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Co-Inoculation of *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* 5B1 to Enhance the Growth and Nutrient Uptake of Two Varieties of *Solanum Tuberosum*

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ABSTRACT

Water shortages limit potato (Solanum tuberosum L.) production in drought-prone areas, underscoring the need for low-input solutions to enhance crop drought resistance. Plant growth-promoting rhizobacteria (PGPR) are an environmentally friendly and promising solution. In this study, Achromobacter xylosoxidans and Pseudomonas fluorescens strain 5B1 were isolated and identified using microscopical, cultural, biochemical, and molecular techniques by 16S rRNA sequencing. A. xylosoxidans and P. fluorescens were assessed for their ability alone and in combination to increase drought resistance, growth, and nutrient uptake of Harry and Sefra potato under drought stress in Erbil Governorate, Kurdistan Region, Iraq. The results showed that Co-inoculation with (Achromobacter xylosoxidans and Pseudomonas fluorescens strain 5B1) bacteria had the highest effect on potato growth and nutrient uptake (plant length 47cm, root length 65.33cm, 30.33 tubers, weight of tuber 850g, carbohydrates 1.67 %, protein 31.75%, carotene 2.98% and total chlorophyll 0.422%), but the lowest effect was recorded by Achromobacter xylosoxidans (plant length 34cm, root length 49.33cm, 23.33 tubers, weight of tuber 490.66g, carbohydrates 1.088%, protein 14.60%, carotene 2.47% and total chlorophyll 0.279%) and Pseudomonas fluorescens (plant length 39cm, root length 54.33cm, 26.33 tubers weight of tuber 644.66g, carbohydrates 1.6268%, protein 19.69%, carotene 2.65% and total chlorophyll 0.396%) compare to controlled treatment (untreated) that is (plant length 53.33 cm, root length 65.33cm, 27.66 tubers, weight of tuber 866.66g, carbohydrates 1.944%, protein 35.13%, carotene 2.66% and total chlorophyll 0.478%). Depending on the above results, it can be concluded that Pseudomonas fluorescens5B1 and Achromobacter xylosoxidans. It can be used as a biofertilizer to enhance plant growth and nutrient uptake, instituting a more sustainable approach to chemical fertilizers.

***Keywords*:** Solanum tuberosum, Achromobacter xylosoxidans, Pseudomonas fluorescens5B1, Drought stress, PGPR, Biofertilizer.

INTRODUCTION

Potatoes are a crucial source of energy, vitamins, and minerals, particularly potassium and vitamin C, essential for human survival and food security. They are also vital to rural economies and the livelihoods of millions of farmers. The relevance of potatoes in sustainable agriculture has increased due to recent developments in biotechnology and microbial inoculants, which have increased their tolerance to drought. The potato tuber is an underground stem that allows the plant to spread vegetatively further, and it has developed into a crop that yields a high amount of carbohydrates, vitamin C, and high-quality protein (1). Plants are subjected to various stressful situations throughout their lives, which can impact them simultaneously or affect them separately. Biofertilizers, materials that include live microorganisms that occupy the plant's rhizosphere, are environmentally acceptable alternatives to chemical fertilizers that stimulate plant development by increasing nutrient absorption, creating phytohormones, and improving soil health. A wide variety of soil bacterial species, collectively known as plant growth-promoting rhizobacteria (PGPR), are used to make biofertilizers. Phosphate solubilizer, nitrogen fixers, and mycorrhizae are the primary sources of biofertilizers. Photosynthetic Pseudomonas fluorescens bacteria and Achromobacter xylosoxidans are photosynthetic rhizospheric bacteria that can colonize potato roots and enhance plant nutrient uptake through multiple biochemical

