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Boosting maize yield and root traits with salt-tolerant plant growth-promoting rhizobacteria in the Indo-Gangetic plain: A microbial solution to soil salinity

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ABSTRACT

Soil salinity, which significantly reduces maize production in the Indo-Gangetic plains, requires continuous and sustained efforts. This study investigated six salt-tolerant bacterial strains and their ability to promote maize growth, yield, and root architecture in saline conditions. Among them, *Bacillus subtilis* ASM7 and *Pseudomonas fluorescens* ASM16 were the most effective, markedly enhancing plant height, dry matter accumulation, and yield attributes such as grain yield by 27% and 23%, respectively. These strains also improved cob traits and root architecture, such as root length and root volume by 77% and 56%, respectively, particularly by stimulating finer root structures that favor more efficient soil exploration under stress. The findings highlight the preferential stimulation of finer root structures over primary development, which optimizes soil exploration during stress. All these results of plant growth-promoting rhizobacteria in saline agro-ecosystems show that *B. subtilis* ASM7 and *P. fluorescens* ASM16 strains act as important environmentally friendly bio-inoculants for maize cultivation in the long term, offering a novel microbial strategy for improving crop resilience and productivity in salt-affected agro-ecosystems.

1. INTRODUCTION

Agricultural productivity worldwide is increasingly constrained by environmental stresses, with salinity being one of the most severe threats to crop growth and yield [1]. Salt stress disrupts plant physiology and metabolism, such as hindering germination, photosynthesis, and nutrient uptake, which results in substantial yield reductions [2]. Globally, more than one billion hectares of land are affected by salinity to varying degrees, with extensive areas across Asia, South America, and Australia facing acute challenges. In India, approximately 6.7 million hectares of agricultural land are salt-affected, of which about 2.9 million hectares have been rendered unproductive due to salinization in coastal and inland regions [3,4]. This escalating problem poses a serious risk to national food security.

Maize (*Zea mays* L.), the third most important cereal crop in India, is particularly sensitive to salt stress. High salinity restricts CO_2 uptake due to stomatal closure, hampers root and shoot growth, and causes overall reductions in biomass and grain yield [5,6]. Improving maize's resilience to salinity, therefore, remains a pressing need, especially in regions critical for cereal production such as the Indo-Gangetic plain (IGP). Recent research emphasizes the essential role of the plant microbiome in mitigating stress impacts. Plant growth-promoting rhizobacteria (PGPR) support crop growth under stress by enhancing nutrient availability, producing phytohormones, synthesizing osmoprotectants, and regulating stress-related enzymes such as 1-aminocyclopropane-1-carboxylate (ACC) deaminase. These microbial interactions improve water relations, nutrient assimilation, and metabolic stability during salinity stress [7-13]. However, few PGPR studies have been conducted in Indian or IGP contexts. Some studies have already shown that salt-tolerant *Bacillus* and *Pseudomonas* strains can enhance maize growth, yield, and stress physiology under saline and sodic conditions, including work with native isolates, seed biopriming, and consortia. For example, [14,15] demonstrate that halotolerant *Bacillus* spp. can improve maize performance under salinity, mostly in pot or controlled experiments. Salt-tolerant PGPR consortia or endophytes can enhance maize growth and soil biological properties in saline and sodic fields [16,17]. Studies such as [18-20] extend halotolerant PGPR research to various crops and regions, including Indian coastal or saline systems.

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This study aims to isolate and characterize salt-tolerant PGPR associated with maize roots from saline soils of the IGP. The central hypothesis is that native PGPR strains can integrate the root yield dataset under field-representative IGP salinity. Comparative screening of multiple native strains isolated directly from maize rhizosphere in IGP saline soil, identification of two high-performing candidates tailored for IGP saline soils. Identifying such efficient microbial inoculants can provide an eco-friendly strategy for improving crop productivity and sustainability in salt-affected ecosystems.

