Interrelationships Between Exogenous Plant Growth-Promoting Rhizobacteria and Wheat Rhizosphere Microbiome

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Abstract: The rhizosphere microbiome is modulated by a diverse array of factors, including exogenous bio-inoculants that can exert either beneficial or detrimental effects on native microorganisms and plant growth. This study aims to clarify the impact of inoculation with plant growth-promoting rhizobacteria (PGPR) on the wheat rhizospheric microbiome under greenhouse conditions. The PGPR strains *Bacillus subtilis*, *Pseudomonas putida*, and *Serratia marcescens*, used in this study, were characterized and found to possess key plant growth-promoting traits: phosphate solubilization, siderophore production, and indole acetic acid synthesis. A quantitative assessment of microbiome activity was conducted in wheat rhizospheric soil, encompassing various microbial populations, including phosphate-solubilizing bacteria, cellulose-degrading microorganisms, ammonium oxidizers, siderophore-producing bacteria, and nitrogen-fixing *Azotobacter*, in addition to total bacterial, actinobacterial, and fungal counts. Moreover, some soil enzyme activities (urease and phosphatases) were measured. The application of PGPR strains exerted a positive influence on all examined beneficial native rhizospheric microbial populations and enzyme activities. The responses of microbial populations varied significantly with plant age and the specific PGPR strain employed. Notably, wheat plants inoculated with *Pseudomonas putida* exhibited the highest microbial populations compared to other strains. Our findings indicate that the type of inoculant strain, plant age, and soil microbial community composition are critical factors influencing the response of the soil microbial community. We recommend further field evaluation of these PGPR strains prior to their widespread adoption as biofertilizers.

Keywords: PGPR, wheat, soil microbial activity, microbiome.

INTRODUCTION

The escalating global population necessitates a substantial increase in the production of primary crops, such as wheat, to meet the increasing demand for food. Consequently, there is an urgent imperative to develop sustainable agricultural practices that prioritize eco-friendly crop production systems. In this context, plant growth-promoting rhizobacteria (PGPR) emerge as a promising biotechnological approach, offering a novel biofertilizer strategy that can potentially replace or complement traditional agrochemicals (**Sati et al., 2023; Sun et al., 2024**). PGPR strains possessing a suite of beneficial traits can enhance plant growth and yield, thereby serving as biofertilizers that provide essential nutrients and facilitate nutrient uptake by plants by solubilizing minerals and producing the vital enzymes that occupying in nutrient cycles in soil. PGPR can also act as phytostimulators that directly promote plant growth through the production of phytohormones, such as indole-3-acetic acid, cytokinin, and gibberellins (**Kumar et al., 2022**; **Hnini et al., 2024; Ghanem et al., 2024**). In addition to their role in plant growth promotion, PGPR can function as biological control agents, protecting root systems from phytopathogenic microorganisms by producing siderophores, hydrogen cyanide, antibiotics, and competing for ecological niches. This biocontrol activity can reduce the need for chemical pesticides and fungicides, thereby minimizing the environmental impact of agricultural practices (**El-Saadony et al., 2022; Al Raish et al., 2025**).

While the beneficial effects of PGPR on plant performance are well-documented, research on their impact on indigenous microbial communities remains limited (**Samain et al., 2023**). Elucidating the consequences of introducing PGPR into soil ecosystems on the activity and dynamics of native microbial populations is crucial for applied soil ecology. Understanding these interactions can help predict the long-term efficacy and sustainability of PGPR-based biofertilizers (**Zhang et al., 2025)**. This study aimed to 1) Investigate the impact of selected PGPR strains on native soil microbial populations; and 2) Examine the interrelationships between microbial populations in the wheat rhizosphere and plant growth. By exploring these interactions, we can gain a deeper understanding of the complex relationships between PGPR, plant growth, and soil microbial communities, ultimately informing the development of more effective and sustainable agricultural practices. The findings of this study will contribute to the research growing on PGPR and their potential applications in sustainable agriculture. By identifying the most effective PGPR strains and understanding their interactions with native microbial populations, we can develop targeted biofertilizer strategies that promote plant growth while minimizing potential risks to the environment.