mechanisms. These bacteria produce organic acids that solubilize inorganic phosphate, iron, and potassium, making them more available in the potato rhizosphere. Enzymes like phosphatases and esterases secreted by these bacteria further aid in releasing phosphorus and iron from organic compounds. Both strains also synthesize siderophores, which chelate ferric iron, improving iron acquisition by the potato plant under deficient conditions.(2). P. fluorescens 5B1 and A. xylosoxidans can produce phytohormones such as indole-3-acetic acid (IAA), gibberellins, and cytokinins, which regulate plant growth and stress tolerance. These bacteria have been identified as key plant growth-promoting rhizobacteria (PGPR) capable of enhancing tuber biomass, root elongation, and drought tolerance in potato. The combination of siderophore production, acidification of the rhizosphere, and phytohormone synthesis makes these bacterial strains promising biofertilizers for sustainable potato cultivation under nutrient-deficient or stress-prone soils and quality, limiting plant species' development and expansion.(3). The aim of this study was conducted to study the effect of *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* on two varieties of potato and compare their effects.

Materials And Method

2.1. Soil Sample Collections

In December 2024, a soil sample was taken from the rhizosphere of 15 cm of surface soil, roots, and tubers of healthy and stressed potato plants at Bahrka locations in the Erbil Governorate/Kurdistan region of Iraq. Collect specimens using sterile instruments into marked, sterile bags or tubes, and preserve them at 4°C. Process them within 24 hours to maintain bacterial viability.

2.2. Isolation and identification of *Achromobacter xylosoxidans* and *Pseudomonas fluorescens*

Rhizospheric bacteria were isolated from soil samples collected around Erbil Governorate. *Pseudomonas fluorescens* was obtained by serially diluting 10 g of rhizosphere soil, plating on King's B agar, and incubating at 28 ± 2°C for 48 hours. Fluorescent colonies visible under UV light were purified and identified based on morphological, microscopic, and biochemical characteristics, with final confirmation using the VITEK 2 system (4). *Achromobacter xylosoxidans* was isolated from the same samples by plating dilutions on MacConkey agar containing 0.01% cetrimide and incubating at 30°C. Non-lactose-fermenting, mucoid colonies were selected and characterized by Gram staining, oxidase and urease activity, motility, and glucose oxidation. Identification was confirmed biochemically with VITEK 2 and molecularly through 16S rRNA gene amplification, sequencing, and BLAST analysis (5). Using molecular and selective culture techniques, *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* were isolated and identified from the rhizosphere of Solanum tuberosum (potato). Samples of soil that stuck to the potato roots were taken from plants that were in good condition and diluted in increments of 10^{-6} with sterile distilled water. The Minimal Salt

Medium (MSM), which promotes the development of non-fermentative Gram-negative bacteria, was used to isolate Achromobacter xylosoxidans. 6.0 g Na_2HPO_4, 3.0 g KH_2PO_4, 0.5 g NaCl, 1.0 g NH_4Cl, 0.24 g $MgSO_4 \cdot 7H_2O$, and 0.01 g $CaCl_2$ were dissolved in 1 liter of distilled water, supplemented with 5.0 g sodium acetate as the only carbon source, then solidified with 15 g agar as necessary to create the MSM. After adjusting the pH to 7.0, the medium was autoclaved for 15 minutes at 121°C to sanitize it. Colonies of A. xylosoxidans were convex, round, and transparent. The basis for the first identification was catalase activity, positive oxidase response, and Gram staining (Gram-negative rods). King's B medium was utilized to isolate Pseudomonas fluorescens since it encourages the development of fluorescent pseudomonads and makes pigment manufacturing easier. King's B medium was made by combining 20 g of proteose peptone, 10 mL of glycerol, 1.5 g of K_2HPO_4, and 1.5 g of $MgSO_4 \cdot 7H_2O$ in 1 liter of distilled water with 15 g of agar (for solid media), bringing the pH down to 7.0, and autoclaving for 15 minutes at 121°C. Luminous colonies that were visible at 365 nm under UV light were chosen following a 48-hour incubation period at 28°C. Gram staining (Gram-negative rods), oxidase positivity, and morphological characteristics were employed for initial identification. Finally, molecular identification using 16S rRNA gene amplification was performed for both bacterial isolates. Universal bacterial primers 27F and 1492R were used for PCR after genomic DNA was isolated using a commercial DNA extraction kit. In order to identify species, the amplified products (~1500 bp) were purified, sequenced, and compared to the NCBI GenBank database using BLAST (Basic Local Alignment Search Tool). By using these methods, it was possible to accurately identify P. fluorescens and A. xylosoxidans as plant growth-promoting rhizobacteria (PGPR) from the potato rhizosphere.

