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Microorganisms associated with epiphytic orchids in southern Ecuador (Loja and Zamora-Chinchi provinces)

Microorganismos asociados con orquídeas epífitas en el sur de Ecuador (provincias de Loja y Zamora-Chinchi)

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Abstract

Orchids (Orchidaceae) are one of the most diverse groups of vascular plants, owing their ability to form mutualistic associations with various microorganisms present in their roots. The objective of this study was to isolate and taxonomically identify fungi and bacteria colonizing the roots of five species of epiphytic orchids from southern Ecuador: *Stelis superbiens* Lindl., *Cyrtorchilum myanthum* (Lindl.) Kraenz, *Masdevallia rosea* Lindl., *Epidendrum rhopalostele* Hágsater & Dodson, and *Cyrtorchilum flexuosum* Kunth. A total of 52 samples were collected at two sites in southern Ecuador. Seventeen fungal isolates were obtained, belonging to the families Dermateaceae, Aspergillaceae, Herpotrichiellaceae, Nectriaceae, and Polyporaceae. In addition, six bacteria belonging to the families Pseudomonadaceae, Burkholderiaceae, and Comamonadaceae were also isolated. The results provide information on the diversity of microorganisms harbored by the roots of the studied species and may serve as a baseline for future

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research on their ecological interactions and potential application in orchid conservation programs.

Keywords: Epiphytic orchids; microbial isolation; roots.

Resumen

Las orquídeas (Orchidaceae) son uno de los grupos más diversos de plantas vasculares, gracias a su capacidad para formar asociaciones mutualistas con diversos microorganismos presentes en sus raíces. Este estudio tuvo como objetivo aislar e identificar taxonómicamente hongos y bacterias asociados a las raíces de cinco especies de orquídeas epífitas del sur de Ecuador: *Stelis superbiens* Lindl., *Cyrtorchilum myanthum* (Lindl.) Kraenz, *Masdevallia rosea* Lindl., *Epidendrum rhopalostele* Hágsater & Dodson y *Cyrtorchilum flexuosum* Kunth. Se recolectaron un total de 52 muestras en dos lugares del sur de Ecuador. Se obtuvieron 17 aislados fúngicos, pertenecientes a las familias Dermateaceae, Aspergillaceae, Herpotrichiellaceae, Nectriaceae y Polyporaceae. Además, se aislaron seis bacterias de las familias Pseudomonadaceae, Burkholderiaceae y Comamonadaceae. Los resultados aportan información sobre la diversidad de microorganismos asociados a las raíces de las especies estudiadas y pueden servir de base para futuras investigaciones sobre sus interacciones ecológicas y su posible aplicación en programas de conservación de orquídeas.

Palabras clave: Orquídeas epífitas; aislamiento microbiano; raíces.

INTRODUCTION

Epiphytic orchids are characterized by establishing themselves on tree branches or bark (Rasmussen & Rasmussen, 2018). In these substrates, their roots meet tree bark, which favours interaction with specific microorganisms and allows them to obtain nutrients. Consequently, this benefits their development and establishment (Ramos *et al.*, 2007; Rasmussen & Rasmussen, 2018).

Among the microorganisms associated with orchids are specific mycorrhizal fungi, which promote seed germination, seedling survival, and in some cases, remain present until the adult stage (Riofrío *et al.*, 2013; Novotná & Suárez, 2018; Alghamdi, 2019; Salazar *et al.*, 2020). Additionally, there are bacteria that interact with orchid roots (Ramos *et al.*, 2007). These bacteria fulfil key functional roles, such as nitrogen fixation and the production of indole-3-acetic acid (IAA, an auxin), which can stimulate various physiological processes in plants, including cell division, differentiation of plant cells and tissues, as well as xylem and root development (Tsavkelova *et al.*, 2007; Etesami & Glick, 2024). There are reports demonstrating that mycorrhizal fungi and bacteria act

synergistically, stimulating plant growth through mechanisms that facilitate nutrient acquisition and pathogen inhibition (Artursson *et al.*, 2006; Sarabia *et al.*, 2010; Zhao *et al.*, 2024).

Microorganisms that interact with plant roots are fundamental for species survival and ecosystem stability (Varela & Trejo, 2001). In orchids, the isolation, identification, and evaluation of fungi and bacteria associated with their roots are key to understanding their role in plant development and ensuring long-term species conservation (Durán *et al.*, 2007).

