



**PHYSICOCHEMICAL PROPERTIES AND DIVERSITY OF MICROBIAL
COMMUNITIES IN SOIL ASSOCIATED WITH FUSARIUM WILT
DISEASE OF BANANA IN SELANGOR, MALAYSIA**

By

FATIN NADIAH BINTI JAMIL

**Thesis Submitted to the School of Graduate Studies, Universiti Putra
Malaysia, in Fulfilment of the Requirements for the Degree of
Master of Science**

November 2021

IB 2022 6

COPYRIGHT

All material contained within the thesis, including without limitation text, logos, icons, photographs, and all other artwork, is copyright material of Universiti Putra Malaysia unless otherwise stated. Use may be made of any material contained within the thesis for non-commercial purposes from the copyright holder. Commercial use of material may only be made with the express, prior, written permission of Universiti Putra Malaysia.

Copyright © Universiti Putra Malaysia



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Master of Science

PHYSICOCHEMICAL PROPERTIES AND DIVERSITY OF MICROBIAL COMMUNITIES IN SOIL ASSOCIATED WITH FUSARIUM WILT DISEASE OF BANANA IN SELANGOR, MALAYSIA

By

FATIN NADIAH BINTI JAMIL

November 2021

Chairman : Associate Professor Noor Baiyya binti Saidi, PhD
Institute : Bioscience

Fusarium wilt (FW) is a soilborne disease caused by the fungal pathogen, *Fusarium oxysporum* f. sp. *cubense* (*Foc*) which jeopardizes the banana industry worldwide including Malaysia. Studies have shown that soil microbiome and its physicochemical properties are associated with the outbreak of FW. Rhizosphere and bulk soil microbiome help in the plant growth and also the defense system. Identification of biomarker identification with strong positive correlation with soil physicochemical properties from the healthy soils of banana is critical for construction of disease suppressive soil. Aside from that, a combination biomarkers of healthy soil with ability to promote plant growth, could be used as a bio-fertilizer and biocontrol agent to control the FW diseased caused by TR4. However, little is known about the diversities of the fungal and bacterial microbiome associated with diseased or healthy sites within the banana field in Malaysia or the difference in soil properties which may lead to poor disease management. This study applied 16S rRNA amplicon and internal transcribed spacer (ITS) sequencing analysis to investigate microbial diversity and community structure in Berangan banana farm in Sabak Bernam, Selangor. Both fungal and bacterial richness and diversity were significantly higher in the FW-infected soils compared to healthy soils. Similar to previously reported studies, the microbial community of healthy and FW-infected soil was more diverse in the rhizosphere than bulk soil. The potential bacterial biomarkers associated with the healthy soil were *Burkholderia* and *Streptomyces* spp., while *Xanthomonadaceae*, *Sphingomonas*, *Azospira oryzae*, *Pseudomonas* and *Acinetobacter tandoii* were highly abundant in FW-infected soil. For fungal biomarker taxa, *Penicillium* sp. was identified as the dominant fungus in healthy soil, while *Trichothecium ovalisporum*, *Nectriaceae* and *Sarocladium strictum* were dominant in FW-infected soil. In physicochemical properties, only magnesium (Mg) and cation exchange capacity (CEC) were found highly significant (t-test, $p < 0.05$) in the healthy soils compared to the infected soils.

For 16S, a Canonical correspondence analysis (CCA) showed a positive correlation of Mg with *Bradyrhizobium* sp. and *Acidobacteriaceae* in rhizosphere healthy (RH) soil for maintaining soil health. Meanwhile in ITS, a positive correlation was found between *Penicillium* sp. with Mg, suggesting the production of Mg was associated with metabolites secreted by *Penicillium* sp., which could control the disease caused by microbes. Overall, this study reported differences in the key taxa of rhizosphere soil microbial communities and soil physicochemical properties between healthy and FW-infected plants, suggesting their potential role as indicators for banana health. This specific information is applicable for constructing a healthy microbial community structure as the sustainable control strategy against TR4. Thus, in order to apply the biofertilizer or biocontrol agent, further study is needed to study the potential of network interaction between the microbial diversities and their functional behaviors and pathways in rhizosphere and bulk soil for long term disease control.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia
sebagai memenuhi keperluan untuk ijazah Master Sains

**SIFAT FIZIKOKIMIA DAN KEPELBAGAIAN KOMUNITI MIKROB
DALAM TANAH YANG BERKAITAN DENGAN PENYAKIT LAYU
FUSARIUM PISANG DI SELANGOR, MALAYSIA**

Oleh

FATIN NADIAH BINTI JAMIL

November 2021

Pengerusi : Profesor Madya Noor Baity binti Saidi, PhD
Institut : Biosains

Layu Fusarium (FW) ialah penyakit bawaan tanah yang disebabkan oleh patogen kulat, *Fusarium oxysporum* f. sp. *ubense* (Foc) yang menjejaskan industri pisang di seluruh dunia termasuk Malaysia. Kajian telah menunjukkan bahawa mikrobiom tanah dan sifat fizikokimianya dikaitkan dengan wabak FW. Rhizosfera dan mikrobiom tanah pukal membantu dalam pertumbuhan tumbuhan dan juga sistem pertahanan. Pengenalpastian biomarker dengan korelasi positif yang kuat dengan sifat fizikokimia tanah daripada tanah pisang yang sihat adalah penting untuk pembinaan tanah penindas penyakit. Selain itu, gabungan biomarker tanah yang sihat dengan keupayaan untuk menggalakkan pertumbuhan tumbuhan, boleh digunakan sebagai bio-baja dan agen biokawalan untuk mengawal FW berpenyakit yang disebabkan oleh TR4. Walau bagaimanapun, sedikit yang diketahui tentang kepelbagaian mikrobiom kulat dan bakteria yang dikaitkan dengan tapak berpenyakit atau sihat dalam ladang pisang di Malaysia atau perbezaan sifat tanah yang mungkin membawa kepada pengurusan penyakit yang lemah. Kajian ini menggunakan analisis penjujukan amplicon 16S rRNA dan spacer transkripsi dalaman (ITS) untuk menyiasat kepelbagaian mikrob dan struktur komuniti di ladang pisang Berangan di Sabak Bernam, Selangor. Kedua-dua kekayaan dan kepelbagaian kulat dan bakteria adalah lebih tinggi dengan ketara dalam tanah yang dijangkiti FW berbanding dengan tanah yang sihat. Sama seperti kajian yang dilaporkan sebelum ini, komuniti mikrob tanah yang sihat dan dijangkiti FW adalah lebih pelbagai di rizosfera daripada tanah pukal. Biomarker bakteria berpotensi yang dikaitkan dengan tanah yang sihat ialah *Burkholderia* dan *Streptomyces* spp., manakala *Xanthomonadaceae*, *Sphingomonas*, *Azospira oryzae*, *Pseudomonas* dan *Acinetobacter tandoii* sangat banyak terdapat dalam tanah yang dijangkiti FW. Untuk taksa biomarker kulat, *Penicillium* sp. dikenal pasti sebagai kulat dominan dalam tanah yang sihat, manakala *Trichothecium ovalisporum*, *Nectriaceae* dan *Sarocladium strictum* dominan dalam tanah yang dijangkiti FW. Dalam sifat

fizikokimia, hanya magnesium (Mg) dan kapasiti pertukaran kation (CEC) didapati sangat signifikan (ujian-t, $p < 0.05$) dalam tanah yang sihat berbanding dengan tanah yang dijangkiti. Untuk 16S, analisis korespondensi Canonical (CCA) menunjukkan korelasi positif Mg dengan *Bradyrhizobium* sp. dan *Acidobacteriaceae* dalam tanah rhizosphere healthy (RH) untuk mengekalkan kesihatan tanah. Manakala di ITS, korelasi positif didapati antara *Penicillium* sp. dengan Mg, mencadangkan pengeluaran Mg dikaitkan dengan metabolit yang dirembeskan oleh *Penicillium* sp., yang boleh mengawal penyakit yang disebabkan oleh mikroba. Secara keseluruhan, kajian ini melaporkan perbezaan dalam taksa utama komuniti mikroba tanah rizosfera dan sifat fizikokimia tanah antara tumbuhan yang sihat dan yang dijangkiti FW, mencadangkan potensi peranan mereka sebagai penunjuk untuk kesihatan pisang. Maklumat khusus ini boleh digunakan untuk membina struktur komuniti mikroba yang sihat sebagai strategi kawalan mampan terhadap TR4. Oleh itu, kajian lanjut diperlukan untuk mengkaji potensi interaksi rangkaian antara kepelbagaian mikroba dan tingkah laku dan laluan fungsinya dalam rizosfera dan tanah pukul untuk kawalan penyakit jangka panjang.

ACKNOWLEDGEMENTS

This dissertation is written to fulfill part of the requirement for Master Science in Molecular Biotechnology. This acknowledgement is to express my gratitude to all important people which I have worked through completing my Master's journey.

First of all, I would like to express my sincere gratitude to my supportive supervisor Assoc. Prof. Dr. Noor Baiti Binti Saidi, for her continuous support, encouragement, patience and motivation at every stage of this dissertation. Without her, I would not have been able to complete my Master research. I also would like to say special thanks to my Co-supervisors, Dr. Amalia Binti Mohd Hashim and Assoc. Prof. Dr. Mohd Termizi bin Yusof. Their immense knowledge and plentiful experience have encouraged me in all the time of my academic research and daily life.

Further, I am also thankful to the Institute of Bioscience, Faculty of Biotechnology and Biomolecular Sciences, Department of Agricultural in Sabak Bernam and all its member's staff for all the considerate guidance. Many thanks to my helpful fellow lab members, Nurul Izzah, Khairil, Zakiah Anis, Azrina, Hidayah, Pavitra, Misfahulhairah, Kharunnisa, Ying and Syazana for all the unconditional support in this study.

I am deeply grateful to my lovely and supportive spouse, Muhammad Afiq for constantly listening to me and talk things out, for proofreading over and over (even after long days at work and during difficult times), and for the sacrifices you have made in order for me to pursue a Master's degree.

Lastly, my family deserves endless gratitude especially my late grandmother, my lovely parents, Mak and Abah, siblings and my nephews for their tremendous support and continuous encouragement they had given to me. Without them, this thesis would not have been possible. Thank you all for the strength you gave me. I love you all!

This thesis was submitted to the Senate of the Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

Noor Baity binti Saidi, PhD

Associate Professor
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Chairman)

Amalia binti Mohd Hashim, PhD

Senior Lecturer
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Member)

Mohd Termizi bin Yusof, PhD

Associate Professor
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Member)

ZALILAH MOHD SHARIFF, PhD

Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date: 14 April 2022

Declaration by graduate student

I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
- this thesis has not been submitted previously or concurrently for any other degree at any institutions;
- intellectual property from the thesis and copyright of thesis are fully-owned by Universiti Putra Malaysia, as according to the Universiti Putra Malaysia (Research) Rules 2012;
- written permission must be obtained from supervisor and the office of Deputy Vice-Chancellor (Research and innovation) before thesis is published (in the form of written, printed or in electronic form) including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials as stated in the Universiti Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld as according to the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software

Signature: _____

Date: _____

Name and Matric No: Fatin Nadiah binti Jamil

Declaration by Members of Supervisory Committee

This is to confirm that:

- the research conducted and the writing of this thesis was under our supervision;
- supervision responsibilities as stated in the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) are adhered to.

