

Andean Rhizospheric Microorganisms as Plant Growth-Promoting Platforms: Characterization of *Pseudomonas Protegens* M2 and *Bacillus Proteolyticus* M9

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The rhizosphere of Andean crops constitutes a unique reservoir of microorganisms with biotechnological potential for boosting plant development and phytopathogen control. In this study, the functional capacities of two microbial strains isolated from Andean tubers were evaluated: *Pseudomonas protegens* M2, from the rhizosphere of oca (*Oxalis tuberosa*), and *Bacillus proteolyticus* M9, isolated from the rhizosphere of mashua (*Tropaeolum tuberosum*). Their molecular identity was confirmed by alignment of the 16S ribosomal marker gene. Strain M2 displayed an outstanding multifunctional profile, with nitrogen-fixing activity, siderophore production, inorganic phosphate solubilization (5.06 ± 0.75 HD/CD ratio), and elevated indoleacetic acid synthesis (60.66 ± 0.44 µg/mL). Furthermore, it exhibited a high antagonistic capacity against *Fusarium oxysporum* ($51.29 \pm 0.73\%$) and *Rhizoctonia* sp. ($59.89 \pm 1.11\%$). In contrast, M9 showed limited behavior, lacking IAA production or antifungal activity. These results position *P. protegens* M2 as a promising microorganism for the development of biological fertilizers and microbial antagonists, promoting eco-friendly agriculture, especially in regions vulnerable to climate change.

1. Introduction

The use of chemicals in agronomy is a major challenge to achieving sustainable agriculture. Furthermore, environmental stress is considered one of the primary barriers to plant development and crop productivity worldwide, significantly affecting various plant species (Sabki et al. 2021). Therefore, bacteria that stimulate plant growth are presented as an effective alternative to enhance plant adaptation and survival in the face of environmental stress conditions (Agunbiade et al., 2024).

The bacteria that inhabit the rhizosphere of plants are a group of microorganisms that promote plant growth (PGPRs) through different direct and indirect mechanisms (Meneguzzi et al., 2024). PGPRs benefit plants by promoting growth and increasing their stress tolerance. These effects are mediated through direct and indirect mechanisms, including bioremediation, phytohormone synthesis, biological nitrogen fixation, siderophore production, pathogen control, nutrient solubilization, and activation of systemic resistance (Etesami & Maheshwari, 2018a). In particular, PGPRs from the *Bacillus* genus, for example, *Bacillus megaterium*, *Bacillus cereus*, *B. licheniformis*, *B. subtilis*, *Bacillus amyloliquefaciens*, and *Bacillus polymyxa*, promote plant development, increase stress tolerance, and strengthen resistance to diseases by establishing themselves in the roots and rhizosphere of crops, also contributing to resilience to drought and to the remediation of heavy metals (Zhou et al., 2016). Thus, the use of PGPRs, also known as biofertilizers, is considered an environmentally friendly and sustainable strategy compared to synthetic pesticides and fertilizers.

Similarly, environmental conditions and its unique ecological niche as in the Andean region, contribute to a wealth of microbial species, making local crops ideal places to find beneficial microorganisms with growth-

