



Review

Abiotic stress and belowground microbiome: the potential of -omics approaches

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Table S1. List of manuscripts that combine the presence of plant, AMF or Actinobacteria and -omics, *i.e.*, RNAseq or untargeted metabolomics/proteomics, in the last ten years.

Reference	Plant	AMF and Actinobacteria	Tissue	-Omics	Stress
AMF					
[132]	Tomato wild-type and <i>rnc</i> mutant	<i>Glomus intraradices</i> (former name)	Roots	Transcriptomics RNAseq	
[133]	Tomato (<i>Solanum lycopersicum</i>)	<i>Funneliformis mosseae</i>	Fruits	Transcriptomics RNA-Seq	
[52]	Rice (<i>Oryza sativa</i>)	<i>Rhizophagus irregularis</i>	Large lateral and fine lateral roots	Transcriptomics RNA-seq	
[134]	<i>Lotus japonicus</i>	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-Seq	
[135]	Litchi (<i>Litchi chinensis</i>)	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-seq	
[54]	Grapevine (<i>Vitis vinifera</i>)	<i>Funneliformis mosseae</i> or mixed commercial inoculum	Roots	Transcriptomics RNA-seq	
[136]	Trifoliate orange (<i>Poncirus trifoliata</i>)	<i>Rhizophagus irregularis</i>	Lateral roots	Transcriptomics RNA-Seq	
[137]	<i>Lotus japonicus</i>	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-Seq	
[55]	Wheat (<i>Triticum aestivum</i>)	<i>Funneliformis mosseae</i>	Roots and leaves	Transcriptomics RNA-seq Proteomics LC-MS/MS	<i>Xanthomonas translucens</i> infection
[138]	Cucumber (<i>Cucumis sativus</i>)	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-seq	Cold stress
[139]	Common bean (<i>Phaseolus vulgaris</i>)	A mix of <i>Glomus clarum</i> , <i>Acaulospora scrobiculata</i> , <i>Gigaspora rosea</i>	Roots/ validation on LMD samples	Transcriptomics RNA-Seq	Water deficit
[140]	Sunflower (<i>Helianthus annuus</i>)	<i>Rhizoglyphus irregularis</i>	Roots	Transcriptomics RNA-Seq	

[141]	<i>Medicago truncatula</i> , <i>Nicotiana benthamiana</i> and <i>Allium schoenoprasum</i>	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-Seq combined with LMD	
[56]	Tomato (<i>Solanum lycopersicum</i>)	<i>Rhizophagus intraradices</i>	Roots	Transcriptomics RNA-seq	Water stress <i>Meloidogyne incognita</i> colonization
[142]	Maize (<i>Zea mays</i>)	<i>Glomus intraradices</i> (former name)	Roots	Transcriptomics RNA-seq	Cadmium
[143]	Maize (<i>Zea mays</i>)	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-Seq	
[144]	Alfalfa (<i>Medicago sativa</i>)	<i>Rhizophagus intraradices</i>	Leaves	Transcriptomics RNA-Seq	<i>Acyrtosiphon pisum</i> attack
[145]	Cassava (<i>Manihot esculenta</i>)	<i>Rhizophagus irregularis</i>	Fine roots	Transcriptomics RNA-Seq	
[146]	<i>Sesbania cannabina</i>	<i>Funneliformis mosseae</i>	Roots/shoots	Transcriptomics RNA-Seq	Salinity
[147]	Sunflower (<i>Helianthus annuus</i>)	<i>Rhizoglyphus irregulare</i>	Roots	Transcriptomics RNA-Seq	
[148]	Asparagus (<i>Asparagus officinalis</i>)	<i>Rhizophagus irregularis</i>	Leaves	Transcriptomics RNA-Seq	Salinity
[149]	garden pea (<i>Pisum sativum</i>)	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-Seq	
[150]	Soybean (<i>Glycine max</i>)	<i>Funneliformis mosseae</i>	Roots	Transcriptomics RNA-Seq Metabolomics UPLC-MS/MS	Root rot disease
[151]	Wheat (<i>Triticum aestivum</i>)	<i>Funneliformis mosseae</i>	Roots	Transcriptomics RNA-seq	Water deficit
[152]	Tomato (<i>Solanum lycopersicum</i>)	<i>Rhizophagus irregularis</i>	Mature, green, red fruits	Transcriptomics RNA-Seq	
[153]	Sunflower (<i>Helianthus annuus</i>)	<i>Rhizoglyphus irregulare</i>	Roots	Transcriptomics RNA-Seq	
[154]	Soybean (<i>Glycine max</i>)	<i>Funneliformis mosseae</i>	Roots	Transcriptomics RNA-Seq Proteomics iTRAQ	
[155]	Pea (<i>Pisum sativum</i>)	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-Seq	