Signature: _____
Name of Chairman
of Supervisory
Committee: Associate Professor Dr. Noor Baity binti Saidi

Signature: _____
Name of Member
of Supervisory
Committee: Dr. Amalia binti Mohd Hashim

Signature: _____
Name of Member
of Supervisory
Committee: Associate Professor Dr. Mohd Termizi bin Yusof

TABLE OF CONTENTS

	Page
ABSTRACT	i
ABSTRAK	iii
ACKNOWLEDGEMENTS	v
APPROVAL	vi
DECLARATION	viii
LIST OF TABLES	xii
LIST OF FIGURES	xiii
LIST OF ABBREVIATIONS	xv
CHAPTER	
1 INTRODUCTION	1
1.1 Introduction	1
1.2 Objectives of the study	2
2 LITERATURE REVIEW	3
2.1 The Bananas and Plantains (<i>Musa</i> spp.)	3
2.1.1 Bananas in Malaysia	3
2.1.2 Origin and Taxonomy	4
2.2 Fusarium Wilt of Banana	5
2.2.1 History	5
2.2.2 Variation in Host and Pathogen	5
2.2.3 Symptoms and Epidemiology	6
2.3 Management of Fusarium Wilt of Banana	7
2.3.1 Biological Control	8
2.3.2 Chemical Control	9
2.3.3 Cultural and Physical Control	9
2.4 Soil Rhizosphere Microbiome	10
2.4.1 Ecology of the Microbial Community in the Rhizosphere	10
2.4.2 Measuring Microbial Diversity	12
2.4.3 Factors Affecting Soil Rhizosphere Microbiome	14
2.4.4 Analysis of Soil Microbiome Using Metagenomics	14
3 MATERIALS AND METHODS	16
3.1 Chemicals	16
3.2 Selection of Sampling Site	16
3.3 Determination of Sampling Frame and Sampling of Plant Tissues	17
3.3.1 DNA Extraction of Plant Sample	19
3.3.2 Polymerase Chain Reaction (PCR)	19
3.4 Rhizosphere and Bulk Soil Sampling and Processing for NGS	20

3.5	Analysis of Physicochemical Properties of Soil	21
3.5.1	Determination of Soil Bulk Density and Air Porosity	22
3.6	Analysis of Bacterial and Fungal Community in Soil Samples	22
3.6.1	DNA Extraction of Soil Samples	22
3.6.2	Next-generation Sequencing	23
3.6.3	Sequence Processing	23
3.6.4	Data Processing and Normalization	24
3.6.5	Data Analysis and Visualization	24
3.7	Statistical Analysis	25
4	RESULTS AND DISCUSSION	26
4.1	Soil Physicochemical Properties Associated with Fusarium Wilt of Bananas	26
4.2	Analysis of Soil Bacterial Community Associated with FW of Bananas	32
4.2.1	Bacterial Sequencing Analysis and Diversity Coverage	32
4.2.2	Bacterial Community Structure of Bulk and Rhizosphere Soil of Banana	34
4.2.3	The Alpha Diversity of Soil Bacterial Communities	35
4.2.4	The Beta Diversity of Soil Bacterial Communities	36
4.2.5	Identification of Bacterial Taxa Biomarker in the Rhizosphere Soil	38
4.2.6	Effects of Mg and CEC on the Abundant Bacterial Taxa in the Rhizosphere Soil	40
4.3	Analysis of Soil Fungal Community Associated with Fusarium Wilt of Bananas	41
4.3.1	Fungal Sequencing Analysis and Diversity Coverage	41
4.3.2	Fungal Community Structure of Bulk and Rhizosphere Soil of Banana	43
4.3.3	The Alpha and Beta Diversity of Soil Fungal Communities	45
4.3.4	Identification of Fungal Taxa Biomarker in the Rhizosphere Soil	48
4.3.5	Effects of Mg and CEC on the Abundant Fungal Taxa in the Rhizosphere Soil	51
5	SUMMARY, CONCLUSION AND RECOMMENDATION FOR FUTURE RESEARCH	52
	REFERENCES	53
	APPENDICES	83
	BIODATA OF STUDENT	92
	LIST OF PUBLICATIONS	93

LIST OF TABLES

Table		Page
1	Soil physicochemical properties between healthy and infected bulk soils	27
2	Heatmap of the Pearson correlation analysis of soil properties in healthy soil	30
3	Heatmap of the Pearson correlation analysis of soil properties in infected soil	31

LIST OF FIGURES

Figure		Page
1	Symptoms of FW in banana	7
2	The tapered zone of soil surrounding the plant root is considered the rhizosphere	11
3	Banana farm in Sabak Bernam, Selangor, Malaysia	16
4	Schematic farm layout from drone view	17
5	External symptoms of FW in cv. 'Berangan' banana	18
6	Internal symptoms of FW in cv. 'Berangan' banana	18
7	Soil sampling	21
8	Rarefaction curves for the bacterial OTUs in all samples clustered at a 97% similarity level	32
9	Common bacterial OTUs recovered from soil. (Venn diagram)	33
10	Relative abundance levels. (Bacterial community)	34
11	Alpha-diversity indexes. (Bacterial community)	36
12	Principal coordinate analysis (PCoA) based on Bray-Curtis. (Bacterial community)	37
13	Differentially abundant taxa. (Bacterial community)	38
14	Canonical Correspondence Analysis (CCA) of the correlation between bacterial taxa and the soil physicochemical properties in healthy and infected soil at the taxa level	40
15	Rarefaction curves for the fungal OTUs in all samples, clustered at a 97% similarity level	42
16	Common fungal OTUs recovered from soil. (Venn diagram)	43
17	Relative abundance levels. (Fungal community)	44
18	Alpha-diversity indexes. (Fungal community)	46
19	Principal coordinate analysis (PCoA) based on Bray-Curtis distance. (Fungal community)	47

20	Differentially abundant taxa. (Fungal community)	49
21	Canonical Correspondence Analysis (CCA) of the correlation between fungal taxa and the soil physicochemical properties in both types of soil samples at the taxa level	51



LIST OF ABBREVIATIONS

%	Percentage
°C	Degree celsius
µL	Microliter
ACE	Abundance-based Coverage Estimator
ANOSIM	Analysis of similarities
B	Boron
BCAs	Biological control agents
BH	Bulk soil healthy
BI	Bulk soil infected
bp	Base pair
Ca	Calcium
CCA	Canonical correspondence analysis
CEC	Cation exchange capacity
Cl	Chlorine
cm	Centimeter
Cu	Copper
DNA	Deoxyribonucleic acid
Fe	Iron
<i>Foc</i>	<i>Fusarium oxysporum</i> f.sp. <i>cubense</i>
FW	Fusarium wilt
G	Gram
ITS	Internal Transcribed Spacer
K	Potassium
Kg	Kilogram
L	Litre
LDA	Linear Discriminant Analysis
LEfSe	Linear discriminant analysis Effect Size
m	Metre

M	Molar
Mg	Magnesium
ml	Millilitre
mm	Millimetre
mM	Millimolar
Mn	Manganese
Mo	Molybdenum
N	Nitrogen
ng	Nanogram
OM	Organic matter
OTU	Operational Taxonomic Unit
P	Phosphorus
<i>P. aeruginosa</i>	<i>Pseudomonas aeruginosa</i>
<i>P. fluorescens</i>	<i>Pseudomonas fluorescens</i>
PCoA	Principal coordinate analysis
PCR	Polymerase chain reaction
PERMANOVA	Permutational ANOVA
PGPF	Plant-growth promoting fungi
PGPR	Plant-growth promoting rhizobacteria
Pte. Ltd.	Private limited
RH	Rhizosphere soil healthy
RI	Rhizosphere soil infected
rpm	Rotation per minute
rRNA	ribosomal RNA
S	Sulphur
Si	Silicone
TR4	Tropical race 4
VCGs	Vegetative compatibility groups
w/v	Weight per volume

WGS	Whole Genome Sequencing
Zn	Zinc
α	Alpha
β	Beta
ρ	Bulk density



CHAPTER 1

INTRODUCTION

1.1 Introduction

Fusarium wilt (FW) is the most destructive fungal disease affecting banana plantations across the globe (Dita et al., 2018). It is caused by a soil-borne fungus called *Fusarium oxysporum* sp. *cubense* (*Foc*). The pathogen penetrates through banana roots and dominates the vascular tissues, disrupting the dissemination of necessary nutrients from roots to the upper parts of the plant (Li et al., 2017). *Foc* is classified into four races, *Foc* race 1 causes damage to Gros Michel cultivar, race 2 affects Bluggoe and Gros Michel cultivars. Meanwhile, race 3 only infect *Heliconia* spp. and the most susceptible race is race 4, which divided into Tropical (TR4) and Subtropical (SR4) variants, where extremely affect Cavendish cultivar in subtropical and tropical area (Ploetz, 2015). Tropical Race 4 (TR4) emerges as the most virulent strain of *Foc*, causing epidemics in countries including China, Taiwan, Malaysia, Indonesia and the Philippines (Jamil et al., 2019). Generally, the richness and diversity of microbiomes in the soil play a vital role in the development and maintenance of healthy soil, which protect it from microbial pathogens and, at the same time, enhance the soil and plant health condition for better production (Pascale et al., 2020; Ray et al., 2020). The beneficial effect is achieved through an interaction between the rhizosphere microbiome and other microbes in the soil, including bacteria, fungi, nematodes, protozoa, algae, and microarthropods (Mohanram & Kumar 2019). In the soil suppressive to FW disease, plant-beneficial rhizobacteria such as *Bradyrhizobium*, *Pseudomonas*, *Burkholderia*, and *Streptomyces* were prevalent (Wang et al., 2022; Zhou et al., 2019; Effendi & Pancoro, 2021). While *Penicillium*, *Aspergillus* and *Trichoderma* were prevalent as beneficial fungi (Bidellaoui et al., 2019; Miao et al., 2019; Zhou et al., 2019). In addition, soil physicochemical properties also affect plant health and influence soil microbial communities (Wang et al., 2022; Sui et al., 2021; Zhao et al., 2018). For example, the microbial composition of the rhizosphere soil of bananas is affected by soil pH, potassium and phosphorus availability in the soil where a high level of the soil properties have been shown to improve the suppression ability against banana FW disease (Wu et al., 2020, Zhou et al., 2019; Shi et al., 2017). The soil microbiomes differ according to climate, ecological fitness, cultivation methods, soil nutrients, pathogens, and field management practices (Shah et al., 2021; Islam et al., 2020; Xue et al., 2018; Lori et al., 2017; Wang et al., 2017). Therefore, a lack of information and understanding on the soil microbial communities associated with FW disease of bananas in a specific location may lead to poor disease management. High-throughput sequencing technology and bioinformatics analysis allowed the discovery of the composition and identity of bacterial and fungal communities in the soil through the sequencing of 16S rRNA of bacteria and internal transcribed spacer (ITS) of fungi (Yuan et al., 2020; Ptaszyńska et al., 2021). Thus, to reveal information and gain an overview of the relationship involving various pathogenic

and beneficial soil microbiome associated with FW disease of banana, 16S rRNA and ITS amplicon metagenomics approaches were applied and explored in this study. It was hypothesized that the diversity and composition of soil bacterial and fungal communities between healthy and FW-infected soil are different in both 16S rRNA and ITS sequencing, where there are differentially abundant microbial taxa that can serve as potential biomarkers for biological control against TR4 in the future. Also hypothesized that, there are correlations between soil physicochemical properties with potential biomarker microbial taxa.

1.2 Objectives of the study

The objectives of this study were:

1. To evaluate soil physicochemical properties of healthy and infected soils associated with banana FW disease.
2. To identify and compare the diversity and composition of soil (bulk and rhizosphere) bacterial and fungal communities of the healthy and FW-infected banana through amplicon metagenomics sequencing of 16S rRNA and internal transcribed spacer (ITS) regions.
3. To determine the potential biomarker taxa for future use as potential biocontrol agents against TR4.

REFERENCES

- Adamiak, J., Otlewska, A., Tafer, H., Lopandic, K., Gutarowska, B., Sterflinger, K., & Piñar, G. (2018). First evaluation of the microbiome of built cultural heritage by using the Ion Torrent next generation sequencing platform. *International Biodeterioration & Biodegradation*, 131, 11-18.
- Afzaal, M., Mukhtar, S., Malik, A., Murtaza, R., & Nazar, M. (2018). Paddy soil microbial diversity and enzymatic activity in relation to pollution. In *Environmental pollution of paddy soils* (pp. 139-149). Springer, Cham.
- Aguilar Morán, J. F. (2011). Improvement of Cavendish banana cultivars through conventional breeding. In *VII International Symposium on Banana: ISHS-ProMusa Symposium on Bananas and Plantains: Towards Sustainable Global Production 986* (pp. 205-208).
- Akila, R., Rajendran, L., Harish, S., Saveetha, K., Raguchander, T., & Samiyappan, R. (2011). Combined application of botanical formulations and biocontrol agents for the management of *Fusarium oxysporum* f. sp. *cubense* (Foc) causing Fusarium wilt in banana. *Biological control*, 57(3), 175-183.
- Al-Shammary, A. A. G., Kouzani, A. Z., Kaynak, A., Khoo, S. Y., Norton, M., & Gates, W. (2018). Soil bulk density estimation methods: a review. *Pedosphere*, 28(4), 581-596.
- Altschul, S. F., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990). Basic local alignment search tool. *Journal of molecular biology*, 215(3), 403-410.
- Ammar, E. D., & Hogenhout, S. A. (2005). Use of immunofluorescence confocal laser scanning microscopy to study distribution of the bacterium corn stunt Spiroplasma in vector leafhoppers (Hemiptera: Cicadellidae) and in host plants. *Annals of the Entomological Society of America*, 98(6), 820-826.
- Asif, M., & Kaur, A. (2018). Biologically Active Phytochemical Contents and Biological Activities of Whole *Musa Acuminata* (Banana) Plant. *International Journal of Recent Advances in Medical & Pharma Research*, 1(1).
- Azcolain Olaondo, J. A. (2016). Biofumigación y Biosolarización Para el Manejo del mal de Panamá en la Platanera de Canarias.
- Bancroft, .I. (1876). Report of the board appointed to enquire into the cause of disease affecting livestock and plants. Queensland, 1876. Votes and Proceedings 1877 3, 1011-38.