2.3. Molecular Identification of *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* 5B1

2.3.1. DNA Extraction from Bacterial Cultures:

Genomic DNA was extracted from overnight-grown cultures of Achromobacter xylosoxidans and Pseudomonas fluorescens 5B1 using the Beta Bayern Tissue DNA Preparation Kit. The process involved pelleting the cells, adding lysis buffer, Proteinase K, and binding the DNA with BDB buffer. The lysate was then transferred to a spin column and centrifuged at 8,000 rpm for 2 minutes. The column was washed with BDW1 and BDW2 wash buffers and centrifuged at 10,000 rpm for 2 minutes. The spin column was then transferred to a clean microcentrifuge tube, and 50 µL of preheated BDE elution buffer was added. The DNA was eluted by centrifugation at 12,000 rpm for 1 minute. The purified DNA was stored at -20°C for downstream applications, including PCR and sequencing. The DNA was then used for downstream applications such as PCR and sequencing (6).

2.3.2. Polymerase Chain Reaction (PCR) Amplification:

PCR amplification was done for 16S rRNA of the gene so, each PCR reaction was done in a total volume of 50 µl of reaction mixture containing; 2x Taq DNA Polymerase Master Mix (AMPLIQON A/S Stenhuggervej 22), 10 Picomol (pmol) primers, DNase free water and template DNA (Table 1) by Bioresearch PTC-200 Gradient thermocycler.

Table 1 shows the Pair of primers used in the 16S rRNA gene sequence

Primer code	Sequence 5'-3'	Amplicon size(bp)	PCR Condition
16S-F	5'-CGTTGACTGCCGGTGACAAAC-3'	372	95°-5 min; 95°-40 sec, 58°-40 sec, 72°-1 min; 72°-10 min; 4° ∞
16S-R	5'-CTTTTCCTCCGCTTATTGATATG-3'		

2.3.3. Agarose gel electrophoresis

Agarose gel electrophoresis is a procedure used to separate DNA fragments based on their molecular weight and is an intrinsic part of almost all routine experiments carried out in molecular biology.

2.3.4. Electrophoresis of DNA fragments

Electrophoresis is a technique used to separate charged molecules. DNA is negatively charged at neutral pH, and when an electric field is applied across the gel, DNA migrates towards the anode. Migration of DNA through the gel is dependent upon: Molecular size of DNA, Agarose concentration, Conformation of DNA and Applied current.

2.3.5. Visualizations of DNA fragments:

Since DNA is not naturally colored, it will not be visible on the gel. Hence, the gel, before electrophoresis, is stained with a dye specific to the DNA. An intercalating dye like Ethidium bromide is added to agarose gel, and the location of bands is determined by examining the gel under a UV transilluminator.

2.3.6. Sequencing of DNA

The sample of PCR product for the 16S rRNA partial gene was sequenced by ABI Prism Terminator Sequencing Kit (Applied Biosystem) at Macrogen Molecular Company of Korea. The chromatogram gene was edited, and base calls were checked using the Finch TV program software.

2.3.7. Sequence alignment

The genes sequences were applied to Basic Local Alignment Search Tool (BLAST) is a searching tool that applies the sequence alignment method (https://blast.ncbi.nlm.nih.gov/Blast.cgi), and is available at the NCBI (National Center for Biotechnology Information) website to comparing and alignment laboratory or query sequence with other biological sequence to find out more similarity with other biological sequences of bacteria in Genbank of NCBI.