MATERIALS AND METHODS

Sample collection

Fifty-two root samples were collected from five species of epiphytic orchids in two localities *Masdevallia rosea*, *Cyrtorchilum myanthum*, and *Cyrtorchilum flexuosum* were obtained in El Tiro (Loja-Zamora-Chinchi Road), while *Epidendrum rhopalostele* and *Stelis superbiens* were collected in San Francisco (Fig. 1).

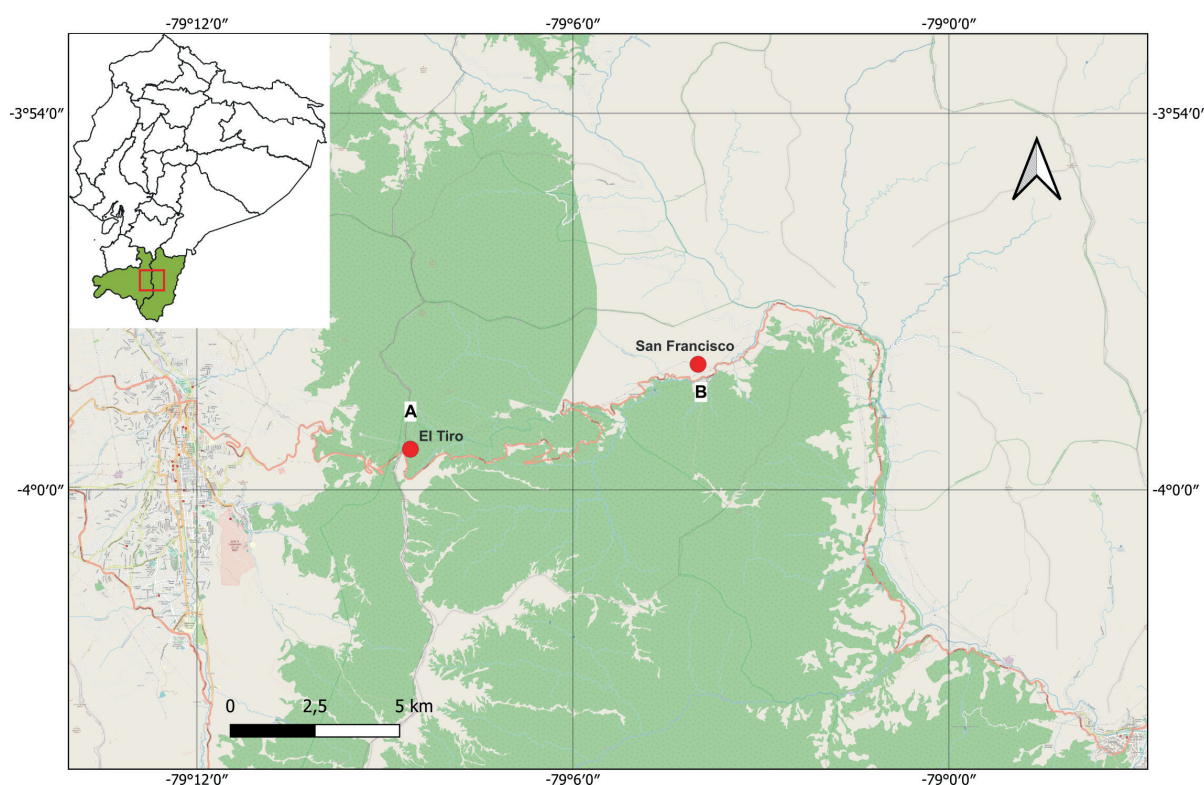


Fig. 1. Root collection sites of five epiphytic orchid species in Loja and Zamora-Chinchi, Ecuador. A) El Tiro: *M. rosea*, *C. myanthum*, and *C. flexuosum*. B) San Francisco: *E. rhopalostele* and *S. superbiens*. The scale bar represents 0, 2.5, and 5 km.

Fig. 1. Localidades de recolección de raíces de cinco especies de orquídeas epífitas en Loja y Zamora-Chinchi, Ecuador. A) El Tiro: *M. rosea*, *C. myanthum* y *C. flexuosum*. B) San Francisco: *E. rhopalostele* y *S. superbiens*. La barra de escala indica 0, 2,5 y 5 km.

