

From hidden allies to precision symbionts: unleashing endophytes for sustainable agroecosystems

Review Published: 30 March 2026

Volume 42, article number 172 (2026) [Cite this article](#)



World Journal of Microbiology and Biotechnology

[Aims and scope](#) →

[Submit manuscript](#) →

[Vivek Kumar](#)  & [Chandra S. Nautiyal](#)

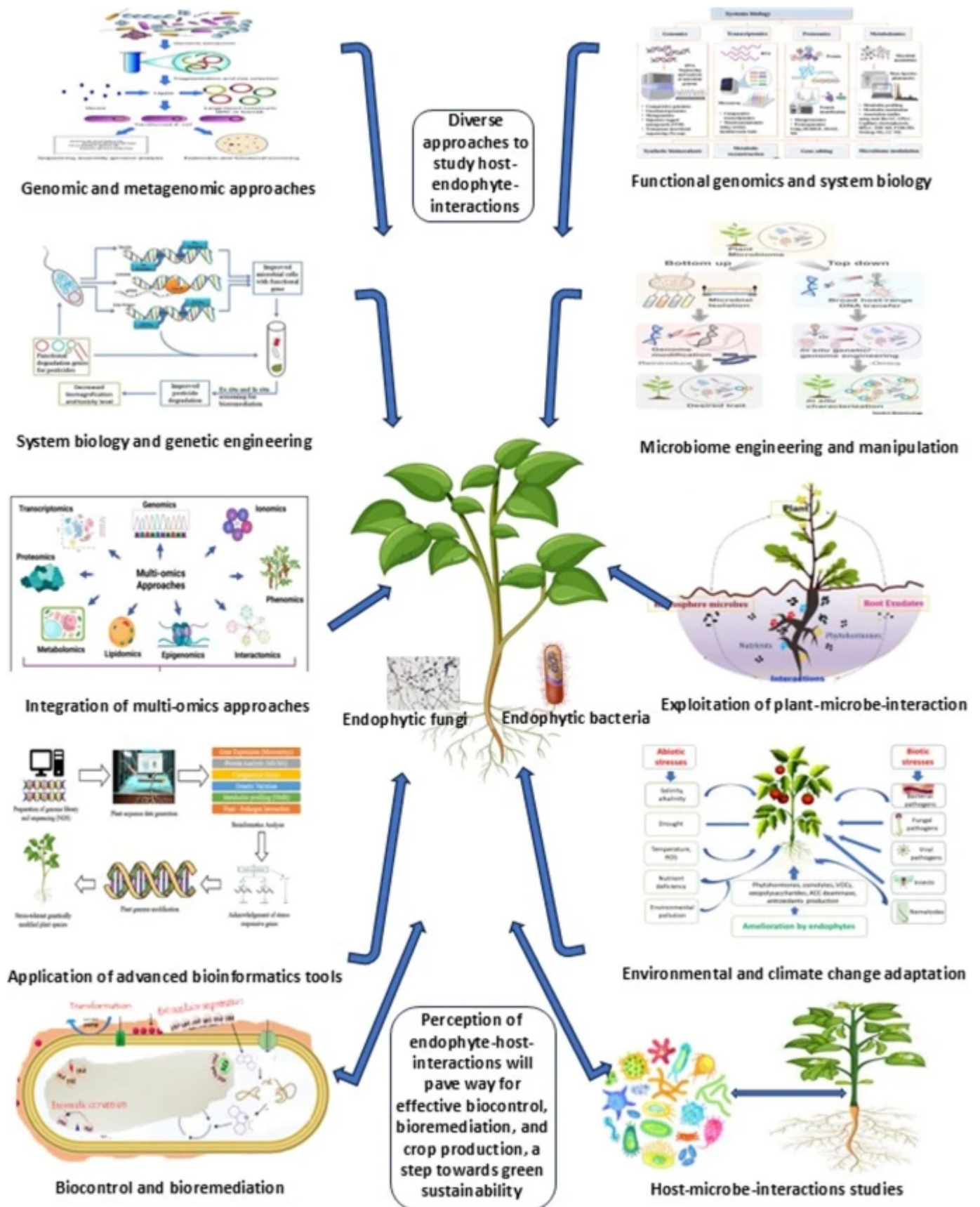
 320 Accesses  1 Citation [Explore all metrics](#) →

Abstract

Plants, together with their resident endophytes, constitute a functional holobiont whose integrated traits enable plant growth, stress resilience, disease resistance, and ecosystem remediation. This review discusses advances across ten converging domains that are reshaping research and applications of endophytes, including the following: genomics and metagenomics that identify core genes for colonization, nitrogen fixation, hormone modulation, and stress adaptation; functional genomics and systems biology deciphering host-microbe signaling networks; synthetic biology and CRISPR-based tools for the rational improvement of beneficial traits; microbiome engineering aimed at designing and stabilizing endophytic consortia; multi-omics integration connecting genomic, transcriptomic, proteomic, and metabolomic layers during colonization and under stress; environmental and climatic factors shaping endosphere diversity; bioinformatic platforms predicting biosynthetic gene clusters, secretomes, and metabolic potential; and agricultural and environmental applications in biocontrol and bioremediation. Remaining

challenges are the uncultured majority of endophytes, context-dependent transitions between mutualism and pathogenicity, limited field validation, and evolving biosafety frameworks. Thus, the forward framework developed here emphasizes the importance of standard strain benchmarking, causal multi-omics workflows, synthetic community design, and multisite agronomic trials. For their part, endophytes form a scalable, climate-resilient platform for the dual purposes of sustainable agriculture and environmental restoration. In the process, endophytes are emerging as a tractable and scalable foundation for climate-resilient biotechnology, wherein molecular innovation connects with field-level sustainability.

Graphical Abstract



 This is a preview of subscription content, [log in via an institution](#)  to check access.

Access this article

[Log in via an institution](#)

Subscribe and save

✓ Springer+

from €37.37 /Month

Starting from 10 chapters or articles per month

Access and download chapters and articles from more than 300k books and 2,500 journals

Cancel anytime

[View plans](#) →

Buy Now

[Buy article PDF 39,95 €](#)

Price includes VAT (India)

Instant access to the full article PDF.

[Institutional subscriptions](#) →

Explore related subjects

Discover the latest articles, books and news in related subjects, suggested using machine learning.

[Arbuscular mycorrhiza](#)

[Horticulture](#)

[Plant Science](#)

[Plant Symbiosis](#)

[Plant Biotechnology](#)[Rhizobial symbiosis](#)[Plant-Microbiome Interactions and Community Dynamics](#)

Data availability

Data sharing does not apply to this article as no datasets were generated or analyzed during the current study.