2. MATERIALS AND METHODS

2.1. Site and Soil Description

The experiment was conducted during the kharif seasons of 2022 and 2023 at ICAR-NBAIM, Mau, under controlled saline conditions representative of the IGP (25°53'55.78 N, 83°29'18.90 E), an area affected by secondary salinization from irrigation, shallow water tables, and intensive agriculture. Bulk saline soil (EC 6.0–8.5 dS/m) was collected from a moderately salt-affected field, air-dried, sieved (2 mm), and characterized as sandy loam with pH 8.5, EC 4.5 dS/m, organic carbon 0.41%, and available N, P, and K of 145.3, 21.2, and 212.8 kg/ha, respectively.

2.2. Experimental Design and Crop Management

The trial was laid out in a randomized block design (RBD) with seven treatments – control, *Bacillus licheniformis* ASM2, *Bacillus subtilis* ASM7, *Pseudomonas koreensis* ASM9, *Pseudomonas fluorescens* ASM16, *Paenibacillus durus* ASM19, and *Bacillus pumilus* AGM27 (NCBI accessions PX525063–PX525068) – each replicated 3 times. Maize cultivar "Kanchan" was sown in the 1st week of July at 60 × 20 cm spacing using surface–sterilized seeds (1% NaOCl, 5 min) soaked for 60 min either in individual bacterial suspensions or sterile 0.85% NaCl (control). Recommended nutrients (120 N, 60 P_2O_5, and 60 K_2O kg/ha) were supplied through urea, diammonium phosphate, and muriate of potash, with half of N and all P and K applied at sowing and the remaining N at tasselling. Standard agronomic practices for maize under saline conditions were followed, and observations were recorded on yield attributes, grain yield, and root architecture.

2.3. Statistical Analysis

Correlation, path, cluster analyses, and principal component analysis (PCA) biplots were performed in R (RStudio, 2023) [21], whereas analysis of variance for the RBD was carried out using SAS (SAS EG 4.3) [22]. Treatment means were compared using the F-test, and least significant differences were calculated at the 5% probability level where treatment effects were significant.

3. RESULTS

3.1. Attribute Characters of Growth

In the present study, maize grown under saline conditions in the Indo-Gangetic region responded positively to inoculation with salt-tolerant bacterial strains. As shown in Table 1, microbial inoculation significantly enhanced plant height, dry matter accumulation (DMA), and growth rate indices compared to the uninoculated control. After 30 days, *P. fluorescens* ASM 16 increased plant height by 11% (from 60.3 to 66.9 cm), whereas after 90 days, *B. subtilis* ASM 7 and *P. fluorescens* ASM 16 extended height to 183.3 cm and 186.5 cm, respectively, relative to the control (160.0 cm). Other strains, such as *P. durus* ASM 19 and *P. koreensis* ASM 9, also promoted comparable

Table 1: Effect of salt-tolerant bacteria on growth attributes of maize under saline soil of Indo-Gangetic plain.

