
Rhizosphere Biology

Series Editor

Anil K. Sharma

Biological Sciences, CBSH, G. B. Pant University of Agriculture & Technology,
Pantnagar, Uttarakhand, India

The Series Rhizosphere Biology, emphasizes on the different aspects of Rhizosphere. Major increase in agricultural productivity, to meet growing food demands of human population is imperative, to survive in the future. Along with methods of crop improvement, an understanding of the rhizosphere biology, and the ways to manipulate it, could be an innovative strategy to deal with this demand of increasing productivity. This Series would provide comprehensive information for researchers, and encompass all aspects in field of rhizosphere biology. It would comprise of topics ranging from the classical studies to the most advanced application being done in the field. Rhizosphere is a dynamic environment, and a series of processes take place to create a congenial environment for plant to grow and survive. There are factors which might hamper the growth of plants, resulting in productivity loss, but, the mechanisms are not very clear. Understanding the rhizosphere is needed, in order to create opportunities for researchers to come up with robust strategies to exploit the rhizosphere for sustainable agriculture.

There are titles already available in the market in the broad area of rhizosphere biology, but there is a major lack of information as to the functions and future applications of this field. These titles have not given all the up-to-date information required by the today's researchers and therefore, this Series aims to fill out those gaps.

More information about this series at <http://www.springer.com/series/15861>

Vadakattu V. S. R. Gupta • Anil K. Sharma
Editors

Rhizosphere Biology: Interactions Between Microbes and Plants

 Springer

Editors

Vadakattu V. S. R. Gupta
Agriculture and Food, CSIRO
Urrbrae, Australia

Anil K. Sharma
Department of Biological Sciences
CBSH, G.B. Pant University of Agriculture &
Technology
Pantnagar, Uttarakhand, India

ISSN 2523-8442

Rhizosphere Biology

ISBN 978-981-15-6124-5

ISSN 2523-8450 (electronic)

ISBN 978-981-15-6125-2 (eBook)

<https://doi.org/10.1007/978-981-15-6125-2>

© Springer Nature Singapore Pte Ltd. 2021, corrected publication 2021

This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed.

The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

The publisher, the authors, and the editors are safe to assume that the advice and information in this book are believed to be true and accurate at the date of publication. Neither the publisher nor the authors or the editors give a warranty, expressed or implied, with respect to the material contained herein or for any errors or omissions that may have been made. The publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

This Springer imprint is published by the registered company Springer Nature Singapore Pte Ltd.

The registered company address is: 152 Beach Road, #21-01/04 Gateway East, Singapore 189721, Singapore

Preface

Rhizosphere plant–microbe interactions are diverse, spatially and temporally dynamic, influenced by plant, soil biophysical environment, and are critical to plant health and crop productivity. It is well established that bacteria and fungi around a plant's root in the rhizosphere, the miniature ecosystem around the root, can influence both the root's form and its physiology. The rhizosphere concept, coined in 1904 by Lorenz Hiltner about the roles of soil microorganisms in plant nutrition and health, has initiated a century-long research and discussion about organismic interactions between plants and microbes. More than 50 years ago, Dr Ralph Foster's (CSIRO, Adelaide) electron micrographs revealed the intricate structure of rhizosphere, rhizoplane, and endosphere environments and the interplay between plant root, microflora, and protozoa. Rhizosphere microbiota provides a valuable potential resource of plant probiotic and growth-promoting functions capable of conjugating crop productivity within sustainable agricultural systems. It is, therefore, important to understand the dynamics of rhizosphere interactions in order to develop practical strategies that would help improving yield and maintain ecosystem health.

During the last decade, there has been a renewed interest in exploring the dynamics of the rhizosphere, using *omics* tools, for its composition and organismal interactions occurring in the complex spatial structuring at the root–soil interface and their key drivers during the crop growth. Recent research has shown structural and functional diversification of root-associated microbial communities of crop varieties, wild and domesticated accessions of barley, maize, canola, peas, and various *Arabidopsis* accessions, etc. Some of these findings also identified bacterial taxa which were positively correlated with crop performance or yield. This led to an intense effort to identify the plant-based traits that modulate the genetic structure and diversity, gene expression, and functional profile from the outer realms of rhizosphere to inside the root. This new understanding has highlighted an attractive avenue that would help to better harness beneficial outcomes from plant–microbiome interactions.