The number of samples collected per species depended on the availability of individuals at each sampling site. Each sample consisted of three to five roots, approximately 3 cm in length, extracted from a single individual. The number of roots collected from each plant varied according to root availability and was limited to minimize damage and avoid compromising plant survival. To preserve the viability of microorganisms to be isolated, the samples were wrapped in aluminium foil and processed in the laboratory on the same day of collection.

Root disinfection

To verify the presence of pelotons, structures formed by hyphae coiled within the cells of the root's cortical tissue, thin root sections (2 to 5 mm) were prepared using a sterile scalpel. These sections were stained with 0.05% methylene blue and examined under a microscope. When the presence of pelotons was confirmed, the roots were subjected to disinfection. First, they were washed with water and neutral soap to remove soil debris. Then, they were submerged in 70% ethanol for 30 seconds and subsequently in 20% sodium hypochlorite for 3 minutes. Afterwards, they were rinsed three times with sterile water for 1 minute each time. Finally, the velamen (the outer layer of the root) was removed using a sterile scalpel and a dissecting microscope.

Isolation of fungi and bacteria

Transverse cuts were made using a sterile scalpel on each root segment, and six sections were individually transferred with sterile forceps to Petri dishes with different culture media. For fungal isolation, FIM (Fungal Isolation Medium) and PDA (Potato Dextrose Agar) were selected because they provide suitable nutrients for fungal growth and have previously been used for the isolation of fungi associated with orchid roots (Tian *et al.*, 2022; Arifin *et al.*, 2021). For bacterial isolation, TSA (Tryptic Soy Agar) and Czapek-Dox Agar were used because they support the growth of a wide range of cultivable bacteria associated with plant tissues and roots (Tsavkelova *et al.*, 2007). All cultures were incubated at 27°C for 24 to 72 hours. When fungi or bacteria reached a growth of at least 1 cm in diameter, subcultures were performed on the same medium to obtain pure cultures. This process was repeated until pure isolates were obtained.

Molecular characterization of isolated microorganisms

For fungi, DNA was extracted from pure cultures using the PureLink Plant Total DNA Purification Kit (Invitrogen), following the manufacturer's protocol. Approximately 100 mg of mycelium was macerated prior to DNA extraction. The ITS1–5.8S–ITS2 region of ribosomal DNA was amplified by PCR using primers ITS1 (5'-TCC GTA GGT GAA CCT GCG-3') and TW14 (5'-GCT ATC AGG CTG GAA ACT TC-3') (White *et al.*, 1990).

In the case of bacteria, Gram staining was first performed to differentiate them into Gram-positive and Gram-negative. Subsequently, they were cultured in liquid TSA and Czapek media under constant agitation (100 rpm) at 27°C for 24 to 72 hours. DNA was then extracted using the Wizard® Genomic DNA Purification Kit (Promega), following the manufacturer's protocol, which includes an initial lysis step that differs depending on whether the isolate is Gram-positive or Gram-negative; no further modifications were made to the manufacturer's protocol. Then, the 16S ribosomal RNA gene region was amplified by PCR, with 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-GGTTACCTTGTTACGACTT-3') primers (Weisburg *et al.*, 1991).

PCR products were verified by gel electrophoresis. Subsequently, they were purified using the Wizard SV Gel and PCR Clean-Up System (Promega). The obtained sequences were sent to MACROGEN (Seoul, South Korea) for sequencing. Sequences were edited with CodonCode Aligner software (v4.2.4) and compared with GenBank databases using the BLAST service (<https://blast.ncbi.nlm.gov>). All the sequences obtained in this study are available in GenBank (accessions: PX238495–PX238508, PX238510–PX238512, PX238682–PX238683, PX238593–PX238596).

Fungi preservation

Pure fungal cultures were replicated in eight test tubes for preservation, using mineral oil and sterile water as protective coverings. Solid media such as Malt Extract Agar (MEA) and Oatmeal Agar (OMA) were employed. For each strain, two tubes with MEA and two with OAT were used. A fraction of the mycelium was inoculated into each tube. Once the fungi had covered approximately 70 to 80% of the agar surface, the culture was covered with mineral oil or sterile water, covering approximately three-quarters of the medium. The tubes were stored at 4°C.