Treatments	Plant Height (cm)			Dry matter accumulation (g)				Crop growth rate				Relative growth rate			
	30 DAS	60 DAS	90 DAS	30 DAS	60 DAS	90 DAS	at harvest	0–30 DAS	30–60 DAS	60–90 DAS	90 DAS - harvest	0–30 DAS	30–60 DAS	60–90 DAS	90 DAS-harvest
Control	60.3	135.8	163.0	48.7	94.1	166.6	221.1	1.62	1.51	2.41	1.81	0.206	0.0219	0.0191	0.0094
Bacillus licheniformis ASM 2	61.3	141.1	169.3	50.8	98.1	173.5	229.1	1.69	1.57	2.51	1.85	0.208	0.0219	0.0190	0.0093
Bacillus subtilis ASM7	66.2	152.7	183.3	62.2	120.3	212.8	281.5	2.07	1.93	3.08	2.29	0.213	0.022	0.0190	0.0093
Pseudomonas koreensis ASM9	64.7	148.8	178.6	55.3	107.2	190.2	251.1	1.84	1.73	2.76	2.03	0.211	0.0218	0.0190	0.0093
Pseudomonas fluorescens ASM 16	66.9	155.4	186.5	60.0	116.1	205.3	275.0	2.00	1.87	2.97	2.323	0.212	0.0220	0.0191	0.0094
Paenibacillus durus ASM 19	65.9	151.5	181.8	58.5	113.7	201.9	265.8	1.95	1.84	2.94	2.13	0.212	0.0220	0.0191	0.0093
Bacillus pumilus ASM27	62.0	142.6	171.1	52.7	101.9	180.3	235.9	1.76	1.64	2.61	1.853	0.209	0.0219	0.0190	0.0093
SEM	1.0	1.7	2.0	1.2	2.2	3.6	6.2	0.05	0.04	0.06	0.052	0.010	0.0010	0.0010	0.0005
LSD (0.005)	3.0	5.1	6.1	3.6	6.8	11.2	19.0	0.16	0.13	0.21	0.162	0.020	0.0020	0.0020	0.001

SEM: Standard error of the mean, LSD: Least significant difference growth, reaching 181.8 cm and 178.6 cm. DMA followed a similar trend. *B. subtilis* ASM 7 recorded the highest biomass (281.5 g), followed by *P. fluorescens* ASM 16 (275.0 g), representing 27.3% and 24.4% increases over the control (221.1 g). *P. durus* ASM 19, *P. koreensis* ASM 9, and *B. pumilis* ASM 27 showed moderate gains (6.7–20.2%). *B. licheniformis* ASM 2 exhibited the least improvement (3.6%), but still outperformed the control. The crop growth rate (CGR) increased substantially in inoculated treatments, with the highest mean CGR between 60 and 90 DAS observed for *B. subtilis* ASM 7 (3.083 g/day), a 27.5% improvement over the control (2.417 g/day). Similarly, *P. fluorescens* ASM 16 (2.973 g/day) and *P. durus* ASM 19 (2.940 g/day) showed notable enhancements. The relative growth rate (RGR) followed a comparable pattern during the vegetative phase, with *B. subtilis* ASM 7 achieving the highest early RGR (0.213 g/g/day) versus control (0.206 g/g/day). These findings suggest that *B. subtilis* ASM 7 and *P. fluorescens* ASM 16 consistently promoted superior growth and biomass accumulation, confirming their adaptability and potential for enhancing maize development under salinity stress.

3.2. Effect of Salt-tolerant Bacteria on Maize Productivity

As shown in Table 2, inoculation with salt-tolerant bacterial strains significantly improved maize yield and cob characteristics under saline soil conditions. *B. subtilis* ASM 7 increased cob length by 28.4%, girth by 32.1%, and grain count per cob by over 30% relative to the control. Similarly, *P. fluorescens* ASM 16 improved cob length and girth by 24.4% and 27.0%, resulting in a 24.6% increase in kernel number per cob. Enhancements in yield attributes translated into substantial gains in economic yield. Grain yield increased by 27.8% with *B. subtilis* ASM 7 (37.33 q) compared to the control (29.22 q), followed by *P. fluorescens* ASM 16 (23.3%) and *P. durus* ASM 19 (21.3%). Even the least effective treatment, *B. licheniformis* ASM 2, improved grain yield modestly (4.2%). Straw yield and total biological yield improved by 25.8% and 26.5%, respectively, while the harvest index (HI) remained relatively stable (38.79–39.16%), indicating balanced biomass partitioning under stress conditions.