This book is a compilation of the latest knowledge on plant and microbial aspects of rhizosphere biology covering different ecological, molecular, and biochemical characteristics of rhizosphere and endosphere interactions. It contains 15 chapters, each prepared by authors who are internationally recognized for their knowledge and

expertise in a particular area of rhizosphere interactions. Additionally, it covers the cross-talk between plants and microbes including quorum-sensing signal molecules, plant interactions with abiotic factors, and potential ways rhizosphere microbial composition and functionality could be manipulated for enhanced and efficient benefits. The different chapters cover key areas such as (1) factors driving rhizosphere biology and interactions, (2) diversity of phenotypic and functional groups, (3) functional significances of rhizosphere interactions, and (4) how best to manipulate rhizosphere interactions. A special feature of the papers is that they highlight the benefits of using the latest omics (metagenomics, transcriptomics, and proteomics) and isotopic tools in dissecting the plethora of mechanisms, genes, and metabolites involved in the multitrophic interactions.

Endophytic bacteria, those that colonize the internal tissue of the plant showing no external sign of infection or negative effect on their host, have been found in all plants and form a range of relationships including symbiotic, mutualistic, commensalistic, and trophobiotic interactions. This type of plant microbiome is now considered as the second genome of the host plant and concepts such as “holobiont” comprising the plant with its endophytic microbiome as an extended phenotype and a unified system. In the chapter on bacterial endophytes, Tosi et al. (Chap. 1) present a comprehensive summary of the latest knowledge about the diversity and functions of bacterial (including actinobacteria) endophytes, their influence on plant fitness, and the potential to manipulate their functions in agroecosystems. The presence of a taxonomic overlap between endophytic and rhizospheric communities and clear community shifts between these compartments confirms the idea that rhizosphere is a key habitat regulating endophytic communities. Although soil type can have a major influence, strong and significant host genotype effects on the diversity resulting in distinct taxonomic composition of endophytic bacteria have been shown with a variety of plants. However, the observation of differential abundance, core microbiomes, new knowledge on the heritability of the specific taxa and their links to plant genotype through genome-wide association studies is needed in order to develop designer plant–microbiome combinations that maximize beneficial functions. The involvement of root exudates as carbon and nutrient sources in modifying the rhizosphere microbial communities, as proposed by Albert Rovira more than 50 years ago, is now extended to include signal molecules and root architecture influencing the microbiome composition. In Chap. 9, Haichar and Achouak describe how newly introduced and modified genes in plants influence the quality and quantity of root exudates and in turn rhizosphere microbiome. It is increasingly becoming clear that the ability of soil microbes to colonize a particular plant species is fuelled and modulated by the release of signals by either or both partners and are only recognized by the right partner. Taking the knowledge from legume–rhizobia and plant–mycorrhizal symbioses, Antar et al. summarize (Chap. 13) the latest knowledge about the signals involved in other beneficial plant–microbe interactions and microbe–microbe signal interactions. In spite of recent findings about the intricacies of rhizosphere interactions, the exact molecular mechanisms governing the complex root–soil–microbe interactions remain largely unknown. Balasubramanian et al. present (Chap. 14) a review of

what is known about the strategies for manipulating the rhizosphere region with a focus on engineering the root H⁺ efflux and organic anions, secondary metabolite composition of root exudates, alterations in root biomass accumulation, and below-ground carbon allocations for improved plant performance.

The carbon inputs by plant roots not only provide the primary source of organic C into the soil modifying rhizosphere microbiome, but the chemical composition of exudates also strongly influences the metabolic potential of rhizosphere-enriched microbes along with mediating nutrient fluxes in the rhizosphere. In Chap. 2, Pett-Ridge et al. provide evidence showing the downstream effects of rhizosphere dynamics on the colonization of nearby soil minerals, degradation of prior season's root litter, and the balance of stabilized versus lost soil carbon. Furthermore, this study provides an excellent example illustrating the benefits of using the latest genomic and isotopic techniques to unravel the mechanisms of C flow between growing plant roots, soil microbial communities, and the surrounding mineral matrix. The beneficial effects of these rhizosphere interactions on nutrient fluxes and availabilities could also improve plant nutrition through increased nutrient use efficiency and, as discussed by Paterson and Mwafurirwa (Chap. 3), provide a realistic means of improving plant health and productivity while potentially also mitigating environmental impacts. Also, recent findings about the diazotrophic communities in the rhizosphere and endosphere in terms of their diversity and functional capacity have rejuvenated the old idea of harnessing the biological N fixation in nonleguminous crops through manipulation of this specific functional group; the chapter by Roley (Chap. 4) presents the latest knowledge on this topic.