promoting properties (Ortiz-Ojeda et al., 2017). Microbial communities associated with native crops are key resources for plant protection and nutritional support, with highly efficient isolates that perform various functions in the rhizosphere (Ogata-Gutiérrez et al., 2017). Mashua (*Tropaeolum tuberosum*) and oca (*Oxalis tuberosa*) are Andean tubers of great nutritional and cultural importance, recognized for their ability to adapt to extreme climatic conditions and low-fertility soils. These characteristics consolidate them as essential crops in the high Andean regions, ensuring their presence in traditional foods and sustainable agricultural practices (García-Díaz et al., 2023). Despite their relevance, studies on the rhizosphere of these crops remain scarce, highlighting a significant gap in our understanding of plant-microorganism interactions. For example, Chica et al. (2019), through a genomic analysis with high-throughput sequencing of 16S rRNA genes (V3-V4 regions), characterized the bacterial communities of the rhizospheres of mashua and oca, finding a higher abundance of bacteria belonging to the phyla Proteobacteria, Actinobacteria, and Bacteroidetes compared to the adjacent soil. The rhizosphere is a zone of soil close to and under the influence of plant roots, where intense biological activity and a close symbiotic relationship with microorganisms develop, playing an essential role in plant health and sustainable agriculture. This zone promotes soil fertility, limits the incidence of disease, and fosters the establishment of specific microbial communities through rhizodeposition and the release of photosynthetically derived compounds (Thepbandit & Athinuwat, 2024). Research into rhizospheric microorganisms associated with mashua and oca would not only strengthen the sustainability of these crops but also support the conservation of native Andean microbial biodiversity. The objective of the research was to identify and characterize bacteria associated the rhizosphere from oca (*Oxalis tuberosa*) and mashua (*Tropaeolum tuberosum*), evaluating their potential as plant growth promoters. Unlike previous metagenomic or descriptive studies, this work provides a functional and quantitative characterization of culturable rhizospheric strains from underexplored Andean tubers, highlighting their multifunctional plant growth promoting traits and biocontrol potential. This approach contributes novel experimental evidence for the selection of native microbial candidates with potential application in sustainable Andean agriculture.

2. Methodology

2.1 Sample Collection

Rhizospheric soil from Oca (*Oxalis tuberosa*) was collected in the province of Huamachuco, Peru (Figure 1) (Latitude -7.85494, Longitude -78.02287). Similarly, rhizospheric soil samples were obtained from Mashua (*Tropaeolum tuberosum*) crops in the province of Santiago de Chuco, Peru (Latitude -8.150233, Longitude -78.163975) (Figure 1).

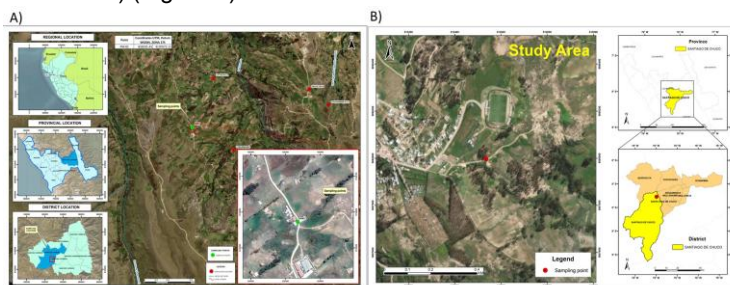


Figure 1: (A) Sampling site of rhizospheric agricultural soil from Oca in the province of Huamachuco (Quiñones-Cerna et al., 2024); and, (B) soil from Mashua in the province of Santiago de Chuco.

2.2 Microbial Isolation

The microbial cultures isolated were obtained following the results reported by Quiñones-Cerna et al. (2024), using their methodology for biodegradative compatibility with hydrocarbons. From 500 g of soil, serial dilutions were made up to 10^{-9} , and the last two (10^{-8} and 10^{-9}) were seeded in Petri dishes with Nutrient Agar (NA). Differentiated colonies were incubated and subcultured on NA at 35°C for 24 h, and were preserved at 5°C.

2.3 Growth-Promoting Characterization

2.3.1 Nitrogen-Fixation Activity Assay

Nitrogen-fixing activity was evaluated by inoculating each bacterial culture in Nfb medium composed of (g/L): Glucose 10, $MgSO_4 \cdot 7H_2O$ 0.3, K_2HPO_4 1.1, KH_2PO_4 0.6, NaCl 0.1, $FeCl_3$ 0.005, $Na_2MoO_4 \cdot 2H_2O$ 0.002, malic acid 2 and $CaCO_3$. Incubation was carried out for 5 days at 30°C, and the formation of a biofilm in the medium was considered indicative of a positive result (González et al., 2023).

