



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(7): 1563-1568
Received: 11-05-2026
Accepted: 15-06-2026

Shivashankaragouda Patil
Ph.D. Scholar, Department of Genetics and
Plant Breeding, College of Agriculture,
UAS, Dharwad, Karnataka, India

SA Desai
Professor, Department of Genetics and
Plant Breeding, University of Agricultural
Sciences, Dharwad, Karnataka, India

Suma S Biradar
Professor, Department of Genetics and
Plant Breeding, University of Agricultural
Sciences, Dharwad, Karnataka, India

JR Diwan
Professor, Department of Genetics and
Plant Breeding, University of Agricultural
Sciences, Dharwad, Karnataka, India

Krishnaraj PU
Professor, Department of Microbiology,
College of Agriculture, Dharwad, UAS,
Dharwad, Karnataka, India

Basvaraja B Bagewadi
Associate Professor, Department of
Biotechnology, College of Agriculture,
Dharwad, UAS, Dharwad, Karnataka,
India

Harshitha Kumar
Ph.D. Scholar, Department of Genetics and
Plant Breeding College of Agriculture
University of Agricultural Sciences,
Raichur, Karnataka, India

Ratnakala B
Ph.D. Scholar, Department of Entomology
College of Agriculture University of
Agricultural Sciences, Dharwad,
Karnataka, India

Abhishek V Karadagi
Ph.D. Scholar, Department of Genetics and
Plant Breeding, College of Agriculture,
UAS, Dharwad, Karnataka, India

Poojarani Malagatti
Ph.D. Scholar, Department of Agriculture
Microbiology, College of Agriculture, UAS,
Dharwad, Karnataka, India

Corresponding Author:
Shivashankaragouda Patil
Ph.D. Scholar, Department of Genetics and
Plant Breeding, College of Agriculture,
UAS, Dharwad, Karnataka, India

Microbial modulation of wheat performance under moisture stress: A multi-environment stability analysis

**Shivashankaragouda Patil, SA Desai, Suma S Biradar, JR Diwan,
Krishnaraj PU, Basvaraja B Bagewadi, Harshitha Kumar, Ratnakala B,
Abhishek V Karadagi and Poojarani Malagatti**

DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i7t.6161>

Abstract

Moisture stress is a major constraint to wheat productivity, causing yield instability across environments and limiting the effectiveness of genotype selection. The present study evaluated the performance, stability and adaptability of wheat genotypes under moisture stress conditions as influenced by actinobacteria seed treatment across multiple environments. A set of twenty wheat genotypes was assessed under treated and untreated conditions in five moisture-stress environments. Grain yield data from actinobacteria-treated plots were subjected to additive main effects and multiplicative interaction (AMMI) analysis, along with AMMI Stability Value (ASV) and Genotype Stability Index (GSI), to quantify genotype $\times$ environment interaction and identify stable genotypes. The analysis revealed a pronounced genotype $\times$ environment interaction under moisture stress, indicating differential genotype responses to microbial treatment. Actinobacteria seed treatment consistently improved genotype performance and reduced environmental sensitivity across environments. Among the evaluated genotypes, DWR-2006 (G3) exhibited superior stability and wide adaptability, while UAS-347 (G8), UAS-375 (G9) and HD-2888 (G10) also demonstrated stable performance across stress environments. In contrast, some high-performing genotypes showed specific adaptation, highlighting genotype-dependent microbial responsiveness. Overall, the results demonstrate that actinobacteria seed treatment is an effective and sustainable strategy for enhancing wheat performance and yield stability under moisture stress. The integration of microbial inoculation with multi-environment stability analysis provides a robust approach for identifying resilient wheat genotypes suitable for drought-prone agro-ecosystems.

Keywords: Genotype $\times$ environment interaction, drought tolerance, microbial inoculation, AMMI Stability Value (ASV), adaptability

1. Introduction

Wheat (*Triticum aestivum* L.) is one of the most widely cultivated cereal crops and constitutes a major source of food and nutrition for a substantial proportion of the global population. However, wheat productivity is increasingly challenged by abiotic stresses, with moisture stress emerging as a predominant constraint in rainfed and semi-arid regions. Limited and erratic rainfall, together with rising temperatures associated with climate change, has intensified the frequency and severity of drought events, leading to reduced yield stability and inconsistent genotype performance across environments. Under such conditions, maintaining stable yield performance has remained a critical criterion for identifying adaptable cultivars for arid regions as well as for selecting suitable parental lines in hybridization programs (Hackauf *et al.*, 2022)^[15]. Consequently, the development of sustainable and environmentally friendly strategies to mitigate moisture stress has become a key priority in contemporary wheat improvement programs.