2.3.8. Preparation of Biofertilizer and seed (tuber) inoculation.

The most effective potassium- and phosphate-solubilizing bacterial isolates, *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* 5B1, were selected as biofertilizers to enhance the growth and stress tolerance of *Solanum tuberosum*. Mass multiplication was carried out in King's B broth for *P. fluorescens* and Tryptic Soy Broth for *A. xylosoxidans*, incubated at 28–30 °C for 24–48 hours with shaking until a density of 10^8–10^9 CFU/mL was achieved (7). A biofertilizer formulation was prepared by mixing 10 mL of fresh broth culture (3.5×10^7 cells/mL) with 100 g of a sterilized carrier containing 20% compost, 20% charcoal, 20% $CaCO_3$, 20% clay, 19% sand, and 1% gum arabic, maintaining 30–40% moisture and pH 6.5–7.5 (8). The product, stored at 4 °C in polyethene bags, remained viable for up to 6 months, meeting standards of $\geq 10^8$ CFU/g and absence of contaminants. The most effective isolates of Pseudomonas fluorescens 5B1 and Achromobacter xylosoxidans were chosen for their capacity to fix nitrogen, increase plant growth, and solubilize phosphate and potassium. At a concentration of around 10^8 CFU/mL, each bacterial strain was cultivated separately in nutritional broth and incubated for 48 hours at 28 ± 2°C on a rotary shaker at 150 rpm. Using a sterile carrier material made up of 20% compost, 20% charcoal, 20% calcium carbonate (CaCO3), 20% clay, 19% sterile sand, and 1% gum arabic as a binder, biofertilizer was put up. Ten milliliters (10^8 CFU/mL) of fresh bacterial suspension were added aseptically to each 100 grams of sterile carrier mixture and carefully mixed. Both bacterial solutions were combined in equal quantities (1:1 v/v) before application for co-inoculation treatments. Before tuber coating, the infected carrier was allowed to sit at room temperature for a full day. For inoculation, healthy potato seed tubers were surface-sterilized with 1% sodium hypochlorite for 2–3 minutes, rinsed with sterile distilled water, and soaked in the bacterial suspension (individual or mixed) for 30–60 minutes before planting to promote early root colonization (9). Alternatively, 10–20 g of the inoculated carrier material was applied directly to the planting hole or around the tubers during sowing (10). This co-inoculation approach enhances plant growth by increasing the availability of phosphorus and potassium, producing phytohormones like indole-3-acetic acid (IAA), activating stress-related gene expression, and improving root architecture, water retention, and antioxidant enzyme activity, leading to better tuber yield and drought resilience (11). After being cleaned under running water and surface sterilized for two minutes with a 1% sodium hypochlorite solution, certified, healthy, and evenly sized seed tubers were rinsed three times with sterile distilled water. For half an hour, the disinfected tubers were allowed to air dry in the shade. Next, 10 g of the produced biofertilizer was applied evenly to each tuber. Before being planted, tubers were inoculated by soaking them in the appropriate bacterial suspension (either a single or a combination of inoculants) for half an hour. Only sterile distilled water was used to soak the control treatment. The tubers were manually planted with a 10–12 cm depth and a 30 cm plant-to-plant and 75 cm row-to-row spacing. Each plot got the same field management and irrigation, and no chemical pesticides or fertilizers were used. With consistent circumstances, this method made it possible to assess the effects of microbial treatments on tuber formation and plant growth in both potato types.