3.3. Effect of Salt-Tolerant Bacteria on Maize Root Architecture

Root analysis [Table 3] revealed marked improvements in the root structure of inoculated maize plants under salinity stress. *B. subtilis* ASM 7 showed the highest enhancement in root length (RL) (106.7 cm), followed by *P. fluorescens* ASM 16 (102.1 cm) and *P. koreensis* ASM 9 (96.8 cm), relative to the control (90.7 cm). Root volume (RV), surface area, and average diameter were also greatest with *B. subtilis* ASM 7 (1.54 cm^3, 42.5 cm^2, and 1.65 mm, respectively). Furthermore, the fractal dimension and root branching metrics (forks, crossings, links, and tips) were substantially greater in inoculated treatments, with *B. subtilis* ASM 7 showing the highest complexity (e.g., 173.5 forks and 166.3 tips versus 122.0 and 98.0 in control). These data collectively indicate that salt-tolerant bacterial inoculation, particularly with *B. subtilis* ASM 7, enhances root system architecture and facilitates better plant adaptation to saline stress, contributing to improved nutrient uptake and yield performance.

3.4. Correlation among the Study Variables

Correlation analysis of different study variables is computed, and the results are depicted in Figure 1. The significance in correlation is depicted in * values, i.e., single * (significant at 5% level of

Table 2: Effect of salt-tolerant bacteria on yield attributes of maize under saline soil of Indo-Gangetic plain.

Treatments	Cob length	Cob girth	Grain per Cob	Grain yield	Straw yield	Biological yield	Harvesting index
Control	11.47	8.63	312.67	29.22	46.11	75.33	38.79
Bacillus licheniformis ASM 2	11.93	9.03	328.00	30.44	47.80	78.24	38.91
Bacillus subtilis ASM7	14.73	11.40	406.33	37.33	58.00	95.33	39.16
Pseudomonas koreensis ASM9	13.17	9.97	358.00	33.37	52.52	85.89	38.85
Pseudomonas fluorescens ASM 16	14.27	10.97	389.67	36.03	56.03	92.06	39.13
Paenibacillus durus ASM 19	13.80	10.60	375.67	35.43	55.74	91.16	38.86
Bacillus pumilus ASM27	12.43	9.40	342.67	31.62	49.74	81.36	38.86
SEM	0.23	0.22	7.21	0.63	0.89	1.51	38.79
LSD (0.005)	0.70	0.68	22.23	1.96	2.73	4.64	38.91

SEM: Standard error of the mean, LSD: Least significant difference

Table 3: Effect of salt-tolerant bacteria on root architecture of maize under saline soil of Indo-Gangetic plain.

Treatments	Root length (cm)	Projected area (cm^2)	Surface area (cm^2)	Avg. diam (mm)	Root volume (cm^3)	No. of forks	No. of crossings	No. of links	No. of tips	Fractal dimension
Control	90.7	9.5	31.7	0.85	0.87	122.0	17.0	280.7	98.0	280.7
Bacillus licheniformis ASM 2	92.5	10.0	33.7	0.96	0.96	123.8	17.7	288.5	107.6	288.5
Bacillus subtilis ASM7	106.7	13.9	42.5	1.65	1.54	173.5	24.3	359.5	166.3	359.5
Pseudomonas koreensis ASM9	96.8	10.4	37.4	1.25	1.18	147.9	19.7	313.3	141.3	313.3
Pseudomonas fluorescens ASM 16	102.1	13.5	40.6	1.44	1.36	164.1	22.3	341.7	162.9	341.7
Paenibacillus durus ASM 19	98.4	11.3	38.9	1.34	1.26	154.8	21.0	326.3	152.2	326.3
Bacillus pumilus ASM27	94.5	9.8	35.8	1.11	1.05	133.3	19.3	297.4	133.3	297.4
SEM	1.7	0.4	0.9	0.05	0.04	3.6	0.7	5.5	23.2	5.5
LSD (0.005)	5.3	1.3	2.8	0.14	0.13	11.0	2.0	17.1	71.5	17.1