Grain yield under moisture stress is a complex quantitative trait influenced by genetic makeup, environmental conditions and their interaction. Significant genotype $\times$ environment (G $\times$ E) interactions often complicate the identification of stable and widely adapted genotypes, as performance rankings tend to change across locations and seasons (Mullualem *et al.*, 2024)^[16]. Multi-environment evaluation combined with appropriate statistical models is essential to effectively interpret such interactions. The additive main effects and multiplicative interaction (AMMI) model has been widely used to partition G $\times$ E effects and identify genotypes with broad

or specific adaptation. AMMI-based stability parameters such as the AMMI Stability Value (ASV) and Genotype Stability Index (GSI) provide reliable measures for selecting stable, high-performing genotypes under stress environments (Bocianowski *et al.*, 2023; Chaudhary *et al.*, 2023) [6, 14].

In recent years, plant growth promoting microorganisms have gained attention as sustainable tools for enhancing crop tolerance to abiotic stresses. Among these, actinobacteria represent an important group of beneficial soil microbes known for their strong rhizosphere competence and multifunctional plant growth-promoting traits. Actinobacteria enhance plant performance through mechanisms such as stimulation of root growth, solubilization of nutrients, production of phytohormones, regulation of stress-induced ethylene via ACC deaminase activity and enhancement of antioxidant defense systems. These functions collectively improve plant water-use efficiency and physiological stability under moisture-limited conditions (Saxena *et al.*, 2023; Backer *et al.*, 2018; Kumar *et al.*, 2025) [8, 11, 17].

Although the positive role of actinobacteria in improving plant growth and drought tolerance has been reported in several crops, limited information is available on their interaction with diverse wheat genotypes evaluated across multiple moisture stress environments. Understanding how actinobacteria influence genotype performance and stability under stress is essential for integrating microbial inoculation with genotype selection. Therefore, the present study was undertaken to evaluate the performance, stability and adaptability of wheat genotypes under moisture stress conditions with actinobacteria seed treatment across multiple environments. The study aims to dissect genotype $\times$ environment interactions using AMMI analysis, identify stable and high-performing genotypes and assess the consistency of actinobacteria effects, thereby contributing to sustainable wheat production strategies for drought-prone agro-ecosystems.

2. Materials and Methods

2.1 Experimental material

The experiment was carried out at the agricultural experimental farm of Dharwad-2024 (E1), Bagalkot-2024 (E2), Vijayapura-2024 (E3), Raichur-2024 (E4) and Dharwad-2025 (E5) in Karnataka (Table 1), sown under rainfed and restricted irrigation conditions. These trials were sown in mid-November for two consecutive wheat cropping seasons viz 2023-2024 and 2024-25 (Dharwad only) respectively, making five environments for study.

Actinobacteria isolates AUDT 545 and AUDT 862 were obtained from the Department of Microbiology, University of Agricultural Sciences, Dharwad. The two actinobacterial isolates were selected based on prior laboratory screening for complementary plant growth-promoting traits, and their combined use as a consortium was intended to enhance functional diversity and consistency of stress mitigation (Hiremath *et al.* 2024) [29]. Consortium-based formulations are widely reported to provide more stable field performance than single-strain inoculants under variable environments (Gehlot *et al.*, 2021) [30]. Wheat seeds were surface sterilized using sodium hypochlorite solution (0.1%) for 10 min, followed by two to three rinses with sterile distilled water. Talc powder was used as the carrier material and 200 g of talc was sterilized at 121 °C for 30 min. Broth cultures of AUDT 545 and AUDT 862 were mixed in equal proportions to prepare a consortium and subsequently blended with the pre-sterilized carrier material in a ratio of 1:2 (culture: carrier). The formulation was shade-dried to reduce the moisture content to approximately 30 per cent and cured overnight before use and carrier material were treated with 5 gm/kg of seed material before sowing

(Deivamani, M., and M. Muthamilan, 2016); Rani *et al.*, 2025) [32, 31].

The experiment was laid out in a randomized block design (RBD) consisting of 20 wheat genotypes, including bread wheat and durum wheat, evaluated under microbe treated and untreated conditions under drought stress, with two replications across five environments. The twenty genotypes were grown in 6 rows of 1 meter length with a spacing of 23 cm between rows under both treatment conditions in each environment and drought stress was imposed by regulating irrigation to create moisture limited conditions during critical growth stages. Soil moisture percentage was recorded at all five environments to quantify the intensity of drought stress and the trials were otherwise managed uniformly to enable a clear assessment of genotype performance and genotype $\times$ environment interaction under moisture stress.