References

Afridi MS, Kumar A, Javed MA, Dubey A, de Meiros FHV, Santoyo G (2024) Harnessing root exudates for plant microbiome engineering and stress resistance in plants. Microbiol Res 279:127564. <https://doi.org/10.1016/j.micres.2023.127564>

Albanese D, Fontana P, De Filippo C, Cavalieri D, Donati C (2015) MICCA: a complete and accurate software for taxonomic profiling of metagenomic data. Sci Rep 5:9743. <https://doi.org/10.1038/srep09743>

Aleynova OA, Kiselev KV (2023) Interaction of plants and endophytic microorganisms: molecular aspects, biological functions, community composition, and practical applications. Plants (Basel) 12(4):714. <https://doi.org/10.3390/plants12040714>

Alsaedi ZS, Ashy RA, Shami AY, Majeed MA, Alswat AM, Baz L, Baeshen MN, Jalal RS (2022) Metagenomic study of the communities of bacterial endophytes in the desert plant *Senna italica* and their role in abiotic stress resistance in the plant. Braz J Biol 82:e267584. <https://doi.org/10.1590/1519-6984.267584>

Álvarez-Loayza P, White JF Jr, Torres MS, Balslev H, Kristiansen T, Svenning JC, Gil N (2011) Light converts endosymbiotic fungus to pathogen, influencing seedling survival

and niche-space filling of a common tropical tree, *Iriartea deltoidea*. PLoS One 6(1):e16386. <https://doi.org/10.1371/journal.pone.0016386>

Anand U, Pal T, Yadav N, Singh VK, Tripathi V, Choudhary KK, Shukla AK, Sunita K, Kumar A, Bontempi E, Ma Y, Kolton M, Singh AK (2023) Current scenario and future prospects of endophytic microbes: promising candidates for abiotic and biotic stress management for agricultural and environmental sustainability. Microb Ecol 86(3):1455–1486. <https://doi.org/10.1007/s00248-023-02190-1>

Aravinthraju K, Shanthi M, Murugan M, Srinivasan R, Maxwell LA, Manikanda Boopathi N, Anandham R (2024) Endophytic entomopathogenic fungi: their role in enhancing plant resistance, managing insect pests, and synergy with management routines. J Fungi 10(12):865. <https://doi.org/10.3390/jof10120865>

Babalola OO, Adeleke BS, Ayangbenro AS (2021) Draft genome sequencing of *Stenotrophomonas indicatrix* BOVIS40 and *Stenotrophomonas maltophilia* JVB5, two strains with identifiable genes involved in plant growth promotion. Microbiol Resour Announc 10(28):e0048221. <https://doi.org/10.1128/MRA.00482-21>

Baetsen-Young A, Man Wai C, VanBuren R, Day B (2020) *Fusarium virguliforme* transcriptional plasticity is revealed by host colonization of maize versus soybean. Plant Cell 32(2):336–351. <https://doi.org/10.1105/tpc.19.00697>.

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA (2012) SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19(5):455–477. <https://doi.org/10.1089/cmb.2012.0021>

Battu L, Reddy MM, Goud BS, Ulaganathan K, Kandasamy U (2017) Genome inside genome: NGS based identification and assembly of endophytic *Spingopyxis granuli* and

Pseudomonas aeruginosa genomes from rice genomic reads. *Genomics* 109:141–146.

<https://doi.org/10.1016/j.ygeno.2017.02.002>

Beghini F, McIver LJ, Blanco-Míguez A, Dubois L, Asnicar F, Maharjan S, Mailyan A, Manghi P, Scholz M, Thomas AM, Valles-Colome M, Weingart G, Zhang Y, Zolfo M, Huttenhower C, Franzosa EA, Segata N (2021) Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. *Elife* 10:e65088. <https://doi.org/10.7554/eLife.65088>

Bhatia A, Pruthi P, Chakraborty I, Shukla N, Narayan J (2025) GetENRICH: A tool for the gene and pathway enrichment analysis of non-model organisms. *Bioinform Adv* 5(1):vbaf023. <https://doi.org/10.1093/bioadv/vbaf023>

Blanco-Míguez A, Beghini F, McIver CF, Thompson LJ, Zolfo KN, Manghi M, Dubois P, Huang L, Thomas KD, Nickols AM, Piccinno WA, Piperni G, Valles-Colomer E, Punčochář M, Tett M, Giordano A, Davies F, Wolf R, Berry J, Spector S, Franzosa TD, Pasolli EA, Asnicar E, Huttenhower F, Segata C N (2023) Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlAn 4. *Nat Biotechnol* 41(11):1633–1644. <https://doi.org/10.1038/s41587-023-01688-w>

Blin K, Shaw S, Kloosterman AM, Charlop-Powers Z, van Wezel GP, Medema MH, Weber T (2021) antiSMASH 6.0: improving cluster detection and comparison capabilities. *Nucleic Acids Res* 49(W1):W29–W35. <https://doi.org/10.1093/nar/gkab335>

Bonab BF, Roveshti AA, Abbasi A (2022) Changes in antioxidant enzymes of barley (*Hordeum vulgare* L.) using the endophytic fungus *Piriformospora indica* and the bacterium *Azospirillum* spp. under drought stress. *Poljoprivreda i Sumarstvo* 68(1):261–283. <https://doi.org/10.17707/AgricultForest.68.1.17>

Carmona-Hernandez S, Reyes-Pérez JJ, Chiquito-Contreras RG, Rincon-Enriquez G, Cerdan-Cabrera CR, Hernandez-Montie LG (2020) Biocontrol of postharvest fruit fungal

diseases by bacterial antagonists: a review. *Agronomy* 9:121.

<https://doi.org/10.3390/agronomy9030121>

Carrión VJ, Perez-Jaramillo J, Cordovez V, Tracanna V, de Hollanr M, Ruiz-Buck D, Mendes LW, van Ijcken WFJ, Gomez-Exposito R, Elsayed SS, Mohanraju P, Arifah A, van der Oost J, Paulson JN, Mendes R, van Wezel GP, Medema MH, Raaijmakers JM (2019) Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. *Science* 366(6465):606–612. <https://doi.org/10.1126/science.aaw9285>

Chaudhary R, Kumar V, Gupta S, Naik B, Prasad R, Mishra S, Saris PEJ, Kumar V (2023) Finger millet (*Eleusine coracana*) plant-endophyte dynamics: plant growth, nutrient uptake, and zinc biofortification. *Microorganisms* 11:973.

<https://doi.org/10.3390/microorganisms11040973>

Chauhan P, Sharma N, Tapwal A, Kumar A, Verma GS, Meena M, Seth CS, Swapnil P (2023) Soil microbiome: diversity, benefits and interactions with plants. *Sustainability* 15(19):14643. <https://doi.org/10.3390/su151914643>

Chavda VR, Bhatt SB, Umaretiya VR, Gajera HP, Padhiyar SM, Kandoliya UK, Parakhia MV (2025) Characterization and metabolomic profiling of endophytic bacteria isolated from *Moringa oleifera* and *Piper betel* leaves. *Sci Rep* 15:632.

