Chapter 4

Results & Discussions

4.1 Characterization of collected soil samples

Among all the Saurashtra region, four areas such as Rajkot, Khijadiya, Veraval and Morbi seven different sampling sites of Saurashtra Region were chosen for soil sample collection.Soil analysis study has been carried out from Gujarat State Fertilizers and Chemical Limited. Various important properties like pH, electrical conductivity (EC), phosphate, potassium content along with presence of micro elements are represented in following series of tables, Table 4.1.1- 4.1.7. Table 4.1 represents a consolidated data of number of agricultural soil samples collected from Khijadiya (3), Veraval (1), Morbi (2) and Rajkot (2) respectively. Majority samples are black clay soils as found to be recorded.

Fig - 4.1 Different areas selected for the collection of samples

Figure 4.1 is a representation of various collected soil samples representing the color and texture of the samples. The black soil is happened to be an accumulation of humus or organic matter. An interesting fact to be shared in this regard is the elements in soil and its influence is dependent on the efficient utilization of microbes present in soil and the law here works in this regard is of Sprengel and Liebig (Kasperi and Power, 2016). Sometimes co limitation of two or more nutrients also influence the population of microbes (Saito *et al.,*2008). A report of Frausto da Silva and Williams (2001) has enlightened on basic roles of soil elements and their chemical nature how influence the microbial population in soil.

Table - 4.1 Sampling trials and sites

Sr No.	Soil Sampling Sites	Number of samples collected
1	Khijadiya	03
2	Veraval	02
3	Morbi	01
4	Rajkot	01

In present study, Table- 4.1.1 to 4.1.7 highlights a quantitative distribution of elemental compositions of soil samples in terms of low, medium and normal range, while the micro elements playing a significant role in crop productivity and microbial growth has been represented in ppm. From three sampling trials it is observed that total nitrogen /organic carbon ranges from 0.50 to 0.30 ppm on an average, while phosphate and potassium vary between 0.10-0.20 ppm except the third trial of sampling where the potassium seems to be high in ppm. The soil pH and EC are in normal range in all three samplings. The interesting finding was intensity of Mn comparatively high than other trace elements like Zn, Fe and Cu, it may be because of major maintenance of buffer in the soil in natural way.

Table – 4.1.1 Soil Sample number-1 From Khijadiya region.

Test	Quantity (ppm)	Quality
Total nitrogen/ organic carbon (OC)%	0.90	High
P_2O_5 Kg/Ac	13.00	Medium
K_2O_7 Kg/Ac	99.00	Medium
pH	7.44	Normal
Electrical conductivity (EC)	1.20	High
S, ppm	100.00	High

Micro elements	Quantity (ppm)	Quality
Zn	1.38	High
Fe	1.04	Low
Mn	15.21	High
Cu	1.11	High

Table - 4.1.2 Soil Sample number-2 From Khijadiya region

Test	Quantity (ppm)	Quality
Total nitrogen/ organic carbon (OC)%	0.51	Medium
P_2O_5 Kg/Ac	15.00	Medium
K_2O_7 Kg/Ac	116.00	Medium
pH	7.65	Normal
Electrical conductivity (EC)	0.54	Normal
S, ppm	9.80	Low

Micro elements	Quantity (ppm)	Quality
Zn	5.47	High
Fe	1.00	Low
Mn	5.74	Medium
Cu	5.04	High

Table - 4.1.3 Soil Sample number-3 From Khijadiya region

Test	Quantity (ppm)	Quality
Total nitrogen/ organic carbon (OC)%	0.53	Medium
P_2O_5 Kg/Ac	15.00	Medium
K_2O_7 Kg/Ac	58.00	Low
pH	7.56	Normal
Electrical conductivity (EC)	0.81	Normal
S, ppm	9.60	Low

Micro elements	Quantity (ppm)	Quality
Zn	2.15	High
Fe	1.21	Low
Mn	12.70	High
Cu	1.31	High

Table - 4.1.4 Soil Sample number-4 From Veraval region

Test	Quantity (ppm)	Quality
Total nitrogen/ organic carbon (OC)%	0.49	Low
P_2O_5 Kg/Ac	10.00	Low
K_2O_7 Kg/Ac	71.00	Medium
pH	7.75	Normal
Electrical conductivity (EC)	0.54	Normal
S, ppm	10.20	Medium

Micro elements	Quantity (ppm)	Quality
Zn	0.59	Medium
Fe	0.54	Low
Mn	9.14	Medium
Cu	0.72	High

4.1.5 Soil Sample number-5 From Veraval region

Test	**Quantity (ppm)**	**Quality**
Total nitrogen/ organic carbon (OC)%	1.08	High
P_2O_5 Kg/Ac	12.00	Medium
K_2O_7 Kg/Ac	76.00	Medium
pH	7.76	Normal
Electrical conductivity (EC)	0.77	Normal
S, ppm	12.40	Medium

Micro elements	**Quantity (ppm)**	**Quality**
Zn	0.72	Medium
Fe	0.49	Low
Mn	6.34	Medium
Cu	1.05	High

4.1.6 Soil Sample number-6 From Morbi region

Test	**Quantity (ppm)**	**Quality**
Total nitrogen/ organic carbon (OC)%	0.36	Low
P_2O_5 Kg/Ac	20.00	Medium
K_2O_7 Kg/Ac	317.00	High
pH	7.73	Normal
Electrical conductivity (EC)	1.50	High
S, ppm	12.50	Medium

Micro elements	**Quantity (ppm)**	**Quality**
Zn	1.15	High
Fe	0.65	Low
Mn	8.32	Normal
Cu	3.19	High

4.1.7 Soil Sample number-7 From Rajkot region

Test	Quantity (ppm)	Quality
Total nitrogen/ organic carbon (OC)%	0.51	Medium
P_2O_5 Kg/Ac	21.00	Medium
K_2O_7 Kg/Ac	34.00	Low
pH	7.63	Normal
Electrical conductivity (EC)	2.10	High
S, ppm	10.20	Medium

Micro elements	Quantity (ppm)	Quality
Zn	0.41	Low
Fe	0.85	Low
Mn	12.16	High
Cu	0.33	Medium

Various microbial activities and soil microbe interactions are well known in agriculture microbiology which emphasize the mineral solubilization, different macro elements hydrolysis, solubilization, accumulation, and degradation by microbial enzyme activity (Hayat *et al.,* 2010), helps to nourish the soil micro flora and fauna and soil stricture too. The soil aggregating and its porosity along with various other important attributes are largely dependent on the availability of soil microbes. One of such important CNPK ratio and its proper balance in soil helps to proliferate the rhizosphere or PGPR traits. The data represented here is an expert for the reflection.

Table - 4.1.8 Detailing on soil isolates of rhizobacteria collected from different soil samples

Sr. No.	Source of soil samples	Number of soil samples collected	Number of isolates obtained
1	Rajkot	02	10
2	Khijadiya	02	35
3	Veraval	01	20
4	Morbi	02	10
Total	**04**	**07**	**75**

The table 4.1.8 represents a numerous bacterial isolates had been collected from various sampling sites with diversity in niche as reflected in the table. The maximum isolates are found to be recorded from Khijadiya site and the least are found to be noted from Rajkot site respectively. The intensity of PGPR strains is found to be more as per literature and various research data in the highest crop productivity areas. Although inappropriate agro techniques sometimes can reduce the load of this micro flora in soil layers (Furtak and Gajra 2017).

4.2 Morphological Identification of PGPR

Table 4.2 Morphological Identification of PGPR

Sample Name	Size	Shape	Pigmentation	Texture	Elevation	Margin
KW1	Large	Circular	Orange	Smooth	Flat	Entire
KW2	Large	Circular	White	Smooth	Flat	Entire
KW3	Large	Irregular	Cream	Dry	Umbonate	Fill form
KW4	Large	Circular	Black	Smooth	Flat	Entire
KW5	Large	Circular	Orange	Smooth	Flat	Entire
KW6	Large	Irregular	Cream	Dry	Umbonate	Fill form
KW7	Large	Circular	Black	Smooth	Flat	Entire
KW8	Large	Circular	Orange	Smooth	Flat	Entire
KW9	Large	Circular	Black	Smooth	Flat	Entire
KW10	Large	Circular	Orange	Smooth	Flat	Entire
KS1	Moderate	Circular	Orange	Dry	Convex	Entire
KS2	Moderate	Circular	Light yellow	Smooth	Convex	Entire
KS3	Large	Irregular	White	Dry	Flat	Entire
KS4	Large	Irregular	Cream	Dry	Umbonate	Filiform
KS5	Large	Irregular	White	Dry	Flat	Entire
KS6	Moderate	Circular	Orange	Dry	Convex	Entire
KS7	Large	Irregular	White	Dry	Flat	Entire
KS8	Large	Irregular	Cream	Dry	Umbonate	Filiform
KS9	Large	Irregular	White	Dry	Flat	Entire

KS10	Moderate	Circular	Orange	Dry	Convex	Entire
KC1	Large	Irregular	White	Smooth	Flat	Entire
KC2	Large	Regular	White	Smooth	Flat	Umbonate
KC3	Large	Circular	White	Smooth	Convex	Entire
KC4	Small	Circular	White	Smooth	Convex	Entire
KC5	Large	Irregular	Yellow	Dry	Fill form	Umbonate
KC6	Large	Irregular	Orange	Smooth	Flat	Entire
KC7	Large	Circular	White	Dry	Flat	Entire
KC8	Small	Circular	White	Smooth	Convex	Entire
KC9	Large	Circular	White	Dry	Flat	Entire
KC10	Small	Circular	Yellow	Smooth	Convex	Entire
KC11	Large	Circular	Orange	Dry	Flat	Entire
KC12	Large	Irregular	Orange	Smooth	Flat	Entire
KC13	Large	Circular	White	Smooth	Convex	Entire
KC14	Large	Irregular	Orange	Smooth	Flat	Entire
KC15	Large	Circular	White	Smooth	Convex	Entire
VO1	Small	Circular	Light yellow	Dry	Raised	Entire
VO2	Large	Irregular	White	Dry	Raised	Fill form
VO3	Moderate	Circular	Orange	Dry	Raised	Entire
VO4	Large	Circular	White	Smooth	Flat	Entire
VO5	Large	Irregular	White	Dry	Raised	Fill form
VO6	Moderate	Circular	Yellow	Dry	Raised	Entire
VO7	Large	Irregular	Orange	Dry	Raised	Fill form
VO8	Moderate	Circular	White	Dry	Raised	Entire
VG1	Large	Circular	White	Smooth	Flat	Entire
VG2	Large	Irregular	White	Smooth	Raised	Fill form
VG3	Large	Circular	Orange	Dry	Flat	Entire
VG4	Small	Circular	White	Dry	Raised	Entire
VG5	Small	Circular	White	Dry	Raised	Entire

VG6	Large	Irregular	White	Dry	Raised	Fill form
VG7	Small	Circular	White	Dry	Raised	Entire
VG8	Large	Circular	White	Smooth	Flat	Entire
VG9	Large	Circular	Black	Smooth	Flat	Entire
VG10	Small	Circular	Light yellow	Dry	Raised	Entire
VG11	Large	Irregular	Cream	Dry	Raised	Fill form
MC1	Large	Irregular	White	Dry	Raised	Fill form
MC2	Moderate	Circular	Yellow	Smooth	Flat	Entire
MC3	Large	Circular	Orange	Dry	Convex	Entire
MC4	Moderate	Circular	White	Smooth	Flat	Entire
MC5	Moderate	Circular	White	Smooth	Flat	Entire
MC6	Large	Irregular	Cream	Dry	Raised	Fill form
MC7	Large	Circular	Black	Smooth	Flat	Entire
MC8	Large	Irregular	Cream	Dry	Raised	Fill form
MC9	Large	Circular	Black	Smooth	Flat	Entire
MC10	Moderate	Circular	Orange	Smooth	Flat	Entire
RC1	Moderate	Circular	Orange	Smooth	Flat	Entire
RC2	Small	Circular	White	Smooth	Convex	Entire
RC3	Large	Circular	White	Smooth	Convex	Entire
RC4	Large	Irregular	Cream	Dry	Raised	Fill form
RC5	Small	Circular	White	Smooth	Convex	Entire
RC6	Moderate	Circular	Orange	Smooth	Flat	Entire
RC7	Large	Irregular	Cream	Dry	Raised	Fill form
RC8	Large	Irregular	Cream	Dry	Raised	Fill form
RC9	Small	Circular	White	Smooth	Convex	Entire
RC10	Large	Irregular	Cream	Dry	Raised	Fill form

The table 4.2 represents an overview of morphological features of the isolates of rhizobacteria gathered from various soil sample of Saurashtra Region. A variation of small to large colonies with circular to irregular margin has been observed. While the color varies

cream to white and shades of brown respectively. The consistency varies on an average from dry to smooth along with entire to fill form margin and elevation of flat, raised to convex colonies. Microscopic identification of various rhizobacterial isolates from different soil samples of Saurashtra Region are represented as follows in Fig 4.3. The table 4.2 colour codes represent the area of the bacterial sampling from the selected seven areas like KW (Khijadiya Wheat soil sample) shows grey in colour, KS (Khijadiya field area of Sorghum) blue in colour, KC (Khijadiya field of Chickpea) in green, VO (Veraval onion field) orange, VG (Veraval garlic field) violet colour, MC (Morbi region corn field) yellow in colour and RC (Rajkot corn field) pink colour.

4.3 Pure culture of rhizobacterial culture strains

By the isolation and pure culture analysis in the nutrient agar medium total 41 isolates have been isolated in single colony each. Pure culture has been obtained from the streak plate method.

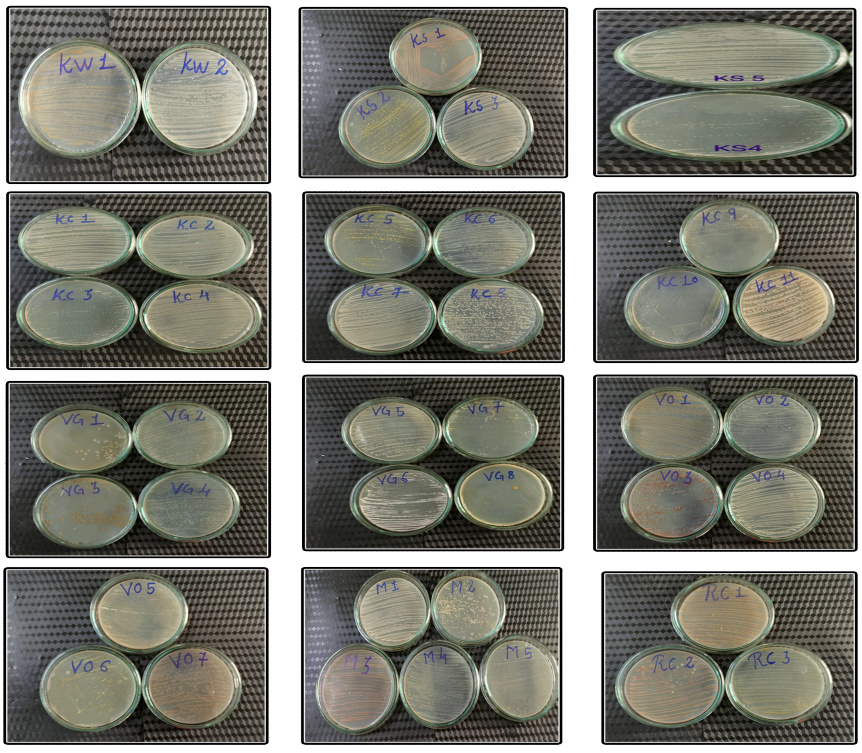
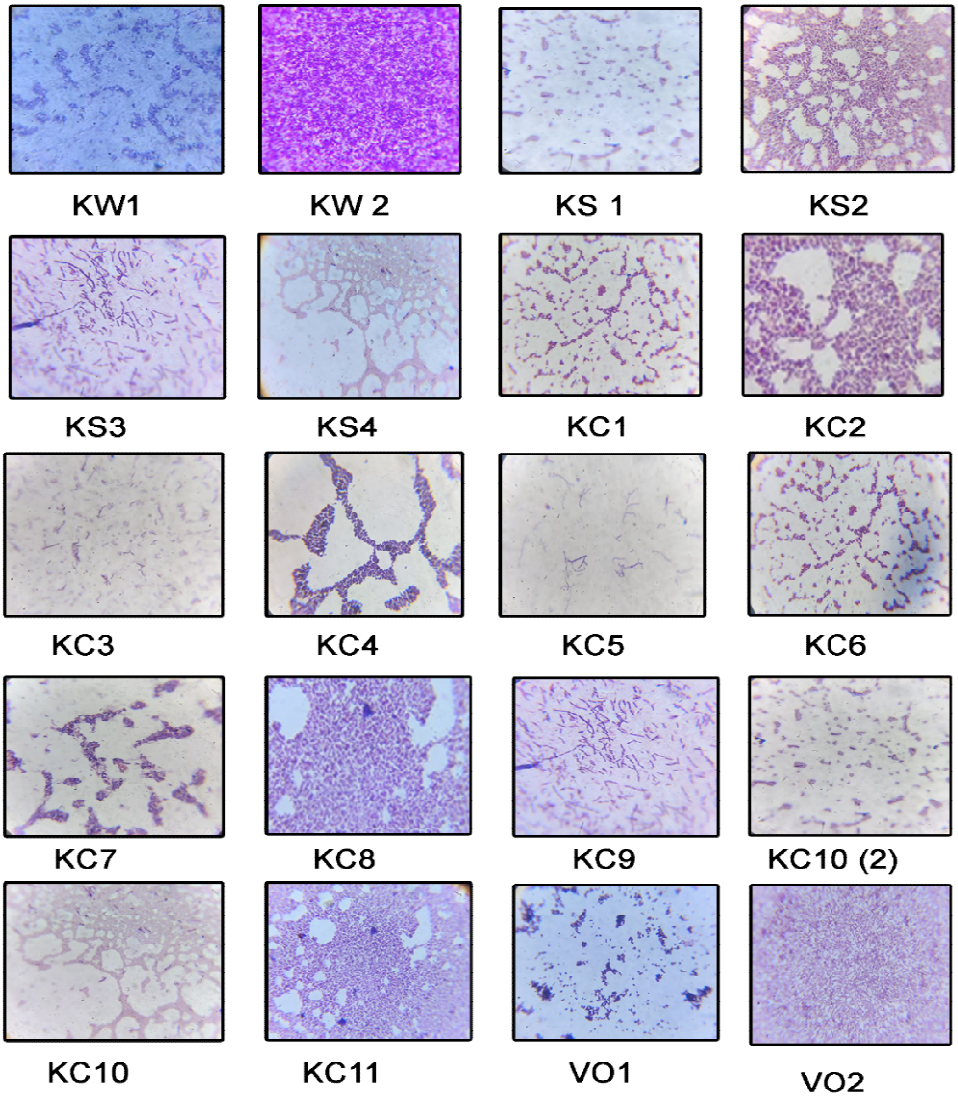


Fig. 4.2 Pure culture of rhizobacterial culture strains


KW1
KW 2
KS 1
KS2
KS3
KS4
KC1
KC2
KC3
KC4
KC5
KC6
KC7
KC8
KC9
KC10 (2)
KC10
KC11
VO1
VO2

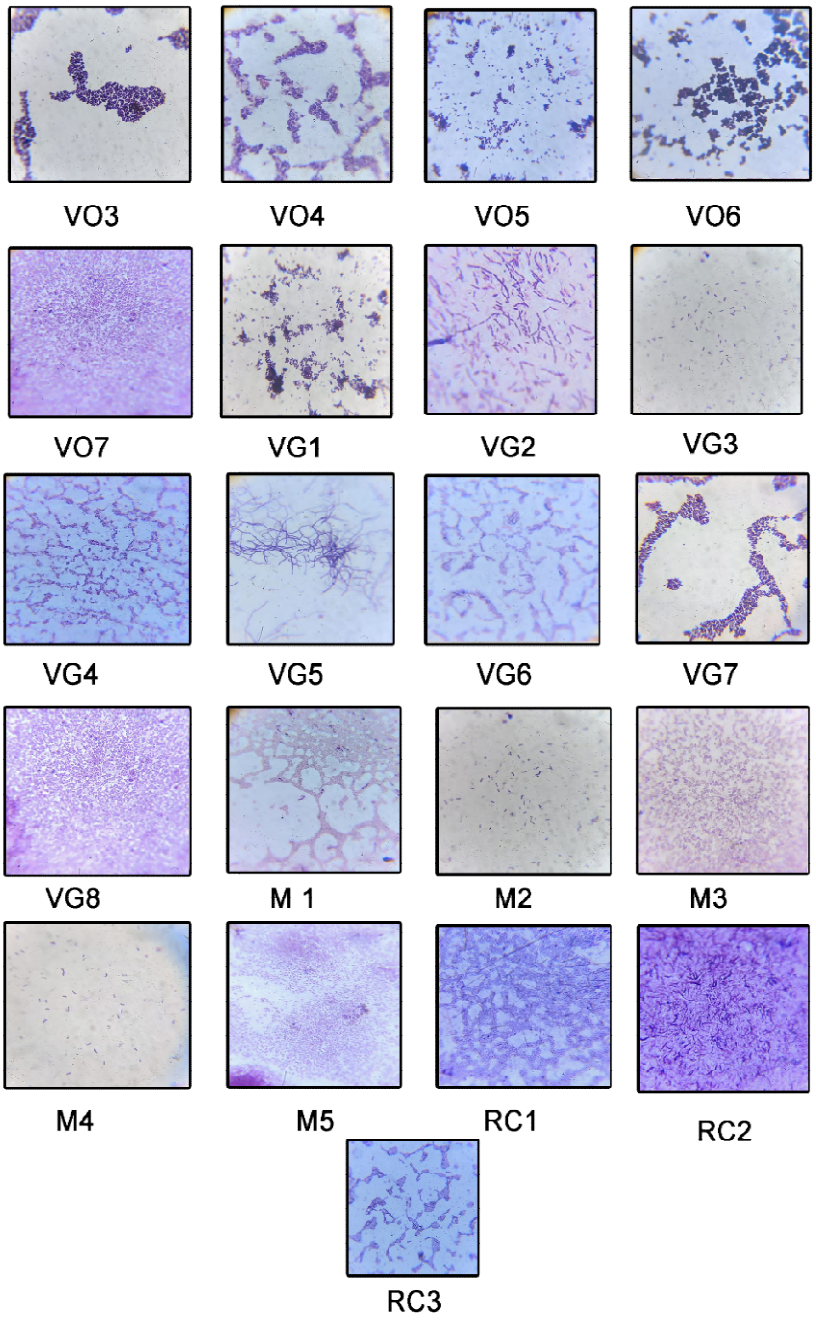


Fig. 4.3 – Gram staining overview of selected isolates of rhizobacteria of soil sample from different agricultural fields

Note KW- Khijadiya Wheat field soil sample, KS - Khijadiya field area of Sorghum, VG- Veraval Garlic crop Field, VO- Veraval Onion crop field, KC- Khijadiya Chickpea crop field. MC- Morbi Corn crop field, RC- Rajkot Corn field represent the +ve Gram Positive and –ve Gram Negative bacterial isolates.

4.4 Growth promotion analysis of PGPR traits

For the growth analysis total 41 isolates have been exposed to the biochemical characterization of growth promotion parameters which can identified for the plant growth promoting rhizobacterial strains. Biochemical characterization such as IAA, HCN test, Siderophore, Chitinase, Ammonia and Phosphate solubilization test was being performed.

4.4.1 HCN production

Microbial cyanides seem to play a role in suppression of many plant diseases. A positive correlation between production of HCN and suppression of root rot by bacterial isolates has been reported (Defago *et al.,* 1990, Rajni and Richa Thakur 2018). In the present study, Sucrose agar medium is used to detect the production of HCN. 4 to 5 drops of picric acid added into the inoculated plate has been changed from yellow to orange-red. Also in present study, 13 isolates were tested for qualitative HCN production on nutrient agar plates supplemented with 2% glycine and 0.5% picric acid. 31.70% out of 41 isolates. KC9 and KC11 is showed maximum HCN production (Fig. - 4.4). Several factors have been reported to influence the rate of HCN production. Glycine has been found to be the direct precursor of microbial cyanide production (Knowles 1976, Voisard *et al*., 1989, Rajni Devi and Richa Thakur 2018) and it has been found in root exudates (Bakker *et al.,* 1989, Curl and Truelove 1986). The induction of plant resistance may be involved by HCN production which was as reported by Rajni Devi and Richa Thakur (2018).