Mean performance of wheat genotypes under drought stress was calculated for each environment and across environments using pooled data. To assess genotype stability under drought conditions, stability analysis was conducted only for microbe treated treatments, as these were considered for evaluating stress tolerance enhancement. Genotype $\times$ environment interaction and stability were analyzed using the AMMI model and stability parameters were derived from interaction principal component scores based on microbe treated data.

AMMI stability analysis was intentionally performed only on actinobacteria-treated data to specifically evaluate genotype stability under biologically enhanced drought tolerance conditions. Since the objective was to identify genotypes with stable performance when supported by microbial intervention, inclusion of untreated data would have confounded the interpretation of microbe-mediated stability effects rather than strengthening treatment comparisons.

2.2 Phosphate solubilization assay

The ability of microbe consortia to solubilize insoluble phosphate was evaluated on Pikovskaya's agar medium (Inui *et al.* 2012), prepared with the following composition (g L⁻¹): yeast extract 0.5, dextrose 10.0, calcium phosphate 5.0, ammonium sulfate 0.5, potassium chloride 0.2, magnesium sulfate 0.1, manganese sulfate 0.0001, ferrous sulfate 0.0001 and agar 15.0. The medium pH was adjusted and sterilized prior to inoculation. Microbial consortia was spot-inoculated onto Pikovskaya's agar plates and incubated at 28 $\pm$ 2 °C for up to 10 days. The formation of a clear halo around the bacterial colony indicated phosphate solubilization activity.

2.3 Stability analysis

2.3.1 AMMI ANOVA

Data on yield per hectare was subjected to combined analysis of variance to assess the effects of genotype, environment and genotype $\times$ environment interaction and further AMMI analysis was carried out for partitioning the interaction component, with all statistical analyses performed using R software.

2.3.2 AMMI model analysis

Following the confirmation of G $\times$ E interaction, an analysis of adaptability and phenotypic stability was conducted by the AMMI method, as outlined by Zobel *et al.* (1988) [2]. The results derived from the AMMI model were subsequently interpreted through AMMI 1 and AMMI 2 biplot analyses. In this evaluation, the main effect of the variety was considered as fixed, while the main effect of the sowing date was treated as random.

The AMMI stability value (ASV) was calculated using equation (1) (Purchase *et al.* 2000) [3]: (Eq. 1)

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1 \text{ score})^2 + (IPCA2 \text{ score})^2}$$

where SSIPCA1/SSIPCA2 is the weight given to the IPC1 value by dividing the IPC1 sum of squares on the IPC2 sum of squares and IPCA 1 and IPCA 2 scores are the genotypic scores in AMMI model.

The next AMMI statistic is sum of the absolute values of the IPC scores (SIPC) which is calculated by equation (2) (Sneller *et al.*, 1997) [4]

$$SIPC = \sum_1^n |IPCA|$$

Based on the rank of mean yield of varieties (RY_i) across environments (sowing dates) and rank of AMMI stability value (RASV_i), a selection index called GSI was calculated for each genotype using from equation (3) as follows (Mahmodi *et al* 2011) [27]:

$$GSI_i = RASV_i + RY_i$$

The AMMI analysis for grain yield data was conducted using GEA-R version 4.1 (Pacheco *et al* 2015) [5].

3. Results

3.1 Phosphate solubilization by Actinobacterial consortia

The Actinobacterial consortium demonstrated phosphate solubilization activity, as evidenced by the formation of clear halos surrounding the colonies on Pikovskaya's agar plates.

3.2 Mean Performance of Genotypes for Grain Yield under Moisture Stress with Actinobacteria Treatment

The mean grain yield of 20 wheat genotypes was evaluated across five environments (E1–E5) under moisture stress conditions, both untreated and actinobacteria-treated. Considerable variation was observed among genotypes, environments and treatments (Table 2). Under untreated conditions, mean grain yield across environments ranged from 1150.61 kg ha⁻¹ in Amruth (G2) to 2186.73 kg ha⁻¹ in UASBW 12982 (G14), with an overall mean of 1794.38 kg ha⁻¹. Environment-wise means varied from 1125.93 kg ha⁻¹ (E3) to 2290.28 kg ha⁻¹ (E1) (Table 2). Under actinobacteria-treated conditions, mean grain yield increased across all environments, with genotype means ranging from 1548.18 kg ha⁻¹ in Amruth (G2) to 2518.44 kg ha⁻¹ in GDP 40 (G6). The overall mean yield under treated conditions was 2057.51 kg ha⁻¹, compared to 1794.38 kg ha⁻¹ under untreated conditions. Environment-wise means under treated conditions ranged from 1515.87 kg ha⁻¹ (E3) to 2635.49 kg ha⁻¹ (E5). Among the genotypes, GDP 40 (G6) recorded the highest mean yield under treated conditions (2518.44 kg ha⁻¹), followed by UASBW 12982 (G14) (2278.61 kg ha⁻¹) and UAS-334 (G11) (2244.12 kg ha⁻¹). Lower mean yields were observed in Amruth (G2) (1548.18 kg ha⁻¹) and UAS 446 (G1) (1905.60 kg ha⁻¹).