- Barka, E. A., Vatsa, P., Sanchez, L., Gaveau-Vaillant, N., Jacquard, C., Klenk, H. P., ... & van Wezel, G. P. (2016). Taxonomy, physiology, and natural products of Actinobacteria. *Microbiology and Molecular Biology Reviews*, 80(1), 1-43.
- Belgrove, A., Steinberg, C., & Viljoen, A. (2011). Evaluation of nonpathogenic *Fusarium oxysporum* and *Pseudomonas fluorescens* for panama disease control. *Plant disease*, 95(8), 951-959.
- Beneduzi, A., Ambrosini, A., & Passaglia, L. M. (2012). Plant growth-promoting rhizobacteria (PGPR): their potential as antagonists and biocontrol agents. *Genetics and molecular biology*, 35(4), 1044-1051.
- Berendsen, R. L., Pieterse, C. M., & Bakker, P. A. (2012). The rhizosphere microbiome and plant health. *Trends in plant science*, 17(8), 478-486.
- Berendsen, R. L., Vismans, G., Yu, K., Song, Y., de Jonge, R., Burgman, W. P., ... & Pieterse, C. M. (2018). Disease-induced assemblage of a plant-beneficial bacterial consortium. *The ISME journal*, 12(6), 1496-1507.
- Berg, G., Rybakova, D., Grube, M., & Köberl, M. (2016). The plant microbiome explored: implications for experimental botany. *Journal of experimental botany*, 67(4), 995-1002.
- Bidellaoui, B., Segarra, G., Hakkou, A., & Trillas, M. I. (2019). Beneficial effects of *Rhizophagus irregularis* and *Trichoderma asperellum* strain T34 on growth and fusarium wilt in tomato plants. *Journal of Plant Pathology*, 101(1), 121-127.
- Bolfarini, A. C. B., Souza, J. M. A., de Souza Silva, M., Ferreira, R. B., Leonel, M., Tecchio, M. A., & Leonel, S. (2020). Ideal harvest stage and quality descriptors of 5 banana cultivars based on 5 fruit diameters. *Emirates Journal of Food and Agriculture*, 220-228.
- Borges, C. V., Amorim, E. P., Leonel, M., Gomez, H. A. G., Santos, T. P. R. D., Ledo, C. A. D. S., ... & Lima, G. P. P. (2019). Post-harvest physicochemical profile and bioactive compounds of 19 bananas and plantains genotypes. *Bragantia*, 78, 284-296.
- Bowen, A., Orr, R., McBeath, A. V., Pattison, A., & Nelson, P. N. (2019). Suppressiveness or conduciveness to *Fusarium* wilt of bananas differs between key Australian soils. *Soil Research*, 57(2), 158-165.
- Brown, A. C. (2018). *Understanding food: principles and preparation*. Cengage learning.

- Bubici, G., Kaushal, M., Prigigallo, M. I., Gómez-Lama Cabanás, C., & Mercado-Blanco, J. (2019). Biological control agents against Fusarium wilt of banana. *Frontiers in microbiology*, 10, 616.
- Bulgarelli, D., Rott, M., Schlaeppi, K., Ver Loren van Themaat, E., Ahmadinejad, N., Assenza, F., & Schulze-Lefert, P. (2012). Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. *Nature*, 488(7409), 91-95.
- Burnham KP, Overton WS (1979). Robust Estimation of Population Size When Capture Probabilities Vary Among Animals. *Ecology* 60:927-936.
- Caporaso, J. G., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F. D., Costello, E. K., ... & Knight, R. (2010). QIIME allows analysis of high-throughput community sequencing data. *Nature methods*, 7(5), 335-336.
- Carrión, V. J., Cordovez, V., Tyc, O., Etalo, D. W., de Bruijn, I., de Jager, V. C., ... & Raaijmakers, J. M. (2018). Involvement of Burkholderiaceae and sulfurous volatiles in disease-suppressive soils. *The ISME journal*, 12(9), 2307-2321.
- Carvalhais, L. C., Dennis, P. G., Badri, D. V., Kidd, B. N., Vivanco, J. M., & Schenk, P. M. (2015). Linking jasmonic acid signaling, root exudates, and rhizosphere microbiomes. *Molecular Plant-Microbe Interactions*, 28(9), 1049-1058.
- Chang, H. X., Haudenschild, J. S., Bowen, C. R., & Hartman, G. L. (2017). Metagenome-wide association study and machine learning prediction of bulk soil microbiome and crop productivity. *Frontiers in Microbiology*, 8, 519.
- Chao, A. (1984). Nonparametric estimation of the number of classes in a population. *Scandinavian Journal of statistics*, 265-270.
- Chao, A., & Lee, S. M. (1992). Estimating the number of classes via sample coverage. *Journal of the American statistical Association*, 87(417), 210-217.
- Cheesman, E. E. (1947). Classification of the Bananas: The Genus Musa L. *Kew Bulletin*, 106-117.
- Chen, (2017). "Fungi on banana in northern Taiwan." PhD diss., National Central University, Taiwan.
- Cheng, J., Lee, X., Tang, Y., & Zhang, Q. (2019). Long-term effects of biochar amendment on rhizosphere and bulk soil microbial communities in a karst region, southwest China. *Applied Soil Ecology*, 140, 126-134.

- Chittarath, K., Mostert, D., Crew, K. S., Viljoen, A., Kong, G., Molina, A. B., & Thomas, J. E. (2018). First report of *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (VCG 01213/16) associated with Cavendish bananas in Laos. *Plant disease*, 102(2), 449.
- Chong, J., Liu, P., Zhou, G., & Xia, J. (2020). Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. *Nature Protocols*, 15(3), 799-821.
- Chuang, T.Y., 1986. Studies on the soils suppressive to banana *Fusarium* wilt. I. Screening soils for suppressiveness to *Fusarium oxysporum* f. sp. *cubense* (E. F. Sm.) Snyder. & Hans. *Plant Protection Bulletin* (Taiwan, R.O.C) 28, 345-352.
- Cody, M. L., MacArthur, R. H., & Diamond, J. M. (1975). *Ecology and evolution of communities*. Harvard University Press.
- Cong, J., Yang, Y., Liu, X., Lu, H., Liu, X., Zhou, J., ... & Zhang, Y. (2015). Analyses of soil microbial community compositions and functional genes reveal potential consequences of natural forest succession. *Scientific reports*, 5, 10007.
- Cook, D. C., Taylor, A. S., Meldrum, R. A., & Drenth, A. (2015). Potential economic impact of Panama disease (tropical race 4) on the Australian banana industry. *Journal of Plant Diseases and Protection*, 122(5-6), 229-237.
- Cordero, O. X., & Datta, M. S. (2016). Microbial interactions and community assembly at microscales. *Current opinion in microbiology*, 31, 227-234.
- Crawford, R. H., Floyd, M., & Li, C. Y. (2000). Degradation of serpentine and muscovite rock minerals and immobilization of cations by soil *Penicillium* spp. *Phyton*, 40(2), 315-322.
- Cui, Y., Fang, L., Guo, X., Wang, X., Zhang, Y., Li, P., & Zhang, X. (2018). Ecoenzymatic stoichiometry and microbial nutrient limitation in rhizosphere soil in the arid area of the northern Loess Plateau, China. *Soil Biology and Biochemistry*, 116, 11-21.
- Dal Bello, G. (2008). First report of *Trichothecium roseum* causing postharvest fruit rot of tomato in Argentina. *Australasian Plant Disease Notes*, 3, 103-104.
- Dale, J., Paul, J. Y., Dugdale, B., & Harding, R. (2017). Modifying bananas: From transgenics to organics?. *Sustainability*, 9(3), 333.

- Daniells, J. W., Geering, A. D., Bryde, N. J., & Thomas, J. E. (2001). The effect of Banana streak virus on the growth and yield of dessert bananas in tropical Australia. *Annals of Applied Biology*, 139(1), 51-60.
- Das, R., Romi, W., Das, R., Sharma, H. K., & Thakur, D. (2018). Antimicrobial potentiality of actinobacteria isolated from two microbiologically unexplored forest ecosystems of Northeast India. *BMC microbiology*, 18(1), 71.
- de Oliveira, E., Magalhães, P. C., Gomide, R. L., Vasconcelos, C. A., Souza, I. R., Oliveira, C. M., ... & Schaffert, R. E. (2002). Growth and nutrition of mollicute-infected maize. *Plant disease*, 86(9), 945-949.
- Debona, D., Rios, J. A., Nascimento, K. J. T., Silva, L. C., & Rodrigues, F. A. (2016). Influence of magnesium on physiological responses of wheat infected by *Pyricularia oryzae*. *Plant Pathology*, 65(1), 114-123.
- Dhariwal, A., Chong, J., Habib, S., King, I. L., Agellon, L. B., & Xia, J. (2017). MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. *Nucleic acids research*, 45(W1), W180-W188.
- Ding, L. J., Cui, H. L., Nie, S. A., Long, X. E., Duan, G. L., & Zhu, Y. G. (2019). Microbiomes inhabiting rice roots and rhizosphere. *FEMS microbiology ecology*, 95(5), fiz040.
- Dita, M. A., Teixeira, L., Li, C., Zheng, S., O'Neill, W., Daniels, J., ... & Roux, N. (2021). Practical guidelines for early screening and field evaluation of banana against Fusarium wilt, *Pseudocercospora* leaf spots and drought.
- Dita, M. A., Waalwijk, C., Buddenhagen, I. W., Souza Jr, M. T., & Kema, G. H. J. (2010). A molecular diagnostic for tropical race 4 of the banana fusarium wilt pathogen. *Plant Pathology*, 59(2), 348-357.
- Dita, M., Barquero, M., Heck, D., Mizubuti, E. S., & Staver, C. P. (2018). Fusarium wilt of banana: current knowledge on epidemiology and research needs toward sustainable disease management. *Frontiers in plant science*, 9, 1468.
- DOA. (2018). "Phytosanitary Requirements for Exportation of Horticulture Product from Malaysia 2018." In. http://www.doa.gov.my/index/resources/aktiviti_sumber/sumber_awam/maklumat_biosekuriti/keperluan_fitok_eksport_produk_horti_2018.pdf.

- Dominguez, J., Negrín, M. A., & Rodriguez, C. M. (2001). Aggregate water-stability, particle-size and soil solution properties in conducive and suppressive soils to *Fusarium* wilt of banana from Canary Islands (Spain). *Soil Biology and Biochemistry*, 33(4-5), 449-455.
- Dong, L., Xu, J., Feng, G., Li, X., & Chen, S. (2016). Soil bacterial and fungal community dynamics in relation to *Panax notoginseng* death rate in a continuous cropping system. *Scientific reports*, 6(1), 1-11.
- Dong, X., Ling, N., Wang, M., Shen, Q., & Guo, S. (2012). Fusaric acid is a crucial factor in the disturbance of leaf water imbalance in *Fusarium*-infected banana plants. *Plant Physiology and Biochemistry*, 60, 171-179.
- Dong, X., Xiong, Y., Ling, N., Shen, Q., & Guo, S. (2014). Fusaric acid accelerates the senescence of leaf in banana when infected by *Fusarium*. *World Journal of Microbiology and Biotechnology*, 30(4), 1399-1408.
- Eckert, I. M., Littlefair, J. E., Zhang, G. K., Chain, F. J., Crease, T. J., & Cristescu, M. E. (2018). Bioinformatics for biomonitoring: Species detection and diversity estimates across Next-Generation Sequencing Platforms. *Advances in Ecological Research*, 59, 1-32.
- Edgar, R. C. (2013). UPARSE: highly accurate OTU sequences from microbial amplicon reads. *Nature methods*, 10(10), 996-998.
- Edgar, R. C., Haas, B. J., Clemente, J. C., Quince, C., & Knight, R. (2011). UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics*, 27(16), 2194-2200.
- Edwards, J., Johnson, C., Santos-Medellín, C., Lurie, E., Podishetty, N. K., Bhatnagar, S., ... & Sundaresan, V. (2015). Structure, variation, and assembly of the root-associated microbiomes of rice. *Proceedings of the National Academy of Sciences*, 112(8), E911-E920.
- Effendi, Y., & Pancoro, A. (2021). Revealing the role of Plant Growth Promoting Rhizobacteria in suppressive soils against *Fusarium oxysporum* f. sp. *cubense* based on metagenomic analysis. *Heliyon*, 7(8), e07636.
- Egamberdieva, D., Jabborova, D., Wirth, S. J., Alam, P., Alyemeni, M. N., & Ahmad, P. (2018). Interactive effects of nutrients and *Bradyrhizobium japonicum* on the growth and root architecture of soybean (*Glycine max* L.). *Frontiers in microbiology*, 9, 1000.
- Egidi, E., Delgado-Baquerizo, M., Plett, J. M., Wang, J., Eldridge, D. J., Bardgett, R. D., & Singh, B. K. (2019). A few Ascomycota taxa dominate soil fungal communities worldwide. *Nature communications*, 10(1), 1-9.