[156]	Alfalfa (<i>Medicago sativa</i>)	<i>Rhizophagus intraradices</i>	Leaves	Transcriptomics RNA-Seq	<i>Phoma medicaginis</i> infection
[157]	Tomato (<i>Solanum lycopersicum</i>)	<i>Rhizophagus irregularis</i>	Roots	Transcriptomics RNA-Seq	
[158]	<i>Medicago truncatula</i>	<i>Glomus intraradices</i> (former name)	LMD cell-type populations from roots	Proteomics LC-MS/MS	
[159]	Sorghum (<i>Sorghum bicolor</i>)	A mix of <i>Glomus aggregatum</i> and <i>Glomus etunicatum</i> , <i>Funneliformis mosseae</i> , <i>Rhizophagus irregularis</i> alone or plus PGPB	Roots	Proteomics LC-MS/MS	
[160]	<i>Medicago sativa</i>	<i>Funneliformis mosseae</i>	Roots	Proteomics iTRAQ HPLC	Atrazine
[161]	Soybean (<i>Glycine max</i>)	<i>Funneliformis mosseae</i>	Roots	Proteomics iTRAQ and LC-MS/MS	Root rot disease
[162]	<i>Echinacea angustifolia</i>	<i>Rhizophagus irregularis</i>	Leaves	Proteomics LC-MS/MS	Salinity
[163]	Pea (<i>Pisum sativum</i>)	<i>Rhizophagus irregularis</i>	Seeds	Proteomics LC-MS	
[164]	Pea (<i>Pisum sativum</i>)	A mix of <i>Claroideoglossum etunicatum</i> , <i>Claroideoglossum claroideum</i> , <i>Rhizophagus irregularis</i> , <i>Funneliformis geosporus</i> , <i>Funneliformis mosseae</i>	Seeds	Proteomics Nano ESI LC-MS/MS Metabolomics MS/MS	<i>Didymella pinodes</i> infection
[165]	<i>Phragmites australis</i>	<i>Rhizophagus irregularis</i>	Root tips	Proteomics iTRAQ	Copper
[166]	<i>Pteris cretica</i> var. <i>nervosa</i>	<i>Funneliformis mosseae</i>	Fronds	Proteomics LC-MS/MS	Antimony
[167]	<i>Medicago truncatula</i>	<i>Rhizophagus irregularis</i>	LMD cell-type populations from roots	Metabolomics GC-EI/TOF-MS	
[45]	Tomato (<i>Solanum lycopersicum</i>)	A mix of <i>Funneliformis mosseae</i> , <i>Rhizoglossum irregulare</i> and <i>Claroideoglossum etunicatum</i>	Roots	Metabolomics LC ESI-MS	Drought and salinity
[102]	Wheat (<i>Triticum durum</i> /T. <i>aestivum</i>)	<i>Funneliformis mosseae</i>	Roots	Metabolomics UHPLC-ESI/QTOF-MS	Water deficit
[168]	Soybean (<i>Glycine max</i>)	A mix of <i>Funneliformis mosseae</i> , <i>Paraglossum</i>	Roots	Metabolomics GC-MS	

		<i>occultum</i> , <i>Diversispora spurca</i> , <i>Glomus</i> sp., <i>Acaulospora scrobiculata</i> , <i>Gigaspora</i> sp.			
[169]	Sweet pepper (<i>Capsicum annuum</i>)	<i>Funneliformis mosseae</i> , <i>Rhizoglossum irregularis</i>	Leaves	Metabolomics UHPLC/Q-TOF	
[170]	Maize (<i>Zea mays</i>)	A mix of <i>Rhizoglossum irregulare</i> , <i>Funneliformis mosseae</i> plus <i>Trichoderma</i>	Leaves and roots	Metabolomics UHPLC/Q-TOF	
[171]	Tomato (<i>Solanum lycopersicum</i>)	A mix of <i>Funneliformis mosseae</i> , <i>Rhizophagus intraradices</i> plus <i>Trichoderma</i> and PGPR	Stems with young and mature leaves, and fine feeding roots	Metabolomics LC-MS	<i>Fusarium</i> crown and root rot diseases
[172]	Trifoliate orange (<i>Poncirus trifoliata</i>)	<i>Rhizophagus intraradices</i>	Roots	Metabolomics LC-MS/MS	Water deficit
Actinobacteria					
[173]	Pedunculate oak (<i>Quercus robur</i>)	<i>Streptomyces</i> sp. strain (AcH 505)	Leaves	Transcriptomics RNA-seq	Oak powdery mildew infection
[174]	<i>Arabidopsis thaliana</i>	<i>Arthrobacter endophyticus</i> ; <i>Nocardiopsis alba</i>	Roots	Transcriptomics RNA-seq	Salinity
[175]	Wheat (<i>Triticum aestivum</i>)	<i>Arthrobacter nitroguajacolicus</i>	Roots	Transcriptomics RNA-seq	Salinity
[176]	Tomato (<i>Solanum lycopersicum</i>)	<i>Streptomyces</i> sp. KLBMP5084	Leaves	Transcriptomic RNA-seq	Salinity
[177]	<i>Arabidopsis thaliana</i>	<i>Streptomyces</i> isolate (KB001)	Whole seedlings	Transcriptomics RNA-seq	<i>Sclerotinia sclerotiorum</i> and <i>Rhizoctonia solani</i> infection
[178]	Rice (<i>Oryza sativa</i>)	<i>Streptomyces hygroscopicus</i> OsiSh-2	Leaves	Proteomics HPLC LC-MS/MS	<i>Magnaporthe oryzae</i> infection
[179]	Oats (<i>Avena barbata</i>)	Rhizosphere microbial community (<i>Actinomyces</i>)	Roots	Metabolomics UHPLC; LC-MS/MS; LC-MS	

[180]	Peppermint (<i>Mentha piperita</i>)	<i>Streptomyces</i> , C-2012 (<i>Streptomyces rimosus</i>) <i>Streptomyces</i> , C-801 (<i>Streptomyces monomycin</i>)	Shoots	Metabolomics GC/MS	Water stress
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Table S2: List of manuscripts that combine the presence of AMF or Actinobacteria and -omics, *i.e.*, genome sequencing, RNAseq or untargeted metabolomics/proteomics, in the last ten years.