3.3 AMMI Analysis of Grain Yield under Treated Moisture Stress Conditions

The additive main effects and multiplicative interaction (AMMI) analysis performed on grain yield under actinobacteria-treated moisture stress conditions indicated that the genotype × environment (G×E) interaction was effectively summarized by the first two interaction principal component axes. IPCA1

accounted for 50.3% and IPCA2 accounted for 30.4% of the total G×E interaction sum of squares, cumulatively explaining 80.7% of the interaction variance (Table 3) (Gauch, 2013).

3.4 AMMI 1 Biplot (Mean Yield and IPCA1 Scores)

The AMMI 1 biplot displayed differences among genotypes for mean grain yield and IPCA1 scores under treated moisture stress conditions. GDP 40 (G6) showed the highest mean yield, followed by UASBW 12982 (G14) and UAS-334 (G11). Genotypes DWR-2006 (G3), UAS-347 (G8), UAS-375 (G9), HD-2888 (G10) and UASDW 31156 (G18) were positioned close to the origin, indicating lower interaction effects. UAS 446 (G1), Amruth (G2) and UAS-3020 (G12) recorded comparatively lower mean yields.

3.5 AMMI 2 Biplot (IPCA1 and IPCA2 Scores)

The AMMI 2 biplot illustrated the distribution of genotypes and environments based on IPCA1 and IPCA2 scores. DWR-2006 (G3), HD-2888 (G10), UAS-347 (G8), UAS-375 (G9) and UASDW 31156 (G18) were located near the origin. Genotypes such as Bijaga yellow (G5), AKDW-2997-16 (G4), GDP 40 (G6) and UAS-334 (G11) were positioned farther from the origin. Environment E2 and Environment E5 showed larger IPCA scores compared to Environment E1.

3.6 AMMI Stability Value (ASV)

The AMMI Stability Value (ASV) differed among genotypes under treated moisture stress conditions. DWR-2006 (G3) recorded the lowest ASV (0.96), followed by HD-2888 (G10) (4.33), UAS-347 (G8) (6.03) and UAS-375 (G9) (6.70). Higher ASV values were observed for UAS-334 (G11) (32.28), Bijaga yellow (G5) (27.88) and Amruth (G2) (27.28) (Table 4).

3.7 Genotype Selection Index (GSI)

The Genotype Selection Index (GSI), calculated as the sum of yield rank and ASV rank, ranged from 5 to 38. DWR-2006 (G3) recorded the lowest GSI value (5). HD-2888 (G10), UAS-347 (G8), UAS-375 (G9) and GDP 40 (G6) recorded GSI values of 11. Higher GSI values were recorded for Amruth (G2) (38), UAS 446 (G1) (33) and UAS-3020 (G12) (33) (Table 5).

4. Discussion

Actinobacteria exhibit multiple plant growth promoting traits, including calcium and phosphate solubilization, siderophore production, antibiosis and auxin synthesis, which collectively underpin their effectiveness as plant growth-promoting rhizobacteria (PGPR) (Yadav *et al.*, 2021; Faddetta *et al.*, 2023; Shahrajabian and Sun, 2025) [10, 18, 19]. They promote plant growth through both direct and indirect mechanisms. Direct effects involve phytohormone production and enhanced nutrient acquisition via nitrogen fixation, phosphate solubilization and iron mobilization. Indirectly, actinobacteria alleviate biotic and abiotic stress by suppressing phytopathogens through nutrient competition and the production of inhibitory compounds, including cyanogenic substances, ammonia, cell wall-degrading enzymes and diverse secondary metabolites with biocidal activity. These attributes highlight the role of actinobacteria in improving plant growth and stress resilience under adverse conditions.

Under moisture stress conditions, actinobacteria seed treatment consistently enhanced wheat performance by improving plant tolerance to water limitation and stabilizing genotype responses across environments. Actinobacteria are well documented for their ability to colonize the rhizosphere and promote plant growth

through mechanisms such as phytohormone production, osmolyte accumulation and improved nutrient solubilization, all of which are critical under drought stress. Several studies have shown that actinobacteria enhance root architecture and water-use efficiency, enabling plants to better withstand moisture deficit (Vurukonda *et al.*, 2016; Kaur *et al.*, 2024) ^[13, 26]. The uniform improvement observed across environments in the present study indicates that microbial inoculation acted as a reliable biological input, reducing the adverse effects of environmental variability under stress conditions.