- Escobar-Zepeda, A., Godoy-Lozano, E. E., Raggi, L., Segovia, L., Merino, E., Gutiérrez-Rios, R. M., & Sanchez-Flores, A. (2018). Analysis of sequencing strategies and tools for taxonomic annotation: defining standards for progressive metagenomics. *Scientific reports*, 8(1), 1-13.
- Espinosa-Victoria, D., López-Reyes, L., Carcaño-Montiel, M. G., & Serret-López, M. (2020). The Burkholderia genus: between mutualism and pathogenicity. *Revista mexicana de fitopatología*, 38(3), 337-359.
- FAO. (2019, August, 28). Banana market review preliminary results for 2019. <http://www.fao.org/3/ca7567en/ca7567en.pdf>
- Fonseca-García, C., Coleman-Derr, D., Garrido, E., Visel, A., Tringe, S. G., & Partida-Martínez, L. P. (2016). The cacti microbiome: interplay between habitat-filtering and host-specificity. *Frontiers in microbiology*, 7, 150.
- Fouda, A., Awad, M. A., Eid, A. M., Saied, E., Barghoth, M. G., Hamza, M. F., ... & Hassan, S. E. D. (2021). An Eco-Friendly Approach to the Control of Pathogenic Microbes and Anopheles stephensi Malarial Vector Using Magnesium Oxide Nanoparticles (Mg-NPs) Fabricated by Penicillium chrysogenum. *International Journal of Molecular Sciences*, 22(10), 5096.
- Freitas, A. S., Pozza, E. A., Alves, M. C., Coelho, G., Rocha, H. S., & Pozza, A. A. (2016). Spatial distribution of Yellow Sigatoka Leaf Spot correlated with soil fertility and plant nutrition. *Precision agriculture*, 17(1), 93-107.
- Fu, L., Penton, C. R., Ruan, Y., Shen, Z., Xue, C., Li, R., & Shen, Q. (2017). Inducing the rhizosphere microbiome by biofertilizer application to suppress banana Fusarium wilt disease. *Soil Biology and Biochemistry*, 104, 39-48.
- Fu, R., Yu, F., Gu, Y., Xue, T., Guo, Y., Wang, Y., ... & Chen, W. (2015). Improvement of antagonistic activity of bacillus megaterium MHT6 against fusarium moniliforme using he-ne laser irradiation. *International Journal of Agriculture and Biology*, 17(6).
- Furtado, E. L., Bueno, C. J., Oliveira, A. L. D., Menten, J. O. M., & Malavolta, E. (2009). Relações entre ocorrência do Mal-de-Panama em bananeira da cv. Nanicão e nutrientes no solo e nas folhas. *Tropical Plant Pathology*, 34(4), 211-215.
- Gaiero, J. R., McCall, C. A., Thompson, K. A., Day, N. J., Best, A. S., & Dunfield, K. E. (2013). Inside the root microbiome: bacterial root endophytes and plant growth promotion. *American journal of botany*, 100(9), 1738-1750.

- Gamez, R., Cardinale, M., Montes, M., Ramirez, S., Schnell, S., & Rodriguez, F. (2019). Screening, plant growth promotion and root colonization pattern of two rhizobacteria (*Pseudomonas fluorescens* Ps006 and *Bacillus amyloliquefaciens* Bs006) on banana cv. Williams (*Musa acuminata* Colla). *Microbiological research*, 220, 12-20.
- García-Bastidas, F., Ordóñez, N., Konkol, J., Al-Qasim, M., Naser, Z., Abdelwali, M., ... & Kema, G. H. J. (2014). First report of *Fusarium oxysporum* f. sp. *cubense* tropical race 4 associated with Panama disease of banana outside Southeast Asia. *Plant Disease*, 98(5), 694-694.
- Garrigues, S., Gandía, M., Castillo, L., Coca, M., Marx, F., Marcos, J. F., & Manzanares, P. (2018). Three antifungal proteins from *Penicillium expansum*: different patterns of production and antifungal activity. *Frontiers in microbiology*, 9, 2370.
- Garrigues, S., Gandía, M., Popa, C., Borics, A., Marx, F., Coca, M., ... & Manzanares, P. (2017). Efficient production and characterization of the novel and highly active antifungal protein AfpB from *Penicillium digitatum*. *Scientific reports*, 7(1), 1-13.
- Gatch, E. W., & du Toit, L. J. (2017). Limestone-mediated suppression of *Fusarium* wilt in spinach seed crops. *Plant disease*, 101(1), 81-94.
- Ge, Y., Chen, Y., Li, C., Wei, M., Lv, J., & Meng, K. (2017). Inhibitory effects of sodium silicate on the fungal growth and secretion of cell wall-degrading enzymes by *Trichothecium roseum*. *Journal of Phytopathology*, 165(9), 620-625.
- Getha, K., & Vikineswary, S. (2002). Antagonistic effects of *Streptomyces violaceusniger* strain G10 on *Fusarium oxysporum* f. sp. *cubense* race 4: indirect evidence for the role of antibiosis in the antagonistic process. *Journal of Industrial Microbiology and Biotechnology*, 28(6), 303-310.
- Getha, K., Vikineswary, S., Wong, W. H., Seki, T., Ward, A., & Goodfellow, M. (2005). Evaluation of *Streptomyces* sp. strain g10 for suppression of *Fusarium* wilt and rhizosphere colonization in pot-grown banana plantlets. *Journal of Industrial Microbiology and Biotechnology*, 32(1), 24-32.
- Geyer, K. M., Altrichter, A. E., Takacs-Vesbach, C. D., Van Horn, D. J., Gooseff, M. N., & Barrett, J. E. (2014). Bacterial community composition of divergent soil habitats in a polar desert. *FEMS microbiology ecology*, 89(2), 490-494.

- Ghag, S. B., Shekhawat, U. K., & Ganapathi, T. R. (2015). Fusarium wilt of banana: biology, epidemiology and management. *International Journal of Pest Management*, 61(3), 250-263.
- Goss-Souza, D., Mendes, L. W., Borges, C. D., Rodrigues, J. L., & Tsai, S. M. (2019). Amazon forest-to-agriculture conversion alters rhizosphere microbiome composition while functions are kept. *FEMS microbiology ecology*, 95(3), fiz009.
- Goss-Souza, D., Mendes, L. W., Rodrigues, J. L. M., & Tsai, S. M. (2020). Ecological processes shaping bulk soil and rhizosphere microbiome assembly in a long-term Amazon forest-to-agriculture conversion. *Microbial ecology*, 79(1), 110-122.
- Groenhagen, U., Baumgartner, R., Bailly, A., Gardiner, A., Eberl, L., Schulz, S., & Weiskopf, L. (2013). Production of bioactive volatiles by different Burkholderia ambifaria strains. *Journal of chemical ecology*, 39(7), 892-906.
- Gu, Z., Wang, M., Wang, Y., Zhu, L., Mur, L. A. J., Hu, J., & Guo, S. (2020). Nitrate stabilizes the rhizospheric fungal community to suppress Fusarium wilt disease in cucumber. *Molecular Plant-Microbe Interactions*, 33(4), 590-599.
- Guo, L., Yang, L., Liang, C., Wang, G., Dai, Q., & Huang, J. (2015). Differential colonization patterns of bananas (*Musa* spp.) by physiological race 1 and race 4 isolates of *Fusarium oxysporum* f. sp.
- Haddad, F., Rocha, L. S., Soares, A. C. F., Martins, I. P. S., Teixeira, L. A. J., Staver, C., & Dita, M. (2016, October). Management of Fusarium wilt of bananas in Minas Gerais, Brazil. In *X International Symposium on Banana: ISHS-ProMusa Symposium on Agroecological Approaches to Promote Innovative Banana 1196* (pp. 137-146).
- Handelsman, J. (2004). Metagenomics: application of genomics to uncultured microorganisms. *Microbiology and molecular biology reviews*, 68(4), 669-685.
- Haney, C. H., Samuel, B. S., Bush, J., & Ausubel, F. M. (2015). Associations with rhizosphere bacteria can confer an adaptive advantage to plants. *Nature plants*, 1(6), 1-9.
- Hassan, M. K., McInroy, J. A., & Kloepper, J. W. (2019). The interactions of rhizodeposits with plant growth-promoting rhizobacteria in the rhizosphere: a review. *Agriculture*, 9(7), 142.

- Heck, D. W., Ghini, R., & Bettiol, W. (2019). Deciphering the suppressiveness of banana Fusarium wilt with organic residues. *Applied Soil Ecology*, 138, 47-60.
- Heltshe JF, Forrester NE (1983). Estimating Species Richness Using the Jackknife Procedure. *Biometrics* 39:1-11.
- Herbert, JA and Marx, D. (1990). Short-term control of Panama disease of bananas in South Africa. *Phytophylactica*, 22(3), 339-341.
- Hermanto, C., Eliza, I. D., & Deni Emilda, M. Subhana.(2012). Pre-planting treatments for management of banana Fusarium wilt. *ARPN Journal of Agriculture and Biological Sciences*, 7, 260-265.
- Heslop-Harrison, J. S., & Schwarzacher, T. (2007). Domestication, genomics and the future for banana. *Annals of botany*, 100(5), 1073-1084.
- Ho, Y. N., Chiang, H. M., Chao, C. P., Su, C. C., Hsu, H. F., Guo, C. T., ... & Huang, C. C. (2015). In planta biocontrol of soilborne Fusarium wilt of banana through a plant endophytic bacterium, Burkholderia cenocepacia 869T2. *Plant and Soil*, 387(1), 295-306.
- Hortal, J., Borges, P. A., & Gaspar, C. (2006). Evaluating the performance of species richness estimators: sensitivity to sample grain size. *Journal of animal ecology*, 75(1), 274-287.
- Hu, W., Yang, B., He, Z., & Li, G. (2021). Magnesium may be a key nutrient mechanism related to Fusarium wilt resistance: a new banana cultivar (Zhongjiao No. 9). *PeerJ*, 9, e11141.
- Huang, X., Liu, S., Liu, X., Zhang, S., Li, L., Zhao, H. & Cai, Z. (2020). Plant pathological condition is associated with fungal community succession triggered by root exudates in the plant-soil system. *Soil Biology and Biochemistry*, 151, 108046.
- Huang, Y. H., Wang, R. C., Li, C. H., Zuo, C. W., Wei, Y. R., Zhang, L., Yi, G. J. (2012). Control of Fusarium wilt in banana with Chinese leek. *European journal of plant pathology*, 128(2), 243-252.
- Zhang, H., Mallik, A., & Zeng, R. S. (2013). Control of Panama disease of banana by rotating and intercropping with Chinese chive (*Allium tuberosum* Rottler): role of plant volatiles. *Journal of chemical ecology*, 39(2), 243-252.
- pathology, 134(1), 87-95.
- Huber, D. M., & Jones, J. B. (2013). The role of magnesium in plant disease. *Plant and Soil*, 368(1), 73-85.