Reference	AMF and Actinobacteria	-Omics	Stress
AMF			
[181]	<i>Rhizophagus irregularis</i> DAOM197198	Genome sequencing	
[182]	<i>Rhizophagus irregularis</i> DAOM197198	Single nucleus genome sequencing	
[183]	<i>Gigaspora rosea</i>	Genome sequencing	
[184]	<i>Acaulospora morrowiae</i> , <i>Diversispora versiforme</i> , <i>Scutellospora calospora</i> , <i>Racocetra castanea</i> , <i>Paraglomus brasili-anum</i> , <i>Ambispora leptoticha</i> , <i>Claroideoglossum claroideum</i> , <i>Funneliformis mosseae</i>	Transcriptomics Ultra-low input RNA-seq	
[185]	<i>Rhizophagus irregularis</i> DAOM197198	Genome assembly and gene annotation, and compared its gene content with five isolates of <i>R. irregularis</i> sampled in the same field.	
[186]	<i>Diversispora epigaea</i> (formerly <i>Glomus versiforme</i>) and its bacterial endosymbionts	Genome assembly and comparative genomics	
[187]	<i>Gigaspora rosea</i>	Comparative genomics	
[188]	<i>Gigaspora margarita</i>	Genome sequencing	
Actinobacteria			
[189]	<i>Planobispora rosea</i> ATCC 53733	Transcriptomics RNA-seq Proteomics nano LC-ESI-LIT-MS/MS	
[190]	<i>Nocardiopsis gilva</i> YIM 90087 ^T	Transcriptomics RNA-seq	Salinity
[191]	<i>Saccharothrix yanglingensis</i> Hhs.015	Transcriptomics RNA-seq	<i>Valsa mali</i>

[192]	<i>Rhodococcus</i> sp. CNS16	Transcriptomics RNA-seq	Temperature gradients
[193]	<i>Nocardiopsis xinjiangensis</i>	Proteomics iTRAQ, LC-MS/MS	Salinity
[194]	<i>Streptomyces</i> spp.	Metabolomics UHPLC Q-TOF	<i>Xanthomonas oryzae</i> pv. <i>Oryzae</i> infection
[195]	<i>Streptomyces fradiae</i> MM456M-mF7	Metabolomics HPLC, LC-ESI-MS/MS	
[196]	<i>Thermobifida cellulosilytica</i>	Metabolomics LC-MS/MS	
[197]	<i>Streptomyces pulveraceus</i> Strain ES16	Metabolomics HPLC-HRMS Volatilomics SPME-GC-MS	

References

- 132) Ruzicka, D.; Chamala, S.; Barrios-Masias, F.H.; Martin, F.; Smith, S.; Jackson, L.E.; Barbazuk, W.B.; Schachtman, D.P. Inside arbuscular mycorrhizal roots - molecular probes to understand the symbiosis. *Plant Genome* **2013**, *6*, 1-13. <https://doi.org/10.3835/plantgenome2012.06.0007>.
- 133) Zouari, I.; Salvioli, A.; Chialva, M.; Novero, M.; Miozzi, L.; Tenore, G.C.; Bagnaresi, P.; Bonfante, P. From root to fruit: RNA-Seq analysis shows that arbuscular mycorrhizal symbiosis may affect tomato fruit metabolism. *BMC Genomics* **2014**, *15*, 221. <https://doi.org/10.1186/1471-2164-15-221>.
- 134) Handa, Y.; Nishide, H.; Takeda, N.; Suzuki, Y.; Kawaguchi, M.; Saito, K. RNA-seq Transcriptonal Profiling of an Arbuscular Mycorrhiza Provides Insights into Regulated and Coordinated Gene Expression in *Lotus japonicus* and *Rhizophagus irregularis*. *Plant Cell Physiol* **2015**, *56*, 1490-1511. <https://doi.org/10.1093/pcp/pcv071>.
- 135) Shu, B.; Li, W.; Liu, L.; Wei, Y.; Shi, S. Transcriptomes of Arbuscular Mycorrhizal Fungi and Litchi Host Interaction after Tree Girdling. *Front Microbiol* **2016**, *7*, 408. <https://doi.org/10.3389/fmicb.2016.00408>.
- 136) Chen, W.; Li, J.; Zhu, H.; Xu, P.; Chen, J.; Yao, Q. Arbuscular Mycorrhizal Fungus Enhances Lateral Root Formation in *Poncirus trifoliata* (L.) as Revealed by RNA-Seq Analysis. *Front Plant Sci* **2017**, *8*, 2039. <https://doi.org/10.3389/fpls.2017.02039>.
- 137) Sugimura, Y.; Saito, K. Transcriptional profiling of arbuscular mycorrhizal roots exposed to high levels of phosphate reveals the repression of cell cycle-related genes and secreted protein genes in *Rhizophagus irregularis*. *Mycorrhiza* **2017**, *27*, 139-146. <https://doi.org/10.1007/s00572-016-0735-y>.
- 138) Ma, J.; Sun, C.; Bai, L.; Dong, R.; Yan, Y.; Yu, X.; He, C.; Zou, Z.; Li, Y. Transcriptome Analysis of Cucumber Roots Reveals Key Cold-Resistance Genes Induced by AM Fungi. *Plant Mol Biol Rep* **2018**, *36*, 135-148. <https://doi.org/10.1007/s11105-018-1066-2>.