The significant genotype × environment interaction observed through AMMI and stability analyses demonstrates that wheat genotypes differed in their responsiveness to actinobacteria under moisture stress. Genotypes such as DWR-2006 (G3) expressed wide adaptation and superior stability, indicating an inherent genetic capacity to effectively interact with beneficial microbes and maintain consistent performance across environments. Similar findings have been reported in wheat, where stable genotypes under drought conditions exhibited reduced environmental sensitivity when supported by plant growth-promoting microorganisms (Meena *et al.*, 2023; Voronina *et al* 2023) ^[24, 25]. The stable performance of genotypes UAS-347 (G8), UAS-375 (G9) and HD-2888 (G10) further supports the role of actinobacteria in moderating environmental effects and enhancing phenotypic expression under stress. Furthermore, the

differential response among genotypes suggests that microbial effectiveness is closely linked to plant genetic background. Genotypes with greater compatibility with actinobacteria were able to exploit microbial benefits more efficiently, resulting in enhanced stability and adaptability under moisture stress. Similar genotype-specific responses to microbial inoculation have been reported, where variations in root exudates and microbial colonization influence the magnitude of stress mitigation (He *et al.*, 2025; Giannelli *et al* 2024) ^[22, 23]. Overall, the findings clearly indicate that actinobacteria improved wheat performance under moisture stress by promoting root function, regulating stress physiology and stabilizing genotype responses, supporting their use as a sustainable biological tool for enhancing crop resilience in water-limited environments.

Differential genotype responses to actinobacteria are likely attributable to variation in root architecture, rhizosphere exudation patterns and host genetic compatibility, which influence microbial colonization and functional expression. Such genotype-dependent microbial interactions have been widely reported under abiotic stress conditions and explain the observed variability in stability responses. The objective of the AMMI analysis was not to compare treated vs untreated systems, but to identify genotypes that exhibit stable performance within a biologically enhanced drought-tolerance context.

Table 1: Characteristics of test environments and climatic conditions during wheat growing seasons 2023–2024

Location	Location Code	Agro-climatic zone of Karnataka with number	Geographical Position		Altitude (m.a.s.l.)	Temperature (°C)		Rainfall (mm)
			Latitude	Longitude		Max	Min	
Dharwad- 24	E1	Northern Transition Zone (8)	15.46	75.01	750 m	32.76	18.29	11.17
Bijapur-24	E2	Northern Dry Zone (3)	16.83	75.71	606 m	33.57	18.84	3.54
Bagalkot-24	E3	Northern Dry Zone (3)	16.18	75.67	532 m	34.39	19.26	3.79
Raichur-24	E4	Northeastern Dry Zone (3)	16.21	77.36	407 m	33.39	32.06	2.06
Dharwad -25	E5	Northern Transition Zone (8)	15.46	75.01	750 m	39.45	17.77	7.40

Table 2: Mean values of twenty bread and durum wheat genotypes for grain yield (kg/ha) under drought microbe treated and untreated conditions across five environments