- Hung, T. N., Hung, N. Q., Mostert, D., Viljoen, A., Chao, C. P., Molina, A. B. (2018). First report of Fusarium wilt on Cavendish bananas, caused by *Fusarium oxysporum* f. sp. cubense tropical race 4 (VCG 01213/16), in Vietnam. *Plant disease*, 102(2), 448-448.
- Igiehon, N. O., Babalola, O. O., Cheseto, X., & Torto, B. (2021). Effects of rhizobia and arbuscular mycorrhizal fungi on yield, size distribution and fatty acid of soybean seeds grown under drought stress. *Microbiological Research*, 242, 126640.
- Imakumbili M. L. E., (2019) Soil Sampling and Preparation for Soil Chemical Analysis. PLoS ONE. <https://dx.doi.org/10.17504/protocols.io.x72frqe>
- Islam, W., Noman, A., Naveed, H., Huang, Z., & Chen, H. Y. (2020). Role of environmental factors in shaping the soil microbiome. *Environmental Science and Pollution Research*, 1-23.
- Jamil, F. N., Tang, C. N., Saidi, N. B., Lai, K. S., & Baharum, N. A. (2019). Fusarium Wilt in Banana: Epidemics and Management Strategies. In *Horticultural Crops*. IntechOpen.
- Jangid, A., & Prakash, T. (2019). Microbial Genome Diversity and Microbial Genome Sequencing. In *Microbial Genomics in Sustainable Agroecosystems* (pp. 175-201). Springer, Singapore.
- Oksanen, J. F. G. B., Friendly, M., Kindt, R., Legendre, P., McGlinn, D., Minchin, P. R., ... & Szoecs, E. (2018). Vegan: community ecology package. R package version, 2(6).
- Jarvis, F. G., & Johnson, M. J. (1950). The mineral nutrition of *Penicillium chrysogenum* Q176. *Journal of bacteriology*, 59(1), 51-60.
- Jayaraman, S., Naorem, A. K., Lal, R., Dalal, R. C., Sinha, N. K., Patra, A. K., & Chaudhari, S. K. (2021). Disease-Suppressive Soils—Beyond Food Production: a Critical Review. *Journal of Soil Science and Plant Nutrition*, 1-29.
- Ji, L., Nasir, F., Tian, L., Chang, J., Sun, Y., Zhang, J., Tian, C. (2021). Outbreaks of Root Rot Disease in Different Aged American Ginseng Plants Are Associated with Field Microbial Dynamics. *Frontiers in Microbiology*, 12, 1634.
- Jiao, X., Lu, X., Chen, A. J., Luo, Y., Hao, J. J., & Gao, W. (2015). Effects of *Fusarium solani* and *F. oxysporum* infection on the metabolism of ginsenosides in American ginseng roots. *Molecules*, 20(6), 10535-10552.

- Jie, L., Zifeng, W., Lixiang, C., Hongming, T., Patrik, I., Zide, J., Shining, Z. (2009). Artificial inoculation of banana tissue culture plantlets with indigenous endophytes originally derived from native banana plants. *Biological control*, 51(3), 427-434.
- Jing, T., Zhou, D., Zhang, M., Yun, T., Qi, D., Wei, Y., Xie, J. (2020). Newly Isolated *Streptomyces* sp. JBS5-6 as a Potential Biocontrol Agent to Control Banana Fusarium Wilt: Genome Sequencing and Secondary Metabolite Cluster Profiles. *Frontiers in microbiology*, 11, 3036.
- Kalam, S., Basu, A., & Podile, A. R. (2020). Functional and molecular characterization of plant growth promoting *Bacillus* isolates from tomato rhizosphere. *Heliyon*, 6(8), e04734.
- Kalam, S., Das, S. N., Basu, A., & Podile, A. R. (2017). Population densities of indigenous Acidobacteria change in the presence of plant growth promoting rhizobacteria (PGPR) in rhizosphere. *Journal of basic microbiology*, 57(5), 376-385.
- Kaushal, M., Mahuku, G., & Swennen, R. (2020). Metagenomic insights of the root colonizing microbiome associated with symptomatic and non-symptomatic bananas in Fusarium wilt infected fields. *Plants*, 9(2), 263.
- Kennedy, A. C., & Smith, K. L. (1995). Soil microbial diversity and the sustainability of agricultural soils. *Plant and soil*, 170(1), 75-86.
- Khaitov, B. (2018). Effects of Rhizobium inoculation and magnesium application on growth and nodulation of soybean (*Glycine max* L.). *Journal of Plant Nutrition*, 41(16), 2057-2068.
- Khazanah Research Institute. 2019. Banana: The World's Most Popular Fruit. Kuala Lumpur: DOA. (2017). "Fruit Crop Statistics 2017." <http://www.doa.gov.my/index.php/pages/view/622?mid=239>.
- Kobayashi, N. (1987). Daikon ioubyou no yokusi dojoyou. *Kongetsunonogyou*. vol.31, no.8, p.85-90.
- Köberl, M., Dita, M., Martinuz, A., Staver, C., & Berg, G. (2017). Members of Gammaproteobacteria as indicator species of healthy banana plants on Fusarium wilt-infested fields in Central America. *Scientific reports*, 7, 45318.
- Koenig, R. L., Ploetz, R. C., & Kistler, H. C. (1997). *Fusarium oxysporum* f. sp. *cubense* consists of a small number of divergent and globally distributed clonal lineages. *Phytopathology*, 87(9), 915-923.

- Kõljalg, U., Nilsson, R. H., Abarenkov, K., Tedersoo, L., Taylor, A. F., Bahram, M., ... & Douglas, B. (2013). Towards a unified paradigm for sequence-based identification of fungi. *Molecular ecology*, 22(21), 5271-5277.
- Kopecky, J., Samkova, Z., Sarikhani, E., Kyselková, M., Omelka, M., Kristufek, V., ... & Sagova-Mareckova, M. (2019). Bacterial, archaeal and micro-eukaryotic communities characterize a disease-suppressive or conducive soil and a cultivar resistant or susceptible to common scab. *Scientific reports*, 9(1), 1-14.
- Krishna, B. M., Khan, M. A., & Khan, S. T. (2019). Next-generation sequencing (NGS) platforms: An exciting era of genome sequence analysis. In *Microbial Genomics in Sustainable Agroecosystems* (pp. 89-109). Springer, Singapore.
- Lan, X., Zhang, J., Zong, Z., Ma, Q., & Wang, Y. (2017). Evaluation of the biocontrol potential of *Purpureocillium lilacinum* QLP12 against *Verticillium dahliae* in eggplant. *BioMed Research International*, 2017.
- Lauber, C. L., Hamady, M., Knight, R., & Fierer, N. (2009). Soil pH as a predictor of soil bacterial community structure at the continental scale: a pyrosequencing-based assessment. *Applied and Environmental Microbiology*.
- Lee, J. Y. N., & Tan, I. K. P. (2018). Bacterial diversity and community structure of banana rhizosphere in orang asli fields and commercial plantations. *Sains Malaysiana*, 47(2), 243-251.
- Leong, S. K., Latiffah, Z., & Baharuddin, S. (2010). Genetic diversity of *Fusarium oxysporum* f. sp. *ubense* isolates from Malaysia. *African Journal of Microbiology Research*, 4(11), 1026-1037.
- Li, C., Chen, S., Zuo, C., Sun, Q., Ye, Q., Yi, G., & Huang, B. (2011). The use of GFP-transformed isolates to study infection of banana with *Fusarium oxysporum* f. sp. *ubense* race 4. *European Journal of Plant Pathology*, 131(2), 327-340. *ubense*. *Journal of Phytopathology*, 163(10), 807-817.
- Li, C., Yang, J., Li, W., Sun, J., & Peng, M. (2017). Direct root penetration and rhizome vascular colonization by *Fusarium oxysporum* f. sp. *ubense* are the key steps in the successful infection of Brazil Cavendish. *Plant Disease*, 101(12), 2073-2078.
- Li, R., Shen, Z., Sun, L., Zhang, R., Fu, L., Deng, X., & Shen, Q. (2016). Novel soil fumigation method for suppressing cucumber *Fusarium* wilt disease associated with soil microflora alterations. *Applied Soil Ecology*, 101, 28-36.

- Li, X., Zhang, Y. N., Ding, C., Jia, Z., He, Z., Zhang, T., & Wang, X. (2015). Declined soil suppressiveness to *Fusarium oxysporum* by rhizosphere microflora of cotton in soil sickness. *Biology and fertility of soils*, 51(8), 935-946.
- Lian, F., Xue, R., Lin, X., Yang, Y., Zhang, H., Zeng, R., & Song, Y. (2019). Inhibitory effects of aqueous leachates and volatiles from *Allium tuberosum* and *Ageratum conyzoides* on *Fusarium oxysporum* f. sp. *cubense*. *Journal of South China Agricultural University*, 40(4), 40-46.
- Liddicoat, C., Bi, P., Waycott, M., Glover, J., Breed, M., & Weinstein, P. (2018). Ambient soil cation exchange capacity inversely associates with infectious and parasitic disease risk in regional Australia. *Science of the Total Environment*, 626, 117-125.
- Lin, Y. T., Lee, C. C., Leu, W. M., Wu, J. J., Huang, Y. C., & Meng, M. (2021). Fungicidal activity of volatile organic compounds emitted by *Burkholderia gladioli* strain BBB-01. *Molecules*, 26(3), 745.
- Lindahl, B. D., Nilsson, R. H., Tedersoo, L., Abarenkov, K., Carlsen, T., Kjoller, R., ... & Kauserud, H. (2013). Fungal community analysis by high-throughput sequencing of amplified markers—a user's guide. *New Phytologist*, 199(1), 288-299.
- Ling, N., Wang, T., & Kuzyakov, Y. (2022). Rhizosphere bacteriome structure and functions. *Nature Communications*, 13(1), 1-13.
- Lundberg, D. S., Lebeis, S. L., Paredes, S. H., Yourstone, S., Gehring, J., Malfatti, S., ... & Dangl, J. L. (2012). Defining the core *Arabidopsis thaliana* root microbiome. *Nature*, 488(7409), 86-90.
- Liu, H., Carvalhais, L. C., Schenk, P. M., & Dennis, P. G. (2017). Effects of jasmonic acid signalling on the wheat microbiome differ between body sites. *Scientific reports*, 7(1), 1-8.
- Liu, H., Carvalhais, L. C., Schenk, P. M., & Dennis, P. G. (2018). Activation of the salicylic acid signalling pathway in wheat had no significant short-term impact on the diversity of root-associated microbiomes. *Pedobiologia*, 70, 6-11.
- Liu, H., Xiong, W., Zhang, R., Hang, X., Wang, D., Li, R., & Shen, Q. (2018). Continuous application of different organic additives can suppress tomato disease by inducing the healthy rhizospheric microbiota through alterations to the bulk soil microflora. *Plant and soil*, 423(1), 229-240.

- Liu, L., Kong, J., Cui, H., Zhang, J., Wang, F., Cai, Z., & Huang, X. (2016). Relationships of decomposability and C/N ratio in different types of organic matter with suppression of *Fusarium oxysporum* and microbial communities during reductive soil disinfestation. *Biological Control*, *101*, 103-113.
- Lori, M., Symnaczik, S., Mäder, P., De Deyn, G., & Gattinger, A. (2017). Organic farming enhances soil microbial abundance and activity—A meta-analysis and meta-regression. *PLoS One*, *12*(7), e0180442.
- Lozupone C, Knight R (2005). UniFrac: a new phylogenetic method for comparing microbial communities. *Appl Environ Microbiol* *71*:8228-8235.
- Lu, Z., Yang, S., Yuan, X., Shi, Y., Ouyang, L., Jiang, S., Zhang, G. (2019). CRISPR-assisted multi-dimensional regulation for fine-tuning gene expression in *Bacillus subtilis*. *Nucleic acids research*, *47*(7), e40-e40.
- Lucaciu, R., Pelikan, C., Gerner, S. M., Zioutis, C., Köstlbacher, S., Marx, H., ... & Rattei, T. (2019). A bioinformatics guide to plant microbiome analysis. *Frontiers in plant science*, *10*, 1313.
- Luo, T., Yang, C., Peng, Y., Lu, L., Sun, G., Wu, J., ... & Gao, Q. (2014). Whole-genome sequencing to detect recent transmission of *Mycobacterium tuberculosis* in settings with a high burden of tuberculosis. *Tuberculosis*, *94*(4), 434-440.
- Lyakh, V. M. (1986). Effectiveness of magnesium fertilizers in plantings of perpetual carnation on substrates containing calcareous loam. *Nauchn Tr Nauchno-Issled Inst Gorn Sadova Tsvtovod*, *33*, 24.
- Ma, Y. N., Chen, C. J., Li, Q. Q., Xu, F. R., Cheng, Y. X., & Dong, X. (2019). Monitoring antifungal agents of *Artemisia annua* against *Fusarium oxysporum* and *Fusarium solani*, associated with *Panax notoginseng* root-rot disease. *Molecules*, *24*(1), 213.
- Magoč, T., & Salzberg, S. L. (2011). FLASH: fast length adjustment of short reads to improve genome assemblies. *Bioinformatics*, *27*(21), 2957-2963.
- Altschul, S. F., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990). Basic local alignment search tool. *Journal of molecular biology*, *215*(3), 403-410.
- Magurran, A. E. (1988). Ecological diversity and its measurement. Princeton university press.
- Magurran, A. E. (2013). *Measuring biological diversity*. John Wiley & Sons.