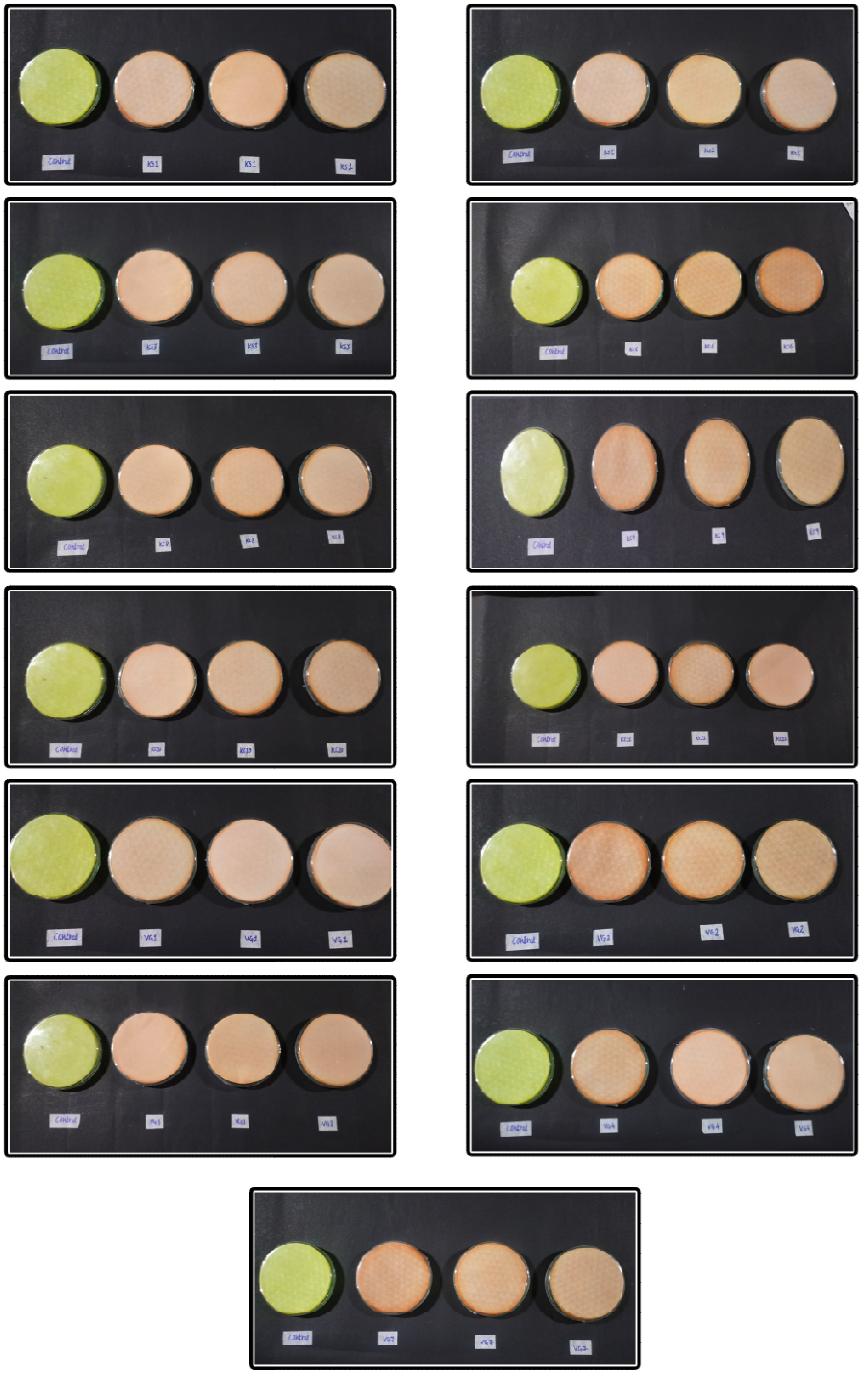


Fig. 4.4 represents HCN Production test for showing positive bacterial isolates

4.4.2 Chitinase production as trait of PGPR

Chitinase activity can exploited for the inhibition of pathogenic growth in plants.

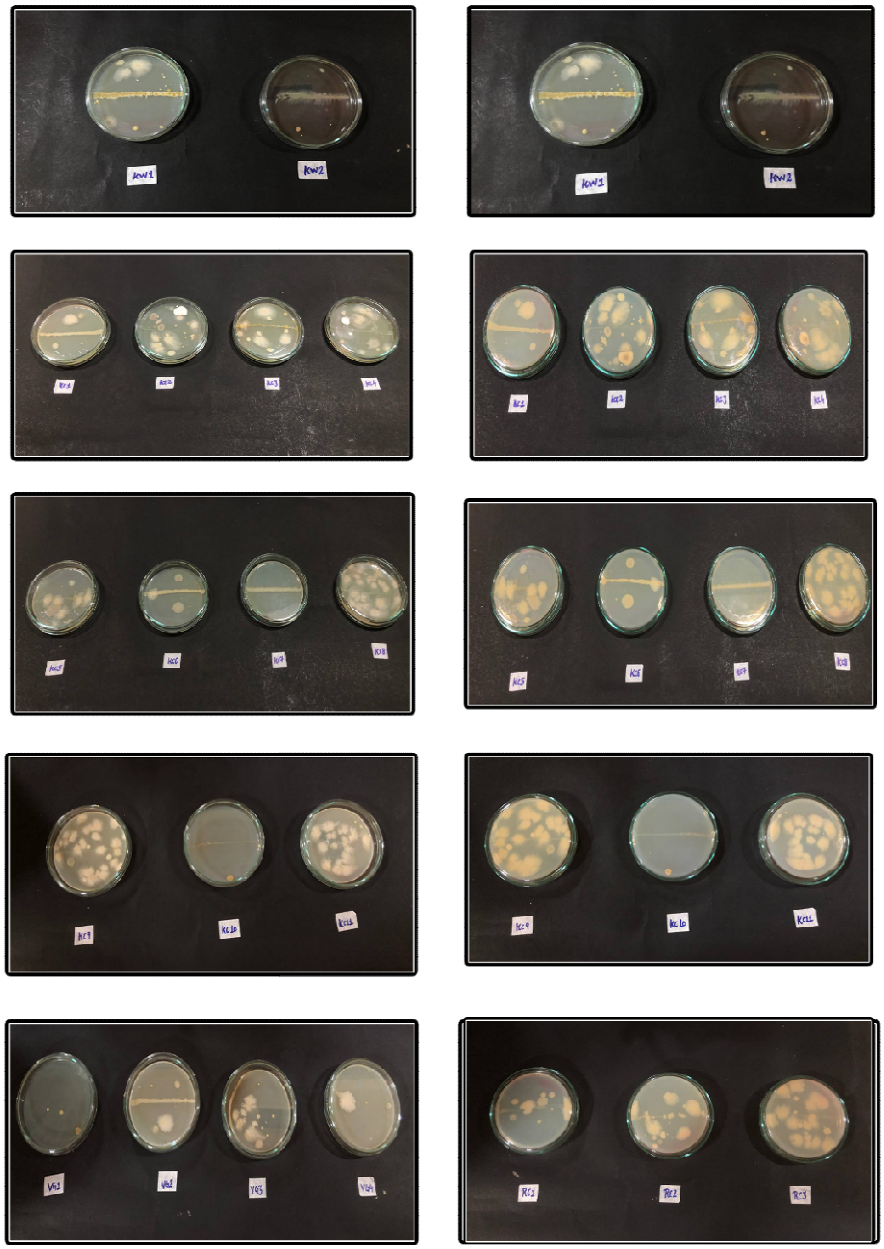


Fig. 4.5 Chitinase Production of all bacterial isolates showing negative result.

Fig. 4.5 shows none of out of 41 isolates displayed chitinase production by obtaining significant zone of chitin degradation on a chitin agar plate. In the report of Joshi and Joshi (2017), chitinase activity is reported to be found 0.35 IU and 0.2 IU respectively.

4.4.3 Siderophore production

Siderophore is an organic compound that is produced by bacterial colonies and can help to grow plants in low iron conditions.

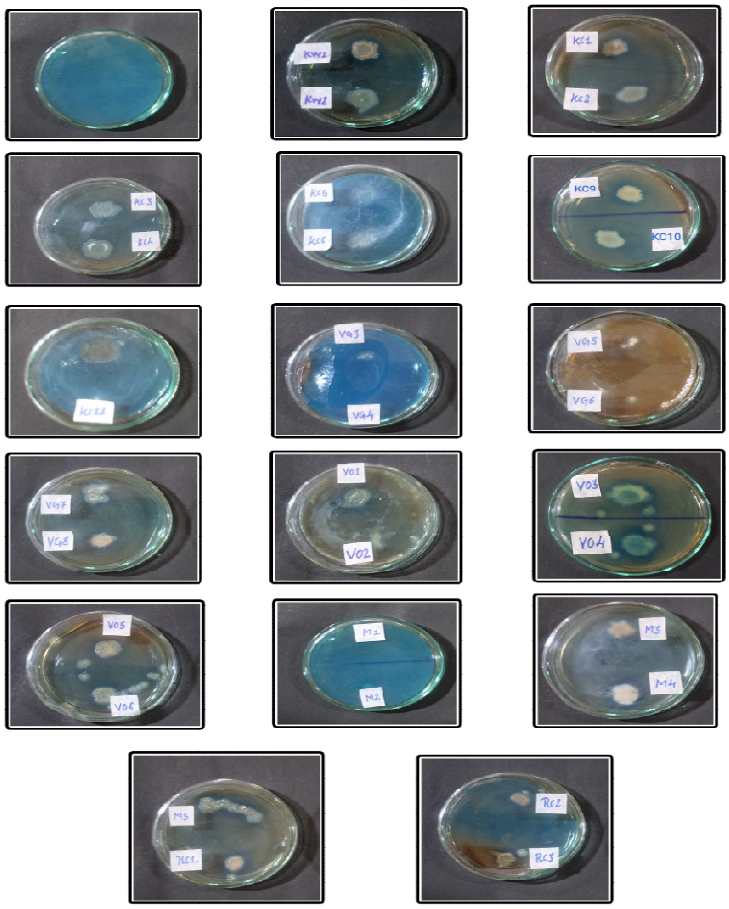


Fig. 4.6 Siderophore production of the selected isolates

Siderophore facilitates iron, which is a cofactor for nitrogenase enzyme essential for atmospheric nitrogen fixation by plants. Only the isolates from Khijadiya displayed siderophore production. Four isolates from Khijadiya – KS2, KC8, KC9 and KC11 displayed siderophore production. Similarly, Shrivastava *et al.,* (2022) studied *Pseudomonas species* is

showing noteworthy contribution in the production ability of siderophore. In her report Pseudomonas has been optimized as a remarkable resource of siderophore which can inhibit the growth of pathogen by quick dropping the ferric ion in the rhizosphere.

4.4.4 Phosphate solubilization

Production of phosphate enzyme be the bacterial isolates. Agar well diffusion method being performed for the detection of phosphate solubilization assay. In the PVK medium bacterial suspension was inoculated in between the well and incubate at 37℃ for 24 hours only few cultures have zoned the zone of hydrolysis (Fig. 4.7).

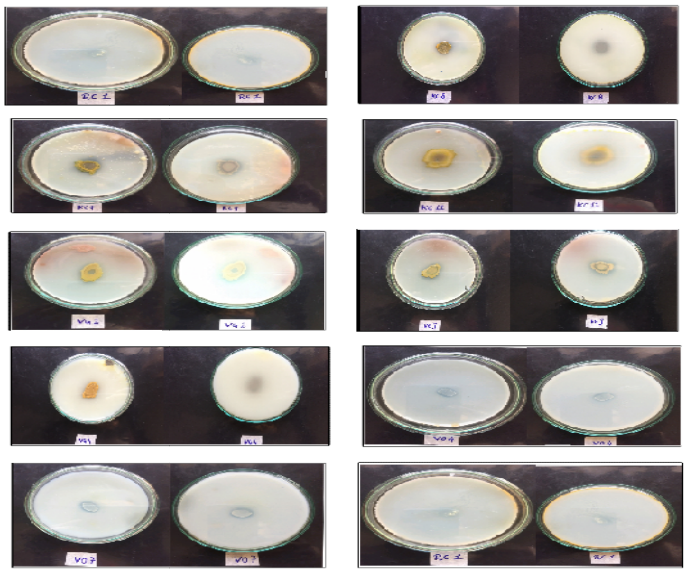


Fig. 4.7 Phosphate Solubilization tests for showing positive bacterial isolates

Among macronutrients required by a high amount for enhancement of plant growth is phosphorus ion, which exists in most cases as an insoluble form. Rhizospheric bacteria have the ability to convert phosphorus from insoluble to soluble form through different mechanisms such as the production of enzymes and /or organic acids (Paul D and Sinha SN 2017). In the current study, the appearance of a clear zone around the bacterial growth on Pikovskaya agar media indicates their success in phosphate solubilizing. The clear zone was observed in KS2, KC8, KC9, KC11, VG2, VG3, VG4, VO4, VO7 and RC1 which correlated with the amount of liberated phosphate. The results showed that the highest phosphate solubilizing was achieved by bacterial isolate VO7 and RC1 followed by VO4. Also, the

difference between the amount of liberated phosphate recorded by bacterial isolates VG4 and VO4 are non-significant (Fig.- 4.7). The production of low molecular weight organic acid is considered the main mechanism for phosphate solubilization by different bacterial species (Khan *et al.,* 2019).

4.4.5. Ammonia production

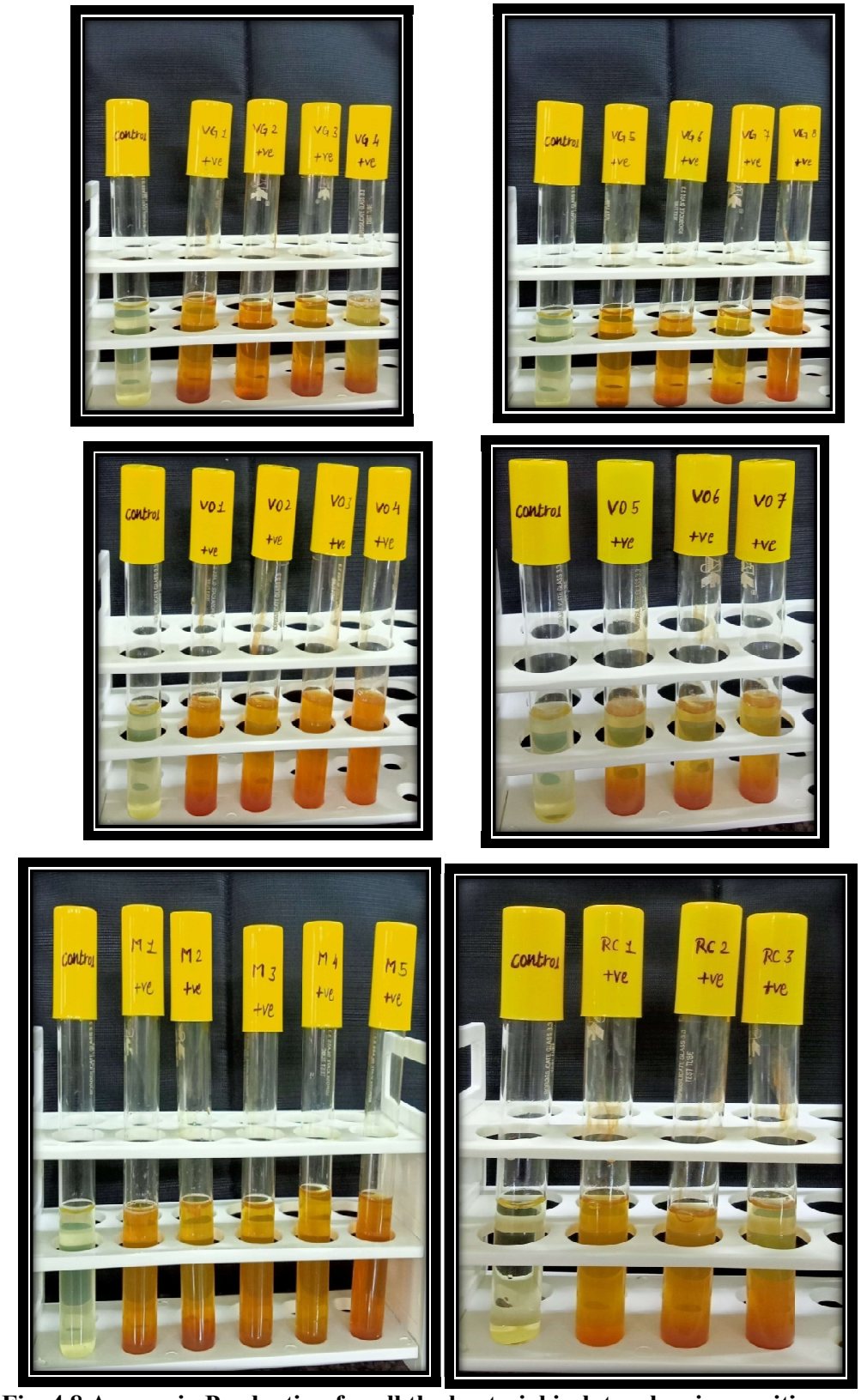


Fig. 4.8 Ammonia Production for all the bacterial isolates showing positive results

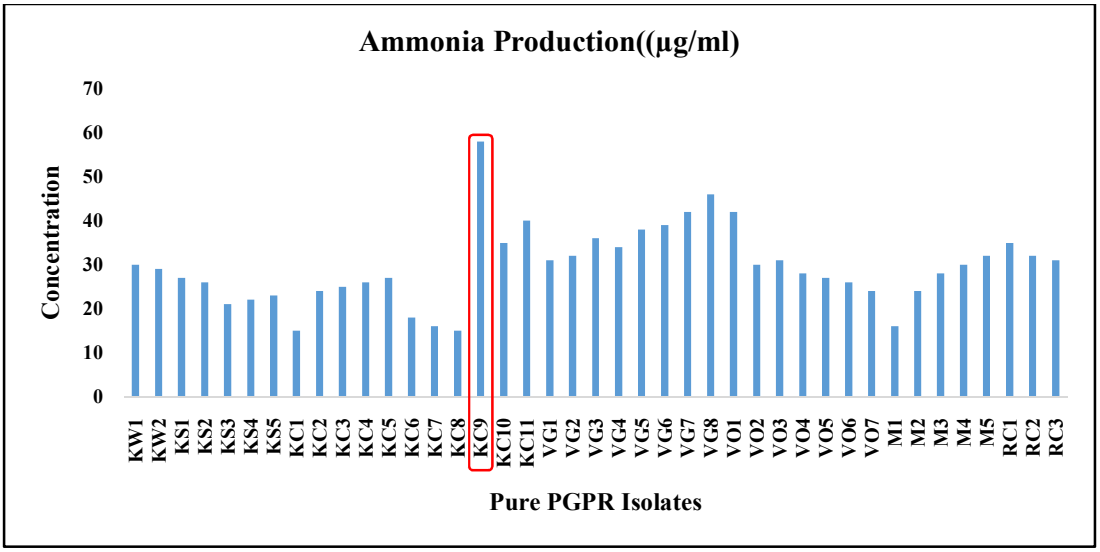


Fig. 4.9 Quantitative estimation of Ammonia Production

Fig. 4.8 indicates nitrogen fixation, ammonia and hydrogen cyanide production by the isolates. All 41 isolates were tested positive for nitrogen fixation, which facilitates the enhanced amount of available nitrogen in the form of ammonia, nitrates or nitrites in the rhizosphere.The ammonia production by the PGPR indirectly affects plant growth and development. The fig. 4.9 depicted brown color development, which indicates the production of ammonia in test tubes by the addition of Nesseler's reagent. The spectrophotometric analysis shows in the figure no. of the brown color developed in all 41 isolates.The maximum amount of ammonia was observed in KC9 (58 µg/ml). According Gosawami *et al.*, (2013) have been reported production of ammonia was noted maximum 36 µg/ml. Similar study of Vasant *et al.*, 2023 reported maximum amount of ammonia produce 55.5 36 µg/ml.Ammonia as important chemical component exert phytopathogenic effect as reported in Fahsi*et al.,* (2021). This paper also highlights an intensified production of ammonia from 0.23 to 0.33 µmol·mL^{-1}. In a report of Tsegaye *et al.,* (2019) the influence of ammonia production as successful PGPR trait had found to be recorded 4.5 % out of 426 samples of *tef* (*Eragrostistef*) collected from rhizosphere soils. As quoted by Tsegaye *et al.,*(2019) "The presence of ammonia producing PGP bacteria is an indicative for ammonification process were takes place in the rhizosphere than non-rhizosphere soil", which clearly indicates the strong influence of Ammonia in PGPR isolation and identification.

4.4.6 IAA production

The result revelead that indolesalkowski reagent has been added to the culture supernatant after the 30 mins pink color is being obtained. Which indicates the production of IAA that stimulate and facilitate the plant growth promotion. In the report of Rani *et al.,*(2011) seven isolates of PGPR bacteria had shown the IAA production ability.

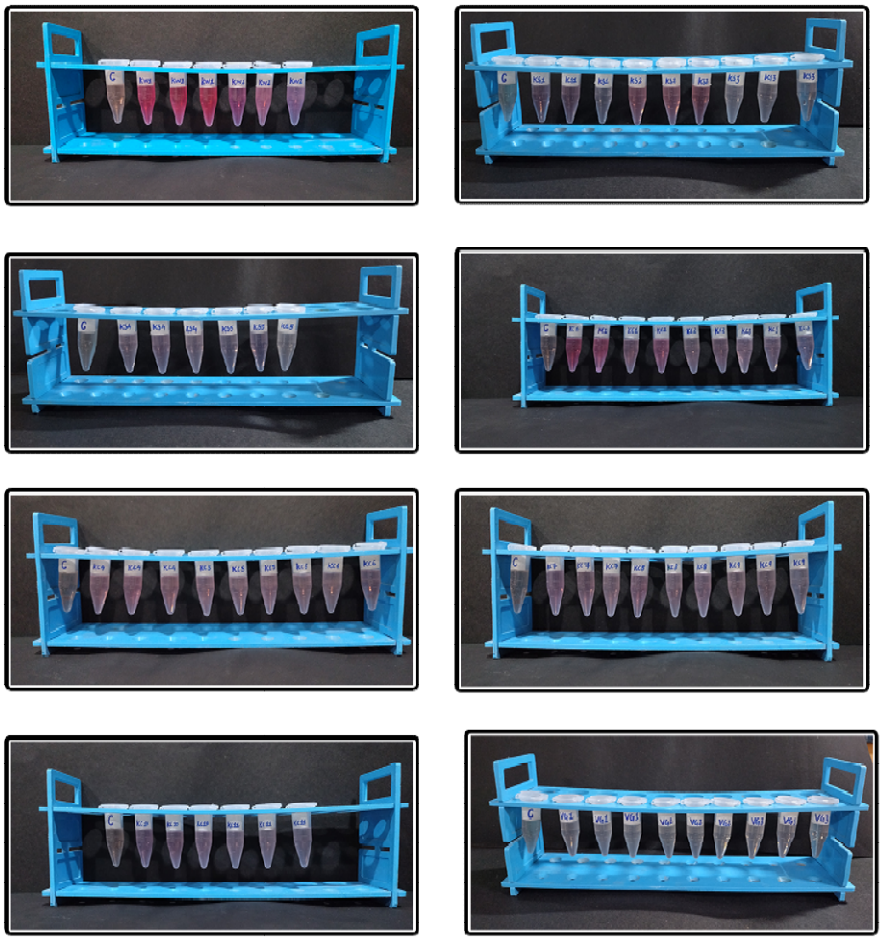


Fig. 4.10 IAA Production test for all bacterial isolates showing positive results

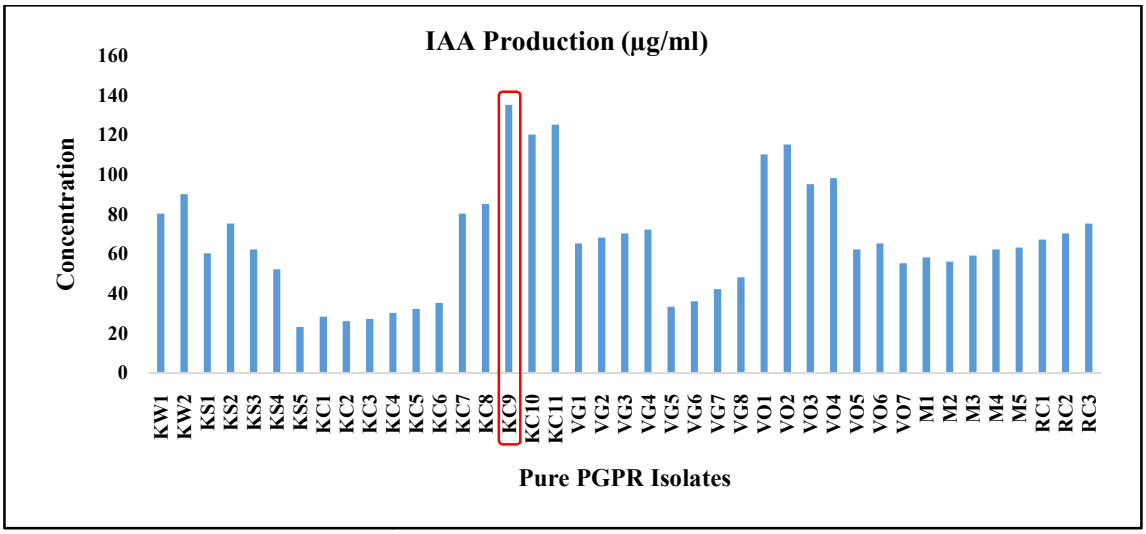


Fig. 4.11Quantitative estimation of IAA Production

All 41 isolates from the different soil samples were screened for the production of IAA (Fig. 4.10). All 41 isolates give production of IAA. L-Tryptophan is generally considered as an IAA precursor; because of its addition to IAA producing bacterial culture enhances IAA biosynthesis (IAA production was found in the medium amended with 0.1% tryptophan for

all isolates Costacurta and Venderleyden, 1995, B. Mohite 2013). All 41 isolates preferred Tryptophan for IAA production Maximum (Figure 4.10). Multifarious factors are responsible for the plant growth promotion employing PGPR and among them one such important contributing factor is IAA (Gold stein 1995). The IAA production is dependent on growth stage of microbes and availability of substrates, and also reports states the high intensity of IAA production in rhizosphere soils, seven isolates of PGPR bacteria had shown the IAA production ability (Rani *et al.,* 2011). IAA is a phytohormone for the separation and differentiation of plant cells and tissues, which can supports plant root elongation. Fig.4.11 shows results of IAA production. 41 isolates produced IAA in the range 23 – 135 µg/ml. Vasant *et al.,* (2023) reported thirty two isolates produced in the range of 20.7-133 µg/ml.