2.3.2 Siderophore Production Assay

The evaluation was performed by inoculating 10 µL of each bacterial culture onto Chromium Azurol S (CAS) agar medium, after incubating for 3 days at 30 °C. The appearance of clear areas was interpreted as evidence of siderophore production (Albdaiwi et al., 2020).

2.3.3 Inorganic Phosphate Solubilization Assay

The test was performed by adding 10 µL of the bacterial inoculum in NBRIP phosphate agar medium. The plates were kept at 32°C for 10 days. Observation of clear areas around the growing colonies confirmed a positive result. For each isolate, the halo diameter (HD) and colony diameter (CD) were recorded, and the HD/CD ratio was calculated (Rehan et al., 2023).

2.3.4 Indole-3-Acetic Acid (IAA) Assay

Microbial cultures were inoculated in Luria Bertani (LB) medium with L-tryptophan and these were grown at 28–30°C for 18 h. IAA synthesis was performed using the Salkowski method, recording absorbance at 530 nm and estimating concentrations based on a standard curve (Cochard et al., 2022).

2.3.5 In Vitro Antagonistic Activity Assay

The plant pathogenic fungi were inoculated in the central zone of potato dextrose agar (PDA) plates, while the test bacteria were placed 2.5 cm away at the edges. These were grown at 28–30°C for 6 days. The inhibitory effect on fungal growth was evaluated by measuring colony diameter and calculating the percentage of inhibition (IP %) (Aallam et al., 2021):

$$IP \% = \frac{T - S}{T} \times 100$$

where T represents the radius of the mycelial colony of the fungus (in mm) in the control, and S the radius of the colony.

2.4 Molecular Characterization and Identification

The microbial culture was subjected to a molecular analysis targeting the 16S rRNA gene using the polymerase chain reaction (PCR), according by Cueva-Almendras et al. (2022). DNA sequencing was performed by Macrogen Inc. (Seoul, South Korea), and the obtained sequences were compared with those available in the EzBioCloud Database (<https://www.ezbiocloud.net/>) using the BLAST (Basic Local Alignment Search Tool) to identify the closest homologous strains. Finally, a phylogenetic tree was constructed from strain-type sequences obtained from EzBioCloud Database and National Center for Biotechnology Information (NCBI) of rRNA using MEGA-X software and edited with FigTree v1.4.4 software.

2.5 Statistical Analysis

The results were presented with their arithmetic mean and standard deviation through the Microsoft Excel v2024 program.

3. Results and discussion

Twelve microbial cultures were obtained; however, only two isolates, designated M2 and M9, were selected for further analysis. This selection was based on preliminary qualitative screening assays, in which these isolates consistently showed positive responses in key plant growth promoting traits, including nitrogen fixation and siderophore production. In contrast, the remaining isolates exhibited weak, inconsistent, or negative responses in these assays. Therefore, M2 and M9 were chosen as representative strains for detailed functional and molecular characterization.

Molecular analysis by 16S rRNA gene sequencing showed that M2 and M9 presented a similarity of 100% and 98.27 %, respectively, with *Pseudomonas protegens* CHA0 and *Bacillus proteolyticus* TD42. The generated amplicons had lengths of 725 bp (M2) and 529 bp (M9), and their sequences were registered in NCBI under accession numbers PP886146 and PQ826256 (Table 1).

Table 1: Results of the alignment and identification of the nucleotide sequences of the 16S rRNA gene of selected bacterial cultures.

Bacterial culture	Genus and species	Similar strain	Pairwise Similarity (%)	Accession number	Source
M2	<i>Pseudomonas protegens</i>	CHA0	99.00	PP886146	Quiñones-Cerna et al. (2024)
M9	<i>Bacillus proteolyticus</i>	TD42	98.27	PQ826256	Performed in this research

Figure 2 shows that isolate M2 clusters with *Pseudomonas protegens* CHA0, sharing a very recent common ancestor due to their minimal evolutionary distance. Likewise, isolate M9 is closely related to *Bacillus proteolyticus* TD42 (distance 0.03), while showing greater divergence from other *Bacillus* species and the outgroup *Deinococcus actinosclerus* BM2(T).