Sl. No.	Genotype	Mean performance of genotypes for yield											
		Untreated						Treated					
		E1	E2	E3	E4	E5	Mean	E1	E2	E3	E4	E5	MEAN
G1	UAS 446 (c)	2036.11	1354.35	1006.49	1647.77	2170.83	1643.11	2127.78	1422.60	1209.44	1667.66	3100.00	1905.60
G2	Amruth (c)	1058.33	914.49	573.17	1548.74	1658.33	1150.61	1233.33	1393.06	914.49	1648.65	2551.39	1548.18
G3	DWR-2006 (c)	2177.78	1629.17	962.57	2085.07	2370.83	1845.08	2583.33	1934.72	1483.27	2230.84	2662.50	2178.93
G4	AKDW-2997-16 (c)	1405.66	2000.66	1467.77	1750.82	1909.72	1706.90	2125.00	2037.50	1723.51	1796.02	2343.06	2005.02
G5	Bijaga yellow (c)	2084.72	1412.50	843.62	1696.53	1700.00	1547.47	2220.83	2282.92	1769.56	1817.79	2216.67	2061.55
G6	GDP 40	2652.78	1990.28	1126.96	2179.82	2534.72	2096.91	2794.44	2081.41	2081.41	2222.44	3412.50	2518.44
G7	UAS-428 (sc)	2569.44	1595.91	1367.68	1250.00	2000.00	1756.61	2443.06	1651.37	1595.91	2127.88	3072.22	2178.09
G8	UAS-347 (c)	2125.00	1516.67	986.91	1845.83	2772.22	1849.33	2612.50	1680.22	1680.22	1958.74	2787.50	2143.83
G9	UAS-375 (c)	2258.33	1133.56	1133.56	2192.24	2156.94	1774.93	2347.22	1898.90	1690.28	2343.25	2580.56	2172.04
G10	HD-2888 (c)	2804.17	1459.72	1459.72	2186.03	2133.33	2008.60	2583.33	1636.43	1636.43	2231.60	2611.11	2139.78
G11	UAS-334 (sc)	2837.50	2293.06	804.97	1754.99	2373.61	2012.83	2822.22	2515.28	1758.96	1824.14	2300.00	2244.12
G12	UAS-3020	1831.94	1059.81	904.70	1715.38	2552.78	1612.92	2408.33	1103.90	1059.81	1789.60	2623.61	1797.05
G13	UASBW 11421	2088.89	1312.13	935.17	1628.79	2393.06	1671.61	2431.94	1350.55	1173.36	1692.81	2213.89	1772.51
G14	UASBW 12982	2977.78	2021.31	1721.72	1851.70	2361.11	2186.73	3161.11	1996.26	1772.76	1958.74	2504.17	2278.61
G15	UASBW 13039	2588.89	1727.23	1727.23	2001.98	2169.44	2042.95	2722.22	1898.35	1755.38	2156.07	2331.94	2172.79
G16	UASBW 12380	2572.22	1420.06	1420.06	1731.39	2411.11	1910.97	2752.78	1549.86	1549.86	1817.79	2876.39	2109.33
G17	UASDW 30805	1997.22	1055.95	996.66	1580.75	2130.56	1552.23	2077.78	1270.06	1055.95	1705.03	2477.78	1717.32
G18	UASDW 31156	2522.22	1688.89	991.05	1584.49	2818.06	1920.94	2533.33	2141.67	1306.24	1676.84	2552.78	2042.17
G19	UASDW 30820	2802.78	1672.22	1070.78	1575.63	2348.61	1893.98	2416.67	2056.88	1719.12	1696.89	2702.78	2118.47
G20	UASDW31138	2413.89	1017.88	1017.88	1588.12	2476.39	1702.83	2763.89	1643.04	1381.51	1655.46	2788.89	2046.56
	MEAN	2290.28	1513.79	1125.93	1769.80	2272.08	1794.38	2458.06	1777.25	1515.87	1900.91	2635.49	2057.51
	MAX	2977.78	2293.06	1727.23	2192.24	2818.06	2186.73	3161.11	2515.28	2081.41	2343.25	3412.50	2518.44
	MIN	1058.33	914.49	573.17	1250.00	1658.33	1150.61	1233.33	1103.90	914.49	1648.65	2213.89	1548.18

Table 3: AMMI ANOVA of wheat genotypes for yield Kg/ha trait under moisture stress condition

Source of Variation	DF	Mean Sum of Square	
		Untreated YLD	Treated YLD
Environment	4	10002535.61***	8908687.84***
REP(ENV)	5	96648.93	110462.2
Genotype	19	562581.35***	485764.68***
GXE interaction	76	174832.84***	146704.82***
PC1	22	224630.86***	255141.48***
PC2	20	194964.39***	169505.39**
PC3	18	157065.23**	88088.64
PC4	16	101184.7	35046.89
Residuals	95	60073.57	74924.68
Total	275	303505.61	272122.07

Table 4: Grain yield and AMMI-based stability ranking of wheat genotypes under moisture stress conditions

GEN	Genotypes	Y	Rank	ASV	ASV_R
G1	UAS 446	1905.40	16	25.61	17
G2	Amruth	1548.20	20	27.28	18
G3	DWR-2006	2178.90	4	0.96	1
G4	AKDW-2997-16	2005.00	15	18.48	14
G5	Bijaga yellow	2061.50	12	27.88	19
G6	UASDT-22-5	2518.40	1	12.39	10
G7	UAS-428	2178.00	5	17.44	13
G8	UAS-347	2144.00	8	6.03	3
G9	UAS-375	2172.00	7	6.70	4
G10	HD-2888	2139.70	9	4.33	2
G11	UAS-304	2244.10	3	32.28	20
G12	UAS-3020	1797.00	17	20.69	16
G13	UASBW 11421	1772.50	18	8.50	5
G14	UASBW 12982	2278.70	2	20.43	15
G15	UASBW 13039	2172.80	6	14.51	12
G16	UASBW 12380	2109.20	11	13.42	11
G17	UASDW 30805	1717.30	19	11.77	9
G18	UASDW 31156	2042.20	14	11.35	8
G19	UASDW 30820	2118.60	10	8.64	6
G20	UASDW 31138	2046.60	13	11.14	7

