & Zhu, J. (2021). Relationship between plant roots, rhizosphere microorganisms, and nitrogen and its special focus on rice. Agriculture 2021, 11, 234.

Yadav, P., Quattrone, A., Yang, Y., Owens, J., Kiat, R., Kuppusamy, T., Russo, S.E. & Weber, K.A. (2023). *Zea mays* genotype influences microbial and viral rhizobiome community structure. *ISME COMMUN*. **3**, 129 (2023). https://doi.org/10.1038/s43705-023-00335-4

Yan, N., Marschner, P., Cao, W., Zuo, C. & Qin, W. (2015). Influence of salinity and water content on soil microorganisms. *Int. Soil Water Conserv. Res.* 3, 316–323. DOI: 10.1016/j.iswcr.2015.11.003

Yin, C., Mueth, N., Hulbert, S., Schlatter, D., Paulitz, T.C., Schroeder, K., Prescott, A. & Dhingra, A. (2017). Bacterial communities on wheat grown under longterm conventional tillage and no-till in the pacific northwest of the United States. *Phytobiomes J*., 1:83–90. https://doi.org/10.1094/PBIOMES-09-16-0008-R.