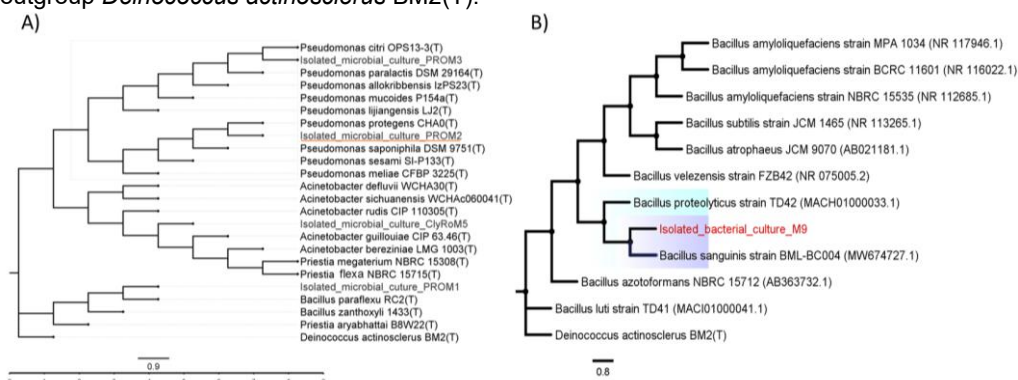


Figure 2: A phylogenetic tree was drawn up by neighborhood joining with 1000 bootstrap replicates, determining the evolutionary distances between nearby sequences with the three-parameter Tamura model.

Culture M2 demonstrated a remarkable ability to fix atmospheric nitrogen, evidenced by a color change in Nfb medium and biofilm formation (Figure 3). Additionally, it showed high siderophore production, confirmed by the formation of clear halos around the colonies, as well as effective inorganic phosphate solubilization. This microorganism also displayed significant antagonistic activity against the phytopathogens *Fusarium sp.* and *Rhizoctonia sp.*, inhibiting their colony growth. On the other hand, culture M9 exhibited moderate but positive changes, with a slight capacity for nitrogen fixation and siderophore production, no halos associated with phosphate solubilization, and lower antagonistic activity compared to M2 (Figure 3).

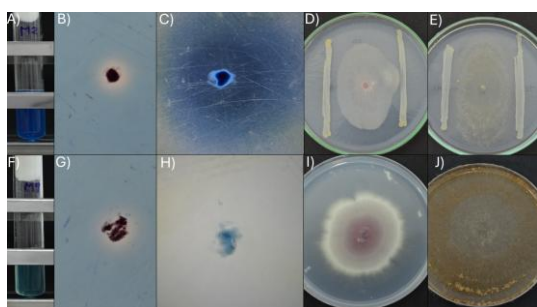


Figure 3: Plant growth enhancement activity assays of the M2 isolate: (A) showing growth with color change and biofilm formation during atmospheric nitrogen fixation in Nfb medium, (B) siderophore production indicated by a halo around the colony, (C) inorganic phosphate solubilization with a halo around the colony, and antagonistic activity against (D) *Fusarium sp.* and (E) *Rhizoctonia sp.* Meanwhile, M9 showed (F) a slight color change and film formation in atmospheric nitrogen fixation, (G) presence of siderophore, (H) negative inorganic phosphate solubilization, and (I-J) no antagonistic activity.

Pseudomonas protegens is known to fix atmospheric nitrogen, thereby improving plant nutrition and growth (Wang et al., 2017). It produces siderophores that facilitate iron uptake in limiting environments (Grosse et al., 2023). Its ability to solubilize phosphates through the secretion of organic acids is also notable, this increases phosphorus availability, promoting plant development (Bakki et al., 2024).