- 139) Recchia, G.H.; Konzen, E.R.; Cassieri, F.; Caldas, D.G.G.; Tsai, S.M. Arbuscular Mycorrhizal Symbiosis Leads to Differential Regulation of Drought-Responsive Genes in Tissue-Specific Root Cells of Common Bean. *Front Microbiol* **2018**, *9*, 1339. <https://doi.org/10.3389/fmicb.2018.01339>.
- 140) Vangelisti, A.; Natali, L.; Bernardi, R.; Sbrana, C.; Turrini, A.; Hassani-Pak, K.; Hughes, D.; Cavallini, A.; Giovannetti, M.; Giordani, T. Transcriptome changes induced by arbuscular mycorrhizal fungi in sunflower (*Helianthus annuus* L.) roots. *Sci Rep* **2018**, *8*, 4. <https://doi.org/10.1038/s41598-017-18445-0>.
- 141) Zeng, T.; Holmer, R.; Hontelez, J.; Te Lintel-Hekkert, B.; Marufu, L.; de Zeeuw, T.; Wu, F.; Schijlen, E.; Bisseling, T.; Limpens, E. Host- and stage-dependent secretome of the arbuscular mycorrhizal fungus *Rhizophagus irregularis*. *Plant J* **2018**, *94*, 411–425. <https://doi.org/10.1111/tpj.13908>.
- 142) Gu, L.; Zhao, M.; Ge, M.; Zhu, S.; Cheng, B.; Li, X. Transcriptome analysis reveals comprehensive responses to cadmium stress in maize inoculated with arbuscular mycorrhizal fungi. *Ecotoxicol Environ Saf* **2019**, *186*, 109744. <https://doi.org/10.1016/j.ecoenv.2019.109744>.
- 143) Han, G.; Cheng, C.; Zheng, Y.; Wang, X.; Xu, Y.; Wang, W.; Zhu, S.; Cheng, B. Identification of Long Non-Coding RNAs and the Regulatory Network Responsive to Arbuscular Mycorrhizal Fungi Colonization in Maize Roots. *Int J Mol Sci* **2019**, *20*, 4491. <https://doi.org/10.3390/ijms20184491>.
- 144) Li, Y.; Nan, Z.; Duan, T. *Rhizophagus intraradices* promotes alfalfa (*Medicago sativa*) defense against pea aphids (*Acyrtosiphon pisum*) revealed by RNA-Seq analysis. *Mycorrhiza* **2019**, *29*, 623–635. <https://doi.org/10.1007/s00572-019-00915-0>.
- 145) Mateus, I.D.; Masclaux, F.G.; Aletti, C.; Rojas, E.C.; Savary, R.; Dupuis, C.; Sanders, I.R. Dual RNA-seq reveals large-scale non-conserved genotype × genotype-specific genetic reprogramming and molecular crosstalk in the mycorrhizal symbiosis. *ISME J* **2019**, *13*, 1226–1238. <https://doi.org/10.1038/s41396-018-0342-3>.
- 146) Ren, C.G.; Kong, C.C.; Yan, K.; Xie, Z.H. Transcriptome analysis reveals the impact of arbuscular mycorrhizal symbiosis on *Sesbania cannabina* exposed to high salinity. *Sci Rep* **2019**, *9*, 2780. <https://doi.org/10.1038/s41598-019-39463-0>.
- 147) Vangelisti, A.; Mascagni, F.; Giordani, T.; Sbrana, C.; Turrini, A.; Cavallini, A.; Giovannetti, M.; Natali, L. Arbuscular mycorrhizal fungi induce the expression of specific retrotransposons in roots of sunflower (*Helianthus annuus* L.). *PLoS One* **2019**, *14*, e0212371. <https://doi.org/10.1371/journal.pone.0212371>.
- 148) Zhang, X.; Han, C.; Gao, H.; Cao, Y. Comparative transcriptome analysis of the garden asparagus (*Asparagus officinalis* L.) reveals the molecular mechanism for growth with arbuscular mycorrhizal fungi under salinity stress. *Plant Physiol Biochem* **2019**, *141*, 20–29. <https://doi.org/10.1016/j.plaphy.2019.05.013>.
- 149) Afonin, A.M.; Leppyanen, I.V.; Kulaeva, O.A.; Shtark, O.Y.; Tikhonovich, I.A.; Dolgikh, E.A.; Zhukov, V.A. A high coverage reference transcriptome assembly of pea (*Pisum sativum* L.) mycorrhizal roots. *Vavilovskii Zhurnal Genet Seleksii* **2020**, *24*, 331–339. <https://doi.org/10.18699/VJ20.625>.
- 150) Lu, C.C.; Guo, N.; Yang, C.; Sun, H.B.; Cai, B.Y. Transcriptome and metabolite profiling reveals the effects of *Funneliformis mosseae* on the roots of continuously cropped soybeans. *BMC Plant Biol* **2020**, *20*, 479. <https://doi.org/10.1186/s12870-020-02647-2>.
- 151) Moradi Tarnabi, Z.; Iranbakhsh, A.; Mehregan, I.; Ahmadvand, R. Impact of arbuscular mycorrhizal fungi (AMF) on gene expression of some cell wall and membrane elements of wheat (*Triticum*