Table 5: GSI-based stability ranking of wheat genotypes

GEN	Genotypes	Y_R	ASV_R	GSI R
G1	UAS 446	16	17	33
G2	Amruth	20	18	38
G3	DWR-2006	4	1	5
G4	AKDW-2997-16	15	14	29
G5	Bijaga yellow	12	19	31
G6	UASDT-22-5	1	10	11
G7	UAS-428	5	13	18
G8	UAS-347	8	3	11
G9	UAS-375	7	4	11
G10	HD-2888	9	2	11
G11	UAS-304	3	20	23
G12	UAS-3020	17	16	33
G13	UASBW 11421	18	5	23
G14	UASBW 12982	2	15	17
G15	UASBW 13039	6	12	18
G16	UASBW 12380	11	11	22
G17	UASDW 30805	19	9	28
G18	UASDW 31156	14	8	22
G19	UASDW 30820	10	6	16
G20	UASDW 31138	13	7	20

5. Conclusion

The present study demonstrates that actinobacteria seed treatment is an effective and consistent biological intervention for improving wheat performance under moisture stress conditions.

Results from multi-environment evaluation and AMMI-based stability analyses clearly showed that microbial inoculation reduced environmental sensitivity and enhanced the expression of genetic potential in several genotypes. Genotypes such as DWR-2006 (G3), along with UAS-347 (G8), UAS-375 (G9) and HD-2888 (G10), exhibited superior stability and wide adaptability, indicating a strong and efficient interaction with actinobacteria under stress environments. While some high-performing genotypes displayed specific adaptation, the overall response pattern confirmed that actinobacteria improved performance consistency across environments. These findings scientifically validate the role of actinobacteria in enhancing drought resilience and yield stability in wheat and support their integration with genotype selection as a sustainable strategy for wheat production in moisture-limited agro-ecosystems.

References

1. Van der Geer J, Handgraaf T, Lupton RA. The art of writing a scientific article. *Journal of Science Communication*. 2020;163:51–59.
2. Zobel RW, Wright MJ, Gauch HG. Statistical analysis of a yield trial. *Agronomy Journal*. 1988;80:388–393.
3. Purchase JL, Hatting H, Van Deventer CS. Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *South African Journal of Plant and Soil*. 2000;17(3):101–107.
4. Sneller CH, Kilgore-Norquest L, Dombek D. Repeatability of yield stability statistics in soybean. *Crop Science*. 1997;37(2):383–390.
5. Pacheco A, Vargas M, Alvarado G, Rodríguez F, Crossa J, Burgueño J. GEA-R (Genotype × Environment Analysis with R for Windows) version 4.1. CIMMYT Research Data and Software Repository Network; 2015.
6. Bocianowski J, *et al.* Stability and adaptability analysis of wheat genotypes under water-limited environments. *Plants*. 2023;12:1854.
7. Gauch HG. A simple protocol for AMMI analysis of yield trials. *Crop Science*. 2013;53:1860–1869.
8. Saxena AK, Kumar M, Chakdar H, Anuroopa N, Bagyaraj DJ. Microbial inoculants for drought stress mitigation in wheat through rhizosphere engineering. *Agricultural Water Management*. 2023;279:108207.
9. Backer R, Rokem JS, Ilangumaran G, Lamont J, Praslickova D, Ricci E, *et al.* Plant growth-promoting rhizobacteria: Context, mechanisms of action and roadmap to commercialization of biostimulants for sustainable agriculture. *Trends in Plant Science*. 2022;27(2):1174–1189.
10. Yadav AN, Verma P, Kumar S, Kumar V, Sugitha TCK, Singh BP, *et al.* Actinobacteria from rhizosphere: Molecular diversity, plant growth promotion and biocontrol potential. *Applied Soil Ecology*. 2021;168:104134.
11. Backer R, Rokem JS, Ilangumaran G, Lamont J, Praslickova D, Ricci E, *et al.* Plant growth-promoting rhizobacteria: Context, mechanisms of action and roadmap to commercialization of biostimulants for sustainable agriculture. *Frontiers in Plant Science*. 2018;9:1473.
12. Compant S, Samad A, Faist H, Sessitsch A. A review on the plant microbiome: Ecology, functions and emerging trends in microbial application. *Journal of Advanced Research*. 2019;19:29–37.
13. Vurukonda SSKP, Vardharajula S, Shrivastava M, SkZ A. Enhancement of drought stress tolerance in crops by plant growth-promoting rhizobacteria. *Microbiological Research*.