Table 2 presents the quantitative evaluation of the growth-promoting characterization of the isolated microbial cultures M2 and M9. Both cultures were diazotrophic (capable of nitrogen fixation) and siderophore producers. Regarding inorganic phosphate solubilization, culture M2 exhibited a high capacity with a value of 5.06 ± 0.75 HD/CD ratio, while culture M9 showed no activity in this test. Likewise, M2 demonstrated notable production of IAA, with a value of 60.66 ± 0.44 $\mu\text{g/mL}$, reinforcing its role in promoting plant growth, whereas M9 did not produce this phytohormone. In antagonism tests (IP %), culture M2 showed significant inhibition against the phytopathogens *Fusarium oxysporum* (51.29 ± 0.73 %) and *Rhizoctonia sp.* (59.89 ± 1.11 %), although it had

no effect on *Botrytis sp.* Conversely, culture M9 exhibited no antagonistic activity against any of the evaluated pathogens.

Table 2: Growth-Promoting Characterization of the isolated microbial cultures M2 and M9.

Isolation	Diazotrophic	Siderophore Production	Inorganic Phosphate Solubilization (HD/CD ratio)	Indole-3-Acetic Acid Production ($\mu\text{g/mL}$)	Antogonic Tests (IP %)		
					<i>Fusarium oxysporum</i>	<i>Botrytis sp.</i>	<i>Rhizoctonia sp.</i>
M2	+	+	5.06 ± 0.75	60.66 ± 0.44	51.29 ± 0.73	0.00	59.89 ± 1.11
M9	+	+	0.00	0.00	0.00	0.00	0.00

In this study, *Pseudomonas* isolate showed a phosphate solubilization efficiency of 5.06 ± 0.75 (HD/CD ratio), a value comparable to those reported in previous research. *Pseudomonas protegens* isolate M2 reached a production of $60.66 \pm 0.44 \mu\text{g/mL}$ of IAA under laboratory conditions, a value that is higher than several previous reports. For example, it exceeds that described by Blanco-Vargas et al. (2020), who obtained a solubilization index (SI) of 2.1 ± 0.2 in *Pseudomonas sp.* isolated from soils with *Allium cepa*, and also differs from that reported by Paul and Sinha (2017) for *Pseudomonas sp.* KUPSB12, with an SI of 2.85 in effluents from the Ganges River. In terms of IAA production, the $60.66 \pm 0.44 \mu\text{g/mL}$ far exceeds the $21.06 \mu\text{g/mL}$ reported by Alcarraz-Curi et al. (2019) in *Pseudomonas putida* 2J, as well as the $5.3 \mu\text{g/mL}$ described by Kuhl-Nagel et al. (2022) in *Pseudomonas sp.* SCA7. According to Hernández-Hernández and Torres-Aquino (2018), isolate M2 is classified in the high IAA production range, far exceeding the thresholds established in the literature.

4. Conclusions

This study demonstrates the strong potential of *Pseudomonas protegens* M2 as a plant growth-promoting rhizobacterium, given its capacity for nitrogen fixation, siderophore production, phosphate solubilization (5.06 ± 0.75 HD/CD ratio), IAA synthesis ($60.66 \pm 0.44 \mu\text{g/mL}$), and antagonism against *Fusarium oxysporum* (51.29 ± 0.73 %) and *Rhizoctonia sp.* (59.89 ± 1.11 %). In contrast, *Bacillus proteolyticus* M9 showed limited activity, lacking phosphate solubilization, IAA production, and pathogen inhibition. Overall, these findings provide a preliminary experimental basis for the selection of native Andean rhizospheric microorganisms, supporting future studies aimed at their formulation and application in sustainable agriculture. However, further validation under greenhouse and field conditions is required to confirm its effectiveness and stability in real agricultural systems.

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