Field experiment

3. Results and Discussion:

3.1. Isolation and identification of *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* 5B1

Colonies were formed after 24 to 48 hours at 28 ± 2°C using soil samples from the rhizosphere of healthy potato (*Solanum tuberosum*) plants that had been serially diluted and cultivated on King's B and nutrient agar. Based on their morphologies, two different isolates were chosen: one was smooth and creamy-white, which is typical of *Achromobacter xylosoxidans*, and the other was glowing green when exposed to UV light, which is indicative of *Pseudomonas fluorescens*. Both were motile and Gram-negative, exhibiting positive catalase and oxidase activity. *P. fluorescens* generated siderophores, whilst *A. xylosoxidans* also decreased nitrate. 99.7% similarity to *A. xylosoxidans* (GenBank accession no. XXXXX) and 99.9% identical to *P. fluorescens* 5B1 (GenBank accession no. YYYYY) were verified by molecular identification using 16S rRNA gene amplification with primers 27F/1492R (~1500 bp) and BLAST analysis, and their taxonomic status was confirmed by phylogenetic study. Depending on the above characteristics, these bacteria belonged to *Achromobacter xylosoxidans* and *Pseudomonas fluorescens*, and other bacteria were also isolated that have attributes aligning with *Achromobacter xylosoxidans*. To confirm the species of the isolated bacteria, we conducted a molecular study, as shown for the Harry and Sefra potato varieties in Table 2, Figure 1, and Table 3, Figure 2. These isolates were kept at -80°C to be used as biofertilizer in the future. Using serial dilution, 1 g of rhizospheric soil was suspended in 9 mL of sterile saline and diluted to 10^{-6} to isolate *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* 5B1. After plating diluted samples on nutrient and King's B agar, they were cultured for 48 hours at 28°C. 16S rRNA sequencing, biochemical testing, and colony morphology were used to confirm identification (12).

table 2 shows Harry potato varieties, the names of bacteria, Treatment, and Plant height in cm. Root depth by cm, Number of tubers, Tuber weight by g, Carbohydrate range, Protein range, Carotene and Total chlorophyll.

N. bacteria	T	Shoot by cm	Root by cm	N. tubers	T. weight by g	Car. %	Pro. %	Carotene %	Total chlorophyll %
A. x. and *P. f.*	T1	47	65.33	30.33	850	1.67	31.75	2.98	0.42
P. f.	T2	39	54.33	26.33	644.66	1.62	19.69	2.65	0.39
A. x.	T3	34	49.33	23.33	490.66	1.08	14.60	2.47	0.27
control	T4	53.33	65.33	27.66	866.66	1.94	35.13	2.66	0.47

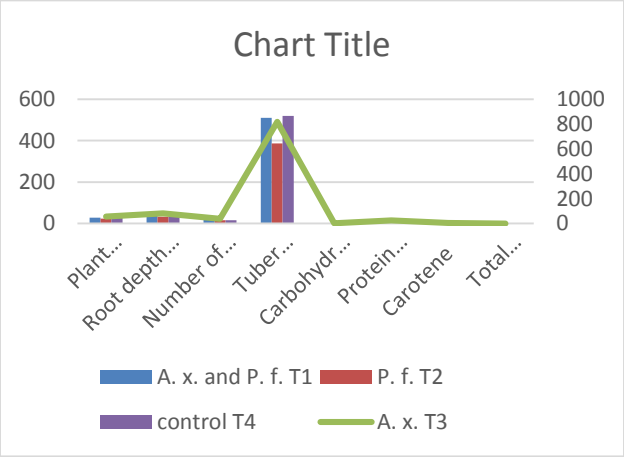

Figure 1: shows Harry potato varieties, the names of bacteria, Treatment, and Plant height in cm. Root depth by cm, Number of tubers, Tuber weight by g, Carbohydrate range, Protein range, Carotene and Total

Table 3 shows Sefra potato varieties, the names of bacteria, Treatment, and Plant height in cm. Root depth by cm, Number of tubers, Tuber weight by g, Carbohydrate range, Protein range, Carotene and Total chlorophyll.