Table 4.3 Summary of observation of PGPR traits with selected isolates of Rhizobacteria

Sr. No.	Sample No.	HCN Production	Chitinase Production	Siderophore Production	IAA Production	Ammonia Production	Phosphate solubilization
1	KW1	-	-	+	+	+	-
2	KW2	-	-	+	+	+	-
3	KS1	+	-	+	+	+	-
4	KS2	+	-	+	+	+	+
5	KS3	+	-	+		+	-
6	KS4	-	-	+	+	+	-
7	KS5	-	-	+	+	+	-
8	KC1	-	-	+	+	+	-

9	KC2	-	-	+	+	+	-
10	KC3	-	-	+	+	+	-
11	KC4	-	-	+	+	+	-
12	KC5	-	-	+	+	+	-
13	KC6	+	-	+	+	+	-
14	KC7	-	-	+	+	+	-
15	KC8	+	-	+	+	+	+
16	KC9	+	-	+	+	+	+
17	KC10	+	-	+	+	+	-
18	KC11	+	-	+	+	+	+
19	VG1	+	-	+	-	+	-
20	VG2	+	-	+	-	+	+
21	VG3	+	-	+	-	+	+
22	VG4	+	-	+	-	+	+
23	VG5	-	-	+	+	+	-
24	VG6	-	-	+	-	+	-
25	VG7	+	-	+	+	+	-

26	VG8	-	-	+	+	+	-
27	VO1	-	-	+	+	+	-
28	VO2	-	-	+	+	+	-
29	VO3	-	-	+	+	+	+
30	VO4	-	-	+	+	+	+
31	VO5	-	-	+	+	+	-
32	VO6	-	-	+	+	+	-
33	VO7	-	-	+	+	+	+
34	M1	-	-	+	+	+	-
35	M2	-	-	+	+	+	-
36	M3	-	-	+	+	+	-
37	M4	-	-	+	+	+	-
38	M5	-	-	+	+	+	+
39	RC1	-	-	+	+	+	-
40	RC2	-	-	+	+	+	-
41	RC3	-	-	+	+	+	-

Note Colour codes showing number of positive isolates for trait identification based screening + all five traits positive; + Only four traits showing positive; + only three traits showing positive

Table 4.4 Summary of determination of potential rhizobacterial isolates

Showing PGPR traits

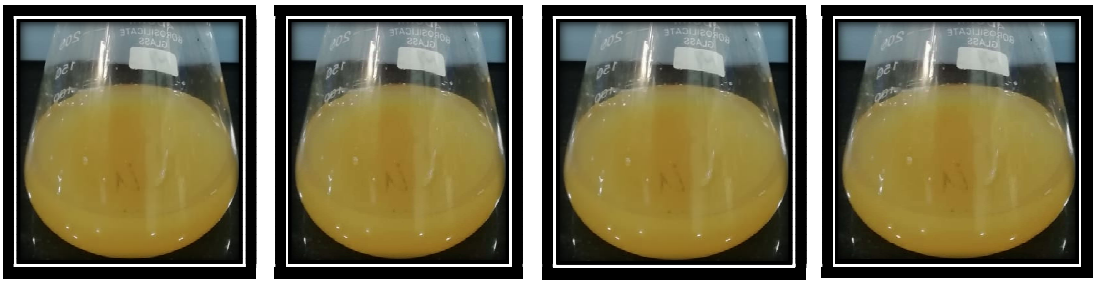
Number of Isolates positive in PGPR trait	Number of growth analysis traits positive
4 isolates (KS2, KC8, KC9 & KC11)	5
11 isolates	4
25 isolates	3
1 isolate	2

The table 4.3 and table 4.4 data is a reflection of various significant number of isolates from different sampling sites. Out of the 41 isolates, positive results of 5 traits are shown in the 4 isolates like, KS2, KC8, KC9 and KC11. 9.76% isolates have shown positive with traits. This is a compiled results of the 41 isolates. 4 traits have shown the positive results with the 11 isolates like, KS1, KC6, KC10, VG2, VG3, VG4, VG7, VO3, VO4, VO7 and M5. 26.83% isolates give 4 trait positive result from the 41 isolates. 2 traits are showing the positive result only in the VG6 isolate with 2.44% out of 41 isolates. The remaining isolates are express positive result with 3 traits with 60.98%. PGPR, can be identified based on an indirectly influencing trait siderophore production plant growth. They usually bind to the available form of iron Fe3+ in the rhizosphere, thus making it unavailable to the phytopathogens and protecting the plant health (Ahmad and Khan, 2008). Siderophore production is an important attribute of PGPR trait as secondary metabolites, the iron fulfilment was mitigated by siderophore production by PGPR, also a protection from phytopathogens provided by siderophore producing isolates. The heavy metal contamination can also be reduced by siderophore producers (Arora and Verma 2017).

4.7 Effect of Seed Inoculation with Plant Growth-Promoting Rhizobacteria (KS2, KC8, KC9 and KC11) by employing bio-priming method

4.7.1 Inoculum Preparation

The PGPR strain (KS2, KC8, KC9 and KC11) were inoculated in 100 Erlenmeyer flask containing 50 ml nutrient broth, flasks were incubated at 37°C for 2 days.During inoculation, the viable cell suspension count was KS2 is 12 x 10^8 CFU/ml, KC8 is 16 x 10^8 CFU/ml, KC9 is 33 x 10^8 CFU/ml, and KC11 is 23 x 10^8 CFU/ml have been found. As per the study of samy *et al.,* 2008 at the movement of inoculation, live cells count varied between 2.8 x 10^9 CFU/ml and 3.6 x 10^9 CFU/ml in the cell suspensions.



KS2 KC8 KC9 KC11

Fig. 4.12 Preparation of Bacterial Inoculum for Potent Selected Isolates

4.7.2 Evaluation study of PGPR trait by individual pot study

An evaluation study at individual pot plant experiment level has successfully revealed the determination of PGPR trait of the four selected isolates reflected in fig. 4.13 – 4.17.

Control KS2 KC8 KC9 KC11

Fig. 4.13 Growth Promotion Activity of <u>Cumin :</u> With and Without Treatment of PGPR Strain (KS2, KC8, KC9 and KC11)

Control KS2 KC8 KC9 KC11

Fig. 4.14 Growth Promotion Activity of <u>Groundnut :</u> With and Without Treatment of PGPR Strain (KS2, KC8, KC9 and KC11)

Control **KS2** **KC8** **KC9** **KC11**

Fig. 4.15 Growth Promotion Activity of Chickpea : With and Without Treatment of PGPR Strain (KS2, KC8, KC9 and KC11)

Control **KS2** **KC8** **KC9** **KC11**

Fig. 4.16 Growth Promotion Activity of Mung : With and Without Treatment of PGPR Strain (KS2, KC8, KC9 and KC11)

Control **KS2** **KC8** **KC9** **KC11**

Fig. 4.17 Growth Promotion Activity of Rice : With and Without Treatment of PGPR Strain (KS2, KC8, KC9 and KC11)

Individual level pot plant experiment with 4 potent PGPR bacteria with control has been shown the growth effect as represented in fig. 4.13 – 4.17. The root and shoot growth with control has clearly been viewed in the figure showing the potential effect of PGPR traits

whose detail representation had been recorded in table 4.5-4.9. In the present study, a series of 8 sets of rhizobacterial consortia has been employed preceded by individual inoculum (Table- 4.5-4.9) development at flask level for determination of root and shoot growth, No. of leaves effect study in monocot & dicot plants.

Table 4.5 Root and shoot length of Cumin plant

Sr. No	Potent Isolate of Rhizobacteria	Root Length (cm)	Shoot Length(cm)
Cumin			
1	Control	6	16
2		6.8	15.2
3		6.4	16.3
	Mean ± SD	6.4±0.4	15.83±0.56
4	KS2	7.0	16
5		7.1	16.2
6		7.2	16.3
	Mean ± SD	7.0±0.26	16.2±0.60
7	KC8	6.7	17.8
8		6.8	17.2
9		6.9	16.5
	Mean ± SD	6.8±0.30	17.16±1.16
10	KC9	10.3	28
11		10.9	29.5
12		10.1	27.8
	Mean ± SD	10.43±0.41	28.43±0.92
13	KC11	8	28
14		9.5	27.3
15		9	27.8
	Mean ± SD	8.83±0.76	26.93±1.05

Table 4.6 Root and shoot length and No. of Leaves of Groundnut Plant

Sr. No.	Potent Isolate of Rhizobacteria	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Groundnut				
1	Control	6	15	40
2		5.2	18	52
3		7	17	42
	Mean ± SD	6.06±0.90	16.66±1.52	44.66±6.42
4	KS2	7.2	17.1	46
5		7.3	17.5	45.8
6		7.8	17.2	46.3
	Mean ± SD	7.1±0.36	17.5±1.75	46.0±4.16
7	KC8	8.1	18.0	46.0
8		8.2	17.9	46.2
9		7.9	182	46.3
	Mean ± SD	8.0±0.76	18.0±1.52	46.3±6.11
10	KC9	8	23	56
11		9	24	60
12		10.5	21	52
	Mean ± SD	9.16±1.25	22.66±1.52	56±4
13	KC11	8	21	58
14		7.5	19	60
15		8	20	64
	Mean ± SD	**7.83±0.2**	**20±1.0**	**60.66±3.05**

Table 4.7 Root Length, Shoot Length and No. of leaves of Chickpea plant

Sr. No	Potent Isolate of Rhizobacteria	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Chickpea				
1	Control	10	22	62
2		9.8	18	65
3		12	20	68
Mean ± SD		10.6±1.21	20±2.0	65.0±3.0
4	KS2	10.1	22.1	60
5		10.5	21.5	69
6		10.2	21.9	66
Mean ± SD		10.1±0.60	21.0±2.08	66.0±3.60
7	KC8	11.1	22.1	62
8		11.3	22.3	70
9		11.2	22.4	67
Mean ± SD		11.2±0.1	22±1.0	66.5±6.50
10	KC9	14	23	68
11		12	27	70
12		16	25	64
Mean ± SD		14±0.2	25±2.0	67.33±3.05
13	KC11	13	21	69
14		11	20	63
15		14.5	26	62
Mean ± SD		12.83±1.75	22.33±3.21	64.66±3.78

Table 4.8 Root Length, Shoot Length and No. of leaves of Mung plant

Sr. No	Potent Isolate of Rhizobacteria	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Mung				
1	Control	6.5	16	10
2		6	18	16
3		6.2	15	12
	Mean ± SD	6.23±0.25	16.33±1.52	12.66±3.05
4	KS2	6.5	16.5	10
5		6.8	16.8	13
6		6.7	16.9	15
	Mean ± SD	6.5±0.40	16.7±2.0	13.33±3.05
7	KC8	7.0	17	17
8		7.1	17.2	17.2
9		7.2	17.3	17.3
	Mean ± SD	7.0±0.1	17±2.0	17±4.58
10	KC9	10	30	38
11		10.5	28	40
12		10.2	32	42
	Mean ± SD	10.23±0.25	30±2.0	40±2.0
13	KC11	9.5	25	26
14		9	20	20
15		8	23	28
	Mean ± SD	8.83±0.76	22.66±2.51	24.66±4.16

Table 4.9 Root Length, Shoot Length and No. of leaves of Rice plant

Sr. No	Potent Isolate of Rhizobacteria	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Rice				
1	Control	8.5	15	12
2		11	17	19
3		6	9	13
Mean ± SD		8.5±2.5	13.66±4.16	14.66±3.78
4	KS2	9.0	14	15
5		9.3	14.3	18
6		9.2	15	16
Mean ± SD		9.0±0.40	14.2±2.51	15.33±1.52
7	KC8	8.5	15.3	16
8		8.8	15	19
9		8.9	15.5	18
Mean ± SD		8.7±0.3	15.2±1.52	15.5±1.52
10	KC9	12	22	22
11		10	18	16
12		10.5	24	20
Mean ± SD		10.83±1.04	21.33±3.05	19.33±3.05
13	KC11	9	15	18
14		8.9	18	16
15		9.5	20	13
Mean ± SD		9.13±0.32	17.66±2.51	15.66±2.51

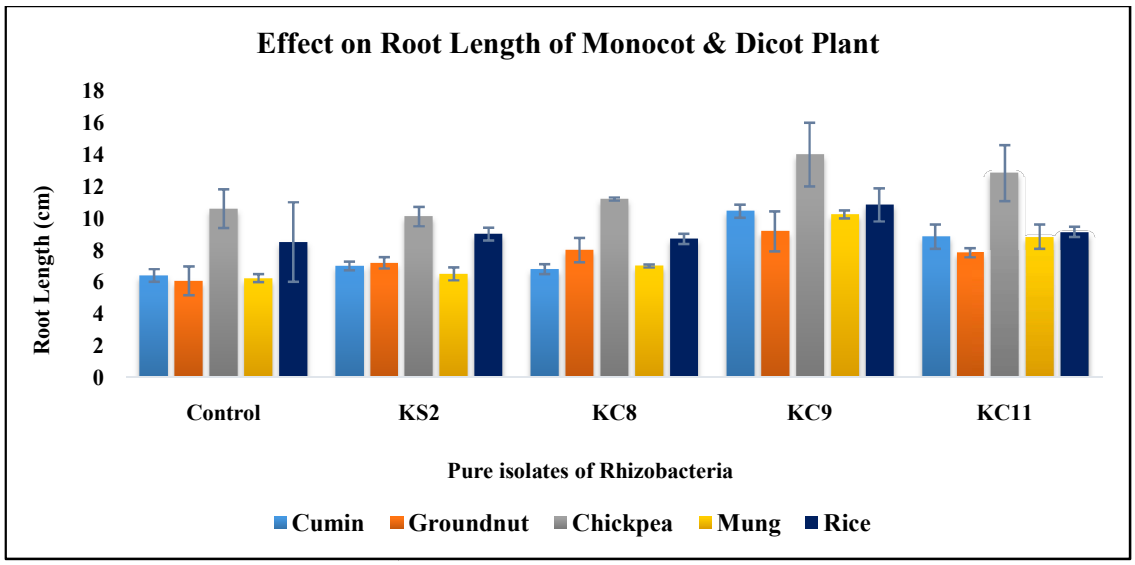


Fig. 4.18 Graphical Representation; *In-vitro* Pot Analysis of PGPR strain on Root Length (cm) of Monocot & Dicot Plant

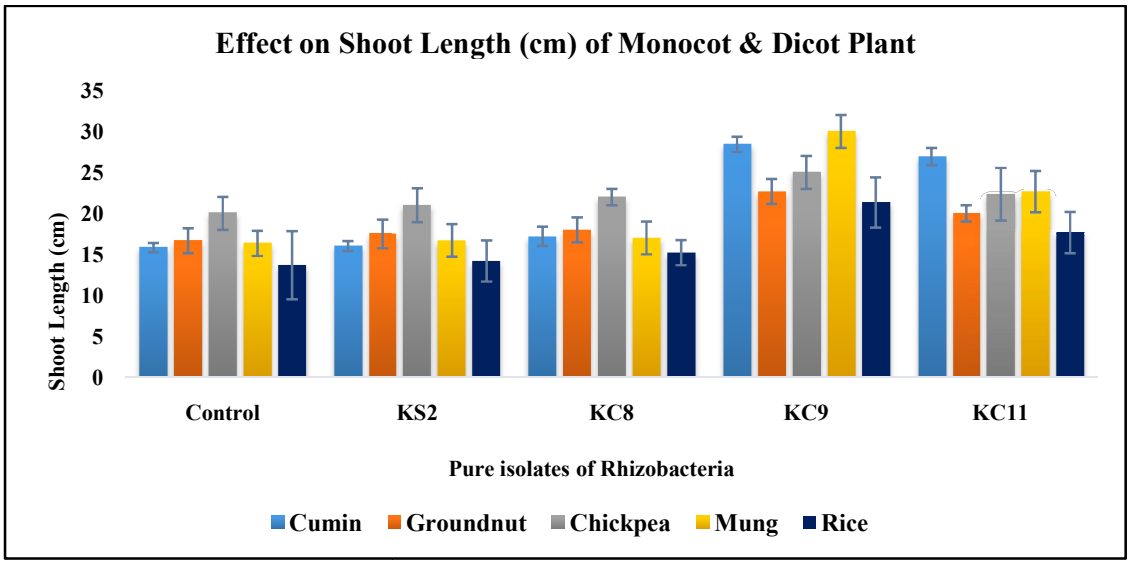


Fig. 4.19 Graphical Representation; *In-vitro* Pot Analysis of PGPR strain on Shoot Length (cm) of Monocot & Dicot Plant

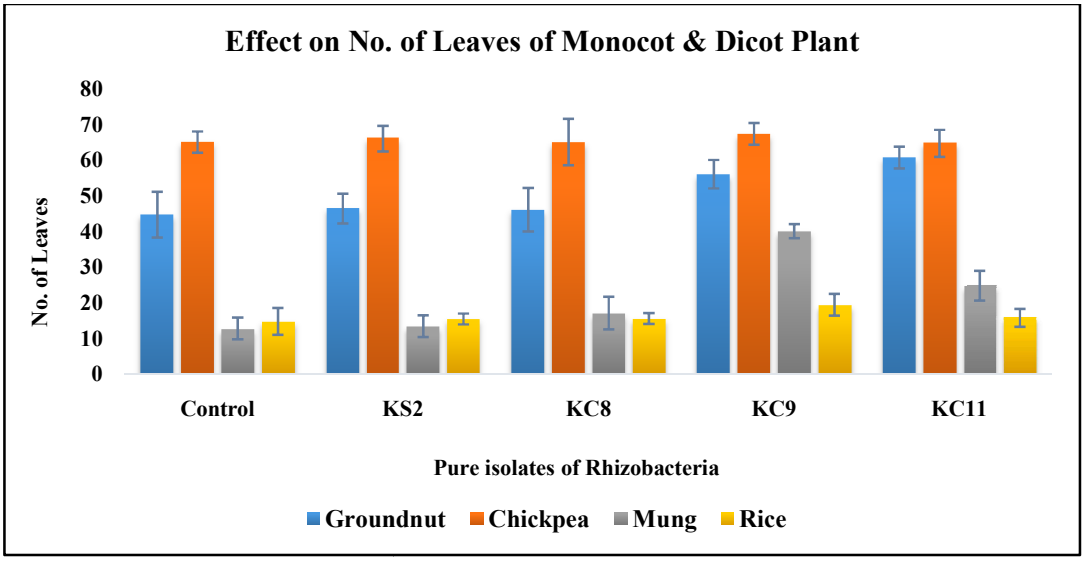


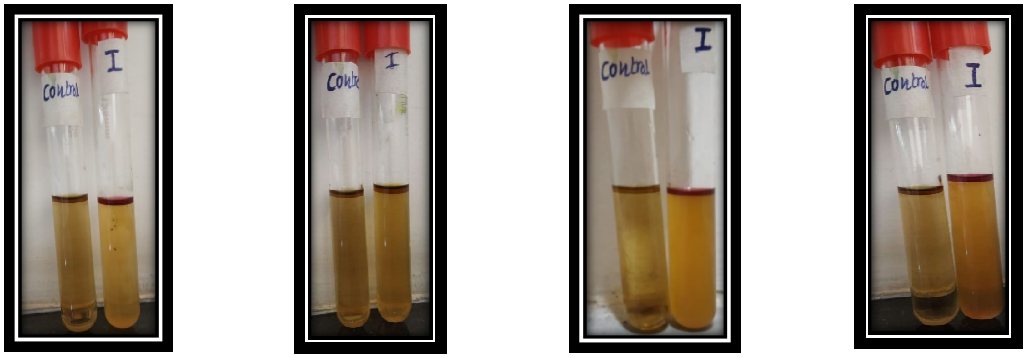
Fig. 4.20 Graphical Representation; *In-vitro* Pot Analysis of PGPR strain on No. of leaves of Monocot & Dicot Plant

In this current study, bio-priming seeds of cumin, groundnut, chickpea, mung and rice were treated with 2.0ml of each PGPR strain (KS2, KC8, KC9, and KC11). The treated and untreated (as control) seeds were planted in the plastic glasses with triplicate manner for seedling germination and observed for another 15 days. After the completion of incubation period, measurements were taken for root length, shoot length and number of leaves of germinated seedlings. The results, as depicted in fig. 4.18showed that the average root length of cumin, groundnut, chickpea, mung, and rice treated with various PGPR inoculants were as follows In cumin KS2 (7.0±0.26 cm), KC8 (6.8±0.30 cm), KC9(10.43±0.41cm) and followed by KC11 (8.83±0.76cm). In the case of groundnut, for KS2 (7.2±0.36 cm), KC8 (8.0±0.76cm), KC9 (9.1±1.25cm), followed by KC11 (7.83±0.28cm).Chickpea root lengths were measured for KS2 (10.1±0.60cm), KC8 (11.2±0.1cm), KC9 (14.0±2.0cm), and followed by KC11 (12.83±1.75cm). In the case of mung beans, the respective root lengths for each PGPR inoculant were KS2 (6.5±0.40cm), for KC8 (7.0±0.1cm), KC9 (10.23±0.25cm), and KC11 (8.83±0.76cm) whereas in rice KS2 (9.0±0.40cm), KC8 (8.7±0.3cm), KC9 (10.83±1.04cm), followed by KC11 (9.13±0.32cm). In contrast, the control group exhibited different growth parameters, with the root length of cumin was (6.4±0.4cm), groundnut (6.04±0.90cm), chickpea (10.6±1.21cm), mung (6.23±0.25cm) and rice was (8.5±2.5cm).Similarly the shoot length of treated cumin seeds was for KS2 (16.0±0.60cm), KC8 (17.2±1.16cm), KC9 (28.43±0.92cm), and followed by KC11 26.93±1.05cm, whereas

in the groundnut, KS2 (17.5±1.75cm), KC8, (18.0±1.52cm) for KC9 (22.66 ±1.52cm), and followed by KC11(20±1.0cm).Chickpea KS2 (21.0±2.08), KC8 (22.0±1.0), KC9 (25±2.0), KC11 (22.33±3.21).Mung plant was recorded maximum in treated with KC11(22.66±2.51) and rice was estimated maximum shoot length in treated with KC9 (21.33±3.05). Result revealed at fig. 4.19the shoot length for cumin in the control group (15.83±0.56cm), groundnut was (16.66±1.52cm), chickpea(20.0±2.0cm),mung(16.33±1.52cm) and rice was 13.66±4.16cm.In the graphical representation, the bacterial strain KC9 was considered as plant growth promoter that significantly enhance the growth of all the plants (Cumin, Chickpea, Groundnut, Mung and Rice) by early seedling development. The number of leaves found maximum in chickpea and groundnut whereas fewer found in mung and rice plant. In control, groundnut(44.66±6.42), chickpea(65.0±3.0), mung(12.66±3.05), rice(14.66±3.78).No. of leaves in groundnut was KS2 (46.33±4.16), KC8 (46.0±6.11), KC9 (56±4.0) and followed by KC11(60.66±3.05) while in chickpea noted for KS2 (66.0±3.60), KC8(65.05±6.50), KC9 (67.33±3.05) and KC11(64.66±3.68).The No. of leaves found in mung KS2 (13.33±3.05), KC8 (17±4.58), KC9 (40±2.0) and followed by KC11 (24.66±4.16),whereas in rice KS2 (15.33±1.52), KC8(15.5±1.52), KC9 (19.33±3.05) and KC11(15.66±2.51)(fig.4.31). Similarly, Dipnwita *et al.,*(2015) has reported, in the pot experiments, it was noted that the inoculation of PGPR substantially enhanced the growth of chickpea plant. Overall, the inoculation led to accelerated seedling growth and development. The present experiment revelled that inoculation with selected isolated bacteria resulted in an increased plant root and shoot length and No. of leaves. Similar enhancements in plant height and leaf area were noted across various crops including potato, radish plants, sorghum, when inoculated with *Pseudomonas* and *Azatobacter* strain (Niranjan *et al.,* 2004).

4.8 Biochemical Characterization of Selected Potent Bacterial Isolates

4.8.1 Indole test : It is screens for the capacity of bacterial colonies to breakdown amino acid tryptophan in the presence of tryptophanase and produce indole.

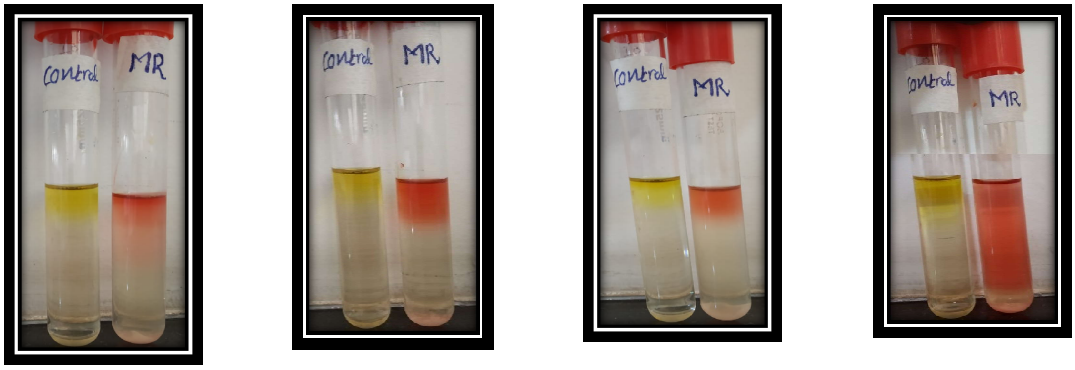


KS2 **KC8** **KC9** **KC11**

Fig. 4.21 Indole test for the selected Bacterial Isolates

4.8.2 Methyl Red test

Methyl red test is for the identification of glucose fermenting bacteria through the pathway of mixed acid fermentation.

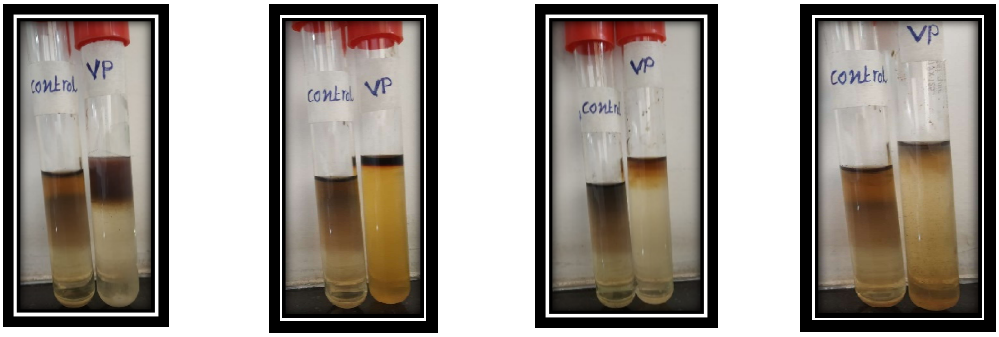


KS2 **KC8** **KC9** **KC11**

Fig. 4.22 Methyl Red Fermentation test for the selected Bacterial Isolates

4.8.3 Voges-Proskaeur test

VP test is employed to detect the acetoin in the bacterial broth cultures. Bacteria having the ability to produce acetylmethylcarbinol.