MATERIALS AND METHODS

Rhizobacterial strains and inoculants preparation:

The PGPR strains, *P. putida*, *B. subtilis* and *S. marcescens* were attained from Microbiological

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Resource Center, Cairo and examined for phosphate solubilization, siderophore production, and indole acetic acid synthesis. Solubilization of tricalcium phosphate was performed using Pikovskaya's broth after 10-day incubation period as described by **Mayadunna *et al.*, (2023)**. The qualitative test of siderophore production was checked by Chromo Azurol S agar as described by **Alexander and Zuberer (1991)**. IAA examination was carried out using Luria-Bertani medium with/without 0.10 % L-tryptophan following **Patten and Glick (2002) (Table 1)**. All PGPR strains were grown in a 100-ml flask containing 50 ml sterile tryptic soy broth (TSB) medium at 28 ºC for 4 days. The cultures were diluted 10 times with sterilized water resulting in 10^8 CFU ml^{-1}.

Greenhouse Trial and Treatments:

A greenhouse pot experiment was conducted in the experimental farm of the Faculty of Agriculture, Suez Canal University, Ismailia, Egypt using sandy soil mixed with 1% sterilized compost. A composite soil and compost samples was air-dried, crushed, sieved and analyzed for physical and chemical properties according to **Jackson (1973)** and **Sparks *et al.* (1996)** as shown in **Table 2**. The mixture of soil and compost (10 g $kg\ soil^{-1}$) was uniformly packed in plastic pots each of 19 cm height and 21.6 cm mean diameter at rate of 5 kg pot^{-1}. The experimental design was randomized complete blocks with three replications. Four treatments were tested: uninoculated control, *Pseudomonas putida*, *Bacillus subtilis* and *Serratia marcescens*.

Five seeds of wheat var. Giza 168 were sown in each pot and irrigated to field capacity using Ismailia canal water (0.35 dSm^{-1}). After two weeks from sowing, the seedlings were thinned to three uniform plants pot^{-1}. The wheat plants were fertilized in accordance with the Ministry of Agriculture's recommendations in Egypt.

Soil and plant analyses:

Rhizospheric soil samples were collected for assaying the microbial community populations and enzyme activities at flowering (90 days after sowing) and ripening stages (120 d post-planting). The microbial populations analysis including the counts of total bacteria, actinobacteria, fungi, P-solubilizing bacteria, siderophore producers and *Azotobacter* were measured using agar plate dilution method for each microorganism following the methods described by **Spark et al., (1996).** Whereas the number of cellulose-decomposing bacteria and NH_4^+-oxidizing bacteria were counted by the most probable number method as detailed by **Spark et al., (1996)**. Urease activity (mg NH_4^+-N released/ g soil/ 2 h) and Phosphatases (alkaline and acid) activities (µg p-nitrophenol released/ g soil/ h) were performed following the procedures presented by **Tabatabai (1994).** Wheat plants were harvested after 130 days (ripeness stage) from sowing to measure grain and straw yields.

Statistical analysis:

The results were processed for analysis of variance and least significant difference ($P < 0.05$) using SPSS software (version 24.0).

Table 1. Some plant promoting traits for bacterial strains used in this study

PGP traits	IAA production		P solubilization	Siderophore production
	Without L-TRP	With L-TRP		
S. marcescens	9.79	25.4	102.79	+
P. putida	8.86	16.52	78.59	+++
B. subtilis	2.70	4.65	191.21	++

IAA: Indole acetic acid
L-TRP: L-tryptophan
- = no production + = low production; ++ = moderate production and +++ = strong production.

Table 2. Some physical and chemical properties of soil and compost used in the current study.