<https://doi.org/10.1038/s41598-024-84840-z>

Chen XL, Sun MC, Chong SL, Si JP, Wu LS (2022) Transcriptomic and metabolomic approaches deepen our knowledge of plant-endophyte interactions. *Front Plant Sci* 12:700200. <https://doi.org/10.3389/fpls.2021.700200>

Chen P, Yu Q, Wang C, Montoya L, West PT, Xu L, Varoquaux N, Cole B, Hixson KK, Kim YM, Liu L, Zhang B, Zhang J, Li B, Purdom E, Vogel J, Jansson C, Hutmacher RB, Dahlberg JA, Coleman-Derr D, Lemaux PG, Taylor JW, Gao C (2025a) Holo-omics disentangle drought response and biotic interactions among plant, endophyte and pathogen. *New Phytol* 246(6):2702–2717. <https://doi.org/10.1111/nph.70155>

Chen Y, Chen L, Lun ATL, Baldoni PL, Smyth GK (2025b) edgeR v4: powerful differential analysis of sequencing data with expanded functionality and improved support for small counts and larger datasets. *Nucleic Acids Res* 53(2):gkaf018. <https://doi.org/10.1093/nar/gkaf018>

del Carmen Orozco-Mosqueda M, Santoyo G (2021) Plant-microbial endophytes interactions: scrutinizing their beneficial mechanisms from genomic explorations. *Curr Plant Biol* 25:100189. <https://doi.org/10.1016/j.cpb.2020.100189>

Digra S, Nonzom S (2023) An insight into endophytic antimicrobial compounds: an updated analysis. *Plant Biotechnol Rep* 14:1–31. <https://doi.org/10.1007/s11816-023-00824-x>

Dogan G, Taskin B (2021) Hydrolytic enzymes producing bacterial endophytes of some poaceae plants. *Pol J Microbiol* 70(3):297–304. <https://doi.org/10.33073/pjm-2021-026>

Eaton CJ, Cox MP, Scott B (2011) What triggers grass endophytes to switch from mutualism to pathogenism? *Plant Sci* 180(2):190–195. <https://doi.org/10.1016/j.plantsci.2010.10.002>

Eichfeld R, Mahdi LK, Quattro CD, Armbruster L, Endeshaw AB, Miyauchi S, Hellmann MJ, Cord-Landwehr S, Peterson D, Singan V, Lail K, Savage E, Ng V, Grigoriev IV, Langen G, Moerschbacher BM, Zuccaro A (2024) Transcriptomics reveal a mechanism of niche defense: two beneficial root endophytes deploy an antimicrobial GH18-CBM5 chitinase to protect their hosts. *New Phytol* 244(3):980–996. <https://doi.org/10.1111/nph.20080>

Emms DM, Kelly S (2019) OrthoFinder: phylogenetic orthology inference for comparative genomics. *Genome Biol* 20:238–244. <https://doi.org/10.1186/s13059-019-1832-y>

Estaki M, Jiang L, Bokulich NA, McDonald D, González A, Kosciulek T, Martino C, Zhu Q, Birmingham A, Vázquez-Baeza Y, Dillon MR, Bolyen E, Caporaso JG, Knight R (2020) QIIME 2 enables comprehensive end-to-end analysis of diverse microbiome data and comparative studies with publicly available data. *Curr Protoc Bioinformatics* 70(1):e100. <https://doi.org/10.1002/cpbi.100>

Fadiji AE, Babalola OO (2020) Metagenomics methods for the study of plant-associated microbial communities: a review. *J Microbiol Methods* 170:105860. <https://doi.org/10.1016/j.mimet.2020.105860>

Fadiji AE, Adeniji A, Lanrewaju AA, Adedayo AA, Chukwuneme CF, Nwachukwu BC, Aderibigbe J, Omomowo IO (2025) Key challenges in plant microbiome research in the next decade. *Microorganisms* 13(11):2546. <https://doi.org/10.3390/microorganisms13112546>

Fidan O, Zhan J (2019) Discovery and engineering of an endophytic *Pseudomonas* strain from *Taxus chinensis* for efficient production of zeaxanthin diglucoside. *J Biol Eng* 13:66–70. <https://doi.org/10.1186/s13036-019-0196-x>

Fung C, Rusling M, Lampeter T, Love C, Karim A, Bongiorno C, Yuan LL (2021) Automation of QIIME2 metagenomic analysis platform. *Curr Protoc* 1(9):e254. <https://doi.org/10.1002/cpz1.254>

Gaiero JR, McCall CA, Thompson KA, Day NJ, Best AS, Dunfield KE (2013) Inside the root microbiome: bacterial root endophytes and plant growth promotion. *Am J Bot* 100(9):1738–1750. <https://doi.org/10.3732/ajb.1200572>

Godara H, Ramakrishna W (2023) Endophytes as nature's gift to plants to combat abiotic stresses. Lett Appl Microbiol 76(2):ovac067. <https://doi.org/10.1093/lambio/ovac067>

Goldstein S, Beka L, Graf J, Klassen JL (2019) Evaluation of strategies for the assembly of diverse bacterial genomes using MinION long-read sequencing. BMC Genomics 20(1):23. <https://doi.org/10.1186/s12864-018-5381-7>

Guan J, Liu J, Gou J, Xu Z, Zhou Y, Zou X (2025) Endophytic colonization via *Cordyceps cateniannulata* induces a growth-enhancing effect and increases the resistance of tomato plants against *Tetranychus urticae* (Koch). Crop Prot 193:107182. <https://doi.org/10.1016/j.cropro.2025.107182>

Himani KV, Sharma C, Rawat G, Naik B, Rajput V, Gupta S, Kumar V (2025) *Bacopa monnieri* bacterial endophytes: regulating plant growth and active phytochemicals. South Asian Eur J Pub Health 26(S2):1572–1584. <https://doi.org/10.70135/seejph.vi.5073>

Huan T, Forsberg E, Rinehart D, Johnson CH, Ivanisevic J, Benton HP, Fang M, Aisporna A, Hilmer B, Poole FL, Thorgersen MP (2017) Systems biology guided by XCMS Online metabolomics. Nat Methods 14:461–462. <https://doi.org/10.1038/nmeth.4260>

Huang YL (2020) Effect of host, environment and fungal growth on fungal leaf endophyte communities in Taiwan. J. Fungi (Basel) 6(4):244. <https://doi.org/10.3390/jof6040244>

Huang PW, Yang Q, Zhu YL, Zhou J, Sun K, Mei YZ, Dai CC (2020) The construction of CRISPR–Cas9 system for endophytic *Phomopsis liquidambaris* and its PmkkA-deficient mutant revealing the effect on rice. Fungal Genet Biol 136:103301. <https://doi.org/10.1016/j.fgb.2019.103301>

Hung KS, Hsiao CC, Pai TW, Hu CH, Tzou WS, Wang WD, Chen YR (2018) Functional enrichment analysis based on long noncoding RNA associations. BMC Syst Biol

24(12(Suppl 4)):45. <https://doi.org/10.1186/s12918-018-0571-0>

Jacob J, Krishnan GV, Thankappan D, Amma DKBNS (2020) Endophytic bacterial strains induced systemic resistance in agriculturally important crop plants. Editor(s): Kumar A, Radhakrishnan EK, Microbial Endophytes, Woodhead Publishing Pp 75–105.

<https://doi.org/10.1016/B978-0-12-819654-0.00004-1>

Jain A, Sarsaiya S, Singh R, Gong Q, Wu Q, Shi J (2024) Omics approaches in understanding the benefits of plant-microbe interactions. Front Microbiol 15:1391059.

<https://doi.org/10.3389/fmicb.2024.1391059>

Jia J, Lu SE (2024) Comparative genome analyses provide insight into the antimicrobial activity of endophytic *Burkholderia*. Microorganisms 12(1):100.