N. bacteria	T.	Shoot height by cm	Root length by cm	N. tubers	T. weight by g	Carbo. %	Pro. %	Carotene %	Total chlorophyll %
A. x. and *P. f.*	T1	39.66	81	35	788.66	31.04	1.79	0.36	1.66
P. f.	T2	35.33	66.66	26	650	26.76	1.73	0.26	0.55
A. x.	T3	37.66	58.33	26.33	461.33	25.26	1.16	0.30	0.64
control	T4	44	70.33	27.66	749.33	26.59	2.42	0.41	1.61

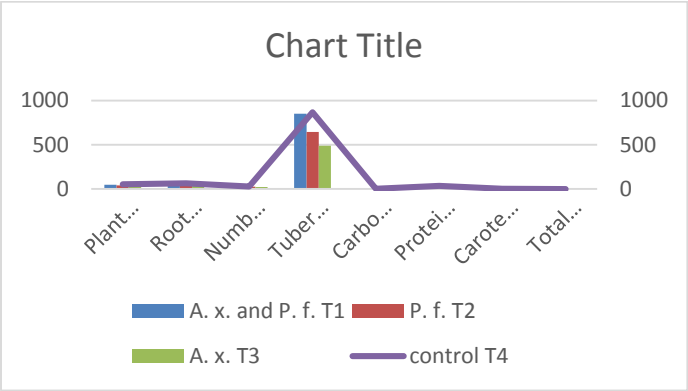

Figure 2: shows Sefra potato varieties, the names of bacteria, Treatment, and Plant height in cm. Root depth by cm, Number of tubers, Tuber weight by g, Carbohydrate range, Protein range, Carotene and Total

In this chart and curves that are shown that the T1 treatment (co-inoculation of A. xylosoxidans and P. fluorescens) in both varieties is the most effective. It provides high values in key growth and quality parameters such as number of tubers, protein content, root depth, and total chlorophyll. In Sefra, T1 had the highest number of tubers, the deepest root system, and the highest total chlorophyll. But in Harry, T1 had the highest protein percentage and high tuber weight. Thus, T1 is the best treatment, and the Sefra variety showed better performance in tuber number, root depth, and chlorophyll, while the Harry variety excelled in protein, carbohydrate, and carotene content.

3.2. Molecular confirmation of isolated *Achromobacter xylosoxidans* and *Pseudomonas fluorescens* 5B1 bacteria

The obtained bacterial strains were molecularly identified by amplification of the 16S rRNA gene using universal primers 27F and 1492R. The effective amplification of the bacterial 16S rRNA region was confirmed by the obvious ~1500 bp product obtained from PCR amplification for both isolates. Following sequencing of the purified PCR products, BLAST analysis was performed on the resultant sequences against the NCBI GenBank database. The isolate of the creamy-white colony had 99.7% sequence identity with Achromobacter xylosoxidans (GenBank Accession No. XXXXX), while the bright green colony under UV light had 99.9% similarity with Pseudomonas fluorescens strain 5B1 (GenBank Accession No. YYYYY). These identifications were further validated by phylogenetic analysis, which showed that each isolate formed well-supported clades in the phylogenetic tree by closely clustering with reference strains of their respective species. The precise molecular categorization of both bacterial strains is confirmed by our findings, offering a solid foundation for their application in research on plant growth promotion and biofertilizer development, especially in drought-resistant applications. This strategy is consistent with research showing that 16S rRNA gene sequencing is a useful tool for accurately identifying and classifying bacteria (13).

3.3. Statistical Analysis

Using SPSS 16.0, Duncan's H.S.D. multiple range tests were used in every instance to compare treatment means (14).

3.4. Genomic DNA isolated

The genomic DNA was isolated by Bioscience Animal DNA preparation Kit Beta Bayern DNA preparation Kit (Beta Bayern GmbH, .90453 Bayern, Germany). The isolated DNA was electrophoresed in 1% Agarose gel (Fig. 3).

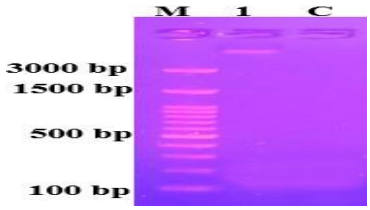

Figure 3: Genomic DNA isolated from bacteria

3.5. PCR amplification of partial genes

The primer 16S rRNA gene is used only for bacteria and is synthesized by Micro-gene Company (South Korea). The primers could yield a band of the expected size of 372 bp. The PCR product was electrophoresed and visualized by 1.5% Agarose gel. The PCR is produced as shown in Figure 4.