- aestivum* L.) under water deficit using transcriptome analysis. *Physiol Mol Biol Plants* **2020**, *26*, 143–162. <https://doi.org/10.1007/s12298-019-00727-8>.
- 152) Schubert, R.; Werner, S.; Cirka, H.; Rödel, P.; Tandron Moya, Y.; Mock, H.P.; Hutter, I.; Kunze, G.; Hause, B. Effects of Arbuscular Mycorrhization on Fruit Quality in Industrialized Tomato Production. *Int J Mol Sci* **2020**, *21*, 7029. <https://doi.org/10.3390/ijms21197029>.
- 153) Vangelisti, A.; Turrini, A.; Sbrana, C.; Avio, L.; Giordani, T.; Natali, L.; Giovannetti, M.; Cavallini, A. Gene expression in *Rhizoglyphus irregularis* at two different time points of mycorrhiza establishment in *Helianthus annuus* roots, as revealed by RNA-seq analysis. *Mycorrhiza* **2020**, *30*, 373–387. <https://doi.org/10.1007/s00572-020-00950-2>.
- 154) Zhang, X.Q.; Bai, L.; Sun, H.B.; Yang, C.; Cai, B.Y. Transcriptomic and Proteomic Analysis Revealed the Effect of *Funneliformis mosseae* in Soybean Roots Differential Expression Genes and Proteins. *J Proteome Res* **2020**, *19*, 3631–3643. <https://doi.org/10.1021/acs.jproteome.0c00017>.
- 155) Zorin, E.A.; Afonin, A.M.; Kulaeva, O.A.; Gribchenko, E.S.; Shtark, O.Y.; Zhukov, V.A. Transcriptome Analysis of Alternative Splicing Events Induced by Arbuscular Mycorrhizal Fungi (*Rhizophagus irregularis*) in Pea (*Pisum sativum* L.) Roots. *Plants (Basel)* **2020**, *9*, 1700. <https://doi.org/10.3390/plants9121700>.
- 156) Li, Y.; Duan, T.; Nan, Z.; Li, Y. Arbuscular mycorrhizal fungus alleviates alfalfa leaf spots caused by *Phoma medicaginis* revealed by RNA-seq analysis. *J Appl Microbiol* **2021**, *130*, 547–560. <https://doi.org/10.1111/jam.14387>.
- 157) Vasan, S.; Srivastava, D.; Cahill, D.; Singh, P.P.; Adholeya, A. Important innate differences in determining symbiotic responsiveness in host and non-hosts of arbuscular mycorrhiza. *Sci Rep* **2021**, *11*, 14444. <https://doi.org/10.1038/s41598-021-93626-6>.
- 158) Gaude, N.; Schulze, W.X.; Franken, P.; Krajinski, F. Cell type-specific protein and transcription profiles implicate periarbuscular membrane synthesis as an important carbon sink in the mycorrhizal symbiosis. *Plant Signal Behav* **2012**, *7*, 461–464. <https://doi.org/10.4161/psb.19650>.
- 159) Dhawi, F.; Datta, R.; Ramakrishna, W. Proteomics provides insights into biological pathways altered by plant growth promoting bacteria and arbuscular mycorrhiza in sorghum grown in marginal soil. *Biochim Biophys Acta Proteins Proteom* **2017**, *1865*, 243–251. <https://doi.org/10.1016/j.bbapap.2016.11.015>.
- 160) Sui, X.; Wu, Q.; Chang, W.; Fan, X.; Song, F. Proteomic analysis of the response of *Funneliformis mosseae*/*Medicago sativa* to atrazine stress. *BMC Plant Biol* **2018**, *18*, 289. <https://doi.org/10.1186/s12870-018-1492-1>.
- 161) Bai, L.; Sun, H.B.; Liang, R.T.; Cai, B.Y. iTRAQ Proteomic Analysis of Continuously Cropped Soybean Root Inoculated With *Funneliformis mosseae*. *Front Microbiol* **2019**, *10*, 61. <https://doi.org/10.3389/fmicb.2019.00061>.
- 162) Jia, T.; Wang, J.; Chang, W.; Fan, X.; Sui, X.; Song, F. Proteomics Analysis of *E. angustifolia* Seedlings Inoculated with Arbuscular Mycorrhizal Fungi under Salt Stress. *Int J Mol Sci* **2019**, *20*, 788. <https://doi.org/10.3390/ijms20030788>.
- 163) Mamontova, T.; Afonin, A.M.; Ihling, C.; Soboleva, A.; Lukasheva, E.; Sulima, A.S.; Shtark, O.Y.; Akhtemova, G.A.; Povydysh, M.N.; Sinz, A.; Frolov, A.; Zhukov, V.A.; Tikhonovich, I.A. Profiling of Seed Proteome in Pea (*Pisum sativum* L.) Lines Characterized with High and Low Responsivity to Combined Inoculation with Nodule Bacteria and Arbuscular Mycorrhizal Fungi. *Molecules* **2019**, *24*, 1603. <https://doi.org/10.3390/molecules24081603>.