<https://doi.org/10.3390/microorganisms12010100>

Jing M, Xu X, Peng J, Li C, Zhang H, Lian C, Chen Y, Shen Z, Chen C (2022) Comparative genomics of three *Aspergillus* strains reveals insights into endophytic lifestyle and endophyte-induced plant growth promotion. J Fungi 8(7):690.

<https://doi.org/10.3390/jof8070690>

Kaminski K, Ludwiczak J, Pawlicki K, Alva V, Dunin-Horkawicz S (2023) pLM-BLAST: distant homology detection based on direct comparison of sequence representations from protein language models. Bioinformatics 39(10):btad579.

<https://doi.org/10.1093/bioinformatics/btad579>

Kandel SL, Joubert PM, Doty SL (2017) Bacterial endophyte colonization and distribution within plants. Microorganisms 5(4):77.

<https://doi.org/10.3390/microorganisms5040077>

Kanehisa M, Furumichi M, Sato Y, Matsuura Y, Ishiguro-Watanabe M (2025) KEGG: biological systems database as a model of the real world. Nucleic Acids Res 53(D1):D672–

D677. <https://doi.org/10.1093/nar/gkae909>

Kashyap N, Singh SK, Yadav N, Singh VK, Kumari M, Kumar D, Shukla L, Kaushalendra Bhardwaj N, Kumar A (2023) Biocontrol screening of endophytes: Applications and limitations. *Plants (Basel)* 12(13):2480. <https://doi.org/10.3390/plants12132480>

Kaul S, Sharma T, K Dhar M (2016) Omics tools for better understanding the plant–endophyte interactions. *Front Plant Sci* 7:955. <https://doi.org/10.3389/fpls.2016.00955>

Kiouri DP, Batsis GC, Chasapis CT (2025) Structure-based approaches for protein–protein interaction prediction using machine learning and deep learning. *Biomolecules* 15(1):141. <https://doi.org/10.3390/biom15010141>

Kirpich AS, Ibarra M, Moskalenko O, Fear JM, Gerken J, Mi X, Ashrafi A, Morse AM, McIntyre LM (2018) SECIMTools: a suite of metabolomics data analysis tools. *BMC Bioinformatics* 19(1):151. <https://doi.org/10.1186/s12859-018-2134-1>

Kovaka S, Zimin AV, Pertea GM, Razaghi R, Salzberg S, Pertea M (2019) Transcriptome assembly from long-read RNA-seq alignments with StringTie2. *Genome Biol* 20(1):278. <https://doi.org/10.1186/s13059-019-1910-1>

Kumar V, Nautiyal CS (2022) Plant abiotic and biotic stress alleviation: from an endophytic microbial perspective. *Curr Microbiol* 79:311–325. <https://doi.org/10.1007/s00284-022-03012-2>

Kumar V, Nautiyal CS (2023) Endophytes modulate plant genes: present status and future perspectives. *Curr Microbiol* 80:353–365. <https://doi.org/10.1007/s00284-023-03466-y>

Kumar M, Sharma S, Gupta S, Kumar V (2018) Mitigation of abiotic stresses in *Lycopersicon esculentum* by endophytic bacteria. *Environmental Sustainability* 1(1):71–

80. <https://doi.org/10.1007/s42398-018-0004-4>

Kumar U, Raj S, Sreenikethanam A, Maddheshiya R, Kumari S, Han S, Kapoor KK, Bhaskar R, Bajhaiya AK, Gahlot DK (2023) Multi-Omics approaches in plant-microbe interactions hold enormous promise for sustainable agriculture. *Agronomy* 13(7):1804. <https://doi.org/10.3390/agronomy13071804>

Kumari P, Deepa N, Trivedi PK, Singh BK, Srivastava V, Singh A (2023) Plants and endophytes interaction: a “secret wedlock” for sustainable biosynthesis of pharmaceutically important secondary metabolites. *Microb Cell Fact* 22:226. <https://doi.org/10.1186/s12934-023-02234-8>

Kuo HC, Hui S, Choi J, Lee YH (2014) Secret lifestyles of *Neurospora crassa*. *Sci Rep* 4(1):5135. <https://doi.org/10.1038/srep05135>

Lahrman U, Ding Y, Banhara A, Rath M, Hajirezaei MR, Döhlemann S, von Wirén N, Parniske M, Zuccaro A (2013) Host-related metabolic cues affect colonization strategies of a root endophyte. *Proc Natl Acad Sci U S A* 110(34):13965–70. <https://doi.org/10.1073/pnas.1301653110>

Lapidus AL, Korobeynikov AI (2021) Metagenomic data assembly – the way of decoding unknown microorganisms. *Front Microbiol* 12:613791. <https://doi.org/10.3389/fmicb.2021.613791>

Li J, Sang Y, Zeng S, Mo S, Zhang Z, He S, Li X, Su G, Liao J, Jiang C (2022) MicrobioSee: a web-based visualization toolkit for multi-omics of microbiology. *Front Genet* 13:853612. <https://doi.org/10.3389/fgene.2022.853612>

Li X, Sun HF, Fan JH, Li YY, Ma LJ, Wang LL, Li XM (2023) Transcriptome modulation by endophyte drives rice seedlings response to Pb stress. *Ecotoxicol Environ Saf* 254:114740. <https://doi.org/10.1016/j.ecoenv.2023.114740>

Li Q, Yao S, Wen H, Li W, Jin L, Huang X (2024) Improving lead phytoremediation using endophytic bacteria isolated from the pioneer plant *Ageratina adenophora* (Spreng.) from a mining area. *Toxics* 12(4):291. <https://doi.org/10.3390/toxics12040291>

Liu Y, Chen N, Gao Y, Bu Z, Niu S, Wang Y, Liu X, Zhu Y (2021) Physiological, biochemical and proteomic insight into the response system of *Streptomyces hygroscopicus* OsiSh-2 to rice blast fungus toxins. *Appl Soil Ecol.* <https://doi.org/10.1016/j.apsoil.2021.104058>

Liu C, Bai Z, Luo Y, Zhang Y, Wang Y, Liu H, Luo M, Huang X, Chen A, Ma L, Chen C, Yuan J, Xu Y, Zhu Y, Mu J, An R et al (2024a) Multiomics dissection of *Brassica napus* L. lateral roots and endophytes interactions under phosphorus starvation. *Nat Commun* 15:9732. <https://doi.org/10.1038/s41467-024-54112-5>

Liu L, Quan S, Li L, Lei G, Li S, Gong T, Zhang Z, Hu Y, Yang W (2024b) Endophytic bacteria improve bio- and phytoremediation of heavy metals. *Microorganisms* 12(11):2137. <https://doi.org/10.3390/microorganisms12112137>

Love MI, Huber W, Anders S (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 15:550. <https://doi.org/10.1186/s13059-014-0550-8>

Lu Y, Zhou G, Ewald J, Pang Z, Shiri T, Xia J (2023) Microbiomeanalyst 2.0: comprehensive statistical, functional and integrative analysis of microbiome data. *Nucleic Acids Res* 51(W1):W310–W318. <https://doi.org/10.1093/nar/gkad407>