Property	Unit	Soil	Compost
Sand	%	94.45	-
Silt	%	3.53	-
Clay	%	2.52	-
Textural class	-	Sand	-
$CaCO_3$	g kg^{-1}	2.68	-
pH	-	7.89†	7.78‡
EC_e§	dSm^{-1}	0.390	9.95
Soluble cations§			
Ca^{2+}	meq l^{-1}	1.51	25.5
Mg^{2+}	meq l^{-1}	0.63	12.2
Na^+	meq l^{-1}	0.94	34.2
K^+	meq l^{-1}	0.82	28.6
Soluble anions§			
HCO_3^-	meq l^{-1}	0.452	20.8
Cl^-	meq l^{-1}	1.30	65.5
SO_4^{-2}	meq l^{-1}	2.15	13.2
Available P	mg kg^{-1}	6.83	136
Available N	mg kg^{-1}	7.91	149
Total P	g kg^{-1}	0. 091	9.31
Total N	g kg^{-1}	0.172	13.8
Organic C	g kg^{-1}	2.39	169

†In soil-water suspension (1:2.5).
‡In compost-water suspension (1:5).
§In compost and soil saturated extracts.

RESULTS AND DISCUSSION

Wheat rhizosphere microbiome:

***Total bacterial count*:** Total bacteria representing the dominant microbial group in agricultural soil, were estimated as a general bioindicator of soil biological activity. It was observed that bacterial populations in the soil during the wheat anthesis stage were higher than those at the ripening stages across all treatments. None of the applied bacterial inoculants exhibited a negative effect on total bacterial counts; instead, increases were observed following inoculation with any of the three tested strains compared to the uninoculated control. Notably, total bacterial counts peaked (7.97 log CFU/g)

in soil inoculated with *Pseudomonas putida*, which significantly surpassed all other treatments (**Table 3**).

Table 3. Effects of inoculation with plant growth promoting rhizobacteria on indigenous rhizosphere microorganisms (log CFU g^{-1} soil; mean ± SE) of wheat at flowering and ripening stages. Different letters indicate statistically significant differences ($p < 0.05$).

Treatments	Total bacteria		Fungi		Actinobacteria		Siderophore producers	
	Flowering	ripening	Flowering	ripening	Flowering	ripening	Flowering	ripening
Untreated	7.56±0.05c	7.44±0.13c	4.28±0.14a	4.32±0.01a	6.90±0.02c	6.75±0.01c	5.44±0.06d	5.52±0.1d
P. putida	7.97±0.05a	7.75±0.04a	4.32±0.01a	4.37±0.07a	7.25±0.04a	7.01±0.01a	6.38±0.06a	6.73±0.05a
B. subtilis	7.70±0.08b	7.66±0.04ab	4.02±0.01b	4.38±0.09a	6.97±0.09b	6.86±0.09b	5.68±0.17c	6.02±0.05c
S. marcescens	7.82±0.03b	7.62±0.05b	4.28±0.14a	4.34±0.1a	7.04±0.02b	6.97±0.01a	6.20±0.13b	6.47±0.02b
	Azotobacter		P-solubilizing bacteria		Cellulose-decomposing bacteria		NH_4^+-oxidizing bacteria	
	Flowering	ripening	Flowering	ripening	Flowering	ripening	Flowering	ripening
Untreated	5.12±0.05c	5.05±0.02b	5.18±0.09c	5.07±0.05c	3.06±0.001c	3.34±0.001c	2.44±0.001c	2.34±0.001d
P. putida	5.73±0.04b	5.53±0.01a	6.12±0.03a	5.42±0.05a	4.34±0.002b	4.55±0.001b	3.25±0.001b	3.14±0.001c
B. subtilis	6.07±0.07a	5.53±0.05a	5.45±0.03b	5.19±0.01b	4.47±0.005a	5.28±0.003a	3.29±0.003b	3.28±0.003b
S. marcescens	5.77±0.04b	5.51±0.04a	5.39±0.05b	5.21±0.02b	4.34±0.001b	4.51±0.001b	3.38±0.001a	3.36±0.001a