- 164) Ranjbar Sistani, N.; Desalegn, G.; Kaul, H.P.; Wienkoop, S. Seed Metabolism and Pathogen Resistance Enhancement in *Pisum sativum* During Colonization of Arbuscular Mycorrhizal Fungi: An Integrative Metabolomics-Proteomics Approach. *Front Plant Sci* **2020**, *11*, 872. <https://doi.org/10.3389/fpls.2020.00872>.
- 165) Wu, J.T.; Wang, L.; Zhao, L.; Huang, X.C.; Ma, F. Arbuscular mycorrhizal fungi effect growth and photosynthesis of *Phragmites australis* (Cav.) Trin ex. Steudel under copper stress. *Plant Biol. (Stuttg)* **2020**, *22*, 62–69. <https://doi.org/10.1111/plb.13039>.
- 166) Xi, L.; Shen, Y.; Zhao, X.; Zhou, M.; Mi, Y.; Li, X.; Chen, H.; Wei, Y.; Su, H.; Hou, H. Effects of arbuscular mycorrhizal fungi on frond antimony enrichment, morphology, and proteomics in *Pteris cretica* var. *nervosa* during antimony phytoremediation. *Sci Total Environ* **2021**, *804*, 149904. <https://doi.org/10.1016/j.scitotenv.2021.149904>.
- 167) Gaude, N.; Bortfeld, S.; Erban, A.; Kopka, J.; Krajinski, F. Symbiosis dependent accumulation of primary metabolites in arbuscule-containing cells. *BMC Plant Biol* **2015**, *15*, 234. <https://doi.org/10.1186/s12870-015-0601-7>.
- 168) Salloum, M.S.; Insani, M.; Monteoliva, M.I.; Menduni, M.F.; Silvente, S.; Carrari, F.; Luna, C. Metabolic responses to arbuscular mycorrhizal fungi are shifted in roots of contrasting soybean genotypes. *Mycorrhiza* **2019**, *29*, 459–473. <https://doi.org/10.1007/s00572-019-00909-y>.
- 169) Bonini, P.; Roupahel, Y.; Miras-Moreno, B.; Lee, B.; Cardarelli, M.; Erice, G.; Cirino, V.; Lucini, L.; Colla, G. A Microbial-Based Biostimulant Enhances Sweet Pepper Performance by Metabolic Reprogramming of Phytohormone Profile and Secondary Metabolism. *Front Plant Sci* **2020**, *11*, 567388. <https://doi.org/10.3389/fpls.2020.567388>.
- 170) Roupahel, Y.; Lucini, L.; Miras-Moreno, B.; Colla, G.; Bonini, P.; Cardarelli, M. Metabolomic Responses of Maize Shoots and Roots Elicited by Combinatorial Seed Treatments With Microbial and Non-microbial Biostimulants. *Front Microbiol* **2020**, *11*, 664. <https://doi.org/10.3389/fmicb.2020.00664>.
- 171) Cai, X.; Zhao, H.; Liang, C.; Li, M.; Liu, R. Effects and Mechanisms of Symbiotic Microbial Combination Agents to Control Tomato *Fusarium* Crown and Root Rot Disease. *Front Microbiol* **2021**, *12*, 629793. <https://doi.org/10.3389/fmicb.2021.629793>.
- 172) Liang, S.M.; Zhang, F.; Zou, Y.N.; Kuča, K.; Wu, Q.S. Metabolomics Analysis Reveals Drought Responses of Trifoliolate Orange by Arbuscular Mycorrhizal Fungi With a Focus on Terpenoid Profile. *Front. Plant Sci* **2021**, *12*, 740524. <https://doi.org/10.3389/fpls.2021.740524>.
- 173) Kurth, F.; Mailänder, S.; Bönn, M.; Feldhahn, L.; Herrmann, S.; Große, I.; Buscot, F.; Schrey, S.D.; Tarkka, M.T. *Streptomyces*-induced resistance against oak powdery mildew involves host plant responses in defense, photosynthesis, and secondary metabolism pathways. *Mol Plant Microbe Interact* **2014**, *27*, 891–900. <https://doi.org/10.1094/MPMI-10-13-0296-R>.
- 174) Dong, Z.Y.; Narsing Rao, M.P.; Wang, H.F.; Fang, B.Z.; Liu, Y.H.; Li, L.; Xiao, M.; Li, W.J. Transcriptomic analysis of two endophytes involved in enhancing salt stress ability of *Arabidopsis thaliana*. *Sci. Total Environ* **2019**, *686*, 107–117. <https://doi.org/10.1016/j.scitotenv.2019.05.483>.
- 175) Safdarian, M.; Askari, H.; Shariati, J.V.; Nematzadeh, G. Transcriptional responses of wheat roots inoculated with *Arthrobacter nitroguajacolicus* to salt stress. *Sci Rep* **2019**, *9*, 1792. <https://doi.org/10.1038/s41598-018-38398-2>.
- 176) Gong, Y.; Chen, L.J.; Pan, S.Y.; Li, X.W.; Xu, J.; Zhang, C.; Xing, K.; Qin, S. Antifungal potential evaluation and alleviation of salt stress in tomato seedlings by a halotolerant plant growth-promoting