Ludueña LM, Anzuay MS, Angelini JG, McIntosh M, Becker A, Rupp O, Goesmann A, Blom J, Fabra A, Taurian T (2019) Genome sequence of the endophytic strain

Enterobacter sp. J49, a potential biofertilizer for peanut and maize. Genomics 111(4):913–920. <https://doi.org/10.1016/j.ygeno.2018.05.021>

Lugli GA, Milani C, Mancabelli L, van Sinderen D, Ventura M (2016) MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. FEMS Microbiol Lett 363(7):fnw049. <https://doi.org/10.1093/femsle/fnw049>

Lyu D, Zajonc J, Pagé A, Tanney CAS, Shah A, Monjezi N, Msimbira LA, Antar M, Nazari M, Backer R, Smith DL (2021) Plant holobiont theory: the phytomicrobiome plays a central role in evolution and success. Microorganisms 9(4):675. <https://doi.org/10.3390/microorganisms9040675>

Maksimov D, Blagova S, Veselova A, Sorokan G, Burkhanova E, Cherepanova E, Sarvarova S, Rumyantsev VY, Alekseev R, Khayrullin (2020) Recombinant *Bacillus subtilis* 26DCryChS line with gene Btcry1Ia encoding Cry1Ia toxin from *Bacillus thuringiensis* promotes integrated wheat defense against pathogen *Stagonospora nodorum* Berk. and greenbug *Schizaphis graminum* Rond. Biol Control 144:104242. <https://doi.org/10.1016/j.biocontrol.2020.104242>

Malgioglio G, Rizzo GF, Nigro S, Lefebvre du Prey V, Herforth-Rahmé J, Catara V, Branca F (2022) Plant-microbe interaction in sustainable agriculture: the factors that may influence the efficacy of PGPM application. Sustainability 14(4):2253. <https://doi.org/10.3390/su14042253>

Manchanda N, Portwood JL, Woodhouse MR, Seetharam AS, Lawrence-Dill CJ, Andorf CM, Hufford MB (2020) GenomeQC: a quality assessment tool for genome assemblies and gene structure annotations. BMC Genomics 21:193. <https://doi.org/10.1186/s12864-020-6568-2>

Meena RS, Kumar S, Datta R, Lal R, Vijayakumar V, Brtnicky M, Sharma MP, Yadav GS, Jhariya MK, Jangir CK et al (2020) Impact of agrochemicals on soil microbiota and management: a review. *Land* 9(2):34. <https://doi.org/10.3390/land9020034>

Mehta S, Bernt M, Chambers M, Fahrner M, Föll MC, Gruening B (2023) A galaxy of informatics resources for MS-based proteomics. *Expert Rev Proteomics* 20:251–266. <https://doi.org/10.1080/14789450.2023.2265062>

Mengistu AA (2020) Endophytes: colonization, behaviour, and their role in defense mechanism. *Int J Microbiol* 6927219. <https://doi.org/10.1155/2020/6927219>

Mishra S, Priyanka Sharma S (2022) Metabolomic insights into endophyte-derived bioactive compounds. *Front Microbiol* 13:835931. <https://doi.org/10.3389/fmicb.2022.835931>

Mishra A, Singh SS, Singh SP, Bhattacharya A, Mishra N, Nautiyal CS (2018) Endophyte-mediated modulation of defense-related genes and systemic resistance in *Withania somnifera* (L.) Dunal under *Alternaria alternata* stress. *Appl Environ Microbiol* 84:e02845–17. <https://doi.org/10.1128/AEM.02845-17>

Mohammadi R, Nami Y, Tajaddod S (2024) Biological pest control potential of symbiotic fungal endophytes of cool-season grasses. *Crop Prot* 183:106751. <https://doi.org/10.1016/j.cropro.2024.106751>

Morales-Vargas AT, López-Ramírez V, Álvarez-Mejía C, Vázquez-Martínez J (2024) Endophytic fungi for crops adaptation to abiotic stresses. *Microorganisms* 12(7):1357. <https://doi.org/10.3390/microorganisms12071357>

Mushtaq S, Shafiq M, Tariq MR, Sami A, Nawaz-Ul-Rehman MS, Bhatti MHT, Haider MS, Sadiq S, Abbas MT, Hussain M, Shahid MA (2023) Interaction between bacterial

endophytes and host plants. *Front Plant Sci* 13:1092105.

<https://doi.org/10.3389/fpls.2022.1092105>

Nielsen H (2019) Predicting secretory proteins with SignalP. *Methods Mol Biol* 1611:59–73. https://doi.org/10.1007/978-1-4939-7015-5_6

Noman M, Ahmed T, Ijaz U, Shahid M, Azizullah Li D, Manzoor I, Song F (2021) Plant–microbiome crosstalk: dawning from composition and assembly of microbial community to improvement of disease resilience in plants. *Int J Mol Sci* 22(13):6852. <https://doi.org/10.3390/ijms22136852>

O'Donnell ST, Ross RP, Stanton C (2020) The progress of multi–omics technologies: determining function in lactic acid bacteria using a systems level approach. *Front Microbiol* 10:3084. <https://doi.org/10.3389/fmicb.2019.03084>

Osborne R, Rehneke L, Lehmann S, Roberts J, Altmann M, Altmann S, Zhang Y, Köpf E, Dominguez–Ferreras A, Okechukwu E, Sergaki C, Rich–Griffin C, Ntoukakis V, Eichmann R, Shan W, Falter–Braun P, Schäfer P (2023) Symbiont–host interactome mapping reveals effector–targeted modulation of hormone networks and activation of growth promotion. *Nat Commun* 14:4065. <https://doi.org/10.1038/s41467-023-39885-5>

Oszust K, Cybulska J, Frąc M (2020) How do *Trichoderma* genus fungi win a nutritional competition battle against soft fruit pathogens? A report on niche overlap nutritional potentiates. *Int J Mol Sci* 21:4235. <https://doi.org/10.3390/ijms21124235>

Pang Z, Chong J, Zhou G, de Lima Morais DA, Chang L, Barrette M, Gauthier C, Jacques PE, Li S, Xia J (2021) MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. *Nucleic Acids Res* 49(W1):W388–W396. <https://doi.org/10.1093/nar/gkab382>

Pang Z, Zhou G, Ewald J, Chang L, Hacariz O, Basu N, Xia J (2022) Using MetaboAnalyst 5.0 for LC–HRMS spectra processing, multi-omics integration and covariate adjustment of global metabolomics data. Nat Protoc 17:1735–1761. <https://doi.org/10.1038/s41596-022-00710-w>

Pawlik M, Płociniczak T, Thijs S, Pintelon I, Vangronsveld J, Piotrowska-Seget Z (2020) Comparison of two inoculation methods of endophytic bacteria to enhance phytodegradation efficacy of an aged petroleum hydrocarbons polluted soil. Agronomy 10(8):1196. <https://doi.org/10.3390/agronomy10081196>

Piasecka A, Kachlicki P, Stobiecki M (2019) Analytical methods for detection of plant metabolomes changes in response to biotic and abiotic stresses. Int J Mol Sci 20:379. <https://doi.org/10.3390/ijms20020379>