These results align with numerous previous studies, where **Meng et al., (2025)** stated that bacterial counts peak at heading and decline post-anthesis which may be due to reduced root exudation (e.g. sugars, organic acids) and nutrient availability. **Papin et al. (2025)** found that inoculation with *Pseudomonas* increased total bacterial counts compared to uninoculated controls, with no suppression of native microbiota. The significant increase in total bacteria following *P. putida* inoculation corroborates its efficacy as a microbiome enhancer. In addition, P. putida produces siderophores and ACC deaminase, enhancing nutrient cycling (P-solubilization, N-fixation) and reducing ethylene stress. This creates a biofertilizer effect that stimulates the entire microbiome (both inoculant and native bacterial growth). **Chebotar et al., (2023)** demonstrated that maximum bacterial abundance in maize fields occurred at flowering stage, coinciding with peak root exudation, fueling bacterial growth, followed by a 40% decline at senescence.

Total fungal count :

Quantification of total fungal populations in soil is critically important, as it reflects the impact of bacterial inoculants applied in this study on distinct microbial groups (e.g., fungi) and enables investigation of potential synergistic or antagonistic interactions. In this study, total fungal counts measured in the wheat rhizosphere generally increased across most treatments until reaching the ripening stage. No significant effect on soil fungal populations was observed compared to the non-inoculated control when using *Pseudomonas putida* or *Serratia marcescens* inoculants. However, inoculation with *Bacillus subtilis* resulted in a reduction in fungal counts at the flowering stage relative to the non-inoculated control. Notably, this suppressive effect diminished by the harvest stage, at which point fungal counts rebounded and exceeded the control (**Table 3**). **Ashour and Afify, (2024)** displayed that inoculation with *Bacillus* reduced rhizosphere fungal populations compared to control. This suppression effect of *Bacillus* might be due to its ability to secrete antifungal lipopeptides that inhibit fungal growth. Suppression effects reverse may be due to degradation of antibiotics by soil enzymes or the shifts in root exudate composition during maturation (**Zahra, et al., 2023**).

Total actinobacteria:

Actinobacteria exhibited a response pattern analogous to total bacteria in soil. No negative effects on actinobacterial populations were observed following application of any of the three inoculants, either at flowering or harvest stages. Instead, a positive impact was recorded and reached its peak (7.25 log CFU/g) in soil inoculated with *Pseudomonas putida* during the flowering stage (**Table 3**).

Similarly, **Nafis et al., (2019)** found that actinobacterial biomass peaked at flowering in wheat fields, coinciding with root exudation compounds that selectively stimulate actinobacterial metabolism. The inoculation with *P. putida* increased actinobacterial counts in wheat rhizosphere via siderophore-mediated iron mobilization, enhancing growth of iron-limited actinobacteria as *Pseudomonas* siderophores solubilize iron, while actinobacteria degrade complex polymers inaccessible to bacteria (**Castro-Sowinski, et al., 2007**).

Siderophore-producing bacteria:

Siderophore-producing bacteria were quantified due to their dynamic role in modifying rhizosphere properties. These compounds facilitate the delivery of insoluble elements e.g. iron to plants via chelation. Additionally, siderophores contribute to plant disease resistance. This study revealed that populations of siderophore-producing bacteria increased until the crop maturity stage. All three bacterial inoculants significantly enhanced the abundance of this bacterial group, with peak counts (6.73 log CFU/g) observed in *Pseudomonas putida*-inoculated soil (**Table 3**).

Sarwar et al., (2022) stated that siderophore-producing bacterial populations in wheat rhizosphere peaked at maturity due to iron demand during grain filling, coinciding with root senescence and iron remobilization. Siderophores (e.g., pyoverdine from *Pseudomonas*) bind Fe^{3+} with high affinity, solubilizing iron in alkaline/calcareous soils. The Fe^{3+}-siderophore

complex is recognized by root transporters, enabling iron uptake (**Xie et al., 2024**). In same context, **Behnoush et al., (2021)** reported that siderophores sequester iron, starving pathogens that require iron for virulence. This reduces pathogen growth by 60–80% and induces systemic resistance (ISR) in plants.