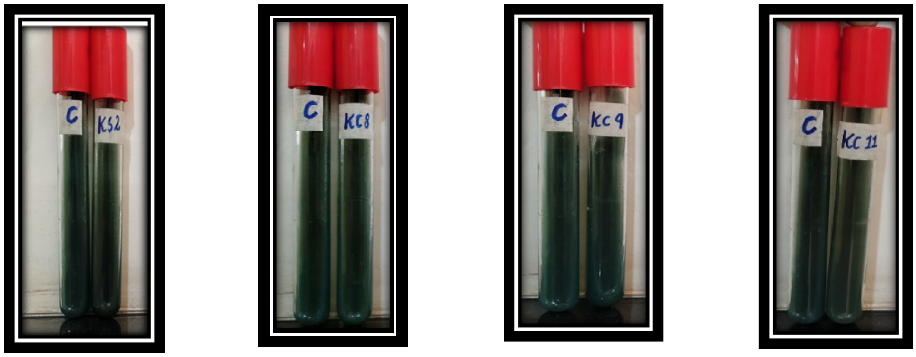


KS2 **KC8** **KC9** **KC11**

Fig. 4.23 VP test for the selected Bacterial Isolates

4.8.4 Utilization of Citrate Test

Citrate utilization test is to identify the organism to use sodium citrate as the only carbon source and ammonium hydrogen phosphate as a nitrogen source by producing citrase enzyme.



KS2 **KC8** **KC9** **KC11**

Fig. 4.24 Citrate Utilization test for the selected Bacterial Isolates

4.8.5 Starch Hydrolysis

Bacteria can hydrolyze starch in the form of amylose and amylopectin in the presence of alpha amylase and oligo-1,6 – glucosidase enzyme.

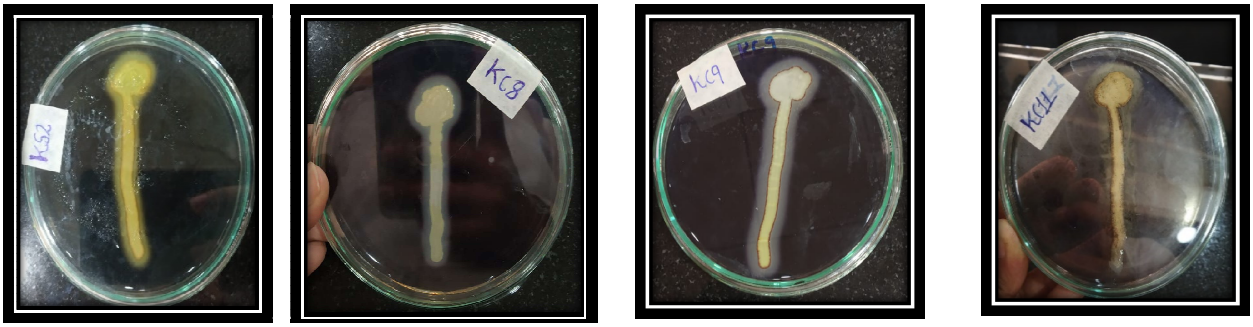


Fig. 4.25 Starch Hydrolysis test for the selected Bacterial Isolates

4.8.6 Carbohydrate Fermentation test

Carbohydrate fermentation test is determined for the identification of bacteria that can utilize carbohydrates to a sole source and result revealed that the presence of acid and gas production from the fermentation by particular carbohydrate by the observation of colour change.

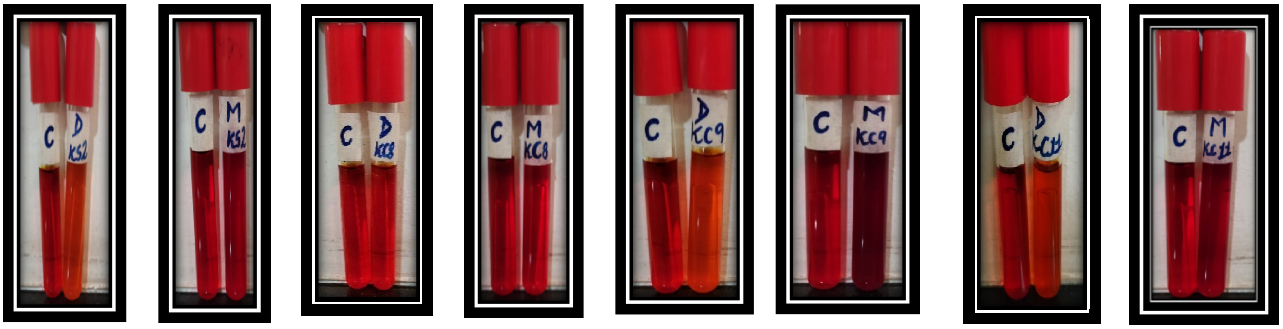


Fig. 4.26 Carbohydrate Fermentation test for the selected Bacterial Isolates

Table 4.10- Representation to the Biochemical Characterization of Selected Potent Bacterial Isolates

Isolates	Indole	MR	VP	Citrate Utilization	Starch	Dextrose	Mannitol
KS2	+	+	-	-	+	+	-
KC8	-	+	-	-	+	+	-
KC9	+	+	-	-	+	+	-
KC11	+	+	-	-	+	+	-

By the performance of biochemical characterizations result revealed in fig. 4.21 - 4.26and table - 4.10, represented that KS2, KC8, KC9 and KC11 isolate exhibited positives results for iodole, methyl-red, catalase, motility, dextrose fermentation and starch utilization give positive tests, while all selected four isolates can't be able to utilize citrate, tryptophan (VP test) and dextrose as substrate for their growth. Shambhavi *et al.,* (2020) reported as *Bacillus sp.* shows positive results of all the biochemical analysis such as catalase, urease, oxidase, citrate utilization, vogues-proskauer, nitrate reduction test, motility and amylase production.

4.9 Molecular Identification of Selected Potent Bacterial Isolates

4.9.1 16S RNA Sequencing

For the molecular identification of mature bacterial isolates of KS2, KC8, KC9 and KC11 were outsourced at Gene Explore Diagnostics & Research Centre Pvt. Ltd. Ahmedabad, Gujarat for 16S RNA sequencing. As per the std protocol of Sanger's method, DNA sequencing reaction of PCR amplicon was carried out with 357F & 1391R primers using BDT v3.1 Cycle Sequencing Kit on ABI 3500xl Genetic Analyzer. The partial 16s rRNA sequence was used to carry out BLAST with the database of NCBI GenBank database. Based on the maximum identity score first ten sequences were selected and aligned using multiple sequence the alignment software programs (Dipanwita *et al.,* 2015).

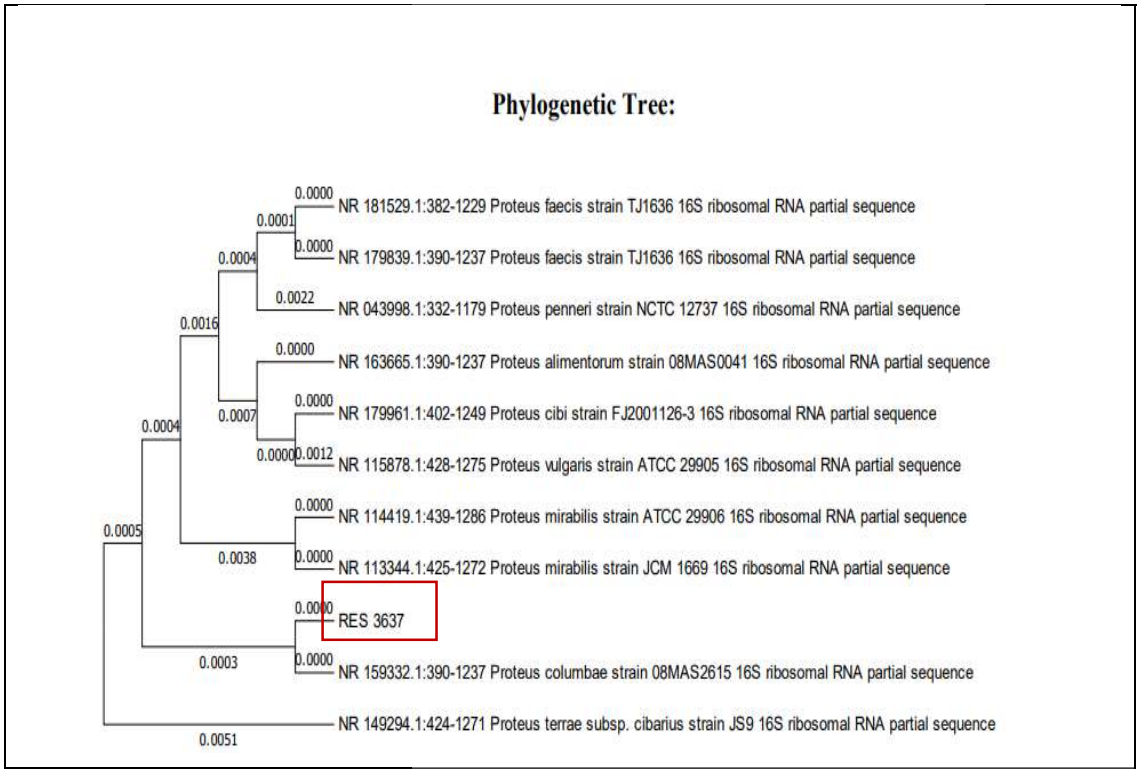


Fig. 4.27 Phylogenetic Tree of KS2 bacterial Strain employing Neighbor-Joining method

Bacterial Sample labeled as AU_CB_MM_KS2, with the reference id RES-3637 was closely related to *Proteus Columbae,* as determined through nucleotide homology analysis. Confirmation of these findings was achieved by 16s Microbial Screening Genetic Typing employing software's that considered E value which shows the 100% match with various *Proteus sp.* The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the maximum composite likelihood method and are in the units of the number of base substitutions per site. The analysis involved 11 nucleotide sequences. There was a total of 847 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.16S rRNA gene sequences by the comparison of available sequences in the database of gene bank with the help of BLAST homology. KS2 was identified as *Proteus sp.* Similarly, Saitou *et al.,* (1987) has reported neighbor-joining method has been utilized for the

reconstructing phylogenetic trees and Kumar *et al.,* (2016) used the MEGA7 bioinformatics tool for molecular evolutionary genetics analysis.

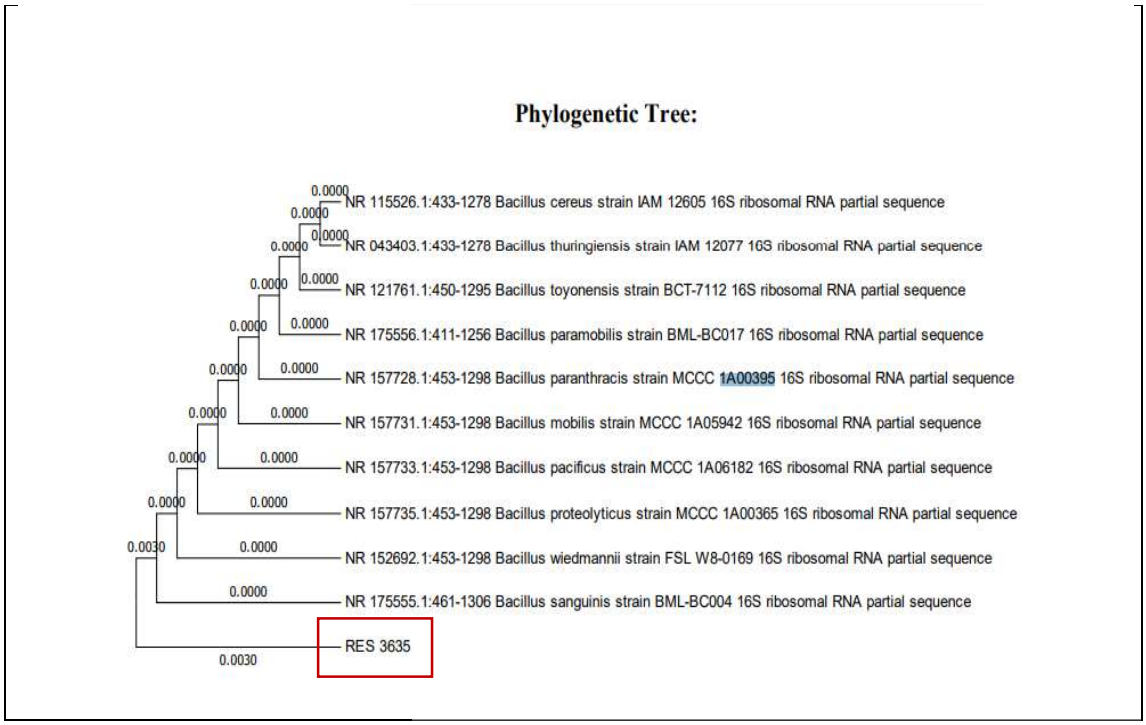


Fig. 4.28 Phylogenetic Tree of of KC8 bacterial Strain employing Neighbor-Joining method

Thebacterial sample designated as AU_CB_MM_KC8, with the reference ID (RES-3635), exhibited a close relationship to Bacillus sp., as determined through nucleotide homology analysis. Confirmation of these findings was achieved by 16S Microbial Screening Genetic Typing, utilizing software was considered E values and confirmed a 100 % match with several Bacillus sp. The evolutionary history was deduced employing the Neighbor- joining method, and the tree was drawn to scale, with branch lengths corresponding to the evolutionary distances used in phylogenetic tree inference. Evolutionary distance were calculated using the maximum composite likelihood method and expressed in the units of base substitutions per site, involving 11 nucleotide sequences with a total of 847 position in the final database. The analysis was carried out using MEGA 7 software. To identify, the *Bacillus sp.* was determined through the comparison of 16S rRNA gene sequences with available sequences in the Gene bank database, employing BLAST homology. Additionally,

Kumar *et al.,* (2016) employed the MEGA 7 software for molecular evolutionary genetics analysis.

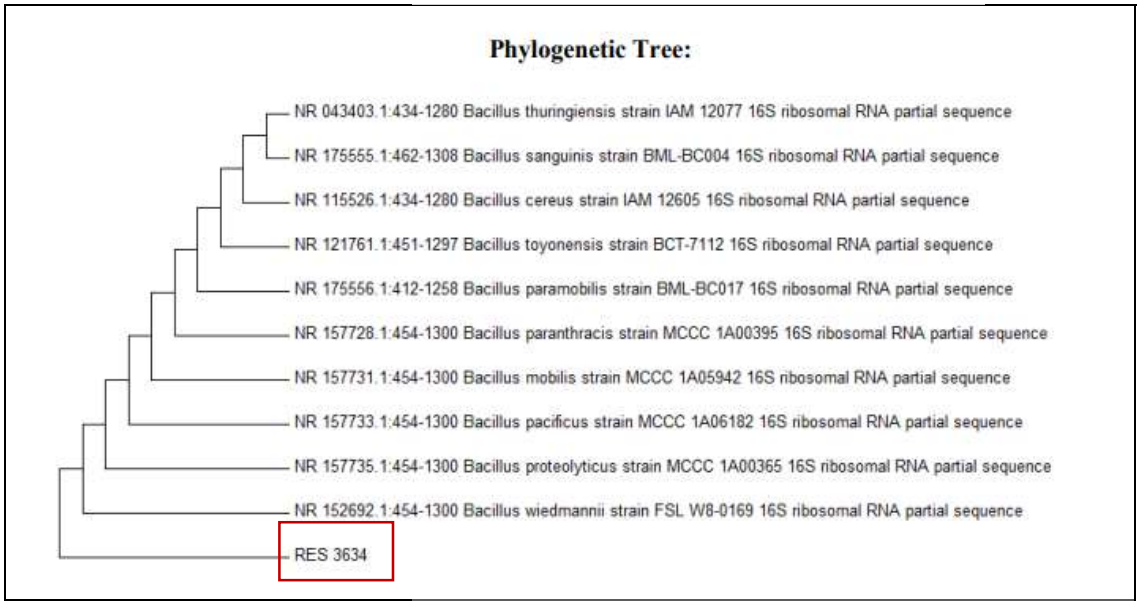


Fig. 4.29 Phylogenetic Tree of *Bacillus sp*. (KC9) employing Neighbor-Joining method with Accession number of OQ654027

Our bacterial sample labelled as AU_CB_MM_KC9 and reference ID RES-3634 is closely related to *Bacillus sp.* based on nucleotide homology analysis. Confirmation by using 16 S Microbial Genetic Typing software, that considered E values, revealing a 100 % match with various *Bacillus sp.* The evolutionary history was inferred using the Neighbor – Joining method. The optimal tree was drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. There was a total of 847 positions in the final dataset. Evolutionary analyses were conducted in MEGA7. 16S rRNA gene sequences by the comparison of available sequences in the database of gene bank with the help of BLAST homology. KC9 was identified as *Bacillus* sp. and deposited to the Gene Bank database with accession number of OQ654027. This identification methodology aligns with previous studies, such as that of Saitou *et al.,* (1987) neighbor-joining method has been utilized for the reconstructing phylogenetic trees and Kumar *et al.,* (2016) used the MEGA7 bioinformatic tool for molecular evolutionary genetics analysis.

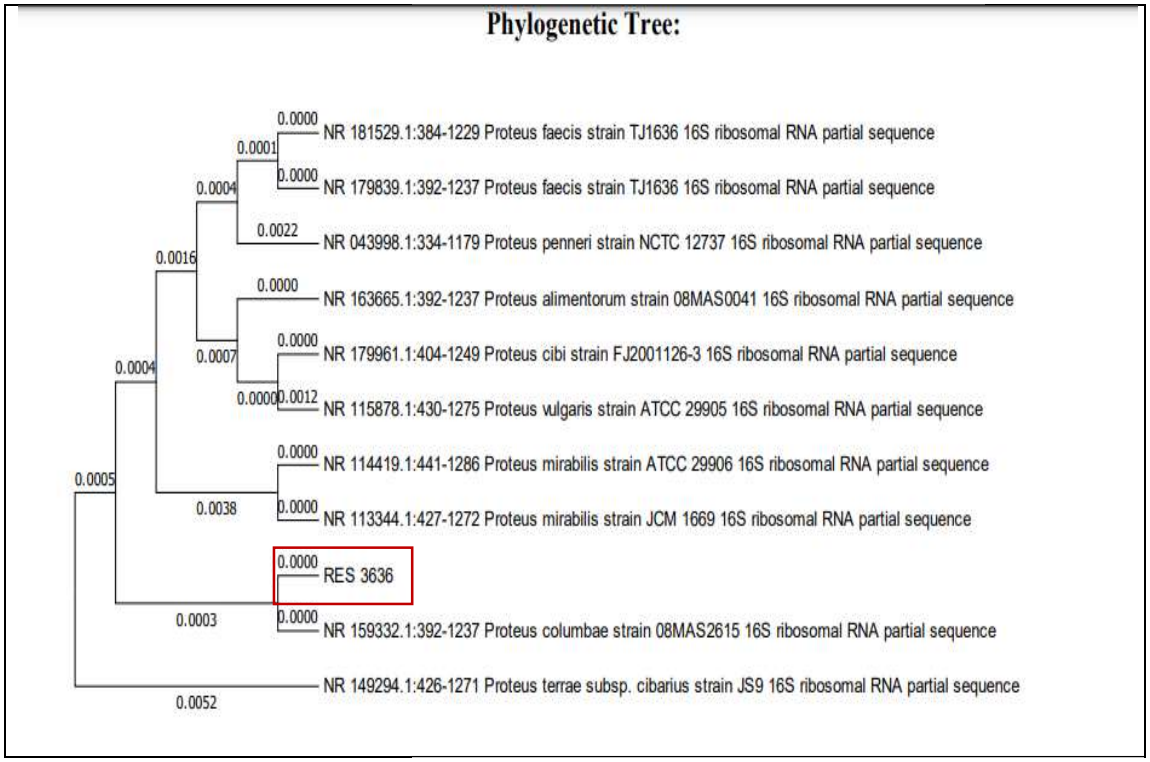


Fig. 4.30 Phylogenetic Tree of *Proteus sp*. (KC11) employing Neighbor-Joining method with Accession number of OQ652027

Our bacterial sample labelled as AU_CB_MM_KC 11 and reference ID RES-3636 is closely related to *Proteus sp*. based on nucleotide homology analysis. Confirmation by using 16 S Microbial Genetic Typing software, that considered E values, which shows a 100 % match with various *Proteus sp.* The evolutionary history was inferred using the Neighbor – Joining method. The optimal tree was drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. There was a total of 847 positions in the final dataset. The evolutionary analyses were executed using MEGA7, comparing 16S rRNA gene sequences with the existing entries in the Gene Bank database through BLAST homology. The strain KC11 was identified as *Proteus columbae* and documented in the Gene Bank database with accession number of OQ652027. This identification methodology aligns with established studies, including Saitou *et al.,* (1987), who employed the neighbor-joining method for the reconstructing phylogenetic trees and Kumar *et al.,* (2016) used the MEGA7 bioinformatics tool for molecular evolutionary genetics analysis.

4.10 Compatibility test

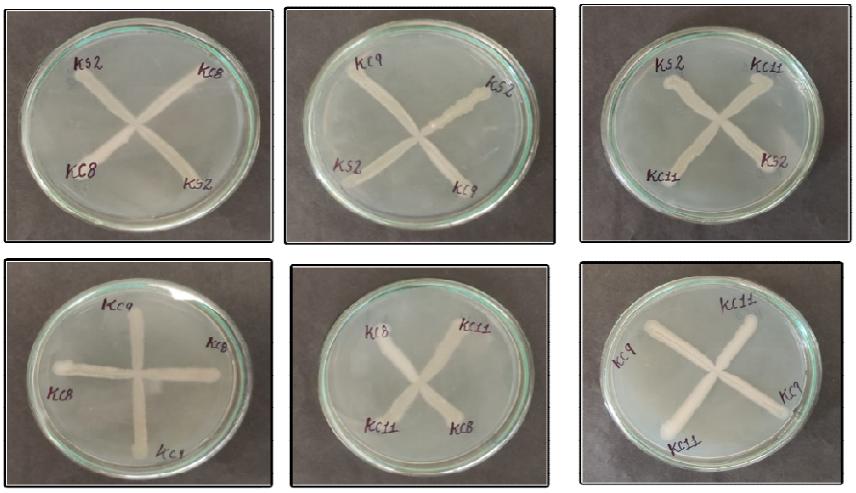
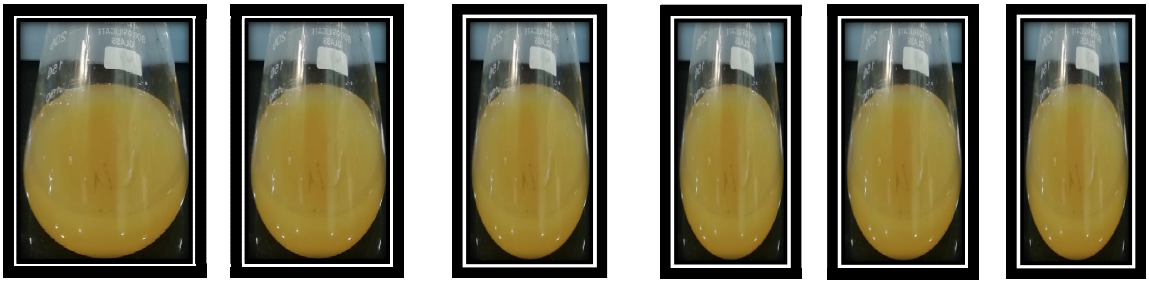


Fig. 4.31 Compatibility Test for Consortia Development

Based on the screening process for plant growth promoting rhizobacterial isolates involved assessing their traits that promote plant growth. The isolates were evaluated and selected for development of consortia based on their efficiency in producing various plant growth promoting factors. The experiment involved testing the compatibility of the microorganisms using a nutrient agar medium. This compatibility assessment was conducted by streaking dual inoculants on nutrient agar medium to determine the compatibility levels among the microorganisms. In the current investigation, the compatibility test utilized four potent isolated bacterial strains KS2, KC8, KC9 and KC11. The dual inoculants were KS2+KC8, KS2+KC9, KS2+KC11, KC8+KC9, KC8+KC11 and followed by KC9+KC11. Marimuthu *et al.,* (2013) have been reported, a selected AZ204 for nitrogen fixation and phosphorus solubilization, and pf1 as a biocontrol agent. They formulated a consortium for application on Gossypium. Various PGPR isolates were employed in the preparation of microbial consortia. *Azospirillum sp.* AZ204 and *pseudomonas sp.*pf 1 exhibited superior performance, effectively suppressing Rhizocotonia bataticola more efficiently than individually inoculated. The consortium demonstrated enhanced plant growth promoting characteristics, performing well when applied.