Pili NN, França SC, Kyndt T, Makumba BA, Skilton R, Höfte M, Mibey RK, Gheysen G (2016) Analysis of fungal endophytes associated with rice roots from irrigated and upland ecosystems in Kenya. Plant Soil 405(1/2):371–380. <http://www.jstor.org/stable/43872721>

Pinski A, Betekhtin A, Hupert-Kocurek K, Mur LAJ, Hasterok R (2019) Defining the genetic basis of plant–endophytic bacteria interactions. Int J Mol Sci 20(8):1947. <https://doi.org/10.3390/ijms20081947>

Qiao L, Liu J, Zhou Z, Li Z, Zhou Y, Xu S, Yang Z, Qu J, Zou X (2023) Positive effects of *Cordyceps cateniannulata* colonization in tobacco: Growth promotion and resistance to abiotic stress. Front Microbiol 14:1131184. <https://doi.org/10.3389/fmicb.2023.1131184>

Raghavan V, Kraft L, Mesny F, Rigerte L (2022) A simple guide to de novo transcriptome assembly and annotation. Briefings Bioinform 23(2):bbab563. <https://doi.org/10.1093/bib/bbab563>

Rakhalaru P, Mampholo BM, Mamphogoro TP, Thantsha MS (2025) Endophytic and epiphytic microorganisms as biocontrol agents: Mechanisms, applications, and metagenomic approaches in tomato cultivation. *Molecules* 30(18):3816.

<https://doi.org/10.3390/molecules30183816>

Rani S, Kumar P, Dahiya P, Maheshwari R, Dang AS, Suneja P (2022) Endophytism: A Multidimensional approach to plant–prokaryotic microbe interaction. *Front Microbiol* 13:861235. <https://doi.org/10.3389/fmicb.2022.861235>

Rathi MS, Paul S, Manjunatha BS, Kumar V, Varma A (2018) Isolation and screening of osmotolerant endophytic bacteria from succulent and non-succulent drought tolerant plants for water stress alleviation in cluster bean (*Cyamopsis tetragonoloba*). *Vegetos* 31(1):57–66. <https://doi.org/10.5958/2229-4473.2018.00008.3>

Rautela I, Poonam Oraon RKK, Kalia S, Sharma MD (2025) Genetic engineering of endophytic fungi for enhanced bioactivity, Editor(s): Dwibedi V, Kapoor N, Gambhir L, Kajale S. In: *Developments in Applied Microbiology and Biotechnology, Navigating Endophytic Research for Next-Generation Therapeutics*, Academic Press, pp 403–417. <https://doi.org/10.1016/B978-0-443-31484-1.00020-7>

Ren X, Shan Y, Li X, Fan J, Li Y, Ma L, Wang L, Li X (2022) Application of RNA sequencing to understand the benefits of endophytes in the salt-alkaline resistance of rice seedlings. *Environ Exp Bot* 196:104820. <https://doi.org/10.1016/j.envexpbot.2022.104820>

Robinson RJ, Fraaije BA, Clark IM, Jackson RW, Hirsch PR, Mauchline TH (2016) Endophytic bacterial community composition in wheat (*Triticum aestivum*) is determined by plant tissue type, developmental stage and soil nutrient availability. *Plant Soil*. <https://doi.org/10.1007/s11104-015-2495-4>

Rodriguez PA, Rothballer M, Chowdhury SP, Nussbaumer T, Gutjahr C, Falter-Braun P (2019) Systems biology of plant-microbiome interactions. *Mol Plant* 12(6):804–821.
<https://doi.org/10.1016/j.molp.2019.05.006>

Roncato-Maccari LD, Ramos HJ, Pedrosa FO, Alquini Y, Chubatsu LS, Yates MG, Rigo LU, Steffens MB, Souza EM (2003) Endophytic *Herbaspirillum seropedicae* expresses nif genes in gramineous plants. *FEMS Microbiol Ecol* 45(1):39–47.
[https://doi.org/10.1016/S0168-6496\(03\)00108-9](https://doi.org/10.1016/S0168-6496(03)00108-9)

Rubio-Santiago J, Hernández-Morales A, Rolón-Cárdenas GA, Arvizu-Gómez JL, Soria-Guerra RE, Carranza-Álvarez C, Rubio-Salazar JE, Rosales-Loredo S, Pacheco-Aguilar JR, Macías-Pérez JR (2023) Characterization of endophytic bacteria isolated from *Typha latifolia* and their effect in plants exposed to either Pb or Cd. *Plants* 12(3):498.
<https://doi.org/10.3390/plants12030498>

Ryu JY, Kim HU, Lee SY (2019) Deep learning enables high-quality and high-throughput prediction of enzyme commission numbers. *Proc Natl Acad Sci U S A* 116(28):13996–14001. <https://doi.org/10.1073/pnas.1821905116>

Salas-Núñez LF, Barrera-Ocampo A, Caicedo PA, Cortes N, Osorio EH, Villegas-Torres MF, González Barrios AF (2024) Machine learning to predict enzyme-substrate interactions in elucidation of synthesis pathways: a review. *Metabolites* 4(3):154.
<https://doi.org/10.3390/metabo14030154>

Santoyo G, Moreno-Hagelsieb G, del Carmen Orozco-Mosqueda M, Glick BR (2016) Plant growth-promoting bacterial endophytes. *Microbiol Res* 183:92–99.
<https://doi.org/10.1016/j.micres.2015.11.008>

Santra HK, Banerjee D (2023) Antifungal activity of volatile and non-volatile metabolites of endophytes of *Chloranthus elatior* Sw. *Front Plant Sci* 14:1156323.
<https://doi.org/10.3389/fpls.2023>

Satam H, Joshi K, Mangrolia U, Waghoo S, Zaidi G, Rawool S, Thakare RP, Banday S, Mishra AK, Das G, Malonia SK (2023) Next-generation sequencing technology: current trends and advancements. *Biology (Basel)* 12(7):997. <https://doi.org/10.3390/biology12070997>

Schönrogge K, Gibbs M, Oliver A, Cavers S, Gweon HS, Ennos RA, Cottrell J, Iason GR, Taylor J (2022) Environmental factors and host genetic variation shape the fungal endophyte communities within needles of Scots pine (*Pinus sylvestris*). *Fungal Ecol* 57–58:101162. <https://doi.org/10.1016/j.funeco.2022.101162>

Schwengers O, Jelonek L, Dieckmann MA, Beyvers S, Blom J, Goesmann A (2021) Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. *Microb Genom* 7(11):000685. <https://doi.org/10.1099/mgen.0.000685>

Seemann T (2014) Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30(14):2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>

Shahzad A, Siddique A, Ferdous S, Amin MA, Qin M, Aslam U, Naeem M, Bashir T, Shakoor A (2023) Heavy metals mitigation and growth promoting effect of endophytic *Agrococcus terreus* (MW 979614) in maize plants under zinc and nickel contaminated soil. *Front Microbiol* 14:1255921. <https://doi.org/10.3389/fmicb.2023.1255921>

Shao Y, Liu T (2025) iNClassSec-ESM: discovering potential non-classical secreted proteins through a novel protein language model. *Comput Struct Biotechnol J* 27:1350–1358. <https://doi.org/10.1016/j.csbj.2025.03.043>