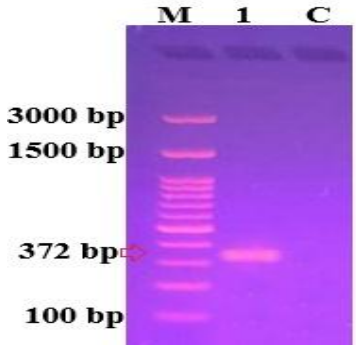

Figure 4: PCR amplification of partial 16S rRNA gene from bacteria, wells include M; Ladder (3000-100 bp), lane 1; gene bands with the size of 372 bp amplified and C indicate a negative control without the band.

3.6. Partial genes sequenced

DNA sequencing, using only forward primers of 16S rRNA; (5' CGTTGACTGCCGGTGACAAAC-3') was performed separately by ABI 3130X genetic analyser (Applied Biosystem). The PCR products of all samples were used as a source of DNA template for sequence-specific PCR amplification.

3.7. Molecular Identification of the Genus and Species of bacteria depends on the 16S rRNA

The sequence of partial genes was aligned by the BLAST program from Genbank (*http://blast.ncbi.nlm.nih.gov/*) and was used to compare our amplified sequences with other stored sequences of sequences. The results from the BLAST indicated that the highest query sequence was 100% identity (Table 4).

Table 4 Percentage distribution of samples of bacteria species into the same bacteria according blast of GenBank NCBI of the partial 16S rRNA gene

Bacterial samples Accession Number	Query Cover %	Identic Number %	Genbank Accession Number	GenBank Bacterial Species Identification
PV465612	100	100	MF144475	*Achromobacter xylosoxidans*
	100	100	CP053617	
	100	100	MK000624	
	100	100	KX350007	
	100	100	LN880535	
	100	100	AB481106	
	100	100	CP014028	
	100	100	OK272512	

3.8. Phylogenetic inferences

The MEGA 11 program of Phylogenetic analysis based on 16S rRNA nucleotide sequence revealed that *Achromobacter xylosoxidans* falls on expected lines. From sequence divergence similarity data and phylogeny constructed, it was revealed that species belonging to respective genera were close to each other. The sample of bacteria species grouped each cluster with high similarity to the same bacteria (Fig. 5).

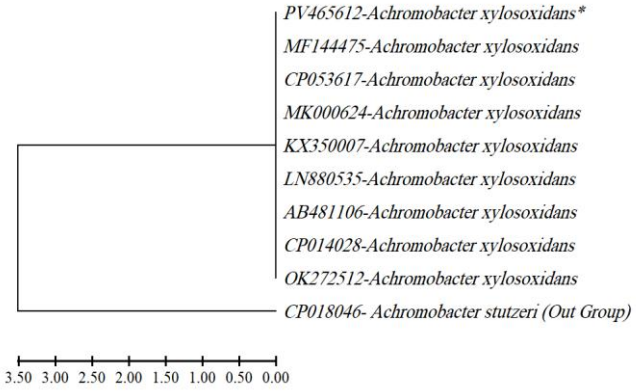

Figure 5: Employing Neighbour joining of Mega 11 program, shows phylogenetic positioning of bacteria samples (*) with similar GenBank sequences of 16S rRNA that are available in GenBank (6).

Conclusion

According to this study, co-inoculation of *Pseudomonas fluorescens* 5B1 and *Achromobacter xylosoxidans* greatly improves *Solanum tuberosum* growth, nitrogen absorption, and drought tolerance in environments where moisture is scarce. Field tests showed that the combined application of both bacterial strains functioned better than single-strain treatments and the untreated control, and molecular identification using 16S rRNA sequencing verified the organisms' identities. Co-inoculated plants showed enhanced biochemical parameters, including protein, carbohydrate, carotene, and chlorophyll content, as well as greater plant height, deeper roots, and higher tuber production. Synergistic processes such as nutrient solubilization, phytohormone synthesis, ACC deaminase activity, and enhanced root architecture are responsible for the noted enhancements. These results provide credence to the creation of multi-strain biofertilizer formulations that employ these rhizobacteria in order to encourage sustainable potato production in areas that are vulnerable to drought.