4.11 Consortia Development



KS2+KC8 KS2+KC9 KS2+KC11 KC8+KC9 KC8+KC11 KC9+KC11

Fig. 4.32 Effect of Consortium on Seed Germination of Monocot & Dicot Plants

The isolates KS2, KC8, KC9 and KC11 were subjected to compatibility testing for the purpose of formulating microbial consortium. In present study, results revealed in fig no. 4.33- 4.37KS2+KC8, KS2+KC9, KS2+KC11, KC8+KC9, KC8+KC11. In a microbial consortium, a diverse group of microorganisms collaborates as a community, working together within a complex system where each member benefits from the activities of others in the community. Microbial consortia exhibit greater efficiency compared to single strains of organisms due to the diversity of their metabolic capabilities. The microorganisms interact synergistically, contributing nutrients and removing inhibitory products. Coinoculation, a common practice, often results in increased growth and yield compared to single inoculation, provided that the plants have balanced nutrition and improved absorption of nitrogen, phosphorus and mineral nutrients. (Laxmi *et al.,* 2013)

KS2+KC8 KS2+KC9 KS2+KC11 KC8+KC9 KC8+KC11 KC9+KC11

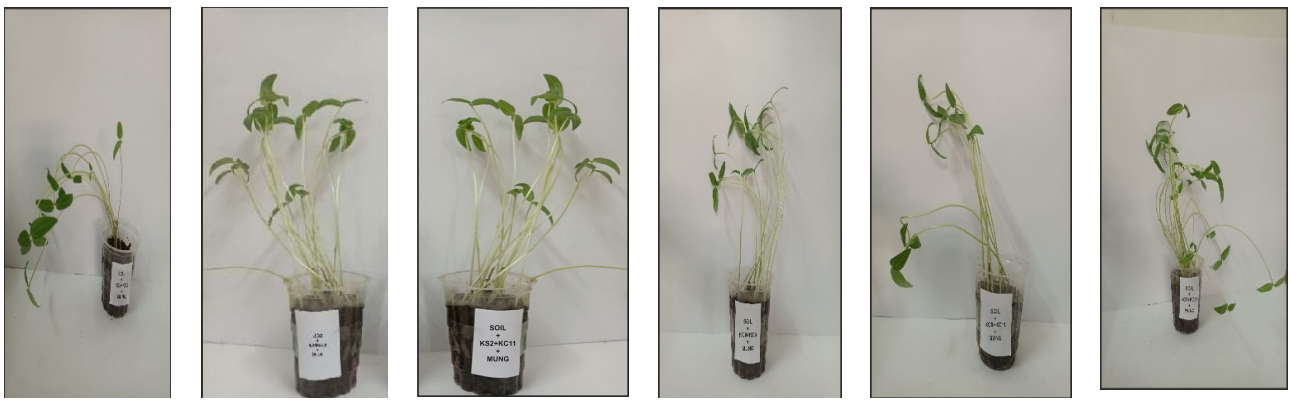
Fig. 4.33 *In – Vitro* Pot Analysis of Consortia Study of Cumin Plant

KS2+KC8 KS2+KC9 KS2+KC11 KC8+KC9 KC8+KC11 KC9+KC11

Fig. 4.34 *In – Vitro* Pot Analysis of Consortia Study of Groundnut Plant

KS2+KC8 KS2+KC9 KS2+KC11 KC8+KC9 KC8+KC11 KC9+KC11

Fig. 4.35 *In – Vitro* Pot Analysis of Consortia Study of Chickpea Plant



KS2+KC8 KS2+KC9 KS2+KC11 KC8+KC9 KC8+KC11 KC9+KC11

Fig. 4.36 *In – Vitro* Pot Analysis of Consortia Study of Mung Plant

KS2+KC8 **KS2+KC9** **KS2+KC11** **KC8+KC9** **KC8+KC11** **KC9+KC11**

Fig. 4.37 *In – Vitro* Pot Analysis of Consortia Study of Rice Plant

Table 4.11 Root Length, Shoot Length and No. of leaves of Cumin plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)
Cumin				
1		Control	6	16
2			6.8	15.2
3			6.4	16.3
		Mean ± SD	6.4±0.4	15.83±0.56
4	Treatment No.1	KS2 + KC8	7.2	19.7
5			7.1	19
6			7.8	20.5
		Mean ± SD	7.36±0.37	19.73±0.75
7	Treatment No.2	KS2 + KC9	7.4	24.2
8			7.8	26.3
9			8.1	25.8
		Mean ± SD	7.76±0.35	25.03±1.11
10	Treatment No.3	KS2 + KC11	8.1	25.7
11			8.2	22
12			7.8	23
		Mean ± SD	8.03±0.2	23.56±1.91
13	Treatment No.4	KC8 + KC9	8.7	23.9
14			8.8	25.1
15			8.9	24.6
		Mean ± SD	8.56±0.41	24.53±0.60
16	Treatment No.5	KC8 + KC11	9.6	26.9
17			9	25.3
18			9.7	26.8
		Mean ± SD	9.43±0.37	26.33±0.89
19	Treatment No.6	KC9 + KC11	12.1	33.2
20			12.3	34.6
21			12.9	35.1
		Mean ± SD	12.43±0.41	34.3±0.9

Table 4.12 Root Length, Shoot Length and No. of leaves of Groundnut plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Groundnut					
1		Control	6	15	40
2			5.2	18	52
3			7	17	42
		Mean ± SD	6.06±0.90	16.66±1.52	44.66±6.42
4	Treatment No.1	KS2 + KC8	6	16	50
5			5	13	45
6			5.5	17	48
		Mean ± SD	5.5±0.5	15.33±2.08	47.66±2.51
7	Treatment No.2	KS2 + KC9	5.5	14	44
8			6.5	15	40
9			5	22	60
		Mean ± SD	5.66±0.76	17±4.35	43.33±3.0
10	Treatment No.3	KS2 + KC11	5.5	15	30
11			5	13	32
12			4.5	10.5	36
		Mean ± SD	5.43±0.86	12.83±2.25	32.66±3.0
13	Treatment No.4	KC8 + KC9	4.5	12	44
14			5.3	13.5	38
15			5.2	16.2	32
		Mean ± SD	5.46±0.37	13.9±2.1	38.0±6.0
16	Treatment No.5	KC8 + KC11	3.8	10	42
17			4.5	13.5	40
18			5.2	15.5	36
		Mean ± SD	4.5±0.7	12.83±2.75	39.33±3.0
19	Treatment No.6	KC9 + KC11	10.5	21	64
20			11.2	26	60
21			11.3	27	68
		Mean ± SD	11±0.43	24.66±3.21	64.0±4.0

Table 4.13 Root Length, Shoot Length and No. of leaves of Chickpea plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Chickpea					
1		Control	10	22	62
2			9.8	18	65
3			12	20	58
		Mean ± SD	10.6±1.21	20±2.0	65±3.0
4	Treatment No.1	KS2 + KC8	9.8	20	42
5			9.7	18	40
6			9.6	17	43
		Mean ± SD	9.7±0.1	18.33±1.52	41.66±1.52
7	Treatment No.2	KS2 + KC9	8.9	18	35
8			8.7	19	38
9			9.2	21	42
		Mean ± SD	8.93±0.25	19.33±1.52	38.33±3.5
10	Treatment No.3	KS2 + KC11	7.5	17	36
11			7.2	15	32
12			6.5	13	30
		Mean ± SD	7.06±0.51	15±2.0	32.66±3.0
13	Treatment No.4	KC8 + KC9	6.5	14	32
14			6.4	12	34
15			6	11	36
		Mean ± SD	6.3±0.26	12.33±1.52	34.0±2.0
16	Treatment No.5	KC8 + KC11	7.8	18	36
17			7.4	14	32
18			7.9	16	38
		Mean ± SD	7.7±0.26	16.0±2.0	35.33±3.0
19	Treatment No.6	KC9 + KC11	16	28	70
20			15	27	74
21			14	30	78
		Mean ± SD	15±1.0	28.33±1.52	74.0±4.0

Table 4.14 Root Length, Shoot Length and No. of leaves of Mung plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Mung					
1		Control	6.5	16	10
2			6	18	16
3			6.2	15	12
		Mean ± SD	6.23±0.25	16.33±1.52	12.66±3.0
4	Treatment No.1	KS2 + KC8	5	12	12
5			5.2	10	18
6			5.3	8	14
		Mean ± SD	5.166±0.15	10±2.0	14.66±3.0
7	Treatment No.2	KS2 + KC9	6	15	20
8			6.5	18	26
9			5.5	14	18
		Mean ± SD	6.0±0.5	15.66±2.08	21.33±4.16
10	Treatment No.3	KS2 + KC11	3.5	13	18
11			4.5	12	23
12			5	9	17
		Mean ± SD	4.33±0.76	11.33±2.0	19.33±3.2
13	Treatment No.4	KC8 + KC9	4.2	14	15
14			4.5	16	24
15			4.8	18	20
		Mean ± SD	4.5±0.3	16.0±2.0	19.66±4.5
16	Treatment No.5	KC8 + KC11	3.5	11.5	12
17			3.8	10	14
18			3.9	13	16
		Mean ± SD	3.73±0.20	11.5±1.5	14.0±2.0
19	Treatment No.6	KC9 + KC11	11	30	44
20			11.5	38	40
21			12	34	48
		Mean ± SD	11.5±05	34±4.0	44.0±4.0

Table 4.15 Root Length, Shoot Length and No. of leaves of Rice plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Rice					
1		Control	8.5	15	12
2			11	17	19
3			6	9	13
Mean ± SD			8.5±2.5	13.66±4.16	14.66±3.78
4	Treatment No.1	KS2 + KC8	5.5	14	11
5			4.2	12	16
6			4.5	8	13
Mean ± SD			4.73±0.68	11.33±3.0	13.33±2.51
7	Treatment No.2	KS2 + KC9	4.5	10	10
8			4.8	12	11
9			4.9	14	9
Mean ± SD			4.73±0.2	12±2.0	10.0±1.0
10	Treatment No.3	KS2 + KC11	4.5	9	12
11			5.5	10	17
12			4	8	10
Mean ± SD			5.0±0.5	9.0±1.0	13.0±3.6
13	Treatment No.4	KC8 + KC9	5.2	12	10
14			5.3	15	9
15			4.5	14	8
Mean ± SD			5.0±0.4	13.66±1.52	9.0±1.0
16	Treatment No.5	KC8 + KC11	4.2	12	8
17			3.5	8	6
18			3.8	7	12
Mean ± SD			3.83±0.35	9.0±2.64	8.66±3.0
19	Treatment No.6	KC9 + KC11	12	26	22
20			15	22	18
21			10	24	20
Mean ± SD			12.33±2.51	24±2.0	20.0±2.0

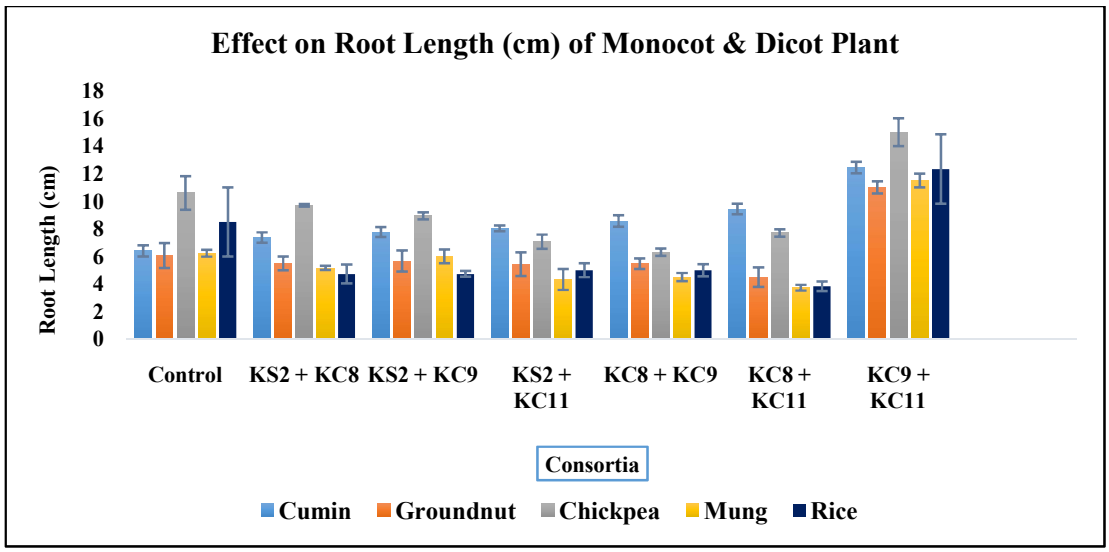


Fig. 4.38 Graphical Representation; *In-vitro* Pot Analysis of Consortia on Root Length (cm) of Monocot & Dicot Plant

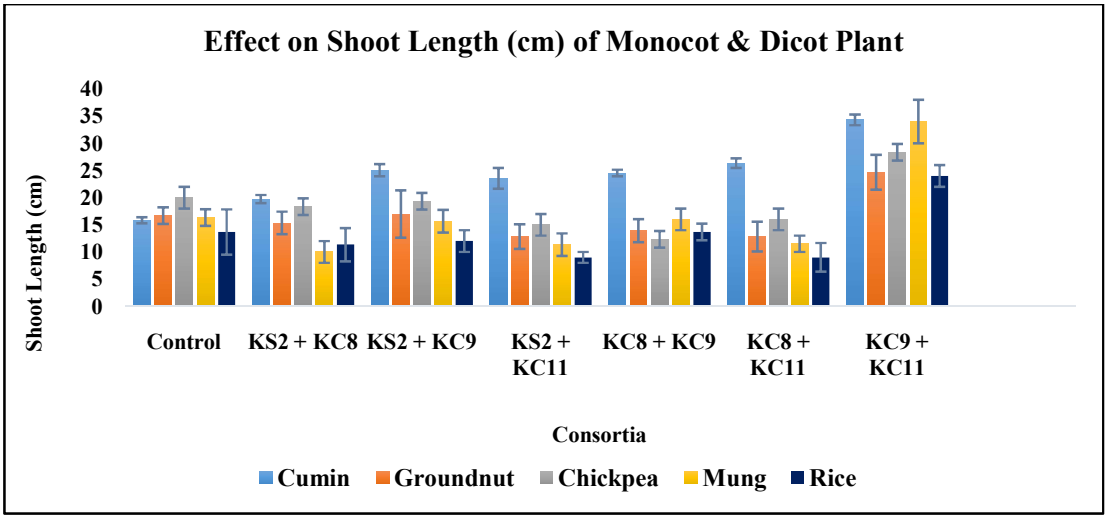


Fig. 4.39 Graphical Representation; *In-vitro* Pot Analysis of Consortia on shoot Length (cm) of Monocot & Dicot Plant

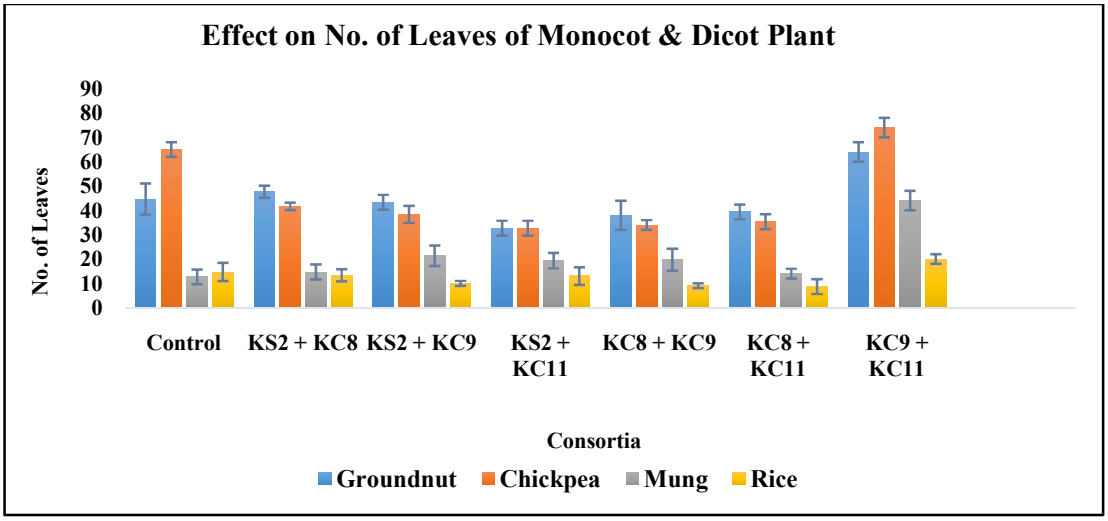


Fig. 4.40 Graphical Representation; *In-vitro* Pot Analysis of Consortia on No. of Leaves of Monocot & Dicot Plant

In this present study, cumin, groundnut, chickpea, mung and rice were treated with 2.0ml of consortium such as KS2+KC8, KS2+KC9, KS2+KC11, KC8+KC9, KC8+KC11, KC9+KC11. The treated and untreated seeds were planted in the plastic glasses with triplicate manner for germination and observed for another 15 days. After the completion of incubation period, measurements were taken for root length, shoot length and number of leaves. The results, as depicted in fig. 4.38showed that the average root length of cumin, groundnut, chickpea, mung, and rice treated with various consortium were as follows In control condition,cumin (6.4±0.4cm), groundnut (6.06±0.90 cm), chickpea (10.6±1.21 cm), mung (6.23±0.25 cm) and followed by rice (8.5±2.5 cm). Treated with KS2+KC8 cumin (7.36±0.37 cm), groundnut (5.5±0.5 cm), chickpea (9.7±0.1 cm), mung (5.16±0.15 cm) and followed by rice (4.73±0.68 cm).Treated with KS2+KC9 cumin (7.76±0.35 cm), groundnut (5.66±0.76 cm), chickpea (8.93±0.25 cm), and mung (6.0±0.5 cm) and followed by rice (4.73±0.2 cm).Treated with KS2+KC11 cumin (8.03±0.2 cm), groundnut (5.43±0.6 cm), chickpea (7.06±0.51 cm), mung (4.33±0.76cm) and followed by rice (5.0±0.5 cm).Treated with KC8+KC9 cumin (8.56±0.41cm), groundnut (5.46±0.37cm), chickpea (6.3±0.26 cm), mung (4.5±0.3 cm) and followed by rice (5.0±0.4 cm). Treated with KC8+KC11 cumin (9.43±0.37cm), groundnut (4.5±0.7cm), chickpea (7.7±0.26 cm), mung (3.73±0.20 cm) and followed by rice (3.83±0.35 cm).Treated with KC9+KC11 cumin (12.43±0.41cm), groundnut (11.0±0.43cm), chickpea (15.0±1.0 cm), mung (11.5±0.5 cm) and followed by rice (12.33±0.51cm).The average shoot length of cumin, groundnut, chickpea, mung, and rice

treated with various consortium were as follows In control condition,cumin (15.83±0.56cm), groundnut (16.66±1.52 cm), chickpea (20.0±2.0 cm), mung (16.33±1.52 cm) and followed by rice (13.66±4.16 cm). Treated with KS2+KC8 cumin (19.73±0.5 cm), groundnut (15.33±2.08 cm), chickpea (18.33±1.52 cm), mung (10.0±2.0 cm) and followed by rice (11.33±3.0 cm).Treated with KS2+KC9 cumin (25.03±1.11 cm), groundnut (17±4.35 cm), chickpea (19.33±1.52 cm), and mung (15.66±2.08 cm) and followed by rice (12.0±2.0 cm).Treated with KS2+KC11 cumin (23.56±1.91 cm), groundnut (12.83±2.25 cm), chickpea (15.0±2.0cm), mung (11.33±2.0cm) and followed by rice (9.0±1.0 cm).Treated with KC8+KC9 cumin (24.53±0.60cm), groundnut (13.9±2.1cm), chickpea (12.33±1.52 cm), mung (16.0±2.0 cm) and followed by rice (13.66±1.52 cm). Treated with KC8+KC11 cumin (26.33±0.89cm), groundnut (12.83±2.75cm), chickpea (16.0±2.0 cm), mung (11.5±1.5cm) and followed by rice (9.0±2.64 cm).Treated with KC9+KC11 cumin (34.3±0.9cm), groundnut (24.66±3.21cm), chickpea (28.33±1.52 cm), mung (34.0±4.0 cm) and followed by rice (24.0±2.0cm)(fig .no. 4.39).The number of leaves groundnut, chickpea, mung, and rice treated with various consortium were as follows In control condition,groundnut (44.66±6.42cm), chickpea (65.0±3.0 cm), mung (12.66±3.0 cm) and followed by rice (14.66±3.78 cm). Treated with KS2+KC8 groundnut (47.66±2.51 cm), chickpea (41.66±1.52 cm), mung (14.66±3.0 cm), and followed by rice (13.33±2.51cm).Treated with KS2+KC9 groundnut (43.33±3.0 cm), chickpea (38.33±3.5 cm), and mung (21.33±4.16 cm) and followed by rice (10.0±1.0 cm).Treated with KS2+KC11 groundnut (32.66±3.0 cm), chickpea (32.66±3.0cm), mung (19.33±3.2cm) and followed by rice (13.0±3.6 cm).Treated with KC8+KC9 groundnut (38.0±6.0cm), chickpea (34.0±2.0 cm), mung (19.66±4.5cm) and followed by rice (9.0±1.0 cm). Treated with KC8+KC11 groundnut (39.33±3.0cm), chickpea (35.33±3.0 cm), mung (14.0±2.0cm) and followed by rice (8.66±3.0 cm).Treated with KC9+KC11 groundnut (64.0±4.0cm), chickpea (74.0±4.0 cm), mung (44.0±4.0 cm) and followed by rice (20.0±2.0cm).

4.12 Isolation and Molecular identification of fungi.

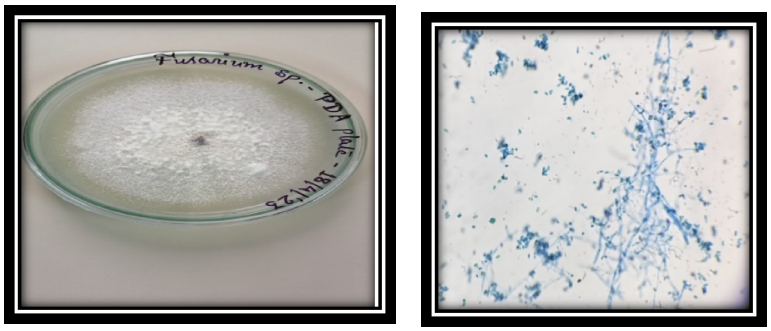


Fig. 4.41 Isolation and identification of fungi.

Fungi were isolated from the soil sample collected from the field at Saurashtra region, Gujarat. Potato dextrose agar medium is a nutrient rich medium for wide range of fungi. The fungal isolate was identified as *Fusarium sp.*by the morphological and microscopic examination. It is having white cottony mycellial growth on PDA plates, by performing staining technique, small portion of fungal growth was placed on glass slide containing lacto phenol cotton blue with placing to the coverslip and was observed in 40X. Results revealed that very short conidiophore, septate were observed. Similarly, Joshi *et al.,* (2013) reported sixty isolates of *Fusarium sp.* from rhizosphere of tomato by using serial dilution method and followed by point inoculation on PDA plate for isolation and identification through lactophenol cotton blue staining.

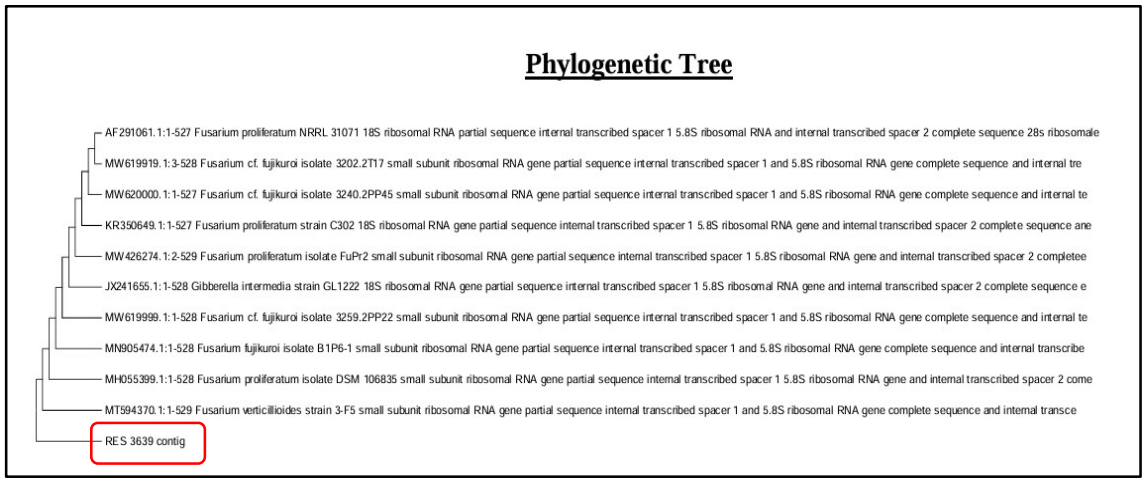


Fig. 4.42 Phylogenetic Tree of *Fusarium sp*. employing Neighbor-Joining method with Accession number of OQ652012

Fungal Sample AU_CB_MM_A is closely related to *Fusarium Species* based on nucleotide homology analysis. Results is confirmed by 16s Microbial Screening Genetic Typing using software's considering E value which shows the 100% match with various *Fusarium sp.* The

evolutionary history was inferred using the Neighbor-Joining method. The optimal tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. There was a total of 501 positions in the final dataset. Evolutionary analyses were conducted in MEGA7. 16S rRNA gene sequences by the comparison of available sequences in the database of gene bank with the help of BLAST homology. Fungal sample was identified as *Fusarium sp*. and deposited to the Gene Bank database with accession number of OQ652012. Similarly, as per the study of Saitou *et al.,* (1987) neighbor-joining method has been utilized for the reconstructing phylogenetic trees and Kumar *et al.,* (2016) used the MEGA7 bioinformatics tool for molecular evolutionary genetics analysis.

4.13 Pathogenicity test

Groundnut Chickpea Rice Mung

Fig.4.43 *Fusarium Sp.* caused Wilt Disease in Groundnut, Chickpea, Rice

The induction of the wilt disease organism on the plants has been indicated in fig. 4.42. The control and the tested plant species growth has been observed with comparative growth study of the induction of *Fusairum sp*. Pathogenicity of the plants has been recorded after the inoculation of *Fusarium sp.* into the healthy plants. It indicates that isolated *Fusarium sp.* from soil samples having the ability to cause disease in all four plants such as Mung, Chickpea, Groundnut, and Rice.

4.14 Antifungal Activity of KS2, KC8, KC9 and KC11 Bacterial Strains against *Fusarium sp.*

Antifungal activity has been performed with KS2, KC8, KC9 and KC11 against *Fusarium sp*. *Bacillus sp.* (KC9) exhibited maximum zone of inhibition of *Fusarium sp*. by the

inhibition of Hyphal growth was 28 mm and showed higher antagonistic activity. Whereas KC11 shows less quiet was 22 mm and less antifungal activity against *Fusarium sp.*

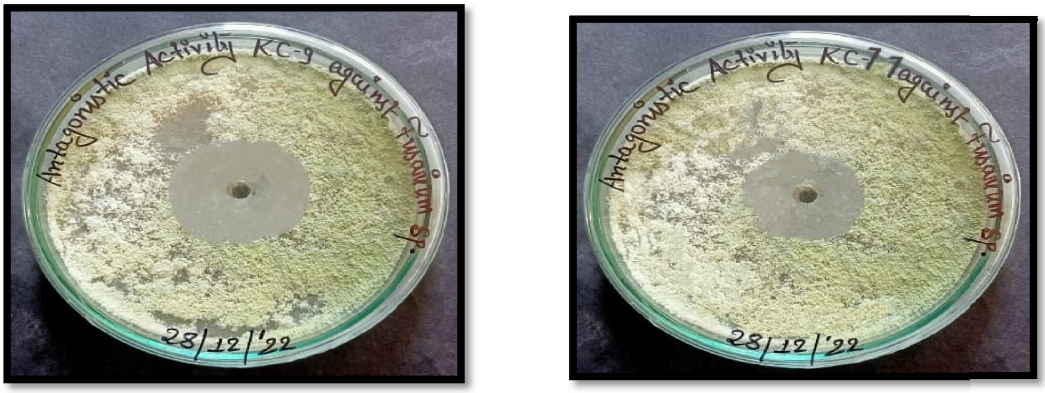


Fig. 4.44 Antifungal Activity of Potent Bacterial Isolates against *Fusarium sp.*

4.15 *In-vitro* Study on the Effect of KC9 and KC11 Bacterial Strains against *Fusarium sp.*

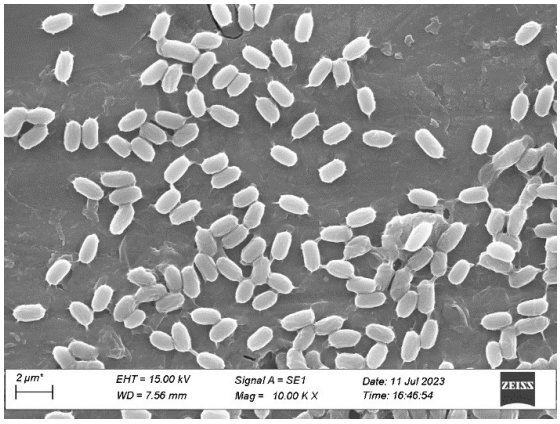
Antifungal activity has been performed with KC9 and KC11 against *Fusarium* sp. *Bacillus sp*. (KC9) exhibited maximum growth inhibition of *Fusarium* . by the inhibition of Hyphal growth and showed higher antifungal activity. Whereas KC11 shows less quiet and less antifungal activity against *Fusarium*. Moreover, *Fusarium sp*. is resistive against KS2 and KC8 inhibition ratio of sporulation gradually decreased.