Shi X, Qin T, Gao Y, Zhao N, Ren A (2025) Comparative genome and transcriptome analysis of the endophytic fungus *Epichloë sibirica* reveals biological control mechanism in host *Achnatherum sibiricum*. *Biol Control* 205:105778 <https://doi.org/10.1016/j.biocontrol.2025.105778>

Shrivastava N, Jiang L, Li P, Sharma AK, Luo X, Wu S, Pandey R, Gao Q, Lou B (2018) Proteomic approach to understand the molecular physiology of symbiotic interaction between *Piriformospora indica* and *Brassica napus*. *Sci Rep* 8(1):5773. <https://doi.org/10.1038/s41598-018-23994-z>

Shymanovich T, Faeth SH (2019) Environmental factors affect the distribution of two *Epichloë* fungal endophyte species inhabiting a common host grove bluegrass (*Poa alsodes*). *Ecol Evol* 9(11):6624–6642. <https://doi.org/10.1002/ece3.5241>

Singh P, Singh R, Madhu GS, Singh VP (2023) Seed biopriming with *Trichoderma harzianum* for growth promotion and drought tolerance in rice (*Oryza sativus*). *Agric Res* 12(2):154–162. <https://doi.org/10.1007/s40003-022-00641-8>

Starr AE, Deeke SA, Li L, Zhang X, Daoud R, Ryan J, Ning Z, Cheng K, Nguyen LVH, Abou-Samra E, Lavallée-Adam M, Figeys D (2018) Proteomic and metaproteomic approaches to understand host-microbe interactions. *Anal Chem* 90(1):86–109. <https://doi.org/10.1021/acs.analchem.7b04340>

Suryanarayanan TS, Uma Shaanker R (2021) Can fungal endophytes fast-track plant adaptations to climate change? *Fungal Ecol* 50:101039. <https://doi.org/10.1016/j.funeco.2021.101039>

Taj B, Adeolu M, Xiong X, Ang J, Nursimulu N, Parkinson J (2023) MetaPro: a scalable and reproducible data processing and analysis pipeline for metatranscriptomic investigation of microbial communities. *Microbiome* 11:143. <https://doi.org/10.1186/s40168-023-01562-6>

Terna PT, Mohamed Nor NMI, Azuddin NF, Azuddin AF, Zakaria L (2024) Molecular identification and pathogenicity of endophytic fungi from corn ears. *Sci Rep* 14:17146. <https://doi.org/10.1038/s41598-024-68428-1>

Teufel F, Almagro Armenteros JJ, Johansen AR, Gíslason MH, Pihl SI, Tsirigos KD, Winther O, Brunak S, von Heijne G, Nielsen H (2022) SignalP 6.0 predicts all five types of signal peptides using protein language models. *Nat Biotechnol* 40(7):1023–1025.
<https://doi.org/10.1038/s41587-021-01156-3>

Tlou M, Ndou B, Mabona N, Khwathisi A, Ateba C, Madala N, Serepa-Dlamini MH (2024) Next generation sequencing-aided screening, isolation, molecular identification, and antimicrobial potential for bacterial endophytes from the medicinal plant, *Elephantorrhiza elephantina*. *Front Microbiol* 15:1383854.
<https://doi.org/10.3389/fmicb.2024.1383854>

Tsipinana S, Husseiny S, Alayande KA, Raslan M, Amoo S, Adeleke R (2023) Contribution of endophytes towards improving plant bioactive metabolites: a rescue option against red-taping of medicinal plants. *Front Plant Sci* 14:1248319.
<https://doi.org/10.3389/fpls.2023.1248319>.

Ujimatsu R, Takino J, Aoki S, Nakamura M, Haba H, Minami A, Hiruma K (2025) A fungal transcription factor converts a beneficial root endophyte into an anthracnose leaf pathogen. *Curr Biol* 35:1989–2005. <https://doi.org/10.1016/j.cub.2025.03.026>

Upadhyay SK, Srivastava AK, Rajput VD, Chauhan PK, Bhojiya AA, Jain D, Chaubey G, Dwivedi P, Sharma B, Minkina T (2022) Root exudates: mechanistic insight of plant growth promoting rhizobacteria for sustainable crop production. *Front Microbiol* 13:916488. <https://doi.org/10.3389/fmicb.2022.916488>

Urhan A, Abeel T (2021) A comparative study of pan-genome methods for microbial organisms: *Acinetobacter baumannii* pan-genome reveals structural variation in antimicrobial resistance-carrying plasmids. *Microb Genom* 7(11):000690.
<https://doi.org/10.1099/mgen.0.000690>

Venkataraman M, Infante V, Sabat G, Sanos-Giles K, Ané JM, Pflieger BF (2025) A novel membrane-associated protein aids bacterial colonization of maize. *ACS Synth Biol*

17(1):206–215. <https://doi.org/10.1021/acssynbio.4c00489>

Verma V, Batta A, Singh HB, Srivastava A, Garg SK, Singh VP, Arora PK (2023) Bioengineering of fungal endophytes through the CRISPR/Cas9 system. *Front Microbiol* 14:1146650. <https://doi.org/10.3389/fmicb.2023>

Verma V, Srivastava A, Garg SK, Singh VP, Arora PK (2024) Incorporating omics-based tools into endophytic fungal research. *Biotechnol Notes* 5:1–7. <https://doi.org/10.1016/j.biotno.2023.12.006>

Vimal SR, Singh JS, Kumar A, Prasad SM (2024) The plant endomicrobiome: structure and strategies to produce stress resilient future crop. *Curr Res Microb Sci* 6:100236. <https://doi.org/10.1016/j.crmicr.2024.100236>

Walia V, Saipradeep VG, Srinivasan R, Sivadasan N (2023) MAGE: strain level profiling of metagenome samples. In: Jahn K, Vinař T (eds) *Comparative Genomics. RECOMB-CG. Lecture Notes in Computer Science*, 13883. Springer, Cham. https://doi.org/10.1007/978-3-031-36911-7_14

Wang T, Chen T, White JF, Li C (2022) Identification of three *Epichloë* endophytes from *Hordeum bogdanii* Wilensky in China. *J. Fungi (Basel)* 8(9):928. <https://doi.org/10.3390/jof8090928>

Wang Y, Li Z, Xu M, Xiao Z, Liu C, Du B, Xu D, Li L (2023) Signal molecules regulate the synthesis of secondary metabolites in the interaction between endophytes and medicinal plants. *Processes* 11(3):849. <https://doi.org/10.3390/pr11030849>

Wang J, Zhao Y, Wu S, Gu X, Liu X, Tian Y, Hu B, Zhao Y (2025) Genome analysis reveals *Erwinia amylovora* in China is closely related to those of Kyrgyzstan and Kazakhstan. *Phytopathol Res* 7:31. <https://doi.org/10.1186/s42483-025-00316-6>

Westreich ST, Treiber ML, Mills DA, Korf I, Lemay DG (2018) SAMSA2: a standalone metatranscriptome analysis pipeline. *BMC Bioinformat* 19:175.