SEM: Standard error of the mean, LSD: Least significant difference

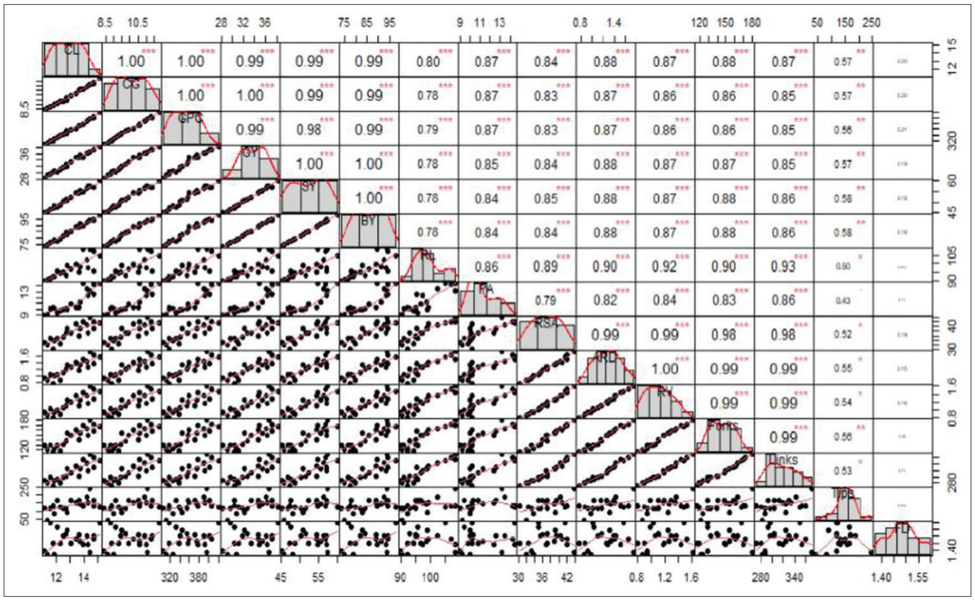

Figure 1: Correlation analysis among the different study variables related to maize cob, root traits, and yield parameters. CL: Cob length, CG: Cob girth, GPC: Grain per cob, GY: Grain yield, SY: Stover yield, BY: Biological yield, RL: Root length, PA: Projected area, RSA: Root surface Area, ARD: Average root diameter, RV: Root volume, FD: Fractal dimension.

significance), two ** (Significant at 1% level of significance), and three *** (significant at 0.01% level of significance). Tight association is proved when correlation analysis is done with coefficient of uniformity (CU), coefficient of biomass (CB), germination percentage (GP), and grain yield (GY) (r > 0.98, ***). Biological and grain yield show a strong connection because of biological yield (BY), and GY are also highly correlated (r = 0.86, ***). In this study, the traits of each plant's pods and their numbers show weak or non-significant correlations between them, which reveals that they are contributing to the unique variance. Correlation values >0.5 and near 1 show a highly positive correlation. Further, the correlation values < 0.5 and closer to 0 are denoted as very low correlation. The tips variable is less correlated with the remaining variables.

3.5. PCA

After correlation analysis, PCA biplot analysis was done to achieve dimension reduction in the original variables [Figure 2]. PC1 (horizontal axis) and PC2 (vertical axis) are the first two principal components, representing the largest variation in the dataset. Observations (numbered points) are plotted based on their scores along these components. The red arrows are variable loadings, which show how each original variable contributes to PC1 and PC2. The length of arrows indicates the strength of the variable's contribution to the principal components.

The longer the arrow, the greater the contribution, and vice versa. The direction of the arrows represents the nature of the correlation between the variables. The variables with arrows pointing in the same direction represent a positive relation, and vice versa. Independent variables are represented through perpendicular arrows. The long arrows are the variables, DMA-80DAS, FD, RL, and PH-60DAS, which explain a lot of the trend. High mutual correlation traits are PH-80DAS, tips, forks, PA, and links clustered together, etc. The variable FD (likely "Flowering Days") points nearly straight up, meaning it loads strongly on PC2.