Bacteria cryopreservation

Pure bacterial cultures, previously grown in liquid medium for 24 hours, were preserved in cryotubes containing Trypticase Soy Broth (TSB) and glycerol as a cryoprotectant, in a 70%-30% ratio with a final volume of 1.6 mL. Four replicates were prepared for each bacterial culture. After inoculating the bacteria, the cryotubes were incubated at room temperature for 24 hours, observing bacterial growth at the bottom of the tube. Subsequently, they were stored at -80°C for preservation.

RESULTS AND DISCUSSION

Mycorrhizal pelotons were observed in 50 of the 52 examined samples. Colonization was absent in two samples: one from *C. myanthum* and another from *C. flexuosum*. Colonization was concentrated in root sectors in direct contact with the substrate, while aerial roots showed no evidence of colonization. From cortical discs plated on culture media, 17 fungal isolates were recovered, with the highest yield on FIM medium. Fungal isolation success varied among orchid species: *C. flexuosum* yielded the highest number of isolates (5), followed by *S. superbiens* (4) and *C. myanthum* (4), while *E. rhopalostele* yielded 3 isolates and *M. rosea* only 1 isolate. El Tiro (*M. rosea*, *C. myanthum*, *C. flexuosum*) yielded a higher total number of fungal isolates (10) than San Francisco (*E. rhopalostele*, *S. superbiens*; 7 isolates). Of these, 16 isolates belonged to the phylum Ascomycota (families Dermateaceae, Aspergillaceae, Nectriaceae, and Herpotrichiellaceae), and one isolate, belonging to the family Polyporaceae, was assigned to the phylum Basidiomycota. At the genus level, *Pezicula* was the most abundant (11 isolates), followed by *Neonectria* (two isolates) and *Aspergillus* (two isolates), with single isolates of *Trametes* and *Cadophora* (Fig. 2).

Six bacterial isolates were identified as *Pseudomonas* (four isolates; Pseudomonadaceae), *Paraburkholderia* (one isolate; Burkholderiaceae), and *Variovorax* (one isolate; Comamonadaceae) (Fig. 3). Bacterial isolation success varied among orchid species. *C. myanthum* and *E. rhopalostele* yielded two bacterial isolates each, whereas *C. flexuosum* and *S. superbiens* yielded one isolate each. No bacterial isolates were recovered from *M. rosea*. The total number of bacterial isolates was the same in both localities, with three isolates recovered from El Tiro and three from San Francisco. *Pseudomonas* was the most frequently recovered bacterial genus, accounting for four of the six isolates obtained (Fig. 3).

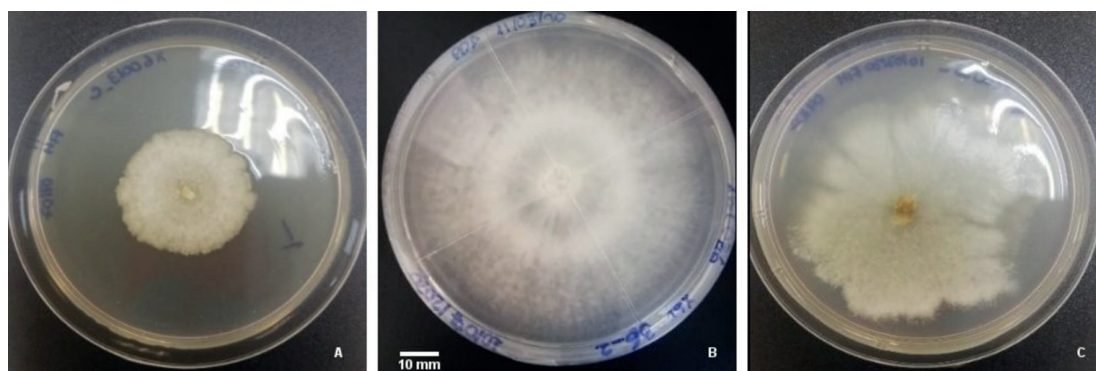


Fig. 2. Fungi isolated from the roots of epiphytic orchids. Colonies corresponding to A) *Pezicula* sp. B) *Aspergillus* sp. grown on FIM medium. C) *Trametes* sp. grown on PDA medium. Scale bar = 10 mm.

Fig. 2. Hongos aislados de raíces de orquídeas epífitas. Colonias correspondientes a: A) *Pezicula* sp. B) *Aspergillus* sp. cultivadas en medio FIM. C) *Trametes* sp. cultivada en medio PDA. Barra de escala = 10 mm.