- actinomycete *Streptomyces* sp. KLBMP5084. *Rhizosphere* **2020**, *16*, 100262. <https://doi.org/10.1016/j.rhisph.2020.100262>.
- 177) Belt, K.; Foley, R.C.; O'Sullivan, C.A.; Roper, M.M.; Singh, K.B.; Thatcher, L.F. A Plant Stress-Responsive Bioreporter Coupled With Transcriptomic Analysis Allows Rapid Screening for Biocontrols of Necrotrophic Fungal Pathogens. *Front Mol Biosci* **2021**, *8*, 708530. <https://doi.org/10.3389/fmolb.2021.708530>.
- 178) Gao, Y.; Ning, Q.; Yang, Y.; Liu, Y.; Niu, S.; Hu, X.; Pan, H.; Bu, Z.; Chen, N.; Guo, J.; Yu, J.; Cao, L.; Qin, P.; Xing, J.; Liu, B.; Liu, X.; Zhu, Y. Endophytic *Streptomyces hygrosopicus* OsiSh-2-Mediated Balancing between Growth and Disease Resistance in Host Rice. *mBio* **2021**, *12*, e0156621. <https://doi.org/10.1128/mBio.01566-21>.
- 179) Zhalnina, K.; Louie, K.B.; Hao, Z.; Mansoori, N.; da Rocha, U.N.; Shi, S.; Cho, H.; Karaoz, U.; Loqué, D.; Bowen, B.P.; Firestone, M.K.; Northen, T.R.; Brodie, E.L. Dynamic root exudate chemistry and microbial substrate preferences drive patterns in rhizosphere microbial community assembly. *Nat Microbiol* **2018**, *3*, 470–480. <https://doi.org/10.1038/s41564-018-0129-3>.
- 180) Esmaeil Zade, N.S.; Sadeghi, A.; Moradi, P. *Streptomyces* strains alleviate water stress and increase peppermint (*Mentha piperita*) yield and essential oils. *Plant Soil* **2019**, *434*, 441–452. <https://doi.org/10.1007/s11104-018-3862-8>.
- 181) Tisserant, E.; Malbreil, M.; Kuo, A.; Kohler, A.; Symeonidi, A.; Balestrini, R.; Charron, P.; Duensing, N.; Frei dit Frey, N.; Gianinazzi-Pearson, V.; Gilbert, L.B.; Handa, Y.; Herr, J.R.; Hijri, M.; Koul, R.; Kawaguchi, M.; Krajinski, F.; Lammers, P.J.; Masclaux, F.G.; Murat, C.; Morin, E.; Ndikumana, S.; Pagni, M.; Petitpierre, D.; Requena, N.; Rosikiewicz, P.; Riley, R.; Saito, K.; San Clemente, H.; Shapiro, H.; van Tuinen, D.; Bécard, G.; Bonfante, P.; Paszkowski, U.; Shachar-Hill, Y.Y.; Tuskan, G.A.; Young, J.P.; Sanders, I.R.; Henrissat, B.; Rensing, S.A.; Grigoriev, I.V.; Corradi, N.; Roux, C.; Martin, F. Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. *Proc Natl Acad Sci USA* **2013**, *110*, 20117–20122. <https://doi.org/10.1073/pnas.1313452110>.
- 182) Lin, K.; Limpens, E.; Zhang, Z.; Ivanov, S.; Saunders, D.G.; Mu, D.; Pang, E.; Cao, H.; Cha, H.; Lin, T.; Zhou, Q.; Shang, Y.; Li, Y.; Sharma, T.; van Velzen, R.; de Ruijter, N.; Aanen, D.K.; Win, J.; Kamoun, S.; Bisseling, T.; Geurts, R.; Huang, S. Single nucleus genome sequencing reveals high similarity among nuclei of an endomycorrhizal fungus. *PLoS Genet* **2014**, *10*, e1004078. <https://doi.org/10.1371/journal.pgen.1004078>.
- 183) Tang, N.; San Clemente, H.; Roy, S.; Bécard, G.; Zhao, B.; Roux, C. A Survey of the Gene Repertoire of *Gigaspora rosea* Unravels Conserved Features among Glomeromycota for Obligate Biotrophy. *Front Microbiol* **2016**, *7*, 233. <https://doi.org/10.3389/fmicb.2016.00233>.
- 184) Beaudet, D.; Chen, E.C.H.; Mathieu, S.; Yildirim, G.; Ndikumana, S.; Dalpé, Y.; Séguin, S.; Farinelli, L.; Stajich, J.E.; Corradi, N. Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. *DNA Res* **2018**, *25*, 217–227. <https://doi.org/10.1093/dnares/dsx051>.
- 185) Chen, E.C.H.; Morin, E.; Beaudet, D.; Noel, J.; Yildirim, G.; Ndikumana, S.; Charron, P.; St-Onge, C.; Giorgi, J.; Krüger, M.; Marton, T.; Ropars, J.; Grigoriev, I.V.; Hainaut, M.; Henrissat, B.; Roux, C.; Martin, F.; Corradi, N. High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*. *New Phytol* **2018**, *220*, 1161–1171. <https://doi.org/10.1111/nph.14989>.
- 186) Sun, X.; Chen, W.; Ivanov, S.; MacLean, A.M.; Wight, H.; Ramaraj, T.; Mudge, J.; Harrison, M.J.; Fei, Z. Genome and evolution of the arbuscular mycorrhizal fungus *Diversispora epigaea* (formerly *Glomus*