Fig. 4.45 Antagonistic Activity of Potent Bacterial Isolates against *Fusarium sp.*

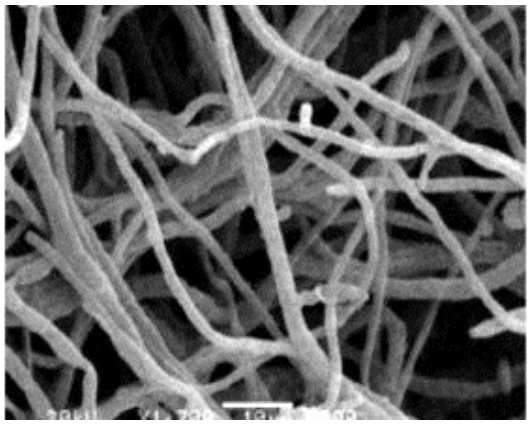
4.16 Ultra Structural Cell Study

SEM Analysis Antagonistic activity of *Bacillus sp.* (KC9) on *Fusarium sp.*

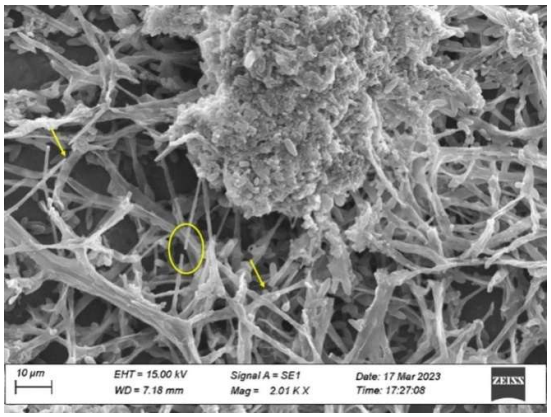
Further, ultrastructural examination by using SEM analysis illustrates that *Bacillus sp.* (KC9) strain induced denudation of *Fusarium sp*. by destroying the hyphal surface of the cellular structure. KC9 strain has been overlapping on *Fusarium* hyphal cells by deforming the hyphal cell from their original state, whenever damage happens in hyphal cell wall surface and inner cytoplasm has been projected that cause cell death. Similar report has been obtained from the Zhao *et al.,* (2014) from the antagonistic activity against *Bacillus subtilis* Strain SG6 on *Fusarium graminearum*. As per his evaluation *B. subtilis* SG6 strain persuaded the husking of *F. Graminearum* hyphal surface which can destroy the cellular structure and lead to cell death.

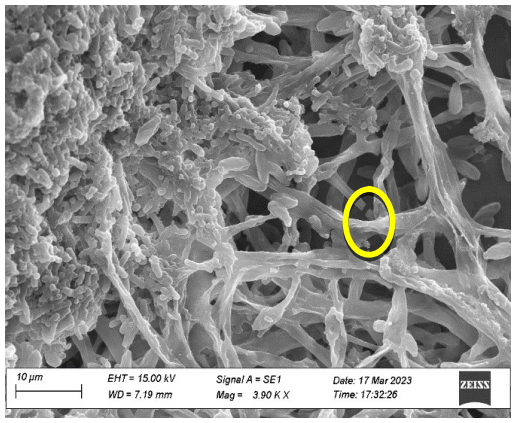


a. KC9 – *Bacillus sp*. cells



b. *Fusarium* Hyphal Cell





c. Deformation occurs in *Fusarium* Hyphal Cells in the Presence of KC9 (*Bacillus sp*.)

Fig.4.46 SEM Analysis of antagonistic activity; bacteria (KC9) interaction with hyphae of *Fusarium sp.* on PDA medium at 5th day after incubation at 28ºC

4.17Study the Effect of Seed and Seedling Germination of monocot and dicot plant

To initiate seed germination, all plants required favourable environmental conditions, including optimum temperature and moisture to overcome exogenic dormancy. Hormones, play crucial role in influencing both the germination rate and maturity of seeds (Begum *et al.,* 2022). Groundnut, chickpea, mung have the high protein source as food materials. In India, there is a significant economic impact due to seed loss at high levels. Therefore there is a need to enhance seed germination rates to ensure optimal crop yield (Makhaye *et al.,* 2021).In the present study, the ability of selected isolate (*Bacillus sp.*- KC9) and (*Proteus columbae sp.*- KC11) to promote groundnut, chickpea , mung and rice seed germination was examined through bio-priming method. 5-5 seeds of groundnut, chickpea, mung and rice were soaked to the bacterial suspension of KC9 and KC11, then placed on the blotting paper containing petri-plate for 7 days to prevent dehydration in fig. 4.47 respectively. The addition of the bacterial suspension to the seeds, which can support the colonization process and increase the bacterial cell number that provide as adhesiveness to seeds. Table 4.16 represented the seeds germination index and relative seed germination in the presence of potential bacterial suspension and fig 4.32illustrates the seed germination within 4 days for the seeds treated with bio-priming method. This research aims to understand the impact of isolate (*Bacillus sp.*- KC9) and (*Proteus columbae sp.*- KC11) on enhancing seed germination, which could have implications for improving crop yield and reducing economic losses associated with seed loss.

Table 4.16 Relative Seed Germination & Germination Index of Various Seeds

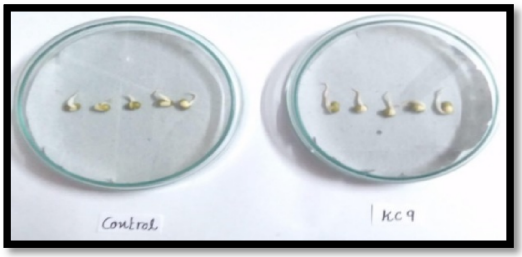
Sr No.	Name of Seeds	Total Number of Seeds	Number of Seeds Germinated	Seed Germination Index	Relative Seed Germination
1.	Groundnut	05	05	100%	100%
2.	Chickpea	05	05	100%	100%
3.	Mung	05	05	100%	100%
4.	Rice	05	05	100%	100%

Groundnut treated with KC9 and untreated as control

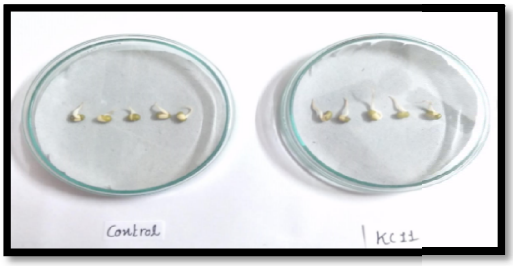
Groundnut treated with KC11 and untreated as control

Chickpea treated with KC9 and untreated as control

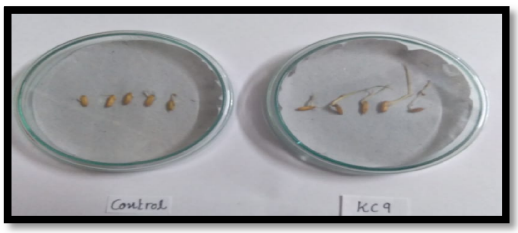
Chickpea treated with KC11 and untreated as control



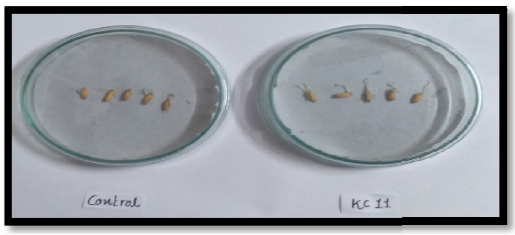
Mung treated with KC9 and untreated as control



Mung treated with KC11 and untreated as control



Rice treated with KC9 and untreated as control



Rice treated with KC11 and untreated as control

Fig. 4.47 Effect of PGPR strain *Bacillus Sp.* and *Proteus sp.* on Seed Germination of Monocot & Dicot seeds

4.17.1 Effect of PGPR strain Inoculant on monocot & dicot plant Seedlings

Rhizobacteria possess significant attributes that contribute to the enhancement of plant growth and the improvement of plant health by Kloepper *et al.,* (1989). Several researchers, such as Zhang *et al.,* (1997) have observed and revealed the capacity of microorganisms, to increase rate of seed germination, expand seedling appearance, develop to stress tolerance factors, increase plants growth yield and promote defence mechanism against various pathogens. Similar findings have been reported in diverse crops including potato, radish plants, pearl millet, wheat, chickpea etc. (Niranjan *et al.,* 2004; Shaukat *et al.,* 2006).Similar findings have been reported by Dobbelaere *et al.,* (2006) conducted a study evaluating the impact of the incorporation of PGPR *Azospirillum brasilense* on the growth yield of spring wheat, revealing effects similar to those reported by other researchers. Additionally, Dipanwita *et al.,* (2015) conducted a similar investigation, studying the activity of the plant growth promoting rhizobacteria*Escherichia coli* and *Pseudomonas fluorescens* on the growth of Cicer arietinum L. (chickpea). Their findings contribute to the growing positive effects of rhizobacteria on various aspects of plant development and health.

4.18 Development of Consortia for Biocontrol Agent employing KC9 & KC11

The selected bacterial consortium were undergone a pot culture experiment study out of 6 consortium has found to reflect crop growth as represented in fig. 4.48 - 4.51.

Soil + *Fusarium sp.* | **Soil + KC9 + *Fusarium sp.*** | **Soil + KC11 + *Fusarium sp.*** | **Soil + KC9 + KC11** | **Soil + KC9+ KC11 +*Fusarium sp.***

Fig. 4.48 *In - Vitro* Pot Analysis of Consortia Study With *Fusarium sp.* of Groundnut Plant

Soil + *Fusarium sp.* **Soil + KC9 + *Fusarium sp.*** **Soil + KC11 + *Fusarium sp.*** **Soil + KC9 + KC11** **Soil + KC9 + KC11 + *Fusarium sp.***

Fig. 4.49 *In - Vitro* Pot Analysis of Consortia Study With *Fusarium sp.* of <u>Chickpea</u> Plant

Soil + *Fusarium sp.* **Soil + KC9 + *Fusarium sp.*** **Soil + KC11 + *Fusarium sp.*** **Soil + KC9 + KC11** **Soil + KC9 + KC11 + *Fusarium sp.***

Fig. 4.50 *In - Vitro* Pot Analysis of Consortia Study With *Fusarium sp.* of <u>Mung</u> Plant

Soil + *Fusarium sp.* | **Soil + KC9 + *Fusarium sp.*** | **Soil + KC11 + *Fusarium sp.*** | **Soil + KC9 + KC11** | **Soil + KC9 + KC11 + *Fusarium sp.***

Fig. 4.51 *In - Vitro* Pot Analysis of Consortia Study With *Fusarium sp.* of Rice Plant

Table 4.17 Root Length, Shoot Length and No. of leaves of Groundnut plant

Sr. N	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Groundnut					
1		Control	6	15	40
2			5.2	18	52
3			7	17	42
		Mean ± SD	6.06±0.90	16.66±1.52	44.66±6.42
4	Treatment No.1	Soil + *Fusarium Sp.*	1	7	32
5			1.2	12	30
6			1.3	9	28
		Mean ± SD	1.16±0.15	9.33±2.51	30.0±2.0
7	Treatment No.2	Soil + KC9	8	23	65
8			9	24	74
9			10.5	21	67
		Mean ± SD	9.16±1.25	22.66±1.52	68.66±4.72
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	2.5	15	40
11			2	16	44
12			3	18	36
		Mean ± SD	2.5±0.5	16.33±1.52	40.0±4.0
13	Treatment No.4	Soil + KC11	8	21	70
14			7.5	19	65
15			8	20	53
		Mean ± SD	7.83±0.28	20.0±1.0	66.0±3.60
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	1.5	12	44
17			2.1	15	38
18			2.3	14	34
		Mean ± SD	1.96±0.4	13.66±1.52	38.66±5.03
19	Treatment No.6	Soil + KC9 + KC11	11.2	28	78
20			12.5	27	68
21			13.2	26	65
		Mean ± SD	12.3±1.01	27.0±1.0	70.33±6.80
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	6.5	18	52
23			5	21	56
24			5.5	20	58
		Mean ± SD	5.66±0.76	19.66±1.52	55.33±3.05

Table 4.18 Root Length, Shoot Length and No. of leaves of Chickpea plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Chickpea					
1		Control	10	22	62
2			9.8	18	65
3			12	20	68
		Mean ± SD	10.6±1.21	20.0±2.0	65.0±3.0
4	Treatment No.1	Soil + *Fusarium Sp.*	2.5	7.5	12
5			2	6.5	10
6			2.1	6	8
		Mean ± SD	2.2±0.26	6.66±0.76	10.0±2.0
7	Treatment No.2	Soil + KC9	14	23	68
8			12	27	70
9			16	25	64
		Mean ± SD	14.0±2.0	25.0±2.0	67.33±3.05
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	4.5	10	22
11			4	9.5	25
12			4.8	8.5	28
		Mean ± SD	4.43±0.4	9.33±0.76	25.0±3.0
13	Treatment No.4	Soil + KC11	8	21	69
14			7.5	19	63
15			8	20	62
		Mean ± SD	7.83±0.28	20.0±1.0	64.66±3.78
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	3.5	9.5	20
17			3	8	23
18			3.2	7.2	15
		Mean ± SD	3.23±0.25	8.23±1.16	19.33±4.04
19	Treatment No.6	Soil + KC9 + KC11	16	28	70
20			15	27	74
21			14	30	78
		Mean ± SD	15±1.0	28.33±1.52	74±4.0
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	5	20	30
23			5.1	19	32
24			5.2	18	36
		Mean ± SD	5.1±0.1	19±1.0	32.66±3.05

Table 4.19 Root Length, Shoot Length and No. of leaves of Mung plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of leaves
Mung					
1		control	6.5	16	10
2			6	18	16
3			6.2	15	12
		Mean ± SD	6.23±0.25	16.33±1.52	12.66±3.05
4	Treatment No.1	Soil + *Fusarium Sp.*	2.5	7	11
5			2	7.5	14
6			2.3	8	8
		Mean ± SD	2.26±0.25	7.5±0.5	11.0±3.0
7	Treatment No.2	Soil + KC9	10	30	38
8			10.5	28	40
9			10.2	32	42
		Mean ± SD	10.23±0.5	30.0±2.0	40.0±2.0
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	3	10	12
11			3.5	16	16
12			3.2	14	14
		Mean ± SD	3.23±0.25	13.33±3.05	14.0±2.0
13	Treatment No.4	Soil + KC11	9.5	25	26
14			9	20	20
15			8	23	28
		Mean ± SD	8.83±0.76	22.66±2.51	24.66±4.16
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	3	10	10
17			3.2	9	12
18			3.1	9.5	8
		Mean ± SD	3.1±0.1	9.5±0.5	10.0±2.0
19	Treatment No.6	Soil + KC9 + KC11	11	30	44
20			11.5	38	40
21			12	34	48
		Mean ± SD	11.5±0.5	34.0±4.0	44.0±4.0
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	5	18	14
23			5.5	12	20
24			5.3	14	12
		Mean ± SD	5.26±0.25	14.66±3.05	15.33±4.16

Table 4.20 Root Length, Shoot Length and No. of leaves of Rice plant

Sr. No	Treatment No.	Consortia	Root Length (cm)	Shoot Length (cm)	No. of Leaves
Rice					
1		Control	8.5	15	12
2			11	17	19
3			6	9	13
		Mean ± SD	8.5±0.32	13.66±4.16	14.66±3.78
4	Treatment No.1	Soil + *Fusarium Sp.*	4	12	15
5			4.5	15	13
6			3.9	10	12
		Mean ± SD	4.13±0.32	12.33±2.51	13.33±1.52
7	Treatment No.2	Soil + KC9	12	22	22
8			10	18	16
9			10.5	24	20
		Mean ± SD	10.83±1.04	21.33±3.05	19.33±3.05
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	6	16	16
11			6.5	18	12
12			5.3	12	14
		Mean ± SD	5.93±0.60	15.33±3.05	14±2.0
13	Treatment No.4	Soil + KC11	9	15	18
14			8.9	18	16
15			9.5	20	13
		Mean ± SD	9.13±0.32	17.66±2.51	15.66±2.51
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	5	15	12
17			5.2	14	15
18			5.3	12	13
		Mean ± SD	5.16±0.15	13.66±1.52	13.33±1.52
19	Treatment No.6	Soil + KC9 + KC11	12	26	22
20			15	22	18
21			10	24	20
		Mean ± SD	12.33±2.51	24.0±2.0	20.0±2.0
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	9	15	20
23			8.5	18	22
24			9.5	24	15
		Mean ± SD	9.0±0.5	19.0±4.25	19.0±3.60

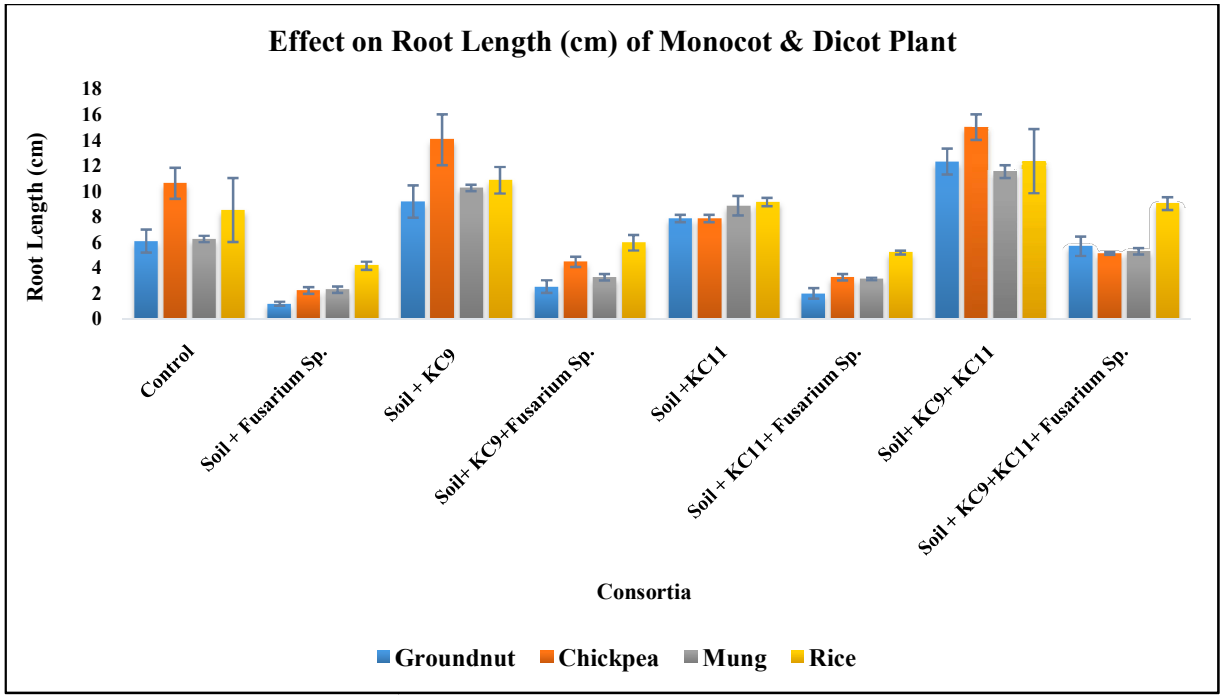


Fig. 4.52 Graphical Representation; *In-vitro* Pot Analysis of consortia on Root Length (cm) of Monocot & Dicot Plant

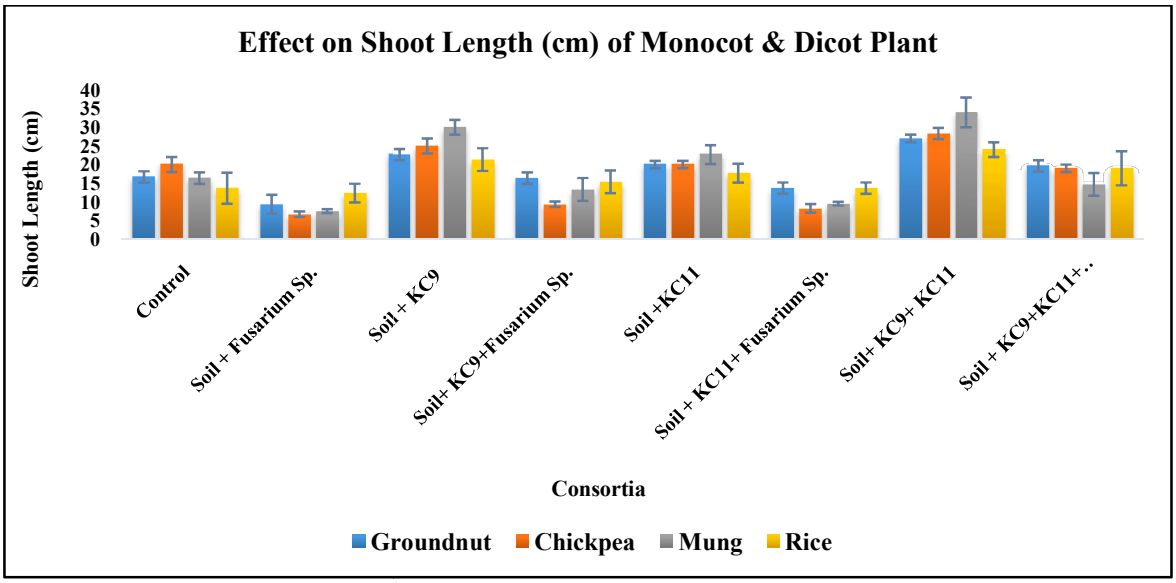


Fig. 4.53 Graphical Representation; *In-vitro* Pot Analysis of Consortia on Shoot Length (cm) of Monocot & Dicot Plant

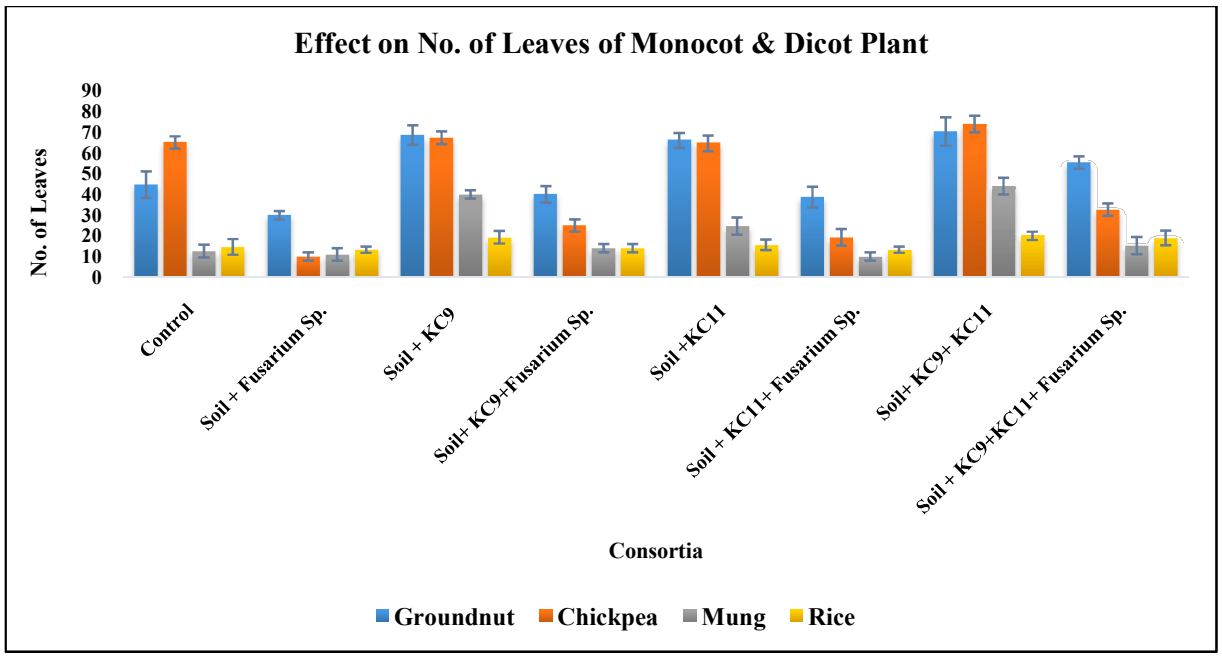


Fig. 4.54 Graphical Representation; *In-vitro* Pot Analysis of Consortia on No. of leaves of Monocot & Dicot Plant