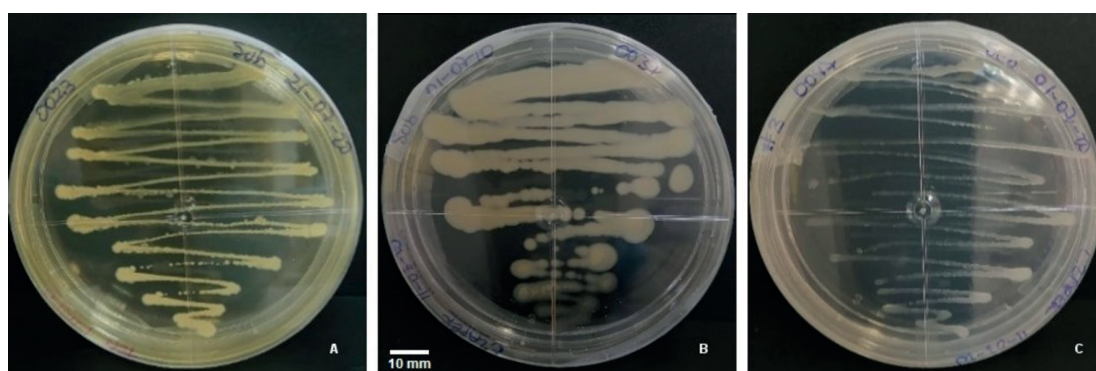


Fig. 3. Bacteria isolated from roots of epiphytic orchids. Colonies corresponding to A) *Paraburkholderia* sp. grown on TSA medium. B) *Pseudomonas* sp. grown on Czapek medium. C) *Variovorax* sp. grown on Czapek medium. Scale bar = 10 mm.

Fig. 3. Bacterias aisladas de raíces de orquídeas epífitas. Colonias correspondientes a: A) *Paraburkholderia* sp. cultivada en medio TSA. B) *Pseudomonas* sp. cultivada en medio Czapek. C) *Variovorax* sp. cultivada en medio Czapek. Barra de escala = 10 mm.

Pezicula is commonly found as an endophyte in the branches and roots of plants in temperate regions. This fungus produces various secondary metabolites with antifungal activity, such as echinocandins, which contribute to the defence against pathogenic fungi and protect its host plant (Chen *et al.*, 2016; Yue *et al.*, 2018; Kochkina *et al.*, 2022). *Trametes*, recovered from *C. myanthum*, is widely recognized as an orchid-associated endophyte; previous work in nearby areas has also documented *Trametes* in roots of related orchid groups, reinforcing its role in orchid–fungus symbioses (Cueva, 2014; Salazar *et al.*, 2020). Members of *Neonectria* are known agents of cankers and root rot in trees and often act as secondary pathogens exploiting natural or artificial wounds.

Notably, *Neonectria punicea* exhibits host- and environment-dependent virulence; its asymptomatic behaviour in some hosts suggests that impacts on orchids may be context specific (Chaverri *et al.*, 2011; Malcolm *et al.*, 2013; Salgado & Crouch, 2019; Karadžić *et al.*, 2020). *Aspergillus flavus* has been associated with the production of aflatoxins, compounds that could play a defensive role by protecting orchids from herbivores and promoting the orchid's survival (Salazar, 2018). More broadly, endophytes can supply essential nutrients during germination and support regeneration and establishment of new plants, underscoring their ecological importance in orchid systems (Salazar, 2018; Selosse *et al.*, 2022).

The bacterial isolates include plant growth-promoting rhizobacteria (PGPR). *Pseudomonas* has been documented to enhance plant development via indole-3-acetic acid (IAA) production, nitrogen fixation, nutrient solubilization, and biocontrol of soilborne phytopathogens (Tsavkelova *et al.*, 2007). In orchids, some strains have improved seed germination and *in vitro* propagation by promoting cell division and root elongation (Tsavkelova *et al.*, 2007; Soto, 2018; Saikia & Thakur, 2024). *Variovorax*, another PGPR with broad metabolic versatility, has helped certain crops tolerate drought stress and is known to produce siderophores and nutrient-mobilizing enzymes, suggesting promise as biofertilizers under adverse conditions and potential applicability in orchids (Sun *et al.*, 2018; Natsagdorj *et al.*, 2019; Kim *et al.*, 2020). *Paraburkholderia* is a commonly reported endophyte associated with plants, recognized for its biocontrol capabilities (Pangastuti *et al.*, 2023), and several studies highlight its ability to promote plant growth and improve plants' tolerance to stress. This is due to its production of volatile organic compounds, which influence plant metabolism and protect the plant against various pathogens (Esmaeel *et al.*, 2018). It can also break down phenolic compounds, tannins, and hydrocarbons, making it useful in soil bioremediation (Herpell *et al.*, 2021).