The rhizobia-legume and mycorrhizae-plant interactions are two well-established examples of plant-microbe symbiosis with extensive research and knowledge about the mechanistic aspects of the beneficial interactions. Recent research has shown that the interactions of "Arbuscular Mycorrhizal Fungi" (AMF), the obligate biotrophs, in the rhizosphere are not just restricted to host plant but involve bacteria in the rhizosphere and hyphosphere; Wang and Feng discussed (Chap. 11) new insights into interactions between AM fungi and other organisms in the rhizosphere.

Plant health status affected by the presence of pathogens and root disease incidence could be a driver for change in the root microbiome as discussed in the chapter by Barnett (Chap. 8) and it was proposed that microsite-based variation between healthy and diseased niches in the root system could ultimately lead to the development of disease suppressive microbiomes; however, the exact mechanisms for such community changes remain elusive at present. Alternatively, plant-microbe interactions in the rhizosphere can have a significant impact on plant health acting as the first line of defense in the rhizosphere. Therefore, identification of plant genetic traits involved in the recruitment of beneficial microorganisms, i.e. promoting probiotic microbial community, would help improve plant defenses against biotic stresses; the chapter by Chiaramonte et al. (Chap. 7) discusses strategies and potential to explore this option through plant breeding programs.

Plant root-biota associations in the rhizosphere involve complex networks and interactions between micro- and macroorganisms across multiple microsites and in intricate spatial structuring that can vary temporally during crop growth from

seedling to maturity. Recent evidence from genomic and transcriptomic studies clearly indicates that there is a strong association between rhizosphere development and taxonomic makeup including the succession in bacterial community in field environments. This has been demonstrated for several crops including cereals, canola, cotton, and other crops (Richardson et al., Chap. 5). The major predators of microorganisms such as protists, faunal nematodes, and microarthropods can modulate the composition of rhizosphere microbiome through preferential feeding, with functional consequences in plant performance by affecting nutrient cycling, pathogen density, etc. (Geisen and Quest, Chap. 12). As rhizosphere food webs are not universally identical, the functional importance of microbial–faunal interactions is modulated by the soil habitat structure and management.

The concept of succession in rhizosphere microbiome dynamics also leads to the idea of “legacy” in that the rhizosphere of crop leaves a footprint in the soil systems affecting the following crops. Since rhizosphere interactions involve modifications in soil physicochemical and biological components, the legacy effects should incorporate physical, chemical, and biological effects that potentially endure beyond the root that created it. In the chapter by Oliver et al. (Chap. 6), they suggest that constraints of destructive sampling can be overcome from the recent advances in micro X-ray computed tomography, but it still requires other complementary techniques to determine the extent of the rhizosphere legacy.

It was considered that the most effective form of manipulation of rhizosphere and endosphere microbiomes is through the use of beneficial microorganisms, “bio-inoculants” either singly or as consortia for biocontrol to reduce or eliminate plant disease effects or effects of abiotic stresses such as from drought/water-stress or salinity effects. Through the use of latest *omics* tools (metagenomic, transcriptomics, and metabolomics), it is now possible to describe in-depth the networks of members of rhizosphere microbiomes including the effects of introducing inoculants as well as identifying mechanisms to manipulate and engineer microbiomes (Franco, Chap. 15). For example, recent evidence suggests that rhizobacteria with the capacity to produce ACC deaminase can initiate a cascade of changes in plant physiological and biochemical responses resulting in increased tolerance to abiotic stresses in a broad range of plant species (Sharma et al., Chap. 10).