- Maron, P. A., Sarr, A., Kaisermann, A., Lévêque, J., Mathieu, O., Guigue, J., & Ranjard, L. (2018). High microbial diversity promotes soil ecosystem functioning. *Applied and Environmental Microbiology*, 84(9), e02738-17.
- Mayers, P. E. (1983). Fusarium wilt of Cavendish bananas in Queensland. In *Proceedings of the international fusarium workshop' Australia* (Vol. 5, p. 60).
- McKinney H., H. (1923). A new system of grading plant diseases. *Journal of Agricultural Research*.
- McMurdie, P. J., & Holmes, S. (2013). phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PloS one*, 8(4), e61217.
- McPherson, M. R., Wang, P., Marsh, E. L., Mitchell, R. B., & Schachtman, D. P. (2018). Isolation and analysis of microbial communities in soil, rhizosphere, and roots in perennial grass experiments. *JoVE (Journal of Visualized Experiments)*, (137), e57932.
- Megersa, H. G. (2017). Propagation methods of selected horticultural crops by specialized organs: review. *J. Horticulture*, 4, 2376-0354.
- Mendes, L. W., de Chaves, M. G., Fonseca, M. D. C., Mendes, R., Raaijmakers, J. M., & Tsai, S. M. (2019). Resistance breeding of common bean shapes the physiology of the rhizosphere microbiome. *Frontiers in microbiology*, 10, 2252.
- Mendes, L. W., Raaijmakers, J. M., de Hollander, M., Mendes, R., & Tsai, S. M. (2018). Influence of resistance breeding in common bean on rhizosphere microbiome composition and function. *The ISME journal*, 12(1), 212-224.
- Mendes, L. W., Kuramae, E. E., Navarrete, A. A., Van Veen, J. A., & Tsai, S. M. (2014). Taxonomical and functional microbial community selection in soybean rhizosphere. *The ISME journal*, 8(8), 1577-1587.
- Miao, G. P., Han, J., Zhang, K. G., Wang, S. C., & Wang, C. R. (2019). Protection of melon against Fusarium wilt-root knot nematode complex by endophytic fungi *Penicillium brefeldianum* HS-1. *Symbiosis*, 77(1), 83-89.
- Milani, C., Duranti, S., Mangifesta, M., Lugli, G. A., Turrone, F., Mancabelli, L., ... & Ventura, M. (2018). Phylotype-level profiling of lactobacilli in highly complex environments by means of an ITS-based metagenomic approach. *Applied and Environmental Microbiology*, 1-29.

- Mohammed, M., Jaiswal, S. K., Sowley, E. N., Ahiabor, B. D., & Dakora, F. D. (2018). Symbiotic N₂ fixation and grain yield of endangered Kersting's groundnut landraces in response to soil and plant associated Bradyrhizobium inoculation to promote ecological resource-use efficiency. *Frontiers in microbiology*, 9, 2105.
- Mohanram, S., & Kumar, P. (2019). Rhizosphere microbiome: revisiting the synergy of plant-microbe interactions. *Annals of Microbiology*, 69(4), 307-320.
- Molina, A. B., Hermanto, C., Pattison, A. B., & Subandiyah, S. (2019). Integrated crop production of bananas in Indonesia and Australia. *Project Report*, ACIAR
- Molina, A., & Williams, R. (2010). Mitigating the threat of banana Fusarium wilt: understanding the agroecological distribution of pathogenic forms and developing disease management strategies.
- Mora-Ruiz, M. D. R., Font-Verdera, F., Orfila, A., Rita, J., & Rosselló-Móra, R. (2016). Endophytic microbial diversity of the halophyte *Arthrocnemum macrostachyum* across plant compartments. *FEMS microbiology ecology*, 92(9), fiw145.
- Moreira WR, Resende RS, Rodrigues FA, Andrade CCL, Nascimento CWA, 2013. Influência do magnésio na resistência do arroz à mancha parda. *Bragantia* 72, 154–61.
- Mostert, D., Molina, A. B., Daniells, J., Fourie, G., Hermanto, C., Chao, C. P., ... & Li, C. (2017). The distribution and host range of the banana Fusarium wilt fungus, *Fusarium oxysporum* f. sp. *cubense*, in Asia. *PLoS one*, 12(7), e0181630.
- Müller, D. B., Vogel, C., Bai, Y., & Vorholt, J. A. (2016). The plant microbiota: systems-level insights and perspectives. *Annual review of genetics*, 50, 211-234.
- Mueller, U. G., & Sachs, J. L. (2015). Engineering microbiomes to improve plant and animal health. *Trends in microbiology*, 23(10), 606-617.
- Nakagawa, H., & Fujita, M. (2018). Whole genome sequencing analysis for cancer genomics and precision medicine. *Cancer science*, 109(3), 513-522.
- Nel, B., Steinberg, C., Labuschagne, N., & Viljoen, A. (2007). Evaluation of fungicides and sterilants for potential application in the management of Fusarium wilt of banana. *Crop Protection*, 26(4), 697-705.

- Netshiheni, R. K., Omolola, A. O., Anyasi, T. A., & Jideani, A. I. (2019). Banana bioactives: absorption, utilisation and health benefits. In *Banana nutrition-function and processing kinetics*. IntechOpen.
- Nishioka, T., Marian, M., Kobayashi, I., Kobayashi, Y., Yamamoto, K., Tamaki, H., & Shimizu, M. (2019). Microbial basis of Fusarium wilt suppression by *Allium* cultivation. *Scientific reports*, 9(1), 1-9.
- NCRS, (February, 2011) Recommended Chemical Soil Test Procedures Retrieved: 18 Feb 2022, https://www.canr.msu.edu/uploads/234/68557/rec_chem_soil_test_proce55c.pdf
- NRCS, U. (2019). Soil Bulk Density/Moisture/Aeration. *USDA NRCS, Washington, DC*.
- O'Donnell, K., Kistler, H. C., Cigelnik, E., & Ploetz, R. C. (1998). Multiple evolutionary origins of the fungus causing Panama disease of banana: concordant evidence from nuclear and mitochondrial gene genealogies. *Proceedings of the National Academy of Sciences*, 95(5), 2044-2049.
- O'Neill, W. T., Henderson, J., Pattermore, J. A., O'Dwyer, C., Perry, S., Beasley, D. R., ... & Hobbs, R. L. (2016). Detection of *Fusarium oxysporum* f. sp. cubense tropical race 4 strain in northern Queensland. *Australasian plant disease notes*, 11(1), 33.
- Oh, S. Y., Fong, J. J., Park, M. S., & Lim, Y. W. (2016). Distinctive feature of microbial communities and bacterial functional profiles in *Tricholoma matsutake* dominant soil. *PLoS One*, 11(12), e0168573.
- Oliveira, E. D., De Oliveira, C. M., Magalhães, P. C., De Andrade, C. L. T., & Hogenhout, S. A. (2005). Spiroplasma and Phytoplasma infection reduce kernel production and nutrient and water contents of several but not all maize cultivars [*Zea mays* L.]. *Maydica (Italy)*.
- Ordóñez, N., Seidl, M. F., Waalwijk, C., Drenth, A., Kilian, A., Thomma, B. P., ... & Kema, G. H. (2015). Worse comes to worst: bananas and Panama disease—when plant and pathogen clones meet. *PLoS pathogens*, 11(11), e1005197.
- Orr, R., & Nelson, P. N. (2018). Impacts of soil abiotic attributes on Fusarium wilt, focusing on bananas. *Applied Soil Ecology*, 132, 20-33.

- Orrù, L. (2018). 7. Sequencing soil samples for qualitative metagenomics–ITS Illumina amplicon protocol. *Crop diversification and low-input farming across Europe: from practitioners' engagement and ecosystems services to increased revenues and value chain organisation*, 71.
- Ossowicki, A., Tracanna, V., Petrus, M. L., van Wezel, G., Raaijmakers, J. M., Medema, M. H., & Garbeva, P. (2020). Microbial and volatile profiling of soils suppressive to *Fusarium culmorum* of wheat. *Proceedings of the Royal Society B*, 287(1921), 20192527.
- Padukkage, D., Geekiyanage, S., Reparaz, J. M., Bezus, R., Balatti, P. A., & Degrassi, G. (2021). *Bradyrhizobium japonicum*, *B. elkanii* and *B. diazoefficiens* Interact with Rice (*Oryza sativa*), Promote Growth and Increase Yield. *Current Microbiology*, 78(1), 417-428.
- Page, E. R. (1962). Studies in soil and plant manganese. *Plant and Soil*, 16(2), 247-257.
- Pandey A, Agrawal GP, Singh SM. Pathogenic fungi in soils of Jabalpur, India. *Mycoses*. 1990 Mar;33(3):116-25. doi: 10.1111/myc.1990.33.3.116. PMID: 2359416.
- Pascale, A., Proietti, S., Pantelides, I. S., & Stringlis, I. A. (2020). Modulation of the root microbiome by plant molecules: the basis for targeted disease suppression and plant growth promotion. *Frontiers in Plant Science*, 10, 1741.
- Paul, E. A. (2016). The nature and dynamics of soil organic matter: plant inputs, microbial transformations, and organic matter stabilization. *Soil Biology and Biochemistry*, 98, 109-126.
- Pegg, K. G., Coates, L. M., O'Neill, W. T., & Turner, D. W. (2019). The epidemiology of *Fusarium* wilt of banana. *Frontiers in plant science*, 10, 1395.
- Peng, H. X., Sivasithamparam, K., & Turner, D. W. (1999). *Chlamydo-spore* germination and *Fusarium* wilt of banana plantlets in suppressive and conducive soils are affected by physical and chemical factors. *Soil Biology and Biochemistry*, 31(10), 1363-1374.
- Pérez Vicente, L. F., Dita, M., & Martínez De La Parte, E. (2014). Technical Manual: Prevention and diagnostic of *Fusarium* Wilt (Panama disease) of banana caused by *Fusarium oxysporum* f. sp. *cubense* Tropical Race 4 (TR4).

- Philippot, L., Raaijmakers, J. M., Lemanceau, P., & Van Der Putten, W. H. (2013). Going back to the roots: the microbial ecology of the rhizosphere. *Nature Reviews Microbiology*, 11(11), 789-799.
- Pieretti, I., Royer, M., Barbe, V., Carrere, S., Koebnik, R., Cociancich, S., ... & Rott, P. (2009). The complete genome sequence of *Xanthomonas albilineans* provides new insights into the reductive genome evolution of the xylem-limited Xanthomonadaceae. *BMC genomics*, 10(1), 1-15.
- Pillay, M., & Tripathi, L. (2007). Banana. In *Fruits and nuts* (pp. 281-301). Springer, Berlin, Heidelberg.
- Pinhassi, J., & Berman, T. (2003). Differential growth response of colony-forming α - and γ -proteobacteria in dilution culture and nutrient addition experiments from Lake Kinneret (Israel), the eastern Mediterranean Sea, and the Gulf of Eilat. *Applied and Environmental Microbiology*, 69(1), 199-211.
- Ploetz, R. C. (1994). Panama disease: return of the first banana menace. *International journal of pest management*, 40(4), 326-336.
- Ploetz, R. C. (2004). Biological control of Fusarium wilt: A review and an evaluation. In *Abstract Booklet, International Congress on Musa: Harnessing Research to Improve Livelihoods. INIBAP (Biodiversity International) Online publication* (p. 141).
- Ploetz, R. C. (2006). Fusarium wilt of banana is caused by several pathogens referred to as *Fusarium oxysporum* f. sp. *cubense*. *Phytopathology*, 96(6), 653-656.
- Ploetz, R. C. (2015a). Fusarium wilt of banana. *Phytopathology*, 105(12), 1512-1521.
- Ploetz, R. C. (2015b). Management of Fusarium wilt of banana: A review with special reference to tropical race 4. *Crop Protection*, 73, 7-15.
- Poli, A., Lazzari, A., Prigione, V., Voyron, S., Spadaro, D., & Varese, G. C. (2016). Influence of plant genotype on the cultivable fungi associated to tomato rhizosphere and roots in different soils. *Fungal biology*, 120(6-7), 862-872.
- Porras-Alfaro, A., Liu, K. L., Kuske, C. R., & Xie, G. (2014). From genus to phylum: large-subunit and internal transcribed spacer rRNA operon regions show similar classification accuracies influenced by database composition. *Applied and environmental microbiology*, 80(3), 829-840.