CONCLUSIONS

This study identified fungi and bacteria associated with the roots of five species of epiphytic orchids. The fungi recovered belonged mainly to the phyla Ascomycota and Basidiomycota, while the bacteria were grouped into the families Pseudomonadaceae, Burkholderiaceae, and Comamonadaceae. *Pezicula* was the most abundant fungal genus identified, while *Pseudomonas* was the predominant bacterial genus. The results contribute to our understanding of the microbial diversity associated with the roots of epiphytic orchids and provide information on the taxa present in the analyzed species.

CONFLICTS OF INTEREST

The authors declared that they have no conflict of interest.

REFERENCES

- Alghamdi, S. A. (2019). Influence of mycorrhizal fungi on seed germination and growth in terrestrial and epiphytic orchids. *Saudi Journal of Biological Sciences* 26 (3): 495-502. <https://doi.org/10.1016/j.sjbs.2017.10.021>
- Arifin, A. R., May, T. W. & Linde, C. C. (2021). New species of *Tulasnella* associated with Australian terrestrial orchids in the Cryptostylidinae and Drakaeinae. *Mycologia* 113: 212-230. <https://doi.org/10.1080/00275514.2020.1813473>
- Artursson, V., Finlay, R. D., & Jansson, J. K. (2006). Interactions between arbuscular mycorrhizal fungi and bacteria and their potential for stimulating plant growth. *Environmental Microbiology* 8 (1): 1-10. <https://doi.org/10.1111/j.1462-2920.2005.00942.x>
- Chaverri, P., Salgado, C., Hirooka, Y., Rossman, A. Y. & Samuels, G. J. (2011). Delimitation of *Neonectria* and *Cylindrocarpon* (Nectriaceae, Hypocreales, Ascomycota) and related genera with *Cylindrocarpon*-like anamorphs. *Studies in Mycology* 68: 57-78. <https://doi.org/10.3114/sim.2011.68.03>
- Chen, C., Verkley, G. J. M., Sun, G., Groenewald, J. Z. & Crous, P. W. (2016). Redefining common endophytes and plant pathogens in *Neofabraea*, *Pezicula*, and related genera. *Fungal Biology* 120 (11): 1291-1322. <https://doi.org/10.1016/j.funbio.2015.09.013>
- Cueva, A. (2014). Caracterización molecular de hongos micorrízicos aislados a partir de cuatro especies de orquídeas epífitas, en dos pisos altitudinales de bosque montano (Undergraduate thesis). Universidad Técnica Particular de Loja, Ecuador. <http://dspace.utpl.edu.ec/handle/123456789/10242>
- Durán, C., Rivero, M. & Seemann, P. (2007). Identification of endomycorrhizae in the native *Gavilea araucana* (Phil.) Correa. *Agro Sur* 35 (2): 67-69. <https://doi.org/10.4206/agrosur.2007.v35n2-32>
- Esmaeel, Q., Miotto, L., Rondeau, M., Leclère, V., Clément, C., Jacquard, C., Sanchez, L. & Barka, E. A. (2018). *Paraburkholderia phytofirmans* PsJN-plants interaction: From perception to the induced mechanisms. *Frontiers in Microbiology* 9. <https://doi.org/10.3389/fmicb.2018.02093>
- Etesami, H. & Glick, B. R. (2024). Bacterial indole-3-acetic acid: A key regulator for plant growth, plant-microbe interactions, and agricultural adaptive resilience. *Microbiological Research* 281. <https://doi.org/10.1016/j.micres.2024.127602>
- Herpell, J. B., Vanwijnsberghe, S., Peeters, C., Schindler, F., Fragner, L., Bejtović, M., Weckwerth, W. & Vandamme, P. (2021). *Paraburkholderia*