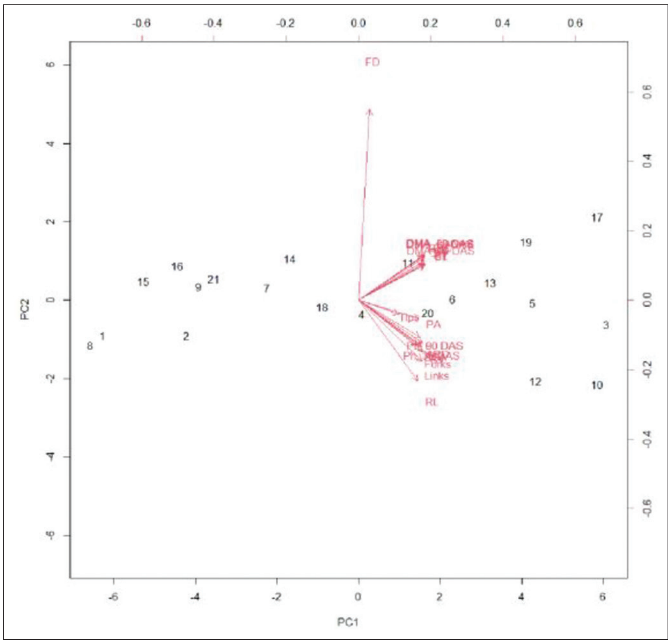

Figure 2: Principal component analysis biplot of maize physiological, yield, and root traits under experimental conditions. CL: Cob length, CG: Cob girth, GPC: Grain per cob, GY: Grain yield, SY: Stover yield, BY: Biological yield, RL: Root length, PA: Projected area, RSA: Root surface area, ARD: Average root diameter, RV: Root volume, FD: Fractal dimension.

3.6. Hierarchical Cluster Analysis

A hierarchical clustering heatmap was generated to observe the relationship between agro-morphological traits and data points, which are mentioned in Figure 3. In moist traits, data 5 and data 6 (clustered together) show highly exhibited values, whereas data 1 and data 2 (clustered together) show the lowest trait expression.

These findings suggest potential redundancy or shared biological functions.

3.7. Path Analysis

Further path analysis between the variables was drawn to map the functional relationships among the different variables [Figure 4]. Green arrows in Figure 4 represent positive effects, and red arrows represent negative effects. In the path analysis diagram, thicker lines represent a stronger effect. Path analysis (path coefficient-1.48) has revealed that the extract of biological yield directly has a very good positive effect on grain yield, making it a major determinant. On the other hand, stover yield (SY) has a direct negative effect on GY (−0.36) but an indirect positive effect on biological yield (0.85). Forks and RV are two traits that indirectly improve GY by having positive effects on SY and BY. RL and root surface area are examples of upstream traits that have weaker and less direct effects on GY. This analysis shows how complicated the interactions are and suggests that to improve GY, we should focus on making BY and its upstream contributors better.

4. DISCUSSION

4.1. Growth Attributing Character

Enhanced maize growth under saline conditions following inoculation with salt-tolerant strains primarily reflects improved physiological stability rather than additive biomass effects [23]. Salinity constrains ion balance and hydration, impairing photosynthesis, whereas inoculation with *B. subtilis* ASM7 and *P. fluorescens* ASM16 sustains metabolic activity through phytohormone synthesis (IAA, cytokinins) and ACC deaminase activity that reduces stress-induced ethylene [16,24-29]. Elevated CGR and RGR during 60–90 days after sowing (DAS) suggest prolonged carbon assimilation, likely supported by chlorophyll retention and osmotic protection via PGPR-derived exopolysaccharides. Variability among other isolates (*P. durus* ASM19, *P. koreensis* ASM9, *B. pumilus* ASM27, and *B. licheniformis* ASM2) reflects differences in root colonization and enzymatic efficiency, indicating that functional performance under salt stress depends on both metabolic adaptability and rhizospheric compatibility [30-35].