- Praeg, N., Pauli, H., & Illmer, P. (2019). Microbial diversity in bulk and rhizosphere soil of *Ranunculus glacialis* along a high-alpine altitudinal gradient. *Frontiers in microbiology*, *10*, 1429.
- Ptaszyńska, A. A., Latoch, P., Hurd, P. J., Polaszek, A., Michalska-Madej, J., Grochowalski, Ł., ... & Starosta, A. L. (2021). Amplicon Sequencing of Variable 16S rRNA from Bacteria and ITS2 Regions from Fungi and Plants, Reveals Honeybee Susceptibility to Diseases Results from Their Forage Availability under Anthropogenic Landscapes. *Pathogens*, *10*(3), 381.
- Puig, C. G., & Cumagun, C. J. R. (2019). Rainforest fungal endophytes for the bio-enhancement of banana toward *Fusarium oxysporum* f. sp. cubense Tropical Race 4. *Archives of Phytopathology and Plant Protection*, *52*(7-8), 776-794.
- Pushpavathi, Y., Dash, S. N., & Reddy, A. (2018). Efficacy of application methods of biocontrol agents and fungicides on *Fusarium* wilt management in banana. *Journal of Pharmacognosy and Phytochemistry*, *7*(6), 2024-2026.
- Qi, Y. X., Zhang, X., Pu, J. J., Xie, Y. X., Zhang, H. Q., & Huang, S. L. (2008). Race 4 identification of *Fusarium oxysporum* f. sp. cubense from Cavendish cultivars in Hainan province, China. *Australasian Plant Disease Notes*, *3*(1), 46-47.
- Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., ... & Glöckner, F. O. (2012). The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic acids research*, *41*(D1), D590-D596.
- Rainey, F. A., Ward-Rainey, N. L., Janssen, P. H., Hippe, H., & Stackebrandt, E. (1996). *Clostridium paradoxum* DSM 7308T contains multiple 16S rRNA genes with heterogeneous intervening sequences. *Microbiology*, *142*(8), 2087-2095.
- Rashid, M. I., Mujawar, L. H., Shahzad, T., Almeelbi, T., Ismail, I. M., & Oves, M. (2016). Bacteria and fungi can contribute to nutrients bioavailability and aggregate formation in degraded soils. *Microbiological research*, *183*, 26-41.
- Ray, P., Lakshmanan, V., Labbé, J. L., & Craven, K. D. (2020). Microbe to microbiome: A paradigm shift in the application of microorganisms for sustainable agriculture. *Frontiers in Microbiology*, *11*, 3323.
- Raza, W., Yang, W., & Shen, Q. R. (2008). *Paenibacillus polymyxa*: antibiotics, hydrolytic enzymes and hazard assessment. *Journal of Plant Pathology*, *419-430*.

- Rousk J, Bååth E, Brookes PC, Lauber CL, Lozupone C, Caporaso JG, Knight R, Fierer N. 2010. Soil bacterial and fungal communities across a pH gradient in an arable soil. *ISME Journal* 4: 1340-1351
- Sabale, S. N., Suryawanshi, P. P., & Krishnaraj, P. U. (2019). Soil metagenomics: concepts and applications. In *Metagenomics-Basics, Methods and Applications*. IntechOpen.
- Sagar, B. S., Raju, B., & Sahithya, B. R. (2018). Physico-chemical evaluation of banana genotypes. *Journal of Pharmacognosy and Phytochemistry*, 7(3), 555-558.
- Salkind, N. J. (2010). *Encyclopedia of research design* (Vols. 1-0). Thousand Oaks, CA: SAGE Publications, Inc. doi: 10.4135/9781412961288
- Santoyo, G., Pacheco, C. H., Salmerón, J. H., & León, R. H. (2017). The role of abiotic factors modulating the plant-microbe-soil interactions: toward sustainable agriculture. A review. *Spanish journal of agricultural research*, 15(1), 13.
- Sawada, E., Koyama, Y., Sato, T., Yonemoto, K., & Toyota, K. (2018). Effect of solarization on the density of *Fusarium oxysporum* in soil and the yield of lotus grown in Naruto area, Tokushima Prefecture, Japan. *Soil Microorganisms*, 72(1), 34-38.
- Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, *et al.* (2009). Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. *Appl Environ Microbiol* 75:7537-7541
- Schmidt, J. E., Kent, A. D., Brisson, V. L., & Gaudin, A. C. (2019). Agricultural management and plant selection interactively affect rhizosphere microbial community structure and nitrogen cycling. *Microbiome*, 7(1), 1-18.
- Segata, N., Izard, J., Waldron, L., Gevers, D., Miropolsky, L., Garrett, W. S., & Huttenhower, C. (2011). Metagenomic biomarker discovery and explanation. *Genome biology*, 12(6), 1-18.
- Senbayram, M., Gransee, A., Wahle, V., & Thiel, H. (2015). Role of magnesium fertilisers in agriculture: plant–soil continuum. *Crop and Pasture Science*, 66(12), 1219-1229.
- Shafi, J., Tian, H., & Ji, M. (2017). *Bacillus* species as versatile weapons for plant pathogens: a review. *Biotechnology & Biotechnological Equipment*, 31(3), 446-459.

- Shah, K. K., Modi, B., Pandey, H. P., Subedi, A., Aryal, G., Pandey, M., & Shrestha, J. (2021). Diversified Crop Rotation: An Approach for Sustainable Agriculture Production. *Advances in Agriculture*, 2021.
- Shang, Q., Yang, G., Wang, Y., Wu, X., Zhao, X., Hao, H., & Wang, R. (2016). Illumina-based analysis of the rhizosphere microbial communities associated with healthy and wilted Lanzhou lily (*Lilium davidii* var. unicolor) plants grown in the field. *World Journal of Microbiology and Biotechnology*, 32(6), 95.
- Sharma-Poudyal, D., Schlatter, D., Yin, C., Hulbert, S., & Paulitz, T. (2017). Long-term no-till: a major driver of fungal communities in dryland wheat cropping systems. *PLoS one*, 12(9), e0184611.
- Sharpton, T. J. (2014). An introduction to the analysis of shotgun metagenomic data. *Frontiers in plant science*, 5, 209.
- Shelef, O., Hahn, P. G., Pineda, A., Tejesvi, M. V., & Martinez-Medina, A. (2019). As Above So Below? Progress in Understanding the Role of Belowground Interactions in Ecological Processes. *Frontiers in Ecology and Evolution*, 7, 318.
- Shen, Z., Ruan, Y., Xue, C., Zhong, S., Li, R., & Shen, Q. (2015). Soils naturally suppressive to banana Fusarium wilt disease harbor unique bacterial communities. *Plant and Soil*, 393(1), 21-33.
- Shi, L., Du, N., Shu, S., Sun, J., Li, S., & Guo, S. (2017). *Paenibacillus polymyxa* NSY50 suppresses Fusarium wilt in cucumbers by regulating the rhizospheric microbial community. *Scientific reports*, 7(1), 1-13.
- Siamak, S. B., & Zheng, S. (2018). Banana Fusarium wilt (*Fusarium oxysporum* f. sp. *cubense*) control and resistance, in the context of developing wilt-resistant bananas within sustainable production systems. *Horticultural Plant Journal*, 4(5), 208-218
- Siegel-Hertz, K., Edel-Hermann, V., Chapelle, E., Terrat, S., Raaijmakers, J. M., & Steinberg, C. (2018). Comparative microbiome analysis of a Fusarium wilt suppressive soil and a Fusarium wilt conducive soil from the Chateaufort region. *Frontiers in Microbiology*, 9, 568.
- Singh, B. & Schulze, D. G. (2015) Soil Minerals and Plant Nutrition. *Nature Education Knowledge* 6(1):1
- Singh, S., Singh, H., Rout, B., Tripathi, R. B. M., Chopra, C., & Chopra, R. S. (2020). The New Science of Metagenomics: Revealing the Secrets of Microbial Physiology. In *Metagenomics: Techniques, Applications, Challenges and Opportunities* (pp. 3-22). Springer, Singapore.

- Singleton DR, Furlong MA, Rathbun SL, Whitman WB (2001). Quantitative comparisons of 16S rRNA gene sequence libraries from environmental samples. *Appl Environ Microbiol* 67:4374-4376.
- Sivamani, E., & Gnanamanickam, S. S. (1988). Biological control of *Fusarium oxysporum* f. sp. *cubense* in banana by inoculation with *Pseudomonas fluorescens*. *Plant and soil*, 107(1), 3-9.
- Smith, E. P., & van Belle, G. (1984). Nonparametric estimation of species richness. *Biometrics*, 119-129.
- Srivastav, R., & Suneja, G. (2019). Recent Advances in Microbial Genome Sequencing. *Microbial Genomics in Sustainable Agroecosystems*, 131-144.
- Stover RH, Simmonds NW. Bananas, 3rd edition. Longman, London 1987.
- Stover, R. H. (1953). The effect of soil moisture on *Fusarium* species. *Canadian Journal of Botany*, 31(5), 693-697.
- Stover, R. H. (1962a). Fusarial wilt (Panama Disease) of bananas and other *Musa* species. *Fusarial wilt (Panama disease) of bananas and other Musa species*.
- Stover, R. H. (1962b). Studies on *Fusarium* wilt of bananas: IX. Competitive saprophytic ability of *F. oxysporum* f. *cubense*. *Canadian Journal of Botany*, 40(11), 1473-1481.
- Stover, R. H. (1990). *Fusarium* wilt of Banana: Some history and current Status of the Disease. *Fusarium wilt of banana.*, 1-7.
- Stover, R. H., & Buddenhagen, I. W. (1986). Banana breeding: polyploidy, disease resistance and productivity. *Fruits*, 41(3), 175-191.
- Su, H. J., Hwang, S. C., & Ko, W. H. (1986). Fusarial wilt of Cavendish bananas in Taiwan. *Plant Disease*, 70(9), 814-818.
- Suárez, J. O., Pajares, J. A., & Diez, J. J. (2018). In vitro antagonism of edible ectomycorrhizal fungi against *Fusarium oxysporum* and *Fusarium verticillioides*. *The Forestry Chronicle*, 94(2), 117-125.
- Sui, X., Zhang, R., Frey, B., Yang, L., Liu, Y., Ni, H., & Li, M. H. (2021). Soil physicochemical properties drive the variation in soil microbial communities along a forest successional series in a degraded wetland in northeastern China. *Ecology and evolution*, 11(5), 2194-2208.

- Sulok, K. M. T., Ahmed, O. H., Khew, C. Y., Zehnder, J. A. M., Jalloh, M. B., Musah, A. A., & Abdu, A. (2021). Chemical and Biological Characteristics of Organic Amendments Produced from Selected Agro-Wastes with Potential for Sustaining Soil Health: A Laboratory Assessment. *Sustainability*, 13(9), 4919.
- Tao, R., Liang, Y., Wakelin, S. A., & Chu, G. (2015). Supplementing chemical fertilizer with an organic component increases soil biological function and quality. *Applied Soil Ecology*, 96, 42-51.
- Taylor & Francis. (2007). *Soil Sampling and Methods of Analysis*. Ed Carter, M.R., Gregorich E.G. CRC Press: Boca Raton, doi.org/10.1201/9781420005271
- Teixeira, L., Heck, D., Nomura, E., Vieira, H., & Dita, M. (2021). Soil attributes, plant nutrition, and Fusarium wilt of banana in São Paulo, Brazil. *Tropical plant Pathology*, 1-12.
- Tenorio-Salgado, S., Tinoco, R., Vazquez-Duhalt, R., Caballero-Mellado, J., & Perez-Rueda, E. (2013). Identification of volatile compounds produced by the bacterium *Burkholderia tropica* that inhibit the growth of fungal pathogens. *Bioengineered*, 4(4), 236-243.
- Thangavelu, R., & Jayanthi, A. (2009). RFLP analysis of rDNA-ITS regions of native non-pathogenic *Fusarium oxysporum* isolates and their field evaluation for the suppression of *Fusarium* wilt disease of banana. *Australasian Plant Pathology*, 38(1), 13-21.
- Thangavelu, R., & Mustafa, M. M. (2010). First report on the occurrence of a virulent strain of *Fusarium* wilt pathogen (Race-1) infecting Cavendish (AAA) group of bananas in India. *Plant Disease*, 94(11), 1379-1379.
- Thangavelu, R., & Mustafa, M. M. (2012). Current advances in the *Fusarium* wilt disease management in banana with emphasis on biological control. In *Plant pathology*. InTech.
- Thangavelu, R., (2016). Status Report on *Fusarium* Wilt Disease in India, 2016 ISHAS ProMusa Symposium, Montpellier, France
- Thangavelu, R., Loganathan, M., Arthee, R., Prabakaran, M., & Uma, S. (2020). *Fusarium* wilt: a threat to banana cultivation and its management. *CAB Reviews*, 15(004), 1-24.
- Thangavelu, R., Palaniswami, A., & Velazhahan, R. (2004). Mass production of *Trichoderma harzianum* for managing *Fusarium* wilt of banana. *Agriculture, ecosystems & environment*, 103(1), 259-263.