<https://doi.org/10.1186/s12859-018-2189-z>

Wilke A, Bischof J, Gerlach W, Glass E, Harrison T, Keegan KP, Paczian T, Trimble WL, Bagchi S, Grama A, Chaterji S, Meyer F (2016) The MG-RAST metagenomics database and portal in 2015. *Nucleic Acids Res* 44:D590–D594.

<https://doi.org/10.1093/nar/gkv1322>

Wolfe ER, Ballhorn DJ (2020) Do foliar endophytes matter in litter decomposition? *Microorganisms* 8(3):446. <https://doi.org/10.3390/microorganisms8030446>

Wu T, Xu J, Xie W, Yao Z, Yang H, Sun C, Li X (2018) *Pseudomonas aeruginosa* L10: a hydrocarbon-degrading, biosurfactant-producing, and plant-growth-promoting endophytic bacterium isolated from a reed (*Phragmites australis*). *Front Microbiol* 9:1087.

<https://doi.org/10.3389/fmicb.2018.01087>

Wu W, Chen W, Liu S, Wu J, Zhu Y, Qin L, Zhu B (2021) Beneficial relationships between endophytic bacteria and medicinal plants. *Front Plant Sci* 12:646146.

<https://doi.org/10.3389/fpls.2021.646146>

Xie H, Chai Y, Liu Z, Hao W, Gai J (2024) Community assembly of endophytic bacteria and fungi differs in soil-root continuum of *Carex cepillacea*. *Appl Soil Ecol* 194:105206.

<https://doi.org/10.1016/j.apsoil.2023.105206>

Xu X, Huang R, Yin WB (2021) An optimized and efficient CRISPR/Cas9 system for the endophytic fungus *Pestalotiopsis fici*. *J Fungi (Basel)* 7(10):809.

<https://doi.org/10.3390/jof7100809>

Yang Y, Chaffin TA, Shao Y, Balasubramanian VK, Markillie M, Mitchell H, Rubio-Wilhelmi MM, Ahkami AH, Blumwald E, Neal Stewart C Jr (2024) Novel synthetic

inducible promoters controlling gene expression during water-deficit stress with green tissue specificity in transgenic poplar. *Plant Biotechnol J* 22(6):1596–1609.

<https://doi.org/10.1111/pbi.14289>

Yongpisanphop J, Babel S, Kurisu F, Kruatrachue M, Pokethitiyook P (2020) Isolation and characterization of Pb-resistant plant growth promoting endophytic bacteria and their role in Pb accumulation by fast-growing trees. *Environ Technol* 41:3598–3606.

<https://doi.org/10.1080/09593330.2019.1615993>

Yuan J, Zhang W, Sun K, Tang M-J, Chen P-X, Li X, Dai CC (2019) Comparative transcriptomics and proteomics of *Atractylodes lancea* in response to endophytic fungus *Gilmaniella* sp. AL12 reveals regulation in plant metabolism. *Front Microbiol* 10:1208.

<https://doi.org/10.3389/fmicb.2019.01208>

Zhang C, Freddolino L (2024) A large-scale assessment of sequence database search tools for homology-based protein function prediction. *Brief Bioinform* 25(4):bbae349.

<https://doi.org/10.1093/bib/bbae349>

Zhang S, Xu B, Gan Y (2019) Seed treatment with *Trichoderma longibrachiatum* T6 promotes wheat seedling growth under NaCl stress through activating the enzymatic and nonenzymatic antioxidant defense systems. *Int J Mol Sci* 20(15):3729.

<https://www.mdpi.com/1422-0067/20/15/3729>

Zhao C, Onyino J, Gao X (2024a) Current advances in the functional diversity and mechanisms underlying endophyte-plant interactions. *Microorganisms* 12(4):779.

<https://doi.org/10.3390/microorganisms12040779>

Zhao S, Yin R, Zhang M, Zhai Z, Shen Z, Mou Y, Xu D, Zhou L, Lai D (2024b) Efficient gene editing in the slow-growing, non-sporulating, melanized, endophytic fungus *Berkleasium* sp. Dzf12 using a CRISPR/Cas9 system. *World J Microbiol Biotechnol* 40:176. <https://doi.org/10.1007/s11274-024-03988-y>

Zhou XR, Dai L, Xu GF, Wang HS (2021) A strain of *Phoma* species improves drought tolerance of *Pinus tabulaeformis*. Sci Rep 11(1):7637. <https://doi.org/10.1038/s41598-021-87105-1>

Zhou G, Pang Z, Lu Y, Ewald J, Xia J (2022) OmicsNet 2.0: a web-based platform for multi-omics integration and network visual analytics. Nucleic Acids Res 50:W527–W533. <https://doi.org/10.1093/nar/gkac376>

Zihad SMNK, Hasan MT, Sultana MS, Nath S, Nahar L, Rashid MA, Uddin SJ, Sarker SD, Shilpi JA (2022) Isolation and characterization of antibacterial compounds from *Aspergillus fumigatus*: an endophytic fungus from a mangrove plant of the Sundarbans. Evid Based Complement Alternat Med 9600079. <https://doi.org/10.1155/2022/9600079>

Zoppi J, Guillaume JF, Neunlist M, Chaffron S (2021) MiBiOmics: an interactive web application for multi-omics data exploration and integration. BMC Bioinformatics 22:6. <https://doi.org/10.1186/s12859-020-03921-8>

Acknowledgements

Thanks are due to Dr. Vijay Dhasmana, President of Swami Rama Himalayan University, Dehradun, for providing invaluable support and resources that contributed significantly to this work.

Funding

No funding was received to assist with the preparation of this manuscript.

Author information

Authors and Affiliations

**School of Biosciences, Swami Rama Himalayan University, Jolly Grant, Dehradun,
Uttarakhand, India**

Vivek Kumar & Chandra S. Nautiyal

Contributions

VK original draft preparation and data curation; CSN intellectualized, reviewed, edited, and made final changes to the manuscript. Both authors checked and certified the final article.

Corresponding author

Correspondence to [Vivek Kumar](#).

Ethics declarations

Ethics approval and consent to participate

Not Applicable.

Consent for publication

Not applicable.

Financial interest

None.

Competing interests

The authors declare no competing interests.

Additional information

Publisher's note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Rights and permissions

Springer Nature or its licensor (e.g. a society or other partner) holds exclusive rights to this article under a publishing agreement with the author(s) or other rightsholder(s); author self-archiving of the accepted manuscript version of this article is solely governed by the terms of such publishing agreement and applicable law.

[Reprints and permissions](#)

About this article

Cite this article

Kumar, V., Nautiyal, C.S. From hidden allies to precision symbionts: unleashing endophytes for sustainable agroecosystems. *World J Microbiol Biotechnol* **42**, 172 (2026).

<https://doi.org/10.1007/s11274-026-04896-z>

Received

14 November 2025

Accepted

05 March 2026

Published

30 March 2026

Version of record

30 March 2026

DOI

<https://doi.org/10.1007/s11274-026-04896-z>

Keywords

[Endophytes](#)

[Microbiome engineering](#)

[Multi-omics](#)

[Plant–microbe interactions](#)

[Rhizosphere](#)

[Sustainable agriculture](#)