- dioscoreae* sp. Nov., a novel plant associated growth promotor. *International Journal of Systematic and Evolutionary Microbiology* 71 (9). <https://doi.org/10.1099/ijsem.0.004969>
- Karadžić, D., Stanivuković, Z., Milanović, S., Sikora, K., Radulović, Z., Račko, V., Kardošová, M., Đurković, J. & Milenković, I. (2020). Development of *Neonectria punicea* pathogenic symptoms in juvenile *Fraxinus excelsior* trees. *Frontiers in Plant Science* 11. <https://doi.org/10.3389/fpls.2020.592260>
- Kim, Y. N., Khan, M. A., Kang, S. M., Hamayun, M. & Lee, I. J. (2020). Enhancement of drought-stress tolerance of *Brassica oleracea* var. *italica* L. by newly isolated *Variovorax* sp. YNA59. *Journal of Microbiology and Biotechnology* 30 (10): 1500-1509. <https://doi.org/10.4014/JMB.2006.06010>
- Kochkina, G. A., Ivanushkina, N. E., Pinchuk, I. P. & Ozerskaya, S. M. (2022). Endophytic Fungi *Pezicula radicicola* in the root nodules of actinorhizal Plants. *Microbiology (Russian Federation)* 91 (6): 750-756. <https://doi.org/10.1134/S0026261722601622>
- Malcolm, G. M., Kulda, G. A., Gugino, B. K. & Jiménez-Gasco, M. D. M. (2013). Hidden host plant associations of soilborne fungal pathogens: An ecological perspective. *Phytopathology* 103 (6): 538-544. <https://doi.org/10.1094/PHYTO-08-12-0192-LE>
- Natsagdorj, O., Sakamoto, H., Santiago, D. M. O., Santiago, C. D., Orikasa, Y., Okazaki, K., Ikeda, S. & Ohwada, T. (2019). *Variovorax* sp. Has an optimum cell density to fully function as a plant growth promoter. *Microorganisms* 7 (3). <https://doi.org/10.3390/microorganisms7030082>
- Novotná, A. & Suárez, J. P. (2018). Molecular detection of bacteria associated with *Serendipita* sp., a mycorrhizal fungus from the orchid *Stanhopea connata* Klotzsch in southern Ecuador. *Botany Letters* 165 (2): 307-313. <https://doi.org/10.1080/23818107.2018.1436087>
- Pangastuti, A., Pitoyo, A., Susilowati, A., Meisari, R., Yuliana, I., Aulia, K., Puspitasari, L. P., Rusiani & Prasajo, H. (2023). Diversity of root bacterial community associated with seven orchid species from Mount Merbabu National Park, Central Java, Indonesia. *Biodiversitas* 24 (10): 5676-5684. <https://doi.org/10.13057/biodiv/d241050>
- Ramos, E., Salgado, T. & Hernández, A. (2007). Estudio de Bacterias asociadas a orquídeas (Orchidaceae). *Lankesteriana International Journal on Orchidology* 7: 322-325. <http://www.redalyc.org/articulo.oa?id=44339813067>
- Rasmussen, H. N. & Rasmussen, F. N. (2018). The epiphytic habitat on a living host: reflections on the orchid-tree relationship. *Botanical Journal of the Linnean Society* 186: 456-472. <https://academic.oup.com/botlinnean/articleabstract/186/4/456/4920859>
- Riofrío, M. L., Cruz, D., Torres, E., de La Cruz, M., Iriondo, J. M. & Suárez, J. P. (2013). Mycorrhizal preferences and fine spatial structure of the