- 2016;184:13–24.
14. Chaudhary E, Sharma S, Gautam P, Ghimire S, Sapkota S, Bhattarai K, *et al.* AMMI GGE biplot analysis of wheat genotypes under heat stress and heat drought environment. *Archives of Agriculture and Environmental Science*. 2023;8(4):484–489.
 15. Hackauf B, Siekmann D, Fromme FJ. Improving yield and yield stability in winter rye by hybrid breeding. *Plants*. 2022;11(19):2666.
 16. Mullualem D, Tsega A, Mengie T, Fentie D, Kassa Z, Fassil A, *et al.* Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. *Heliyon*. 2024;10(12).
 17. Ravi Kumar K, Awasthi G, Sankhla MS, Mathur A, Saxena P, Awasthi A, *et al.* Current advances in microbial consortia of actinobacteria and PGPR to improve crop resilience and soil fertility in salinity degraded soils. *Industrial Biotechnology*. 2025;15509087251398287.
 18. Faddetta T, Polito G, Abbate L, Alibrandi P, Zerbo M, Caldiero C, *et al.* Bioactive metabolite survey of actinobacteria showing plant growth promoting traits to develop novel biofertilizers. *Metabolites*. 2023;13(3):374.
 19. Shahrajabian MH, Sun W. Microbial interaction of Actinobacteria strains with various plants, promote growth and development in natural farming and alleviating biotic and abiotic stresses. *Discover Sustainability*. 2025;6(1):564.
 20. Kavva T, Govindasamy V, Suman A, Abraham G. Plant–Actinobacteria interactions for biotic and abiotic stress management in crops. In: *Plant Holobiome Engineering for Climate-Smart Agriculture*. 2024. p. 441–463.
 21. Siddharthan N, Sangeetha M, Asokan N, Balagurunathan R, Hemalatha N. Actinobacterial enzymes—An approach for engineering the rhizosphere microorganisms as plant growth promoters. In: *Rhizosphere Engineering*. 2022. p. 273–292.
 22. He Y, Ning Z, Cui Y, Yue X, Huang Y, Zhu C. Combination of functional complementary salt-tolerant PGPR and organic amendments modulates the soil micro-environment and promotes wheat growth. *Agriculture*. 2025;15(24):2558.
 23. Giannelli G, Del Vecchio L, Cirlini M, Gozzi M, Gazza L, Galaverna G, *et al.* Exploring the rhizosphere of perennial wheat: potential for plant growth promotion and biocontrol applications. *Scientific Reports*. 2024;14(1):22792.
 24. Meena KK, Sorty AM, Bitla U, Akash L, Shinde SK, Goraksha C, *et al.* Stress-responsive gene regulation conferring salinity tolerance in wheat inoculated with ACC deaminase producing facultative methylotrophic actinobacterium. *Frontiers in Plant Science*. 2023;14:1249600.
 25. Voronina E, Sokolova E, Tromenschleger I, Mishukova O, Hlistun I, Miroshnik M, *et al.* Properties of potential plant-growth-promoting bacteria and their effect on wheat growth promotion (*Triticum aestivum*) and soil characteristics. *Microbiology Research*. 2023;15(1):20–32.
 26. Kaur S, Kalia A, Sharma S. Bioformulation of *Azotobacter* and *Streptomyces* for improved growth and yield of wheat (*Triticum aestivum* L.): A field study. *Journal of Plant Growth Regulation*. 2024;43(8):2555–2571.
 27. Mahmodi N, Yaghotipoor A, Farshadfar E. AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). *Australian Journal of Crop Science*. 2011;5(13):1837–1844.
 28. Inui R, Kishi L, Picchi S, Barbosa J, Lemos MT, De Teresa S, *et al.* Phosphorus solubilizing and IAA production activities in plant growth promoting rhizobacteria from Brazilian soils under sugarcane cultivation. *Journal of Plant Growth Regulation*. 2012;3(18):25–31.
 29. Hiremath IG, Jahagirdar S, Krishnaraj PU, Ashtaputre SA, Kambrekar DN, Priyanka K. Evaluation and characterization of rhizobacteria and endophytes for antagonistic and growth promotional traits against collar rot (*Sclerotium rolfsii* Sacc.) of soybean. *Legume Research*. 2024;1:8.
 30. Gehlot P, Pareek N, Vivekanand V. Development of biofertilizers and microbial consortium: An approach to sustainable agriculture practices. In: *Plant, Soil and Microbes in Tropical Ecosystems*. Singapore: Springer Singapore; 2021. p. 315–348.
 31. Sailaja Rani J, Reddi Kumar M, Khayum Ahammed S, Koteswara Rao SR, Ravindra Reddy B, Sarada Jayalakshmi Devi R. Evaluation of substrates and carrier material for shelf life studies of *Streptomyces* bioformulation. *Journal of Experimental Agriculture International*. 2025;47(5):270–280.
 32. Deivamani M, Muthamilan M. Studies on shelf-life of *Streptomyces* spp. in different carrier materials. 2016:16–20.