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|  | **Main Author** | **Abstract Title** |
| **1** | **Ahkami, Amir H.\*** (amir.ahkami@pnnl.gov) | Investigating a genome-to-phenotype pipeline for model grasses |
| **2** | **Anderton, Christopher R.\*** (Christopher.Anderton@pnnl.gov) | Exploring the soybean microbiome using complementary spatial metabolomics techniques |
| **3** | **Armanhi, Jaderson\*** (jader.armahi@gmail.com) | Community-based culture collection as a strategy for targeting beneficial plant-associated bacteria from the sugarcane microbiome |
| **4** | **Billingsley, John\*** (johnbillingsley@ucla.edu) | Engineering the biocatalytic selectivity of iridoid production in Saccharomyces cerevisiae |
| **5** | **Bingol, Kerem\*** (blairpm@ornl.gov) | Identification of Unknown Secondary Metabolites by Hybrid NMR/MS Approach: Application to Studying the Flowering Time in Arabidopsis thaliana |
| **6** | **Blair, Patricia\*** (blairpm@ornl.gov) | Characterization of the microviridin biosynthetic gene cluster from Chryseobacterium |
| **7** | **Brisson, Vanessa L.\*** (vlbrisson@lbl.gov) | Changes in Root Exudation and Microbiome Recruitment by Maize in Response to Phosphate Limitation |
| **8** | **Chin, Elizabeth L.\*** (elichin@ucdavis.edu) | Metabolomics to understand and detect C. Liberibacter asiaticus infection |
| **9** | **Chooi, Yit-Heng\*** (yitheng.chooi@uwa.edu.au) | Functional genomics-guided discovery of cryptic metabolites involved in pathogenic plant-microbe interactions |
| **10** | **Damasceno, Natalia B.\*** (nbdbio@gmail.com) | Mapping the colonization of a synthetic microbial community inoculum from sugarcane microbiome in maize and soybean plants |
| **11** | **de Souza, Rafael Soares Correa\*** (scs.rafael@gmail.com) | GenomeÂ sequence of an abundance-driven microbiome synthetic community with beneficial effect to plant development |
| **12** | **Gao, Minglu Z.\***( hugogao@uga.edu) | Seeds of antagonism: An ABC transporter and its adjacent transcription factor in Fusarium verticillioides are required for pyrrocidine B tolerance |
| **13** | **Helmann, Tyler C.\*** (thelmann@berkeley.edu) | Efflux transporters contribute to virulence and host compatibility of Pseudomonas syringae B728a |
| **14** | **Heyman, Heino M.\*** (heino.heyman@pnnl.gov) | Metabolomics guided isolation of significant biological plant, soil and microbial secondary metabolites |
| **15** | **Hotton, Sara K.\*** (sara.hotton@bayer.com) | Use of LC-MS/MS in the characterization of protein bioactives from Bacillus spores |
| **16** | **Igwe, Alexandria N. \***  (aigwe@ucdavis.edu) | Assessing Microbial Community Contribution to Plant Abiotic Stress Tolerance: A Case Study in Serpentine Soils |
| **17** | **Izquierdo, Javier A.\*** (javier.izquierdo@hofstra.edu) | The rhizosphere of the beachgrass Ammophila breviligulata as a model for plant-microbiome interactions |
| **18** | **Kistler, H. Corby \*** (hckist@umn.edu) | Nanoscale clustering of enzymes in a fungal sesquiterpene biosynthetic pathway |
| **19** | **Korenblum, Elisa\*** (elisa.korenblum@weizmann.ac.il) | Tomato Rhiz'OMICS |
| **20** | **Liechty, Zachary S.\*** (zsliechty@ucdavis.edu) | Microbial variation among high and low methane emitting rice cultivars |
| **21** | **Lin, Yu-Ju Lulu \*** (superolulu@gmail.com) | Metabolic Engineering a Probiotic Yeast to Increase Astaxanthin Production |
| **22** | **Liu, Fang NO.\*** (fliu21@vols.utk.edu) | Strigolactone impacts on soybean rhizosphere microbial community assembly |
| **23** | **McNeil, Christopher J.\*** (cjmcneil@ucdavis.edu) | Impact of HLB on the Metallome and Metabolome of Citrus |
| **24** | **Murphy, Katherine M.\*** (kmmurphy@ucdavis.edu) | Root-associated microbiome of a diterpene deficient maize mutant |
| **25** | **Noirot, Marie-Francoise S.\*** (mnoirot@anl.gov) | A protein-protein interaction network centered on c-di-GMP signaling in the Plant Growth Promoting rhizobacteria P. fluorescens. |
| **26** | **Okrent, Rachel A.\*** (Rachel.Okrent@ars.usda.gov) | Evolution and diversity of a biosynthetic gene cluster for production of a vinylglyine |
| **27** | **Padhi, Emily MT.\*** (epadhi@ucdavis.edu) | Changes in the root metabolome of citrus plants infected with Candidatus Liberibacter asiaticus |
| **28** | **Pelletier, Dale L.\*** (pelletierda@ornl.gov) | Survey of the biosynthetic potential of the Populus microbiome |
| **29** | **Rosahl, Sabine L. \*** (srosahl@ipb-halle.de) | Hydroxycinnamic acid amides are exported by a MATE transporter in Arabidopsis |
| **30** | **Santos MedellÃ­n, Christian M.\*** (cmsantosm@ucdavis.edu) | Drought stress results in a compartment-specific restructuring of the rice root-associated microbiomes |
| **31** | **Schmidt, Eric W.\*** (ews1@utah.edu) | Chemical diversity generation using RiPP pathways |
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| **33** | **Swift, Candice L.\*** (cswift@umail.ucsb.edu) | Deciphering the role of fungal secondary metabolites within anaerobic microbial communities |
| **34** | **Tholl, Dorothea BC.\*** (tholl@vt.edu) | Volatile Terpene Secondary Metabolism in Switchgrass Roots in the Biotic/Abiotic Environment |
| **35** | **Trail, Frances\*** (trail@msu.edu) | Examining the secondary metabolite activity in the lichen community |
| **36** | **Yan, Yan\*** (mywillflint@gmail.com) | Developing Herbicide with New Mode of Action: Target-guided Genome Mining of Fungus |
| **37** | **Ying-Ning, Ho\*** (silentboyryan0109@gmail.com) | Enzymatic transformation of the siderophore, pyochelin through imaging mass spectrometry of bacteria-fungi interaction |
| **38** | **Zhalnina, Kateryna V.\*** (kzhalnina@lbl.gov) | Chemistry of the plant exudation and substrate utilization preferences of soil microorganisms underlying rhizosphere microbiome assembly in annual and perennial grasses |
| **39** | **Zhang, Jia Jia R\*** (jaz010@ucsd.edu) | Broad-host-range expression reveals native and host regulatory elements influencing heterologous antibiotic production in Gram-negative bacteria |