- epiphytic orchid *Epidendrum rhopalostele*. *American Journal of Botany* 100 (12): 2339-2348. <https://doi.org/10.3732/ajb.1300069>
- Saikia, J. & Thakur, D. (2024). A review on endophytic bacteria of orchids: functional roles toward synthesis of bioactive metabolites for plant growth promotion and disease biocontrol. *Planta* 260 (70). <https://doi.org/10.1007/s00425-024-04501-3>
- Salazar, S. (2018). Aislamiento e identificación de cepas fúngicas de *Stanhopea tigrina* productoras de giberelinas con efecto benéfico para la orquídea. (Doctoral dissertation). Benemérita Universidad Autónoma de Puebla, México. <https://hdl.handle.net/20.500.12371/7956>
- Salazar, J., Pomavilla, M., Pollard, A., Chicca, E. & Peña, D. (2020). Endophytic fungi associated with roots of epiphytic orchids in two Andean forests in southern Ecuador and their role in germination. *Lankesteriana* 20 (1): 37-47. <https://doi.org/10.15517/LANK.V20I1.41157>
- Salgado, C. & Crouch, J. A. (2019). Genome resources for the stem and bark canker pathogens *Corinectria fuckeliana*, *Neonectria hederæ* and *N. punicea*. *Plant Disease* 103 (3): 389-391. <https://doi.org/10.1094/PDIS-05-18-0904-A>
- Sarabia, M., Madrigal, R. & Martínez Miguel. (2010). Plantas, hongos micorrízicos y bacterias: su compleja red de interacciones. *Biológicas* 12: 65-71.
- Selosse, M., Petrolli, R., Mujica, M. I., Laurent, L., Perez, B., Figura, T., Bourceret, A., Jacquemyn, H., Li, T., Gao, J., Minasiewicz, J. & Martos, F. (2022). The Waiting Room Hypothesis revisited by orchids: Were orchid mycorrhizal fungi recruited among root endophytes? *Annals of Botany* 129 (3): 259-270. <https://doi.org/10.1093/aob/mcab134>
- Soto, J. (2018). Biochemical and molecular characterization of bacteria associated with nodules from four legumes in the province of Santa Elena, Ecuador. *Ciencia Ergo Sum* 25 (1). <http://cienciaergosum.uaemex.mx/article/view/9173>
- Sun, S.-L., Yang, W.-L., Fang, W.-W., Zhao, Y.-X., Guo, L. & Dai, Y.-J. (2018). The plant growth-promoting rhizobacterium *Variovorax boronicumulans* CGMCC 4969 regulates the level of Indole-3-Acetic acid synthesized from Indole-3-acetonitrile. *Applied and Environmental Microbiology* 84 (16). <https://doi.org/10.1128/aem.00298-18>
- Tian, F., Liao, X.-F., Wang, L.-H., Bai, X.-X., Yang, Y.-B., Luo, Z.-Q. & Yan, F.-X. (2022). Isolation and identification of beneficial orchid mycorrhizal fungi in *Paphiopedilum barbigerum* (Orchidaceae). *Plant Signaling & Behavior* 17: e2005882. <https://doi.org/10.1080/15592324.2021.2005882>
- Tsavkelova, E., Cherdyntseva, T., Botina, S. & Netrusov, A. (2007). Bacteria associated with orchid roots and microbial production of auxin. *Microbiological Research* 162 (1): 69-76. <https://doi.org/10.1016/j.micres.2006.07.014>

- Varela, L. & Trejo, D. (2001). Los hongos micorrizógenos arbusculares como componentes de la biodiversidad del suelo en México. *Acta Zoológica Mexicana (n.s.)*: 39-51. <https://doi.org/10.21829/azm.2001.8401845>
- Weisburg, W. G., Barns, S. M., Pelletier, D. A. & Lane, D. J. (1991). 16S ribosomal DNA amplification for phylogenetic study. *Journal of Bacteriology* 173 (2): 697-703. <https://doi.org/10.1128/jb.173.2.697703.1991>
- White, T., Bruns, T., Lee, S. & Taylor, J. (1990). Amplification and Direct Sequencing of Fungal Ribosomal RNA Genes for Phylogenetics. En M. A. Innis, D. H. Gelfand, J. J. Sninsky y T. J. White (Eds.), *PCR Protocols: A Guide to Methods and Applications* (pp. 315-322). Academic Press.
- Yue, Q., Li, Y., Chen, L., Zhang, X., Liu, X., An, Z. & Bills, G. (2018). Genomics-driven discovery of a novel self-resistance mechanism in the echinocandin-producing fungus *Pezicula radicola*. *Environmental Microbiology* 20 (9): 3154-3167. <https://doi.org/10.1111/1462-2920.14089>
- Zhao, Z., Yang, L., Wang, Y., Qian, X., Ding, G., Jacquemyn, H. & Xing, X. (2024). Shifts in bacterial community composition during symbiotic seed germination of a terrestrial orchid and effects on protocorm development. *Microbiology Spectrum* 12 (12). <https://doi.org/10.1128/spectrum.02185-24>