As a result of fast-changing global climate scenario with predictions for reduced rainfall and increased effects of other abiotic stresses across many agricultural regions worldwide, exploitation of such beneficial plant–microbe interactions to alleviate abiotic stress effects in crops should be one of the key approaches to promote resilience and improve global food production. A majority of the recent research on the makeup and dynamics of rhizosphere microbiome until now has concentrated on taxonomic/phylogenetic makeup of the microbiome mainly about who is present and variations with plant type, management, and soil environment. In view of the extensive diversity and the dynamic spatial and temporal structure of the microbiome, interpretation and extrapolation of variations in phylogenetic makeup in terms of their functional potential and resilience have been found to be not straightforward. Hence future research on plant-trait based microbiome interactions requires investigations targeting specific functional groups associated with key

plant traits to help with the development of management interventions that can improve productivity in agricultural systems. Through a combination of genomic, transcriptomic, and isotopic tools, it should be possible to directly follow the dynamics of specific microbial functional group and link it with associated functional fluxes. Such research would facilitate the identification of key drivers from plant, microbial, and process perspectives, thereby assisting in the development of new designer plant holobionts that utilize native soil microbiome through next-generation crop breeding, “syncoms” or synthetic communities and management practices for sustainable and resilient food production systems.

Urrbrae, Australia
Pantnagar, Uttarakhand, India

Vadakattu V. S. R. Gupta
Anil K. Sharma

Acknowledgements

With its complexity and diversity of life it hosts, the topic of rhizosphere attracts the interest of many disciplines. As the co-editors of this book, we acknowledge all the authors for preparing excellent summaries with thought provoking discussions on the various topics of rhizosphere interactions. We extend our sincere appreciation to the various reviewers of the manuscripts for their diligence in helping to improve the contributions. Ms. Ranjita Vadakattu provided invaluable help by providing logistical support through the compilation and revision process keeping track of all the contributions. We also thank our parent organizations CSIRO Agriculture and Food in Australia and G.B. Pant University of Agriculture & Technology in India for their support to our participation in preparing this publication.

Contents

1	Bacterial Endophytes: Diversity, Functional Importance, and Potential for Manipulation	1
	Micaela Tosi, Jonathan Gaiero, Nicola Linton, Tolulope Mafa-Attoye, Anibal Castillo, and Kari Dunfield	
2	Rhizosphere Carbon Turnover from Cradle to Grave: The Role of Microbe–Plant Interactions	51
	Jennifer Pett-Ridge, Shengjing Shi, Katerina Estera-Molina, Erin Nuccio, Mengting Yuan, Ruud Rijkers, Tami Swenson, Kateryna Zhalnina, Trent Northen, Jizhong Zhou, and Mary K. Firestone	
3	Root–Soil–Microbe Interactions Mediating Nutrient Fluxes in the Rhizosphere	75
	Eric Paterson and Lumbani Mwafulirwa	
4	Diazotrophic Nitrogen Fixation in the Rhizosphere and Endosphere	93
	Sarah S. Roley	
5	Root Microbiome Structure and Microbial Succession in the Rhizosphere	109
	Alan E. Richardson, Akitomo Kawasaki, Leo M. Condrón, Peter R. Ryan, and Vadakattu V. S. R. Gupta	
6	Rhizosphere Legacy: Plant Root Interactions with the Soil and Its Biome	129
	Ivanah C. Oliver, Oliver G. G. Knox, Richard J. Flavel, and Brian R. Wilson	
7	Rhizosphere Microbiome and Soil-Borne Diseases	155
	Josiane Barros Chiaramonte, Lucas William Mendes, and Rodrigo Mendes	
8	Root Disease Impacts on Root-Rhizosphere Microbial Communities	169
	Stephen Barnett	

9	Newly Introduced or Modified Genes in Plants Potentially Modulate the Host Microbiome	185
	Feth el Zahar Haichar and Wafa Achouak	
10	Rhizosphere Plant–Microbe Interactions Under Abiotic Stress	195
	Suvigya Sharma, Dinesh Chandra, and Anil K. Sharma	
11	Arbuscular Mycorrhizal Fungi Interactions in the Rhizosphere . . .	217
	Fei Wang and Gu Feng	
12	Microbial–Faunal Interactions in the Rhizosphere	237
	Stefan Geisen and Casper W. Quist	
13	Inter-Organismal Signaling in the Rhizosphere	255
	Mohammed Antar, Parghat Gopal, Levini Andrew Msimbira, Judith Naamala, Mahtab Nazari, William Overbeek, Rachel Backer, and Donald L. Smith	
14	Molecular Mechanisms of Plant–Microbe Interactions in the Rhizosphere as Targets for Improving Plant Productivity	295
	Vimal Kumar Balasubramanian, Christer Jansson, Scott E. Baker, and Amir H. Ahkami	
15	Inoculation Effects in the Rhizosphere: Diversity and Function . . .	339
	Christopher M. M. Franco	
	Correction to: Newly Introduced or Modified Genes in Plants Potentially Modulate the Host Microbiome	C1
	Feth el Zahar Haichar and Wafa Achouak	