Phosphate solubilizing bacteria:

Phosphate-solubilizing bacteria (PSB) play a vital role in alkaline-prone soils, such as most Egyptian agricultural soils, where the majority of phosphates exist in plant-unavailable forms. These bacteria solubilize phosphorus from sparingly soluble sources through multiple mechanisms. In this study, PSB populations peaked at the flowering stage and subsequently declined at harvest. No inhibitory effects on PSB counts were observed following application of any inoculant. As shown in **Table 3**, all inoculants increased PSB counts, with the highest value (6.12 log CFU/g) recorded in *Pseudomonas putida*-inoculated soil.

This result agreed with the study of **Yahya et al., (2021**) who found that PSB populations in wheat rhizosphere peaked at flowering due to root exudate-driven stimulation (e.g., malate, citrate), then declined at harvest as root senescence reduced carbon availability. Inoculation with PGPR increased P solubilization via organic acid secretion (e.g. gluconic acid, pKa 3.4) that dissolves Ca-phosphates and stimulation of native PSB through cross-feeding on organic acids (**Panda et al. 2025**).

Azotobacter:

Azotobacter populations were quantified in this study as an indicator of non-symbiotic biological nitrogen fixation (BNF) of atmospheric nitrogen. Across all evaluated treatments, Azotobacter counts reached their maximum at the flowering stage, with the highest value (6.07 log CFU/g) recorded in soil inoculated with *Bacillus subtilis* as displayed in **Table 3**. *B. subtilis* outperformed other inoculants in enhancing Azotobacter, likely due to its dual role in phytohormone-mediated root stimulation and O_2 management via biofilms which enhance nitrogenase enzyme activity (O_2-sensitive, requires microaerophilic conditions) (**Hashem et al., 2019**).

Cellulose decomposing bacteria:

Cellulose-degrading bacteria exemplify specialists performing critical decomposition functions, as they uniquely target the most complex and recalcitrant soil organic compounds. Their role is indispensable for sustained nutrient supply to plants following the depletion of readily decomposable organic matter. As shown in **Table 3**, populations of cellulolytic bacteria were lower than those of other microbial groups, likely reflecting their specialization in degrading a specific complex polymer. Across all treatments, their abundance peaked at the end of the growth season, with *Bacillus subtilis* inoculation yielding the highest counts (5.28 log CFU/g). PGPR was reported to enhance cellulolytic bacteria due to its dual capacity for direct cellulase production and biofilm-mediated enzyme stabilization (**Tang et al., 2020**).

Ammonium-oxidizing bacteria:

Ammonium-oxidizing bacteria play a critical role in soil nitrogen cycling by converting reduced ammonium (NH_4^+) to oxidized nitrate (NO_3^-). While this process prevents nitrogen loss as ammonia (NH_3) volatilization in alkaline soils, it is undesirable in sandy soils where nitrate leaching into groundwater can occur (**Shrivastava et al., 2021**). The latter issue can be mitigated through controlled irrigation and organic matter amendments in sandy soils. Notably, plants require both nitrogen forms (NH_4^+ and NO_3^-) for optimal growth. As shown in **Table 3**, AOB populations were the lowest among all microbial groups examined, likely reflecting their autotrophic metabolism and specialization. All tested inoculants increased AOB counts compared to the uninoculated control, with *Serratia marcescens* proving most effective (3.38 log CFU/g).

Soil enzymatic activity:

The activities of urease, acid phosphatase, and alkaline phosphatase were evaluated in this study due to their critical roles in soil nitrogen and phosphorus cycling. As shown in **Table 4**, the activity of all three enzymes peaked 90 days after planting (flowering stage) and subsequently declined by crop ripeness (120 days post-sowing). Inoculation with all tested PGPR strains significantly enhanced the activities of these enzymes compared to the uninoculated control, although the differences between the effects of the three bacterial strains were not always statistically significant.