4.2. Impact on Maize Production through Salt-Tolerant Bacteria

Yield enhancement through bacterial inoculation arises from hormonal and ionic regulation sustaining reproductive growth under salinity. *B. subtilis* ASM7 and *P. fluorescens* ASM16 likely promote vascular differentiation and nutrient translocation through auxin-mediated signaling and phosphate solubilization, whereas ACC deaminase and osmolyte production alleviate oxidative stress during flowering [36-40]. The concurrent increase in biomass and grain yield with a stable HI indicates improved photosynthetic efficiency rather than altered assimilate partitioning. Variation among other strains reflects differences in compatible solute and siderophore secretion, supporting the concept that PGPR tolerance derives from integrated root–shoot signaling optimizing metabolic balance under stress [41-46].

4.3. Structure of Maize's Root

Root structural improvement under salinity reflects molecular reprogramming of developmental genes governed by microbial signaling. Inoculation with *B. subtilis* ASM7 and *P. fluorescens* ASM16 activates auxin–cytokinin crosstalk, enhancing the expression of root meristem regulators (WOX5, PIN1, and LAX3) and cell-cycle genes (CYCD3), resulting in greater branching and cortical expansion [47-51]. EPS-mediated biofilm formation enhances root–soil adhesion and strengthens Na^+ exclusion zones by maintaining K^+/Na^+ homeostasis. Microscopic evidence of increased root diameter and tip density aligns with the upregulation of aquaporin genes (PIP1 and PIP2), which improve water uptake efficiency. Moderate strains (*P. koreensis* ASM9 and *P. durus* ASM19) may induce partial responses depending on their root colonization patterns and signaling compatibility [17,52-55].

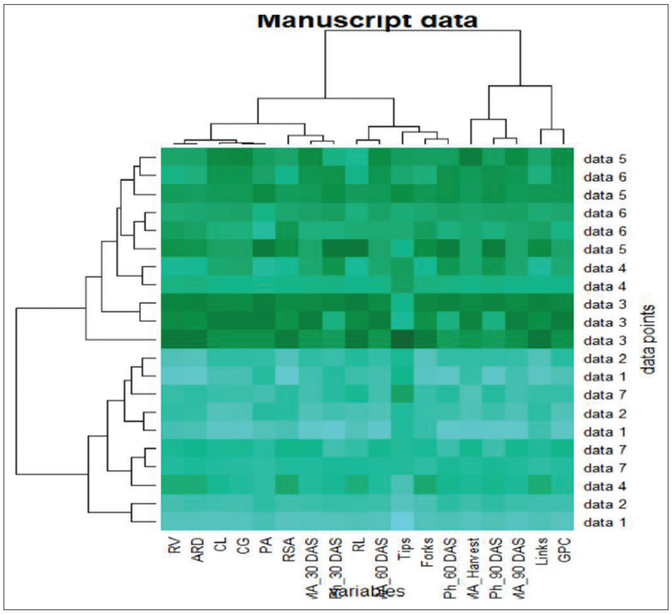

Figure 3: Hierarchical cluster analysis of manuscript data based on morphometric and agronomic traits. The heatmap and dendrogram illustrate clustering patterns among data points and variables including (CL: Cob length, CG: Cob girth, GPC: Grain per cob, GY: Grain yield, SY: Stover yield, BY: Biological yield, RL: Root length, PA: Projected area, RSA: Root surface area, ARD: Average root diameter, RV: Root volume, FD: Fractal dimension).