- versiforme*) and its bacterial endosymbionts. *New Phytol* **2019**, *221*, 1556–1573. <https://doi.org/10.1111/nph.15472>.
- 187) Morin, E.; Miyauchi, S.; San Clemente, H.; Chen, E.C.H.; Pelin, A.; de la Providencia, I.; Ndikumana, S.; Beaudet, D.; Hainaut, M.; Drula, E.; Kuo, A.; Tang, N.; Roy, S.; Viala, J.; Henrissat, B.; Grigoriev, I.V.; Corradi, N.; Roux, C.; Martin, F.M. Comparative genomics of *Rhizophagus irregularis*, *R. cerebriiforme*, *R. diaphanus* and *Gigaspora rosea* highlights specific genetic features in Glomeromycotina. *New Phytol* **2019**, *222*, 1584–1598. doi: 10.1111/nph.15687.
- 188) Venice, F.; Ghignone, S.; Salvioli di Fossalunga, A.; Amselem, J.; Novero, M.; Xianan, X.; Sędziewska Toro, K.; Morin, E.; Lipzen, A.; Grigoriev, I.V.; Henrissat, B.; Martin, F.M.; Bonfante, P. At the nexus of three kingdoms: the genome of the mycorrhizal fungus *Gigaspora margarita* provides insights into plant, endobacterial and fungal interactions. *Environ Microbiol* **2020**, *22*, 122–141. <https://doi.org/10.1111/1462-2920.14827>.
- 189) Tocchetti, A.; Bordoni, R.; Gallo, G.; Petiti, L.; Corti, G.; Alt, S.; Cruz, J.C.; Salzano, A.M.; Scaloni, A.; Puglia, A.M.; De Bellis, G.; Peano, C.; Donadio, S.; Sosio, M. A Genomic, Transcriptomic and Proteomic Look at the GE2270 Producer *Planobispora rosea*, an Uncommon Actinomycete. *PLoS One* **2015**, *10*, e0133705. <https://doi.org/10.1371/journal.pone.0133705>.
- 190) Han, J.; Gao, Q.X.; Zhang, Y.G.; Li, L.; Mohamad, O.A.A.; Rao, M.P.N.; Xiao, M.; Hozzein, W.N.; Alkhalifah, D.H.M.; Tao, Y.; Li, W.J. Transcriptomic and Ectoine Analysis of Halotolerant *Nocardiopsis gilva* YIM 90087T Under Salt Stress. *Front Microbiol* **2018**, *9*, 618. <https://doi.org/10.3389/fmicb.2018.00618>.
- 191) Liu, C.; Fan, D.; Li, Y.; Chen, Y.; Huang, L.; Yan, X. Transcriptome analysis of *Valsa mali* reveals its response mechanism to the biocontrol actinomycete *Saccharothrix yanglingensis* Hhs.015. *BMC Microbiol* **2018**, *18*, 90. <https://doi.org/10.1186/s12866-018-1225-5>.
- 192) Wang, C.; Chen, Y.; Zhou, H.; Li, X.; Tan, Z. Adaptation mechanisms of *Rhodococcus* sp. CNS16 under different temperature gradients: Physiological and transcriptome. *Chemosphere* **2020**, *J238*, 124571. <https://doi.org/10.1016/j.chemosphere.2019.124571>.
- 193) Zhang, Y.; Li, Y.; Zhang, Y.; Wang, Z.; Zhao, M.; Su, N.; Zhang, T.; Chen, L.; Wei, W.; Luo, J.; Zhou, Y.; Xu, Y.; Xu, P.; Li, W.; Tao, Y. Quantitative Proteomics Reveals Membrane Protein-Mediated Hypersaline Sensitivity and Adaptation in Halophilic *Nocardiopsis xinjiangensis*. *J Proteome Res* **2016**, *15*, 68–85. <https://doi.org/10.1021/acs.jproteome.5b00526>.
- 194) Lee, M.Y.; Kim, H.Y.; Lee, S.; Kim, J.G.; Suh, J.W.; Lee, C.H. Metabolomics-Based Chemotaxonomic Classification of *Streptomyces* spp. and Its Correlation with Antibacterial Activity. *J Microbiol Biotechnol* **2015**, *25*, 1265–1274. <https://doi.org/10.4014/jmb.1503.03005>.
- 195) Takehana, Y.; Umekita, M.; Hatano, M.; Kato, C.; Sawa, R.; Igarashi, M. Fradiamine A, a new siderophore from the deep-sea actinomycete *Streptomyces fradiae* MM456M-mF7. *J Antibiot (Tokyo)* **2017**, *70*, 611–615. <https://doi.org/10.1038/ja.2017.26>.
- 196) Elmahdy, M.H.; Azmy, A.F.; El-Gebaly, E.; Saafan, A.; Gaber, Y. A Comparative Proteomic Study of *Thermobifida cellulosilytica* TB100T Secretome Grown on Carboxymethylcellulose and Rice Straw. *Open Biotechnol J* **2020**, *14*, 42–51. <https://doi.org/10.2174/1874070702014010042>.
- 197) Armin, R.; Zühlke, S.; Grunewaldt-Stöcker, G.; Mahnkopp-Dirks, F.; Kusari, S. Production of Siderophores by an Apple Root-Associated *Streptomyces ciscaucasicus* Strain GS2 Using Chemical and Biological OSMAC Approaches. *Molecules* **2021**, *26*, 3517. <https://doi.org/10.3390/molecules26123517>.