Editors and Contributors

About the Editors

Vadakattu V. S. R. Gupta is a Senior Principal Research Scientist at the CSIRO Agriculture and Food unit at the Waite campus in Adelaide, South Australia. He has more than 20 years of experience in fundamental and applied, field-based functional microbial ecology research in soil and water ecosystems in Australia, Canada, and India. His research interests include unraveling the complexities of microbial diversity, functional capability, and resilience of microbe–soil–plant interactions for disease suppression and plant nutrition as a key for developing sustainable agricultural systems. His research has identified changes in soil biology in genetically modified crop systems and the impacts of herbicides on soil biological functions. He has published over 100 refereed articles in scientific journals and books and developed soil biology research investment priorities for government and industry funding bodies in Australia. He was awarded the 2015 Prescott Medal by the Soil Science Society of Australia for his outstanding contribution to Soil Science.

Anil K. Sharma is a Professor at the Department of Biological Sciences, CBSH G.B. Pant University of Agriculture & Technology, Pantnagar. He was a Visiting Scientist at the University of Basel, Switzerland from July 2003 to November, 2003, and at the University of Helsinki, Finland in 2013. He completed his postdoctoral studies at GSU, Louisiana, USA, and he has extensive research and teaching experience. He is a reviewer for DBT, DST, and MOEF projects and for journals such as the Biocontrol Journal, International Journal of Agriculture, and Microbiology. He holds three patents in the field of plant biology and microbiology and has received a number of prestigious grants. His laboratory is involved in various international collaborations, and he has published more than 84 research articles, 32 review articles, and two books with renowned publishers. He has presented his research on several internationally acclaimed platforms.

Contributors

Wafa Achouak Aix Marseille Univ, CNRS, CEA, UMR 7265 BVME, LEMIRE, ECCOREV FR 3098, Saint-Paul-lez-Durance, France

Amir H. Ahkami Environmental Molecular Sciences Laboratory (EMSL), Pacific Northwest National Laboratory (PNNL), Richland, WA, USA

Scott E. Baker Environmental Molecular Sciences Laboratory (EMSL), Pacific Northwest National Laboratory (PNNL), Richland, WA, USA

Vimal Kumar Balasubramanyam Environmental Molecular Sciences Laboratory (EMSL), Pacific Northwest National Laboratory (PNNL), Richland, WA, USA

Stephen Barnett Medical Biotechnology, Flinders University, Bedford Park, SA, Australia

South Australian Research and Development Institute, Hartley Grove, Urrbrae, SA, Australia

Anibal Castillo Environmental Microbiology of Agro-Ecosystems, School of Environmental Sciences, Guelph, ON, Canada

Josiane Barros Chiaramonte Embrapa Meio Ambiente, Jaguariúna, SP, Brazil

Leo Condrón Faculty of Agriculture and Life Sciences, Lincoln University, Christchurch, New Zealand

Kari Dunfield Environmental Microbiology of Agro-Ecosystems, School of Environmental Sciences, Guelph, ON, Canada

Feth el Zahar Haichar Univ Lyon, Université Claude Bernard Lyon 1, UMR CNRS 5557, Laboratoire d'Ecologie Microbienne, UMR INRA 1418, Villeurbanne Cedex, France

INSA-Lyon, Université Claude Bernard Lyon1, CNRS, UMR5240, Microbiologie, Adaptation, Pathogénie, Univ Lyon, 10 rue Raphaël Dubois, 69622, Villeurbanne, France

Katerina Estera-Molina Department of Environmental Science, Policy and Management, University of California, Berkeley, CA, USA

Gu Feng College of Resources and Environmental Sciences, China Agricultural University, Beijing, People's Republic of China

Mary K. Firestone Department of Environmental Science, Policy and Management, University of California, Berkeley, CA, USA

Earth and Environmental Sciences, Lawrence Berkeley National Laboratory, Livermore, CA, USA