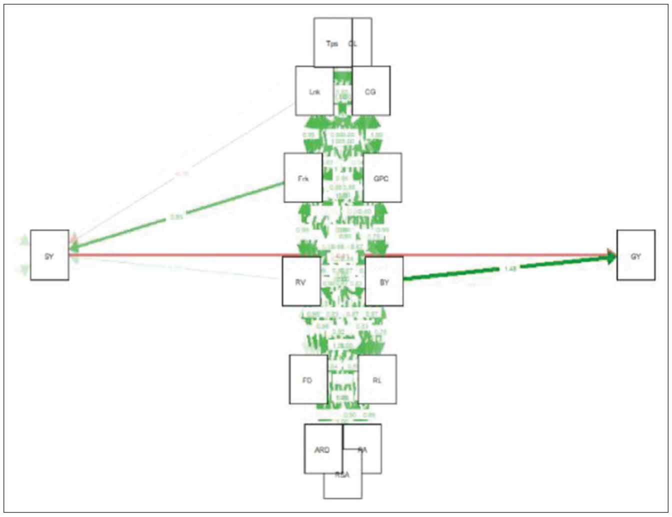

Figure 4: Path analysis diagram illustrating the direct and indirect relationships among maize yield components and root morphological traits. CL: Cob length, CG: Cob girth, GPC: Grain per cob, GY: Grain yield, SY: Stover yield, BY: Biological yield, RL: Root length, PA: Projected areca, RSA: Root surface area, ARD: Average root diameter, RV: Root volume, FD: Fractal dimension.

Overall, the enhanced maize performance under salinity is attributed to integrated molecular, physiological, and structural adaptation triggered by salt-tolerant PGPR. By modulating hormone signaling, ion transport, and gene expression linked to stress resilience, *B. subtilis* ASM7 and *P. fluorescens* ASM16 act as bio-stimulators of holistic plant homeostasis. Their deployment, either alone or in synergy, represents a molecularly informed biotechnological approach to mitigate salinity-induced yield losses in the IGP [56-59].

4.4. Novelty and Implications

Earlier studies [14,15] demonstrate that halotolerant *Bacillus* spp. can improve maize performance under salinity, mostly in pot or controlled experiments with emphasis on physiological and biochemical traits rather than high-resolution root system architecture and trait-yield path analysis. Salt-tolerant PGPR consortia or endophytes can enhance maize growth and soil biological properties in saline and sodic fields [16,17], but their focus is on enzyme activities, antioxidant defense, and ecological fitness rather than detailed quantification of root fractal traits and their statistical linkage to yield components. Some other studies, such as Kapadia *et al*., AbuQamar *et al*., and Gupta *et al*. [18-20], extend halotolerant PGPR research to various crops and regions, including Indian coastal or saline systems, but they do not provide an Indo-Gangetic maize dataset that couples native isolates, detailed root architecture, and multivariate yield-path analysis under the specific EC and pH conditions used here

5. CONCLUSION

This study demonstrates the potential of salt-tolerant PGPR, particularly *B. subtilis* ASM7 and *P. fluorescens* ASM16, in enhancing maize growth and yield under saline conditions of the IGP. These strains improved root architecture and physiological vigor, resulting in greater biomass and grain yield without affecting the HI. The findings highlight the promise of PGPR-based strategies for sustainable soil and nutrient management in salt-affected regions. Future work should focus on field-scale validation and the development of microbial consortia to strengthen crop resilience and productivity. Overall, the main outcome of this study is that inoculation with *B. subtilis* ASM7 and *P. fluorescens* ASM16 significantly improved maize growth and yield performance under salinity stress, demonstrating their practical potential as bioinoculants for salt-affected soils.

6. ACKNOWLEDGMENT

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7. AUTHORS' CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work. All the authors are eligible to be author as per the International Committee of Medical Journal Editors (ICMJE) requirements/guidelines.

8. FUNDING

There is no funding to report.

9. CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

10. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

11. DATA AVAILABILITY

All datasets generated or analyzed during this study are included in the manuscript.

12. PUBLISHER'S NOTE

13. USE OF ARTIFICIAL INTELLIGENCE (AI)-ASSISTED TECHNOLOGY

The authors declare that they have not used artificial intelligence (AI)-tools for writing and editing of the manuscript, and no images were manipulated using AI.

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