Microbial consortia are farmers in supplying both micro and macro nutrients to crop, while also enhancing disease resistance through antagonistic activity of PGPR. The developed consortia benefits plants and soil by delivering a diverse array of nutrients in unified formulation (Kavya *et al.,* 2020).In control condition,groundnut (6.06±0.90 cm), chickpea (10.6±1.21 cm), mung (6.23±0.25 cm) and followed by rice (8.5±0.32 cm). Treated with KC9 groundnut (9.16±1.25 cm), chickpea (14.0±2.0 cm), mung (10.23±0.5 cm) and followed by rice (10.83±1.04 cm).Treated with KC11 groundnut (7.83±0.28 cm), chickpea (7.83±0.28 cm), and mung (8.83±0.76 cm) and followed by rice (9.13±0.32cm).Treated with KC9+KC11 groundnut (12.3±1.01 cm), chickpea (15.0±1.0 cm), mung (11.5±0.5cm) and followed by rice (11.33±2.51cm).Treated with *Fusarium Sp*. groundnut (1.16±0.15cm), chickpea (2.2±0.26 cm), mung (2.26±0.25 cm) and followed by rice (4.13±0.32cm). Treated with KC9+*Fusarium Sp*. groundnut (2.5±0.5cm), chickpea (4.43±0.4 cm), mung (3.23±0.25 cm) and followed by rice (5.93±0.60cm).Treated with KC11+*Fusarium Sp.* groundnut (1.96±0.4cm), chickpea (3.23±0.25 cm), mung (3.1±0.1 cm) and followed by rice (5.16±0.15cm).Treated with KC9+ KC11+*Fusarium Sp.* groundnut (5.66±0.76cm), chickpea (5.1±0.1cm), mung (5.26±0.25cm) and followed by rice (9.0±0.5cm)(Fig. 4.52).The average shoot length of groundnut, chickpea, mung, and rice treated with various consortium were as follows In control condition, groundnut (16.66±1.52 cm), chickpea (20.0±2.0 cm), mung

(16.33±1.52 cm) and followed by rice (13.66±4.16 cm). Treated with KC9 groundnut (22.66±1.52 cm), chickpea (25.0±2.0cm), mung (30.0±2.0 cm) and followed by rice (21.33±3.05 cm).Treated with KC11 groundnut (20.0±1.0 cm), chickpea (20.0±1.0 cm), and mung (22.66±2.51cm) and followed by rice (17.66±2.51cm).Treated with KC9+KC11 groundnut (27.0±1.0 cm), chickpea (28.33±1.52cm), mung (34.0±4.0cm) and followed by rice (24.0±2.0 cm).Treated with *Fusarium sp*. groundnut (9.33±2.51cm), chickpea (6.66±0.76cm), mung (7.5±0.5 cm) and followed by rice (12.33±2.51 cm). Treated with KC9+*Fusarium sp*. groundnut (16.33±1.52cm), chickpea (9.33±0.76 cm), mung (13.33±3.05cm) and followed by rice (15.33±3.05 cm).Treated withKC11+*Fusarium Sp.*groundnut (13.66±1.52cm), chickpea (8.23±1.16cm), mung (9.5±0.5 cm) and followed by rice (13.16±1.52cm). Treated with KC9+ KC11+*Fusarium sp.* groundnut (19.66±1.52cm), chickpea (19.0±1.0cm), mung (14.66±3.05cm) and followed by rice (19.0±4.25cm) (Fig.4.53).The number of leaves groundnut, chickpea, mung, and rice treated with various consortium were as followsIn control condition,groundnut (44.66±6.42cm), chickpea (65.0±3.0 cm), mung (12.66±3.0 cm) and followed by rice (14.66±3.78 cm). Treated with KC9 groundnut (68.66±4.72 cm), chickpea (67.33±3.05 cm), mung (40.±2.0 cm), and followed by rice (19.33±3.05cm).Treated with KC11 groundnut (66.0±3.60 cm), chickpea (64.66±3.78cm), and mung (24.66±3.16 cm) and followed by rice (15.66±2.51 cm).Treated with KC9+KC11 groundnut (70.33±6.80 cm), chickpea (74.0±4.0cm), mung (44.0±4.0cm) and followed by rice (20.0±2.0 cm).Treated with *Fusarium Sp*. groundnut (30.0±2.0cm), chickpea .(10.0±2.0 cm), mung (11.0±3.0cm) and followed by rice (13.33±1.52cm). Treated with KC9+*Fusarium Sp*. groundnut (40.0±4.0cm), chickpea (25.0±3.0 cm), mung (14.0±2.0cm) and followed by rice (14.0±2.0 cm).Treated with KC11+*Fusarium Sp.* groundnut (38.66±5.03cm), chickpea (19.33±4.04cm), mung (10.0±2.0 cm) and followed by rice (13.33±1.52cm).Treated with KC9+ KC11+*Fusarium Sp.* groundnut (55.33±3.05cm), chickpea (32.66±3.05cm), mung (15.33±4.16cm) and followed by rice (19.0±3.60cm) (Fig. 4.54).Based on the antagonistic activity, consortia of KC9 (*Bacillus sp.)* and KC11 (*Proteus columbae*) was observed maximum biocontrol agent activity and performed pot study of groundnut, chickpea, mung and rice plant, we checked all parameters such as root and shoot length of plant, chlorophyll content, total free amino acids, total phenolic compound, total flavonoid content etc. Similar study have been reported in Singh *et al*. (2013) produced and investigated microbial consortium activity on *Cicer arietinum* against *Sclerotiumrolfsii*. The

organisms used in consortia development were *Pseudomonas aeruginosa sp., Trichoderma harzianum sp.* and *Mesorhizobium sp.* The best action of microbial consortia compared to individual inoculation were due to activation of antioxidant mechanisms and shown in the pot study. Kavya *et al.,* 2020 reported microbial consortia Azotobacter, Psolubilizer, K-releaser, Zn-solubilizer and PGPR isolate.

4.19 Effect of Seedling Germination of Consortia on monocot and dicot seeds

Table 4.21 Chlorophyll Content of Groundnut Plant

Sr. No	Treatment No.	Consortia	Chlorophyll a	Chlorophyll b	Total Chlorophyll
Groundnut					
1		Control	3.44106	6.0782	9.312
2			3.55192	6.1748	9.5134
3			3.76438	6.23876	9.77896
		Mean ± SD	3.586±0.16	6.169±0.080	9.534±0.23
4	Treatment No.1	Soil + *Fusarium Sp.*	2.19475	3.37154	5.43724
5			2.23016	3.3822	5.4815
6			2.26557	3.39286	6.34923
		Mean ± SD	2.230±0.03	3.382±0.01	5.75±0.51
7	Treatment No.2	Soil + KC9	4.24455	7.5609	11.5494
8			4.40815	7.7287	11.8717
9			4.43011	7.85386	12.01696
		Mean ± SD	4.360±0.10	7.716±0.14	11.812±0.23
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	3.19932	5.84736	8.85276
11			3.49605	5.81814	9.10584
12			3.4333	5.72812	8.95672
		Mean ± SD	3.37±0.15	5.79±0.06	8.97±0.12
13	Treatment No.4	Soil + KC11	3.63112	5.70864	9.12544
14			3.69925	5.75286	9.23116
15			3.74199	5.80524	9.32684
		Mean ± SD	3.690±0.05	5.75±0.04	9.22±0.1
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	2.18399	3.46314	5.51884
17			2.39795	3.30626	5.56556
18			2.44606	3.31284	5.64784
		Mean ± SD	2.34±0.13	3.360±0.08	5.57±0.063
19	Treatment No.6	Soil + KC9 + KC11	5.79325	5.5295	10.9775
20			5.79338	6.02764	11.49824
21			5.86645	5.7177	11.2597
		Mean ± SD	5.81±0.04	5.75±0.25	11.24±0.26
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	3.66733	3.73582	7.19932
23			3.73008	3.82584	7.34844
24			3.81166	3.75556	7.35616
		Mean ± SD	3.73±0.07	3.772±0.04	7.301±0.088

Table 4.22 Chlorophyll Content of Chickpea Plant

Sr. No	Treatment No.	Consortia	Chlorophyll a	Chlorophyll b	Total Chlorophyll
Chickpea					
1		Control	3.08745	4.4069	7.3149
2			2.89845	4.24726	6.97656
3			2.94118	4.29964	7.06924
		Mean ± SD	2.97±0.09	4.31±0.081	7.12±0.17
4	Treatment No.1	Soil + *Fusarium Sp.*	2.08958	2.81036	4.42668
5			1.98604	2.75548	4.62658
6			1.97872	2.71376	4.57816
		Mean ± SD	2.018±0.06	2.75±0.04	4.54±0.1
7	Treatment No.2	Soil + KC9	3.77408	6.67636	10.22306
8			3.90765	6.7877	10.4607
9			3.95307	6.81718	10.53318
		Mean ± SD	3.87±0.09	6.76±0.07	10.40±0.1
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	2.30235	2.45554	4.6294
11			2.37092	2.80812	5.04482
12			2.31668	2.95776	5.14196
		Mean ± SD	2.32±0.036	2.74±0.25	4.93±0.27
13	Treatment No.4	Soil + KC11	2.89801	3.9389	6.6697
14			2.94418	3.85796	6.63316
15			2.99229	3.86454	6.68544
		Mean ± SD	2.94±0.04	3.88±0.04	6.662±0.02
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	2.24048	2.98224	5.09384
17			2.28742	3.06976	5.18266
18			2.08958	2.81036	4.77956
		Mean ± SD	2.20±0.10	2.95±0.13	5.01±0.2
19	Treatment No.6	Soil + KC9 + KC11	4.30805	7.5405	11.5895
20			4.2311	7.6754	11.6504
21			4.41622	7.66	8.7211
		Mean ± SD	4.31±0.09	7.62±0.07	10.65±1.67
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	3.52225	3.8265	7.1515
23			3.44142	3.78636	7.03476
24			3.47489	3.7095	6.9902
		Mean ± SD	3.47±0.04	3.77±0.05	7.05±0.08

Table 4.23 Chlorophyll Content of Mung Plant

Sr. No	Treatment No.	Consortia	Chlorophyll a	Chlorophyll b	Total Chlorophyll
Mung					
1		Control	4.12916	3.65356	7.55666
2			4.14918	3.6912	7.6131
3			4.18459	3.70186	7.05736
		Mean ± SD	4.15±0.02	3.68±0.02	7.40±0.30
4	Treatment No.1	Soil + *Fusarium Sp.*	2.9807	1.46637	4.29116
5			2.94335	1.36818	4.15808
6			2.7969	2.40684	5.05104
		Mean ± SD	2.90±0.09	1.74±0.5	4.50±0.48
7	Treatment No.2	Soil + KC9	4.1945	7.4668	11.4083
8			4.39845	7.2911	11.4276
9			4.34571	7.2199	11.31472
		Mean ± SD	4.31±0.10	7.32±0.12	11.38±0.06
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	3.25268	5.081	8.1419
11			3.22265	5.02455	8.05724
12			3.23266	2.3453	8.08546
		Mean ± SD	3.23±0.01	4.15±1.56	8.09±0.04
13	Treatment No.4	Soil + KC11	3.55298	5.6456	8.9885
14			3.60109	5.652	9.04708
15			4.1711	5.7322	8.9487
		Mean ± SD	3.77±0.34	5.67±0.04	8.99±0.04
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	2.3464	3.433	5.6425
17			2.37105	3.5352	5.7675
18			2.3883	3.5958	5.8436
		Mean ± SD	2.36±0.02	3.52±0.08	5.75±0.1
19	Treatment No.6	Soil + KC9 + KC11	5.117	8.448	13.26
20			5.258	8.292	13.24
21			5.289	8.238	13.21
		Mean ± SD	5.22±0.09	8.32±0.10	13.23±0.02
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	4.598	7.6675	11.992
23			4.636	7.609	11.975
24			4.642	7.499	11.866
		Mean ± SD	4.62±0.03	7.59±0.08	11.94±0.06

Table 4.24 Chlorophyll Content of Groundnut Plant

Sr. No	Treatment No.	Consortia	Chlorophyll a	Chlorophyll b	Total Chlorophyll
Rice					
1		Control	3.0255	2.333	5.1954
2			3.105	2.483	5.4211
3			3.0755	2.427	5.336
		Mean ± SD	3.06±0.04	2.41±0.07	5.31±0.11
4	Treatment No.1	Soil + *Fusarium Sp.*	2.0622	2.731	4.674
5			1.997	2.553	4.436
6			1.98	2.492	4.36
		Mean ± SD	2.01±0.04	2.59±0.12	4.49±0.16
7	Treatment No.2	Soil + KC9	3.673	6.488	9.94
8			3.807	6.599	10.178
9			3.894	6.791	10.452
		Mean ± SD	3.79±0.1	6.62±0.15	10.19±0.25
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	2.137	2.524	4.4929
11			2.116	2.581	4.5775
12			2.232	2.632	4.7385
		Mean ± SD	2.16±0.06	2.57±0.05	4.60±0.12
13	Treatment No.4	Soil + KC11	2.814	4.6488	7.2959
14			2.819	4.7134	7.3654
15			2.868	4.917	7.6146
		Mean ± SD	2.83±0.02	4.75±0.13	7.42±0.16
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	2.313	2.672	4.855
17			2.34	2.751	4.9601
18			2.345	2.816	5.0287
		Mean ± SD	2.33±0.01	2.74±0.07	4.94±0.08
19	Treatment No.6	Soil + KC9 + KC11	3.8156	6.53	10.1179
20			3.845	6.587	10.2025
21			3.888	6.639	10.2952
		Mean ± SD	3.84±0.03	6.58±0.05	10.20±0.08
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	2.941	4.608	7.3761
23			2.981	4.683	7.488
24			3.242	4.643	7.6978
		Mean ± SD	3.054±0.16	4.64±0.03	7.52±0.16

Table 4.25 Relative water Content (RWC) of Groundnut plant

Sr. No	Treatment No.	Consortia	Fresh Weight	Turgid Weight	Dry Weight	RWC
Groundnut						
1		Control	5	6.2	2.5	67.56
2			5	6.1	2.3	71.05
3			5	6.5	2.1	65.9
Mean ± SD						68.17±2.62
4	Treatment No.1	Soil + *Fusarium Sp.*	5	6.5	2.8	59.45
5			5	6.3	2.9	61.76
6			5	7.2	3	47.61
						56.27±7.59
7	Treatment No.2	Soil + KC9	5	5.8	1.8	80
8			5	5.5	1.2	88.37
9			5	5.3	1.9	91.17
Mean ± SD						86.51±5.8
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	5	6.2	3.5	55.55
11			5	5.9	3.8	57.14
12			5	5.8	3.3	68
						60.23±6.7
13	Treatment No.4	Soil + KC11	5	6.2	2.5	67.56
14			5	6.3	2.1	69.04
15			5	5.8	2.3	77.14
Mean ± SD						71.2±5.1
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	5	6.1	3.7	54.16
17			5	6.4	3.9	44
18			5	6.2	3.4	57.14
Mean ± SD						51.7±6.8
19	Treatment No.6	Soil + KC9 + KC11	5	5.3	1.7	94.28
20			5	5.6	1	88.88
21			5	5.4	1.8	91.42
Mean ± SD						91.5±2.70
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	5	5.2	1.7	91.66
23			5	5.5	1	86.95
24			5	5.3	1.8	88.88
Mean ± SD						89.16±2.36

Table 4.26 Relative water Content (RWC) of Chickpea plant

Sr. No	Treatment No.	Consortia	Fresh Weigh t	Turgi d Weigh t	Dry Weigh t	RWC
Chickpea						
1		Control	5	6.4	3.5	51.72
2			5	6.8	3.8	40
3			5	6.6	3.4	50
Mean ± SD						47.24±6.3
4	Treatment No.1	Soil + *Fusarium Sp.*	5	6.5	3.5	50
5			5	6.7	3.7	43.33
6			5	6.3	4.2	38.09
Mean ± SD						43.80±5.9
7	Treatment No.2	Soil + KC9	5	5.3	3.5	83.33
8			5	5.6	1.9	83.78
9			5	5.8	1	83.33
Mean ± SD						83.48±0.2
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	5	6.2	2.8	78.57
11			5	6.3	3.2	58.06
12			5	6.4	2.6	63.15
Mean ± SD						66.59±10.
13	Treatment No.4	Soil + KC11	5	5.8	1.5	81.39
14			5	5.2	3.1	61.29
15			5	5.5	3.5	75
Mean ± SD						72.56±10.
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	5	5.9	3.8	57.14
17			5	6	3.5	60
18			5	6.5	3.2	54.54
Mean ± SD						57.22±2.7
19	Treatment No.6	Soil + KC9 + KC11	5	5.3	3	86.95
20			5	5.4	2.5	86.2
21			5	5.5	1	88.88
Mean ± SD						87.34±1.3
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	5	5.1	3.5	93.75
23			5	5.6	3	76.92
24			5	5.8	1.8	80
Mean ± SD						83.55±8.9

Table 4.27 Relative water Content (RWC) of Mung plant

Sr. No	Treatment No.	Consortia	Fresh Weight	Turgid Weight	Dry Weight	RWC
Mung						
1		Control	5	6.3	2.6	64.86
2			5	6.2	2.4	68.42
3			5	6.6	2.5	60.97
		Mean ± SD				64.75±3.72
4	Treatment No.1	Soil + *Fusarium Sp.*	5	6.6	2.9	56.75
5			5	6.4	2.8	61.11
6			5	7.3	2.5	46.51
		Mean ± SD				54.79±7.49
7	Treatment No.2	Soil + KC9	5	5.9	1.9	77.5
8			5	5.6	2.8	78.57
9			5	5.4	2.5	86.2
		Mean ± SD				80.75±4.7
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	5	6.2	2.9	63.63
11			5	6.5	3.5	50
12			5	6.7	3.2	56.25
		Mean ± SD				56.62±6.8
13	Treatment No.4	Soil + KC11	5	5.9	2	76.92
14			5	5.3	3.2	85.71
15			5	5.6	3.5	71.42
		Mean ± SD				78.01±7.2
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	5	6.4	3.8	46.15
17			5	6.3	2.1	69.04
18			5	6.8	3.3	48.57
		Mean ± SD				54.58±12.5
19	Treatment No.6	Soil + KC9 + KC11	5	6.2	1.5	74.46
20			5	5.8	1.7	80.48
21			5	5.6	1.8	84.21
		Mean ± SD				54.58±12.5
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	5	5.5	3.2	78.26
23			5	5.8	3.8	60
24			5	6	1.5	77.77
		Mean ± SD				72.01±10.4

Table 4.28 Relative water Content (RWC) of Rice plant

Sr. No	Treatment No.	Consortia	Fresh Weight	Turgid Weight	Dry Weight	RWC
Rice						
1		Control	5	6.5	3.8	44.44
2			5	6.9	3.5	42.85
3			5	6.7	3.3	51.51
		Mean ± SD				46.26±4.60
4	Treatment No.1	Soil + *Fusarium Sp.*	5	6.5	3.8	44.44
5			5	6.3	3.9	45.83
6			5	6.7	4.3	29.16
		Mean ± SD				39.81±9.24
7	Treatment No.2	Soil + KC9	5	5.4	3.4	80
8			5	5.7	1.8	82.05
9			5	5.8	1.2	82.6
		Mean ± SD				81.55±1.37
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	5	6.5	2.5	62.5
11			5	5.8	3.8	60
12			5	5.2	4.5	71.42
		Mean ± SD				64.64±6.0
13	Treatment No.4	Soil + KC11	5	5.7	1.8	82.05
14			5	5.5	3.9	68.75
15			5	5.8	2.8	73.33
		Mean ± SD				74.71±6.7
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	5	6	3.7	56.52
17			5	6.2	3.3	58.62
18			5	6.4	3.8	31.57
		Mean ± SD				48.90±15.0
19	Treatment No.6	Soil + KC9 + KC11	5	5.8	2.3	77.14
20			5	6.2	2.8	78.57
21			5	5.5	3.5	75
		Mean ± SD				76.90±1.79
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	5	6.4	2.6	63.15
23			5	6.2	2.5	67.56
24			5	6.2	2.4	68.42
		Mean ± SD				66.37±2.82

Table 4.29 Total Free amino acids of monocot & dicot plant

Sr. No	Treatment No.	Consortia	Absorbance at 570nm	Absorbance at 570nm	Absorbance at 570nm	Absorbance at 570nm
			Groundnut	Chickpea	Mung	Rice
1		Control	0.258	0.105	0.256	0.31
2			0.254	0.11	0.257	0.315
3			0.253	0.15	0.259	0.328
		Mean ± SD	91.06±0.94	43.45±8.80	91.9±054	113.45±3.31
4	Treatment No.1	Soil + *Fusarium Sp.*	0.352	0.215	0.358	0.412
5			0.358	0.225	0.36	0.425
6			0.375	0.228	0.369	0.431
		Mean ± SD	129.16±4.25	79.51±2.42	129.4±2.09	150.9±3.4
7	Treatment No.2	Soil + KC9	0.852	0.485	0.867	0.51
8			0.851	0.488	0.85	0.512
9			0.85	0.489	0.862	0.513
			303.7±0.5	174.04±0.7	307.02±3.1	182.73±0.5
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	0.932	0.585	0.95	0.612
11			0.945	0.586	0.959	0.625
12			0.951	0.589	0.96	0.628
		Mean ± SD	336.6±3.4	209.5±0.7	341.5±1.9	222.02±3.03
13	Treatment No.4	Soil + KC11	0.745	0.385	0.725	0.418
14			0.749	0.389	0.718	0.42
15			0.742	0.382	0.72	0.425
		Mean ± SD	266.19±1.25	137.61±1.25	257.49±1.28	150.35±1.28
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	0.82	0.42	0.8	0.532
17			0.818	0.425	0.81	0.531
18			0.815	0.428	0.813	0.533
		Mean ± SD	292.02±0.89	151.54±1.43	288.44±2.42	189.99±0.35
19	Treatment	Soil +	1.033	0.89	1.067	0.76

20	No.6	KC9 + KC11	1.285	0.895	1.185	0.768
21			1.289	0.898	1.19	0.775
		Mean ± SD	429.39±52.3	319.4±1.44	409.76±24.8	274.16±2.68
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	1.385	0.912	1.218	0.865
23			1.303	0.915	1.215	0.868
24			1.33	0.918	1.208	0.875
		Mean ± SD	478.33±14.9	326.78±1.07	427.44±12.15	310.47±1.83

Table 4.30 Total Phenolic Compound of monocot & dicot plant

Sr. No	Treatment No.	Consortia	Absorbance at 760 nm	Absorbance at 760 nm	Absorbance at 760 nm	Absorbance at 760 nm
			Groundnut	Chickpea	Mung	Rice
1		Control	3.21	2.32	3.25	2.32
2			3.19	2.45	2.5	2.15
3			3.25	2.58	3.29	2.58
		Mean ± SD	7.24±0.07	5.48±0.3	6.77±1.02	5.25±0.49
4	Treatment No.1	Soil + *Fusarium Sp.*	2.15	1.12	2	0.28
5			2	0.25	2.52	0.25
6			2.1	0.52	1.15	0.52
		Mean ± SD	4.64±0.1	1.29±1.0	4.19±1.5	0.65±0.33
7	Treatment No.2	Soil + KC9	7.25	5.14	6.25	5.12
8			7.26	5.25	6.24	5.25
9			7.32	5.23	6.23	5.13
		Mean ± SD	16.58±0.08	11.81±0.13	14.19±0.02	11.73±0.16
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	5.25	3.14	4.28	3.21
11			5.14	3.15	4.3	3.19
12			5.12	3.18	4.25	3.25
		Mean ± SD	11.73±0.16	7.10±0.04	9.68±0.05	7.24±0.07
13	Treatment No.4	Soil + KC11	6.1	4.25	5.25	4.25
14			6.14	4.21	5.1	4.3

15			6.12	4.16	5.12	4.28
		Mean ± SD	13.91±0.04	9.52±0.1	11.70±0.1	9.68±0.05
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	4.12	2.12	4.08	2.12
17			4.32	2.18	3.9	2.8
18			4.15	2.13	3.8	2.13
		Mean ± SD	13.91±0.04	4.7±0.07	8.88±0.32	5.25±0.89
19	Treatment No.6	Soil + KC9 + KC11	8.12	6.25	7.25	5.25
20			8.25	6.23	7.28	5.1
21			8.2	6.24	7.32	5.12
		Mean ± SD	18.68±0.15	14.19±0.02	16.59±0.08	16.59±0.18
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	6.61	4.56	6.15	3.14
23			6.25	5.2	6.12	3.15
24			6.42	4.85	6.25	3.18
		Mean ± SD	14.62±0.4	11.04±0.7	14.04±0.1	7.10±0.04

4.31 Total Flavonoid Content of monocot & dicot plant

Sr. No	**Treatment No.**	**Consortia**	**Absorbance at 415 nm**	**Absorbance at 415 nm**	**Absorbance at 415 nm**	**Absorbance at 415 nm**
			Groundnut	**Chickpea**	**Mung**	**Rice**
1		Control	0.852	0.651	0.732	0.595
2			0.875	0.612	0.712	0.592
3			0.823	0.689	0.725	0.598
		Mean ± SD	1.452±0.02	1.09±0.03	1.223±0.01	0.991±0.003
4	Treatment No.1	Soil + *Fusarium Sp.*	0.512	0.513	0.413	0.313
5			0.513	0.514	0.415	0.315
6			0.514	0.515	0.414	0.314
		Mean ± SD	0.843±0.001	0.844±0.001	0.664±0.00	0.483±0.001
7	Treatment No.2	Soil + KC9	0.952	0.745	0.812	0.712
8			0.912	0.762	0.821	0.721
9			0.975	0.789	0.814	0.714

		Mean ± SD	1.626±0.03	1.298±0.022	1.389±0.00	1.208±0.004
10	Treatment No.3	Soil + KC9 + *Fusarium Sp.*	0.752	0.618	0.652	0.519
11			0.753	0.612	0.653	0.518
12			0.751	0.613	0.651	0.52
		Mean ± SD	1.275±0.001	1.025±0.003	1.094±0.00	0.854±0.001
13	Treatment No.4	Soil + KC11	0.812	0.531	0.728	0.628
14			0.815	0.535	0.723	0.623
15			0.818	0.534	0.725	0.625
		Mean ± SD	1.389±0.003	0.879±0.002	0.464±0.00	1.045±0.002
16	Treatment No.5	Soil + KC11 + *Fusarium Sp.*	0.651	0.418	0.551	0.451
17			0.612	0.425	0.555	0.455
18			0.625	0.43	0.558	0.458
		Mean ± SD	1.0529±0.019	0.682±0.006	0.917±0.00	0.732±0.001
19	Treatment No.6	Soil + KC9 + KC11	1.25	0.852	0.952	0.81
20			1.258	0.851	0.951	0.812
21			1.252	0.85	0.953	0.813
		Mean ± SD	2.181±0.00	1.454±0.001	1.637±0.00	1.382±0.001
22	Treatment No.7	Soil + KC9 + KC11+ *Fusarium Sp.*	0.915	0.625	0.714	0.614
23			0.898	0.634	0.695	0.618
24			0.895	0.63	0.69	0.613
		Mean ± SD	1.546±0.01	1.052±0.004	1.179±0.01	1.0276±0.002