Richard J. Flavel Faculty of Science, Agriculture, Business and Law, School of Environmental and Rural Science, The University of New England, Armidale, NSW, Australia

Chris Franco Medical Biotechnology, College of Medicine and Public Health, Flinders University, Bedford Park, SA, Australia

Jonathan Gaiero Environmental Microbiology of Agro-Ecosystems, School of Environmental Sciences, Guelph, ON, Canada

Stefan Giesen Department of Terrestrial Ecology, Netherland Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands

Christer Jansson Environmental Molecular Sciences Laboratory (EMSL), Pacific Northwest National Laboratory (PNNL), Richland, WA, USA

Akitomo Kawasaki CSIRO Agriculture and Food, Canberra, ACT, Australia

Oliver G. G. Knox Faculty of Science, Agriculture, Business and Law, School of Environmental and Rural Science, The University of New England, Armidale, NSW, Australia

Nicola Linton Environmental Microbiology of Agro-Ecosystems, School of Environmental Sciences, Guelph, ON, Canada

Tolulope Mafa-Attoye Environmental Microbiology of Agro-Ecosystems, School of Environmental Sciences, Guelph, ON, Canada

Lucas William Mendes Centro de Energia Nuclear na Agricultura, Universidade de São Paulo, Piracicaba, SP, Brazil

Rodrigo Mendes Embrapa Meio Ambiente, Jaguariúna, SP, Brazil

Lumbani Mwafulirwa The James Hutton Institute, Aberdeen, UK

Global Academy of Agriculture and Food Security, University of Edinburgh, Midlothian, UK

Department of Animal and Plant Sciences, University of Sheffield, Sheffield, UK

Trent Northen Environmental Genomics and Systems Biology Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

Erin Nuccio Physical and Life Sciences, Lawrence Livermore National Laboratory, Livermore, CA, USA

Ivanah C. Oliver Faculty of Science, Agriculture, Business and Law, School of Environmental and Rural Science, The University of New England, Armidale, NSW, Australia

Eric Paterson The James Hutton Institute, Craigiebuckler, Aberdeen, UK

Jennifer Pett-Ridge Physical and Life Sciences, Lawrence Livermore National Laboratory, Livermore, CA, USA

Casper W. Quist Department of Terrestrial Ecology, Netherland Institute of Ecology (NIOO-KNAW) and Laboratory of Nematology, Wageningen University and Research Centre (WUR), Wageningen, The Netherlands

Alan E. Richardson CSIRO Agriculture and Food, Canberra, ACT, Australia

Ruud Rijkers Systems Ecology, Department of Ecological Science, VU University, Amsterdam, Netherlands

Sarah S. Roley School of the Environment, Washington State University, Richland, WA, USA

Peter R. Ryan CSIRO Agriculture and Food, Canberra, ACT, Australia

Dinesh Sharma Department of Biological Sciences, CBSH, G.B. Pant University of Agriculture & Technology, Pantnagar, India

Suvigya Sharma Department of Biological Sciences, CBSH, G.B. Pant University of Agriculture & Technology, Pantnagar, India

Shengjing Shi Science Center, AgResearch Ltd., Christchurch, New Zealand
Department of Environmental Science, Policy and Management, University of California, Berkeley, CA, USA

Tami Swenson Environmental Genomics and Systems Biology Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

Micaela Tosi Environmental Microbiology of Agro-Ecosystems, School of Environmental Sciences, Guelph, ON, Canada

Fei Wang School of Resource and Environmental Sciences, Henan Institute of Science and Technology, Xinxiang, People's Republic of China

Brian R. Wilson Faculty of Science, Agriculture, Business and Law, School of Environmental and Rural Science, The University of New England, Armidale, NSW, Australia

NSW Office of Environment and Heritage, University of New England, Armidale, NSW, Australia

Mengting Yuan Department of Environmental Science, Policy and Management, University of California, Berkeley, CA, USA

Kateryna Zhalnina Environmental Genomics and Systems Biology Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

Earth and Environmental Sciences, Lawrence Berkeley National Laboratory, Livermore, CA, USA

Jizhong Zhou Earth and Environmental Sciences, Lawrence Berkeley National Laboratory, Livermore, CA, USA

Institute for Environmental Genomics, Department of Microbiology and Plant Science, University of Oklahoma, Norman, OK, USA