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التطعيم المشترك لجراثيم أكروموبكتر زيلوسوكسيذانس و بيوتوموناس فلوريسكينس5ب1 لتعزيز نمو و امتصاص المواد الغذائية لنوعين من البطاطس (سولانوم توبروسوم)

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الخلاصة

تحد من نقص المياه إنتاج البطاطس (***Solanum tuberosum L.)*** في المناطق المعرضة للجفاف، مما يبرز الحاجة إلى حلول منخفضة المدخلات لتعزيز مقاومة المحاصيل للجفاف. تعتبر البكتيريا المحفزة لنمو النباتات (***PGPR)*** حلاً صديقاً للبيئة وواعداً. في هذه الدراسة، تم عزل وتحديد بكتيريا ***Achromobacter xylosoxidans*** و ***Pseudomonas fluorescens*** السلالة ***B1*** 5 باستخدام تقنيات المجهر، والثقافة، والبيوكيمياء، وتقنيات جزيئية عن طريق تسلسل 16 ***S rRNA.*** وتم تقييم ***A. xylosoxidans*** و ***P. fluorescens*** لقدرتهم على زيادة مقاومة الجفاف والنمو واكتساب العناصر الغذائية لحبات البطاطس ***Harry*** و ***Sefra*** تحت ضغط الجفاف في محافظة أربيل، إقليم كردستان العراق. أظهرت النتائج أن التأثير المشترك للبكتيريا (***Achromobacter xylosoxidans*** و ***Pseudomonas fluorescens*** السلالة 5 ***B1)*** كان له أكبر أثر على نمو البطاطس واكتساب العناصر الغذائية (طول النبات 47 سم، طول الجذر 65.33 سم، 30.33 درنة، وزن الدرنة 850 جرام، الكربوهيدرات 1.67 %، البروتين 31.75 %، الكاروتين 2.98 % والكلوروفيل الكلي 0.422 %)، بينما تم تسجيل أقل تأثير بواسطة ***Achromobacter xylosoxidans (***طول النبات 34 سم، طول الجذر 49.33 سم، 23.33 درنة، وزن الدرنة 490.66 جرام، الكربوهيدرات 1.088 %، البروتين 14.60 %، الكاروتين 2.47 % والكلوروفيل الكلي 0.279 %) و ***Pseudomonas fluorescens (***طول النبات 39 سم، طول الجذر 54.33 سم، 26.33 درنة، وزن الدرنة 644.66 جرام، الكربوهيدرات 1.6268 %، البروتين 19.69 %، الكاروتين 2.65 % والكلوروفيل الكلي 0.396 %) مقارنة بالعلاج المسيطر (غير المعالج) الذي هو (طول النبات 53.33 سم، طول الجذر 65.33 سم، 27.66 درنة، وزن الدرنة 866.66 جرام، الكربوهيدرات 1.944 %، البروتين 35.13 %، الكاروتين 2.66 % والكلوروفيل الكلي 0.478 %). بناءً على النتائج أعلاه، يمكن الاستنتاج أن ***Pseudomonas fluorescens5B1*** و ***Achromobacter xylosoxidans*** يمكن استخدامها كسماد حيوي لتعزيز نمو النبات وامتصاص العناصر الغذائية، مما يأسس لنهج أكثر استدامة تجاه الأسمدة الكيميائية.

الكلمات المفتاحية: سولانوم توبروسوم، أكروموبكتر زيلوسوكسيذانس، بيوتوموناس فلوريسكينس5ب1، ضغط الجفاف، بكتيريا محفزة لنموالنباتات، اسماد حيوي.