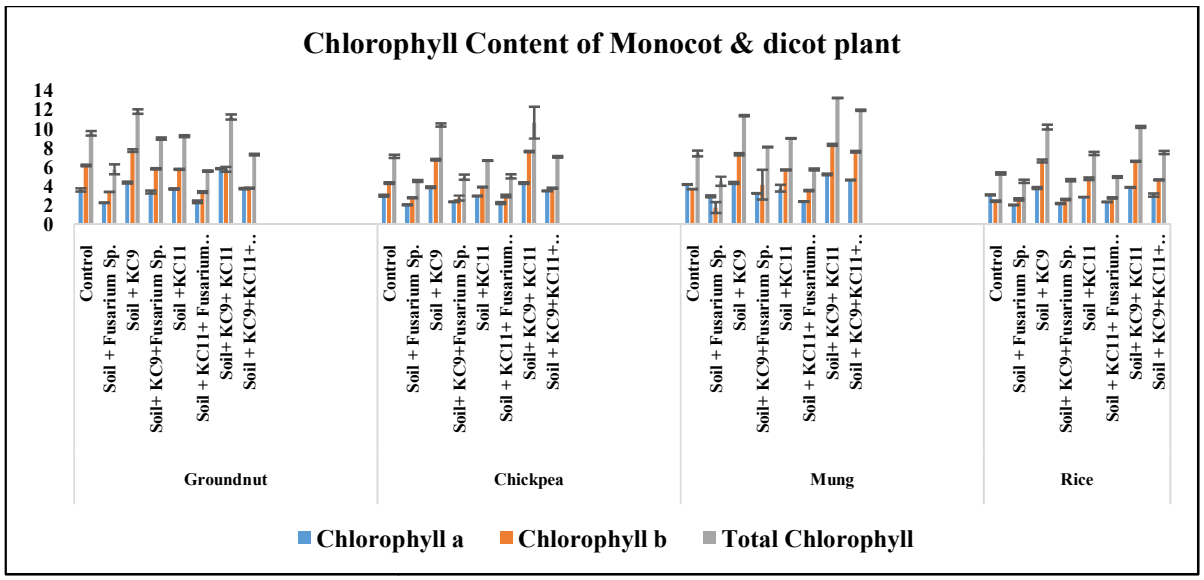


Fig. 4.55 Graphical Representation; Total Chlorophyll Content of Monocot & Dicot Plant

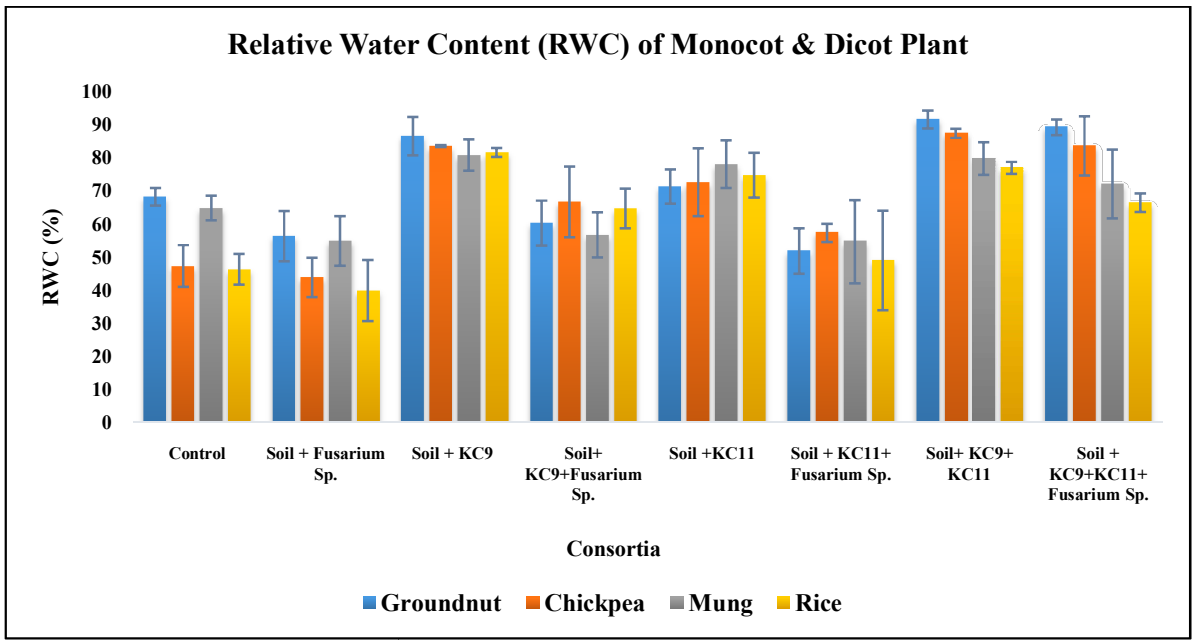


Fig. 4.56 Graphical Representation; Relative Water Content (RWC) of Monocot & Dicot Plant

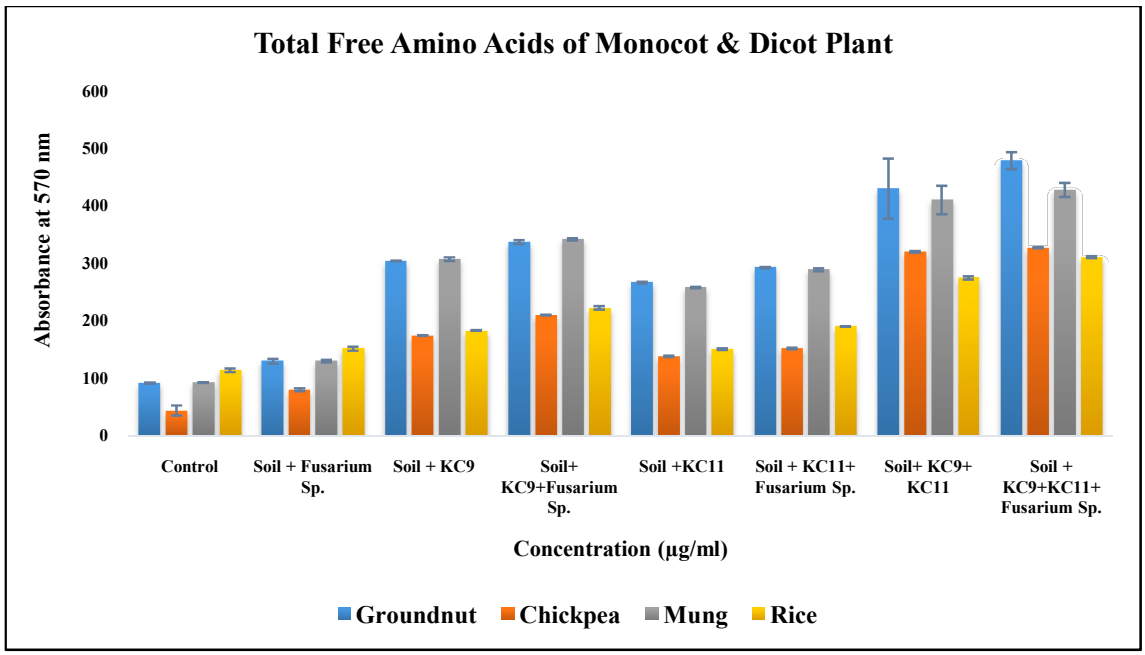


Fig. 4.57 Graphical Representation; Total Free amino acids of Monocot & Dicot Plant

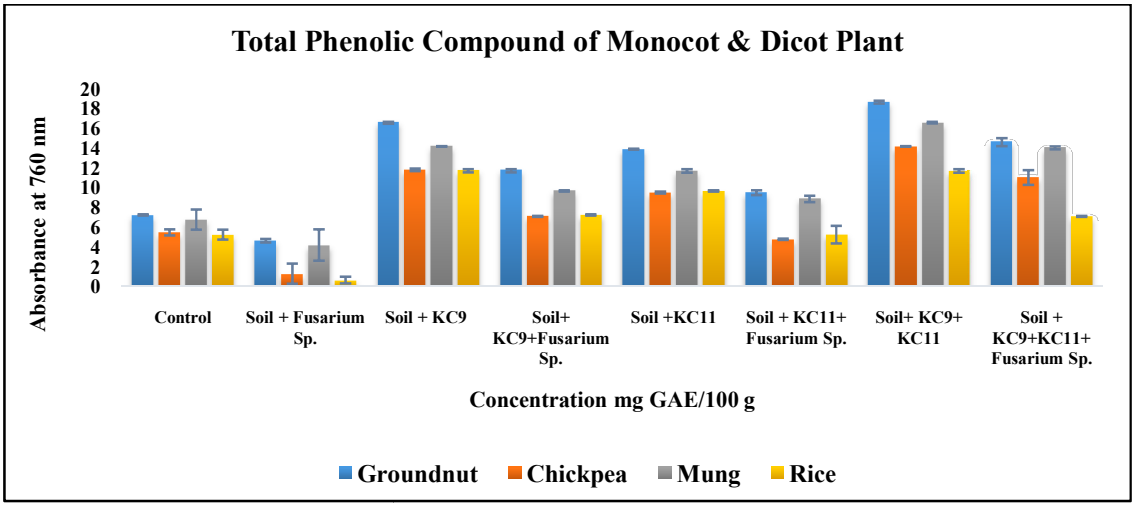


Fig. 4.58 Graphical Representation; Total Phenolic Compound of Monocot & Dicot Plant

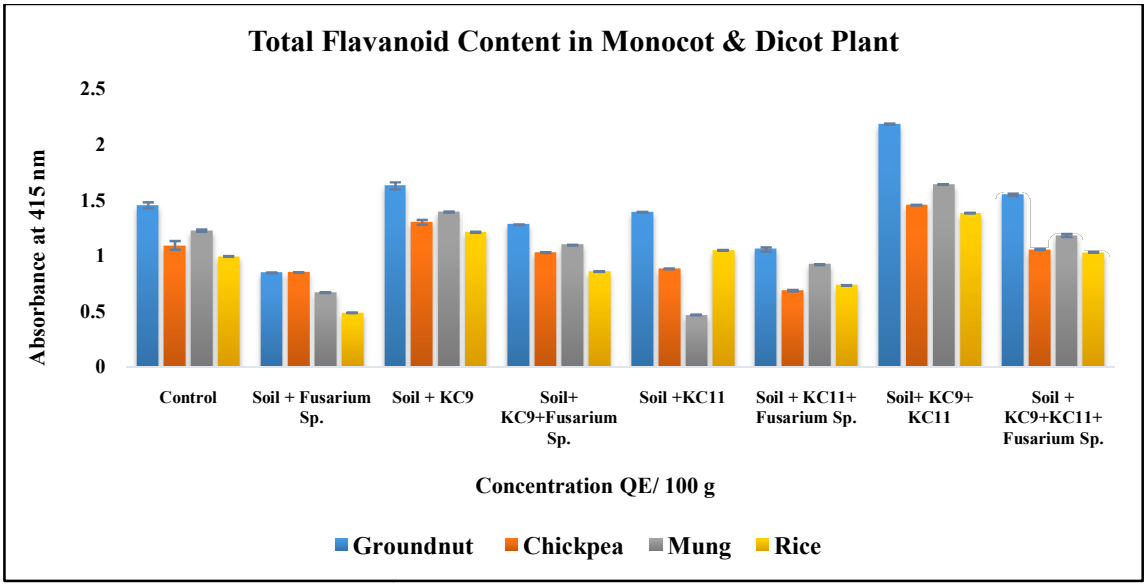


Fig. 4.59 Graphical Representation; Total Flavonoid Content of Monocot & Dicot Plant

In control condition, groundnut (chlorophyll a – 3.58±0.16 µg/ml, chlorophyll b – 6.16 ± 0.080, total Chlorophyll – 9.53±0.23µg/ml), chickpea (chlorophyll a – 2.97±0.09, chlorophyll b – 4.31±0.08µg/ml, total chlorophyll – 7.12±0.17µg/ml), mung (chlorophyll a – 4.15±0.028µg/ml, chlorophyll b – 3.68±0.028µg/ml, total chlorophyll – 7.4±0.30µg/ml), rice (chlorophyll a – 3.06±0.040µg/ml, chlorophyll b – 2.41±0.075µg/ml, total chlorophyll – 5.3±0.11µg/ml), whereas in pathogenic condition, groundnut had (chlorophyll a – 2.23±0.03 µg/ml, chlorophyll b – 3.3 ± 0.01µg/ml, total Chlorophyll – 5.75±0.5µg/ml), chickpea (chlorophyll a – 2.01±0.06µg/ml, chlorophyll b – 2.75±0.04µg/ml, total chlorophyll – 4.54±0.1µg/ml), mung (chlorophyll a – 2.90±0.09µg/ml, chlorophyll b – 1.74±0.5µg/ml, total chlorophyll – 4.5±0.48µg/ml), rice (chlorophyll a –2.01±0.04µg/ml, chlorophyll b – 2.59±0.12µg/ml, total chlorophyll – 4.49±0.16µg/ml).Consortium treated plants had significantly higher total chlorophyll content than single inoculated plants. Single bacterial strain KC9 inoculated plant were as follows groundnut had (chlorophyll a – 4.36±0.10 µg/ml, chlorophyll b – 7.71 ± 0.14µg/ml, total chlorophyll – 11.81±0.23µg/ml), chickpea had (chlorophyll a – 3.87±0.09µg/ml, chlorophyll b – 6.76±0.07µg/ml, total chlorophyll –

10.40±0.16µg/ml), mung had (chlorophyll a – 4.31±0.10µg/ml, chlorophyll b – 7.32±0.12µg/ml, total chlorophyll – 11.38±0.06µg/ml), rice had (chlorophyll a – 3.79±0.11µg/ml, chlorophyll b – 6.62±0.15µg/ml, total chlorophyll – 10.19±0.25µg/ml), while treated with KC11 groundnut had (chlorophyll a – 3.69±0.05 µg/ml, chlorophyll b – 5.75 ± 0.04µg/ml, total chlorophyll – 9.22±0.1µg/ml), chickpea (chlorophyll a – 2.94±0.04µg/ml, chlorophyll b – 3.88±0.04µg/ml, total chlorophyll – 6.66±0.02µg/ml), mung (chlorophyll a – 3.77±0.34µg/ml, chlorophyll b – 5.67±0.04µg/ml, total chlorophyll – 8.99±0.04µg/ml), rice (chlorophyll a – 2.83±0.02µg/ml, chlorophyll b – 4.75±0.13µg/ml, total chlorophyll – 7.4±0.16µg/ml), when treated with consortium KC9+KC11 groundnut had (chlorophyll a – 5.81 ±0.04 µg/ml, chlorophyll b – 5.75 ± 0.25µg/ml, total Chlorophyll – 11.24±0.26µg/ml), Chickpea had (chlorophyll a – 4.31±0.09µg/ml, chlorophyll b – 7.62±0.07µg/ml, total chlorophyll – 10.65±1.67µg/ml), mung had (chlorophyll a – 5.22±0.09µg/ml, chlorophyll b – 8.32±0.10µg/ml, total chlorophyll – 13.23±0.025µg/ml), rice had (chlorophyll a – 3.84±0.03µg/ml, chlorophyll b – 6.58 ±0.05µg/ml, total chlorophyll – 10.20±0.088µg/ml).Single bacterial strain KC9 inoculated with *Fusarium Sp.*groundnut had (chlorophyll a – 3.37±0.15 µg/ml, chlorophyll b – 5.79 ± 0.06µg/ml, total Chlorophyll – 8.97±0.12µg/ml), chickpea (chlorophyll a – 2.32±0.03µg/ml, chlorophyll b – 2.74±0.25µg/ml, total chlorophyll – 4.93±0.27µg/ml), mung (chlorophyll a – 3.23±0.05µg/ml, chlorophyll b – 4.15±1.5µg/ml, total chlorophyll – 8.09±0.04µg/ml), rice (chlorophyll a – 2.16±0.06µg/ml, chlorophyll b – 2.57±0.054µg/ml, total chlorophyll – 4.60±0.12µg/ml), when treated with KC11 + *Fusarium Sp.*groundnut had (chlorophyll a – 2.34±0.13µg/ml, chlorophyll b – 5.79 ± 0.06µg/ml, total Chlorophyll – 5.57±0.06µg/ml), chickpea (chlorophyll a – 2.20±0.10µg/ml, chlorophyll b – 2.95±0.13µg/ml, total chlorophyll – 5.01±0.21µg/ml), mung (chlorophyll a – 2.36±0.02µg/ml, chlorophyll b – 3.52±0.08µg/ml, total chlorophyll – 5.75±0.10µg/ml), rice (chlorophyll a – 2.33±0.01µg/ml, chlorophyll b – 2.74±0.07µg/ml, total chlorophyll – 4.94±0.08µg/ml) showing in fig no. 4.55. Patel *et al.,* 2023 reported in salt stress condition, total chlorophyll content reduced in both uninoculated saline condition and as compared to saline and non – saline, while increased in consortia treated with saline condition. In context, our findings recorded total chlorophyll content was increased in consortia (KC9+KC11) condition.

Relative water content is significantly representing for the water status in plants. The plant inoculated with only double distilled water shown relative water content (RWC) of groundnut (68%), Chickpea (47%), mung (64%) and followed by rice (46%), whereas monocot and dicot plant treated with fungal pathogen (*Fusarium sp.*)., noted relative water content of groundnut (56%), chickpea (43%), mung (54 %), and rice (39%).The plants when treated with individual bacterial strains KC9, KC11 and with consortia (KC9+KC11) the significant percentage of relative water content had been increased than control. The relative water content (RWC) of Groundnut (86 %), Chickpea (83%), mung (80%) and rice (81%)was estimated in treated with KC9, while in treated condition with KC11 showing groundnut (71 %), chickpea (72 %), rice (74 %) and maximum estimated in mung was 78 %.Results revealed at fig no. 4.56& table no.4.25 – 4.28 groundnut was recorded higher relative water content 91% in consortia (KC9+KC11) , Chickpea (87%), mung (79%) and rice was measured (76%).Conversely, a decrease was observed in plants treated with bacteria infected by fungal pathogen *Fusarium sp.* with KC9, *Fusarium Sp.* With KC11 Similarly, a decline in relative water content was noted in consortia treated with the fungal pathogen (KC9+KC11+*Fusarium Sp*.). Under the inoculated condition (KC9+ *Fusarium sp.* , the RWC of groundnut, chickpea, mung and rice was 60 %, 66%, 56 % and 64 % measured whereas, (KC11+ *Fusarium sp.*) observed, the relative water content of groundnut (51%), chickpea (57%) , mung (54%), and rice was (39 %) in treated with *Fusarium sp.* while in consortia (KC9+KC11+ *Fusarium sp.*) 89 % (groundnut), 83 % chickpea ,72 % mung and rice was 66 % . Previous research has found water availability significantly decreased under abiotic stress condition. The significant increase in RWC in PGPR infected wheat and mung grown under salt stress conditions (Ahmed *et al.,* 2013). In the present study, bacterial stress instigated a higher increase in RWC (groundnut, chickpea, mung, rice).

Total free amino acids significantly decreased in plants when treated with single strains and consortia. The result depicted in fig no. 4.57 and table no.4.29 total free amino acid estimated in uninoculated condition groundnut was (91.06±0.94 µg/ml), chickpea (43.45±0.08 µg/ml), mung and rice estimated 91.9±0.54 µg/ml and 113.45±1.20 µg/ml respectively. Fungal pathogen with plant showed total free amino acid content in groundnut was 129.16±4.25 µg/ml chickpea 79.51±2.42 µg/ml, mung 129.4±2.09µg/ml and rice 150.9±3.4 µg/ml respectively. The graphical representation showed maximum change in each plant treated with KC9 observed in groundnut (303.7±0.5 µg/ml), chickpea (174.04±.0.7 µg/ml), mung (307.02±3.1 µg/ml) and rice (182.73±0.5 µg/ml) while in KC11, groundnut (266.19±1.25 µg/ml), chickpea (137.61±1.25 µg/ml), mung (257.49±1.28 µg/ml) and rice (150.35±1.28

µg/ml), whereas (KC9+KC11) showed in groundnut(429.39±1.20 µg/ml), chickpea (319.4±1.44 µg/ml),mung (409.76±1.25µg/ml) and rice (274.16±2.68 µg/ml). Among all selected monocot and dicot plant, total free amino acids were found higher in inoculated with fungal pathogen groundnut was recorded (336.6±3.4), chickpea (174.04±0.7µg/ml), mung (307.02±3.1µg/ml) and rice (182.73±0.5 µg/ml) while in (KC11+ *Fusarium sp.*) recorded groundnut was (292.02±0.89 µg/ml), chickpea (151.54±1.43 µg/ml), mung (288.44±2.42µg/ml) and rice (189.99±0.35 µg/ml) respectively. (KC9+KC11+ *Fusarium sp.*) groundnut (478.33±0.08 µg/ml), chickpea (326.78±0.04 µg/ml), mung (427.44±0.05 µg/ml) and rice (310.47±1.83 µg/ml). When consortium strains were infused rather than individual strains in plant, test revealed a significant increase in plant growth during bacterial stress condition. Similar study of Patel *et al.,* 2023 has reported total free amino acid concentration was measured highest in consortia, followed by individual strain in salt stress condition. In this context, we investigate the concentration of total free amino acids higher increase in consortia treated with pathogen and followed by individual strain with pathogen and higher decrease in plants treated with individual strain and consortia also.

During the growth and development stages of plant, phenolic compounds are produced naturally. The total phenolic compound of groundnut (7.24±0.07 mg GAE/100g), chickpea (5.48±0.3 mg GAE/100g), mung (6.77±1.02 mg GAE/100g), and followed by rice (5.25±0.49 mg GAE/100g) whereas pathogen only groundnut had (4.64±0.1 mg GAE/100g), chickpea (1.29±1.0 mg GAE/100g), mung (4.19±1.5 mg GAE/100g), and rice (0.65±0.33 mg GAE/100g). When treated with KC9 groundnut had (16.58±0.08 mg GAE/100g), chickpea (11.81±0.13 mg GAE/100g), mung (14.19±0.02 mg GAE/100g), (rice 11.73±0.16 mg GAE/100g) respectively, while treated with KC11 bacterial strain groundnut had (13.91±0.04 mg GAE/100g), chickpea (9.52±0.1 mg GAE/100g), mung (11.70±0.1 mg GAE/100g), rice(9.68±0.05 mg GAE/100g).The plant treated with (KC9+KC11) noted maximum phenolic content in all plants, groundnut (18.68±0.15 mg GAE/100g), chickpea (14.19±0.02 mg GAE/100g), mung (16.59±0.08 mg GAE/100g), rice (16.59±0.18 mg GAE/100g) respectively.Under the inoculated condition (KC9+*Fusarium sp.*) estimated less amount of total phenolic compound was groundnut had (16.58±0.08 mg GAE/100g) and chickpea (11.81±0.13 mg GAE/100g), mung (14.19±0.02 mg GAE/100g), rice (11.73±0.16 mg GAE/100g) whereas the graphical representation showed in fig. no.4.58&table no. 4.30 treated with (KC11+ *Fusarium sp.*) of groundnut plant (13.91±0.04 mg GAE/100g),chickpea (9.52±0.1 mg GAE/100g),mung (11.70±0.1 mg GAE/100g), and followed by rice (9.68±0.05 mg GAE/100g).The total phenolic content of groundnut measured as (14.62±0.4 mg GAE/100g) and chickpea (11.04±0.7 mg GAE/100g), mung (14.04±0.1 mg GAE/100g), rice (7.10±0.01 mg GAE/100g), when inoculated condition (KC9+KC11+ *Fusarium sp.*). Various research has shown increased phenolic content during germination, as per the study of Naz *et al.,* 2023 has reported mung bean, chickpea , soyabean and lentil , which showed a similar inclining trend of total phenolic content at various level of germination. Our findings, TPC had increased in both individual bacterial strain and consortia while decreased in pathogenic condition.

Total flavonoids are secondary metabolites, which are mostly used in plants to produce yellow and other pigment which play important role in the colors of plants. They have

antioxidant, anti –allergic properties also (Rebaya *et al.,* 2014). Results revealed in fig no.4.59& table no. 4.31 In control condition, the total flavonoid content of groundnut (1.452±0.02 QE/100g), chickpea (1.09±0.03 QE/100g), mung (1.22±0.01 QE/100g), and followed by rice (0.99±0.003QE/100g) whereas pathogen only groundnut had (0.843±0.001QE/100g), chickpea (0.884±0.001 QE/100g), mung (0.664±0.001 QE/100g), and rice (0.483±0.001 QE/100g). When treated with KC9 groundnut had (1.626±0.01 QE/100g), chickpea (1.298±0.02 QE/100g), mung (1.389±0.004 QE/100g), rice (1.208±0.004 QE/100g) respectively, while treated with KC11 bacterial strain groundnut had (1.389±0.003 QE/100g), chickpea (0.879±0.002 QE/100g), mung(0.464±0.001 QE/100g), rice(1.045±0.002 QE/100g).The plant treated with (KC9+KC11) noted maximum flavonoid content in all plants, groundnut (2.181±0.004 QE/100g), chickpea (1.454±0.001QE/100g), mung (1.637±0.001 QE/100g), rice (1.382±0.001 QE/100g) respectively. Under the inoculated condition (KC9+ *Fusarium sp.*) estimated less amount of total flavonoid was groundnut had (1.275±0.001 QE/100g), chickpea (1.025±0.003 QE/100g), mung (1.094±0.001 QE/100g), rice (0.854±0.001 QE/100g) whereas the graphical representation showed in fig. treated with (KC11+ *Fusarium sp.*) of groundnut plant (1.052±0.001 QE/100g),chickpea (0.682±0.006 QE/100g),mung (0.917±0.003 QE/100g), and followed by rice (0.932±0.001QE/100g).The total flavonoid content of groundnut measured as (1.546±0.01 QE/100g) and chickpea(1.052±0.004 QE/100g), mung (1.179±0.001 QE/100g), rice (1.0276±0.001 QE/100g), when inoculated condition (KC9+KC11+*Fusarium sp.*). According to Sharma *et al.,* 2022, the result revealed that showed legumes were rich sources of flavonoid contents, such as mung bean ((173.16±6.72 QE/100g), soya bean (191.70±8.73 QE/100g) and followed by chickpea (177.4±4.55 QE/100g).