This enhancement may be attributed to the secretion of extracellular enzymes by soil microorganisms, which are the primary source due to their substantial biomass and high metabolic activity (**Singh et al., 2019**). Relating to the previous results, all inoculated soils exhibited increased microbial population counts relative to the uninoculated control, with most microbial populations also peaking at the flowering stage. This indicates that the introduced PGPR strains successfully proliferated in the rhizosphere without antagonistic effects on the indigenous microbial community. The observed decline in enzymatic activities at 120 days post-planting likely resulted from a corresponding decrease in microbial populations. This microbial reduction may have been caused by unfavorable soil moisture conditions and diminished root exudate production as the wheat crop approached harvest.

Specifically, urease activity reached its highest levels in soil inoculated with *Bacillus subtilis*, showing increases of 19.6% and 14.6% over the uninoculated control at the flowering and ripeness stages, respectively (**Table 4**). Across all treatments, alkaline phosphatase consistently exhibited higher activity than acid phosphatase. Peak phosphatase activities occurred in soil inoculated with *Pseudomonas putida*, reaching 182 µg pNP/g soil/h for alkaline phosphatase and 102 µg pNP/g soil/h for acid phosphatase. The dominance of alkaline phosphatase activity could be attributed to the alkaline tendency of the experimental soil (**Table 2**). This observation aligns with the established principle that acid phosphatase dominates in acidic soils, while alkaline

phosphatase prevails in neutral to alkaline soils (**Tabatabai, 1994**).

Table 4. Effect of inoculation with plant growth promoting rhizobacteria on urease (mg NH_4^+ -N released/ g soil/ 2h) and phosphatase (µg pNP/g soil/h) activity in wheat rhizosphere at flowering and ripening stages.

Treatments	Urease		Alkaline phosphatase		Acid phosphatase	
	Flowering	ripening	Flowering	ripening	Flowering	ripening
Untreated	291c	233c	128c	109c	72.3d	58.7c
P. putida	322b	267b	182a	133a	102a	91.1a
B. subtilis	348a	294a	156b	122b	93.6b	69.3b
S. marcescens	318b	272b	144b	124b	81.7c	64.2b

Wheat yield components:

As shown in **Fig. 1**, the application of all three bacterial inoculants increased both straw and grain yields of wheat compared to the uninoculated control. *Bacillus subtilis* proved to be the most effective inoculant, enhancing straw and grain yields by 22.7% and 19.8%, respectively, over the control treatment. The improvement of wheat yield because of microbial inoculants may be attributed to their plant growth promoting traits. All tested PGPR strains were previously confirmed to have the capability to synthesis indole acetic acid (IAA) and siderophores as well to solubilize inorganic insoluble phosphate (**Table 1**). These results agreed with the study of **Wahid et al., (2020)** who found that inoculation of wheat seeds with PGPR boosted wheat yield via increasing root colonization by native microorganisms. They found that the maximum root colonization was detected in the treatment received *Bacillus* sp. Furthermore, several researchers attributed the increased yield in PGPR-inoculated plants to their development of a larger root surface area which enhances water and nutrient uptake and increase the interactions with the adjacent rhizospheric soil and microbiota (**Ortiz-Castro et al., 2020; Khoso et al., 2024**).

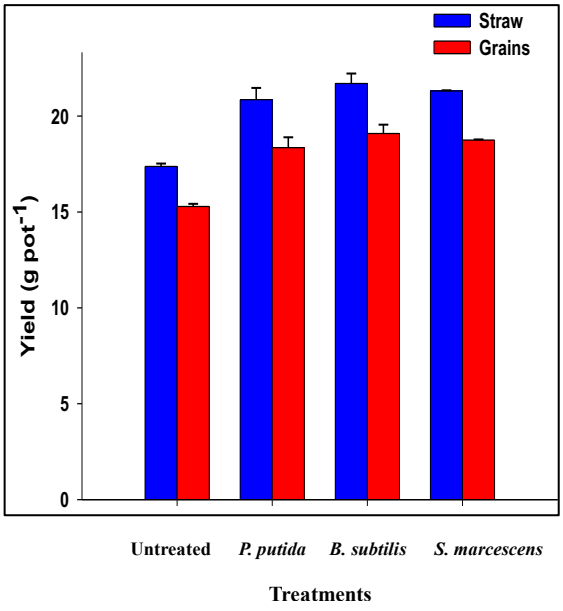

Fig. 1: Straw and grain yields (g pot^{-1}) of wheat in response to inoculation with plant growth promoting rhizobacteria

CONCLUSION

The present study demonstrated that targeted bacterial inoculation significantly enhances both wheat productivity and rhizosphere microbiome functionality. All three inoculants (*Pseudomonas putida*, *Serratia marcescens*, and *Bacillus subtilis*) increased straw and grain yields compared to the uninoculated control, with *B. subtilis* proving most effective (22.7% and 19.8% increases, respectively). This yield enhancement is correlated with positive shifts in key microbial indicators, revealing a strong link between soil microbiome activity and crop performance. The results suggest that the type of PGPR strain and plant age are significant factors influencing indigenous soil microbial community. Further long-term field studies are needed to confirm these benefits under diverse agroclimatic conditions. Investigating the molecular mechanisms underlying the specific interactions between inoculants and native microbial groups will provide deeper insights into microbiome engineering for sustainable agriculture. Exploring the impact of these inoculants on other soil health indicators beyond microbial counts and enzyme activities is also recommended.

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العلاقات المتبادلة بين بكتريا الجذور المنشطة لنمو النبات والمجموع الميكروبي في ريزوسفير القمح

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المستخلص : تهدف هذه الدراسة إلى استكشاف تأثير التلقيح ببكتيريا الجذور المنشطة لنمو النبات (PGPR) على المجموع الميكروبي في ريزوسفير نبات القمح. تم استخدام ثلاث سلالات من بكتيريا الجذور المنشطة لنمو النبات في هذه الدراسة، وهي *Bacillus subtilis* و *Pseudomonas putida* و *Serratia marcescens* ، والتي تم اختبار قدرتها علي اذابة الفوسفات غير العضوي غير الذائب وانتاج مركبات السيدروفورس وانتاج اندول حمض الخليك. تم إجراء تقييم كمي للمجموع الميكروبي في منطقة الجذور لنبات لقمح وكذلك نشاط بعض الانزيمات في التربة، وكانت المجموعات الميكروبية تشمل بكتيريا إذابة الفوسفات، والبكتريا المُحللة للسيلولوز، والبكتريا المؤكسدة للأمونيوم، والبكتيريا المنتجه للسيدروفورس، والأزوتوبكتر المثبت للنيتروجين، بالإضافة إلى إجمالي أعداد البكتيريا والأكتينوبكتيريا والفطريات. كذلك تم تقدير نشاط بعض الانزيمات مثل اليوريز والفوسفاتيز لارتباطها الوثيق بدورتي النيتروجين والفوسفور في التربة. وقد لوحظ أن استخدام اللقاحات البكتيرية أدى إلى تأثير إيجابي على اعداد المجموعات الميكروبية في التربة وكذلك علي زيادة نشاط الانزيمات التي تم فحصها في منطقة الريزوسفير. وانعكس هذا التأثير الايجابي علي تحسن محصولي الحبوب والقش نتيجة للتلقيح ببكتريا الجذور المنشطة لنمو النبات. اختلفت استجابات المجموعات الميكروبية باختلاف عمر النبات واللقاح البكتيري المستخدم. ومن الجدير بالذكر أن هناك ارتباط معنوي قوي بين أعداد المجموعات الميكروبية والأنشطة الانزيمية وبين محصول القمح مما يشير الي أهمية النشاط البيولوجي في التربة كعامل مؤثر وفاعل في نمو وانتاجية النباتات. وتشير النتائج إلى أن نوع اللقاح، وعمر النبات، وتكوين المجموع الميكروبي في التربة هي عوامل أساسية تؤثر على استجابة المجاميع الميكروبية في ريزوسفير نبات القمح عند التلقيح باللقاحات الخارجية. ونوصي بإجراء المزيد من التقييمات الحقلية لهذه السلالات قبل تعميمها على نطاق واسع كأسمدة حيوية.