- Ting, A. S. Y., Mah, S. W., & Tee, C. S. (2009). Prevalence of endophytes antagonistic towards *Fusarium oxysporum* f. sp. *cubense* race 4 in various plants. *American-Eurasian Journal of Sustainable Agriculture*, 3(3), 399-406.
- Ting, A. S. Y., Mah, S. W., & Tee, C. S. (2011). Detection of potential volatile inhibitory compounds produced by endobacteria with biocontrol properties towards *Fusarium oxysporum* f. sp. *cubense* race 4. *World Journal of Microbiology and Biotechnology*, 27(2), 229-235.
- Ting, A. S., Meon, S., Kadir, J., Radu, S., & Singh, G. (2008). Endophytic microorganisms as potential growth promoters of banana. *BioControl*, 53(3), 541-553.
- Tkacz, A., & Poole, P. (2015). Role of root microbiota in plant productivity. *Journal of experimental botany*, 66(8), 2167-2175.
- Toyota, K., Kimura, M., Takechi, S., & Kuninaga, S. (2000). Comparison of microbial community structure between soils suppressive and conducive to Fusarium-wilt of radish. *Soil Microorganisms*, 54(1), 69-79.
- Uma, S., Saraswathi, M. S., & Durai, P. (2019). Banana Genetic Resources. In *Conservation and Utilization of Horticultural Genetic Resources* (pp. 321-361). Springer, Singapore.
- Vaario, L. M., Yang, X., & Yamada, A. (2017). Biogeography of the Japanese gourmet fungus, *Tricholoma matsutake*: a review of the distribution and functional ecology of matsutake. *Biogeography of mycorrhizal symbiosis*, 319-344.
- Venter, Z. S., Jacobs, K., & Hawkins, H. J. (2016). The impact of crop rotation on soil microbial diversity: A meta-analysis. *Pedobiologia*, 59(4), 215-223.
- Viaene, T., Langendries, S., Beirinckx, S., Maes, M., & Goormachtig, S. (2016). *Streptomyces* as a plant's best friend?. *FEMS microbiology ecology*, 92(8).
- Viljoen, A., Mahuku, G. S., Massawe, C., Tendo Ssali, R., Kimunye, J. N., Mostert, G., ... & Coyne, D. L. (2017). Banana diseases and pests: Field guide for diagnostics and data collection.
- Waite, B. H. (1963). Wilt of *Heliconia* spp. caused by *Fusarium oxysporum* f. sp. *cubense* race 3. *Tropical Agriculture Trinidad*, 40, 299-305.

- Wang, B., Li, R., Ruan, Y., Ou, Y., Zhao, Y., & Shen, Q. (2015). Pineapple–banana rotation reduced the amount of *Fusarium oxysporum* more than maize–banana rotation mainly through modulating fungal communities. *Soil Biology and Biochemistry*, *86*, 77-86.
- Wang, Q., Garrity, G. M., Tiedje, J. M., & Cole, J. R. (2007). Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and environmental microbiology*, *73*(16), 5261-5267.
- Wang, R., Zhang, H., Sun, L., Qi, G., Chen, S., & Zhao, X. (2017). Microbial community composition is related to soil biological and chemical properties and bacterial wilt outbreak. *Scientific Reports*, *7*(1), 1-10.
- Wei, X., Wang, X., Cao, P., Gao, Z., Chen, A. J., & Han, J. (2020). Microbial community changes in the rhizosphere soil of healthy and rusty Panax ginseng and discovery of pivotal fungal genera associated with rusty roots. *BioMed research international*, 2020.
- Weiss, S., Xu, Z. Z., Peddada, S., Amir, A., Bittinger, K., Gonzalez, A., ... & Hyde, E. R. (2017). Normalization and microbial differential abundance strategies depend upon data characteristics. *Microbiome*, *5*(1), 27.
- Whittaker, R. H. (1972). Evolution and measurement of species diversity. *Taxon*, *21*(2-3), 213-251.
- Wilson, M. V., & Shmida, A. (1984). Measuring beta diversity with presence-absence data. *The Journal of Ecology*, 1055-1064.
- Win, T. T., Bo, B., Malec, P., & Fu, P. (2021). The effect of a consortium of *Penicillium* sp. and *Bacillus* spp. in suppressing banana fungal diseases caused by *Fusarium* sp. and *Alternaria* sp. *Journal of Applied Microbiology*.
- Woese, C. R., & Fox, G. E. (1977). Phylogenetic structure of the prokaryotic domain: the primary kingdoms. *Proceedings of the National Academy of Sciences*, *74*(11), 5088-5090.
- Wu, D., José, J. V., Nurnberger, J. I., & Torres, E. B. (2018). A biomarker characterizing neurodevelopment with applications in autism. *Scientific reports*, *8*(1), 1-14.
- Wu, X., Shan, Y., Li, Y., Li, Q., & Wu, C. (2020). The soil nutrient environment determines the strategy by which *Bacillus velezensis* HN03 suppresses *Fusarium* wilt in banana plants. *Frontiers in plant science*, *11*, 1801.

- Xia, X., Zhang, P., He, L., Gao, X., Li, W., Zhou, Y., & Yang, L. (2019). Effects of tillage managements and maize straw returning on soil microbiome using 16S rDNA sequencing. *Journal of integrative plant biology*, 61(6), 765-777.
- Xiong, W., Li, R., Ren, Y., Liu, C., Zhao, Q., Wu, H., & Shen, Q. (2017). Distinct roles for soil fungal and bacterial communities associated with the suppression of vanilla Fusarium wilt disease. *Soil Biology and Biochemistry*, 107, 198-207.
- Xu, L., Cui, G., Ke, C., Fan, Y., & Yan, Y. (2018). Immobilized Burkholderia cepacia lipase on pH-responsive pullulan derivatives with improved enantioselectivity in chiral resolution. *Catalysts*, 8(1), 13.
- Xu, Y., Wang, G., Jin, J., Liu, J., Zhang, Q., & Liu, X. (2009). Bacterial communities in soybean rhizosphere in response to soil type, soybean genotype, and their growth stage. *Soil Biology and Biochemistry*, 41(5), 919-925.
- Xue, C., Penton, C. R., Shen, Z., Zhang, R., Huang, Q., Li, R., & Shen, Q. (2015). Manipulating the banana rhizosphere microbiome for biological control of Panama disease. *Scientific reports*, 5(1), 1-11.
- Xue, P. P., Carrillo, Y., Pino, V., Minasny, B., & McBratney, A. B. (2018). Soil properties drive microbial community structure in a large scale transect in South Eastern Australia. *Scientific reports*, 8(1), 1-11.
- Yang, B., Yang, D. P., Gao, Z. Y., Li, M., Zhang, Z. K., & Hu, M. J. (2013). Toxicity test of 8 fungicides against *Trichothecium roseum* causing mango fruit rot. *Journal of Tropical Biology*, 4(1), 45–49.
- Yang, D., Wang, L., Wang, T., Zhang, Y., Zhang, S., & Luo, Y. (2021). Plant Growth-Promoting Rhizobacteria HN6 induced the change and reorganization of Fusarium microflora in the rhizosphere of banana seedlings to construct a healthy banana microflora. *Frontiers in Microbiology*, 12.
- Yang, J., Huang, J., Wang, C., & Feng, Y. (2015). Effects of *Allium tuberosum* juice on the activities of two cell wall degrading enzymes produced by *Fusarium oxysporum* f. sp. *cubense*. *Journal of Zhongkai University of Agriculture and Engineering*, 28(1), 64-66.
- Yasmin, L., Ali, M. A., & Khan, F. N. (2017). Efficacy of fungicides in controlling fusarium wilt of gladiolus. *Bangladesh Journal of Agricultural Research*, 42(4), 599-607.

- Yongmei Liao, Chengwu Zou, Qi Huang & Zhongwen Wang. (2020). Analysis of fungi diversity in root zone soil of banana plants. *Guihaia*, 40(1), 99-107.
- Yuan, J., Wen, T., Zhang, H., Zhao, M., Penton, C. R., Thomashow, L. S., & Shen, Q. (2020). Predicting disease occurrence with high accuracy based on soil macroecological patterns of Fusarium wilt. *The ISME Journal*, 14(12), 2936-2950.
- Yuan, J., Zhao, J., Wen, T., Zhao, M., Li, R., Goossens, P., & Shen, Q. (2018). Root exudates drive the soil-borne legacy of aboveground pathogen infection. *Microbiome*, 6(1), 1-12.
- Yun, T., Zhang, M., Zhou, D., Jing, T., Zang, X., Qi, D., & Xie, J. (2021). Anti-Foc RT4 Activity of a Newly Isolated Streptomyces sp. 5–10 From a Medicinal Plant (*Curculigo capitulata*). *Frontiers in microbiology*, 11, 3544.
- Zhang, C., Lin, Y., Tian, X., Xu, Q., Chen, Z., & Lin, W. (2017). Tobacco bacterial wilt suppression with biochar soil addition associates to improved soil physicochemical properties and increased rhizosphere bacteria abundance. *Applied Soil Ecology*, 112, 90-96.
- Zhang, D., Ge, S., Wang, C., Jiang, Y., Li, X., Xia, S., & Wang, X. (2020). The relationship between soil bacteria and metal nutrient availability for uptake of apple trees in Chinese orchards. *Plant Growth Regulation*, 92, 181-193.
- Zhang, L., Yuan, T., Wang, Y., Zhang, D., Bai, T., Xu, S., ... & Zheng, S. J. (2018). Identification and evaluation of resistance to *Fusarium oxysporum* f. sp. *cubense* tropical race 4 in *Musa acuminata* Pahang. *Euphytica*, 214(7), 1-12.
- Zhang, M. X., Zhang, M. C., Chen, P., Ruan, Y. Z., Zhu, Y. Y., & Shen, Q. R. (2013). Influence of nitrate/ammonium ratio on the plant growth of banana and related wilt disease development. *Journal of Plant Nutrition and Fertilizer*, 19(5), 1241-1247.
- Zhao, Q., Tang, J., Li, Z., Yang, W., & Duan, Y. (2018). The influence of soil physico-chemical properties and enzyme activities on soil quality of saline-alkali agroecosystems in western Jilin Province, China. *Sustainability*, 10(5), 1529.
- Zhao, S., Chen, X., Deng, S., Dong, X., Song, A., Yao, J., & Chen, F. (2016). The effects of fungicide, soil fumigant, bio-organic fertilizer and their combined application on chrysanthemum Fusarium wilt controlling, soil enzyme activities and microbial properties. *Molecules*, 21(4), 526.

- Zhao, S., Liu, D., Ling, N., Chen, F., Fang, W., & Shen, Q. (2014). Bio-organic fertilizer application significantly reduces the *Fusarium oxysporum* population and alters the composition of fungi communities of watermelon *Fusarium* wilt rhizosphere soil. *Biology and Fertility of Soils*, 50(5), 765-774.
- Zhao, X., Liu, X., Zhao, H., Ni, Y., Lian, Q., Qian, H., & Ma, Q. (2021). Biological control of *Fusarium* wilt of sesame by *Penicillium bilaiae* 47M-1. *Biological Control*, 158, 104601.
- Zheng, S. J., García-Bastidas, F. A., Li, X., Zeng, L., Bai, T., Xu, S., & Yang, L. (2018). New geographical insights of the latest expansion of *Fusarium oxysporum* f. sp. *cubense* tropical race 4 into the Greater Mekong Subregion. *Frontiers in plant science*, 9, 457.
- Zhou, D., Jing, T., Chen, Y., Wang, F., Qi, D., Feng, R., & Li, H. (2019). Deciphering microbial diversity associated with *Fusarium* wilt-diseased and disease-free banana rhizosphere soil. *BMC microbiology*, 19(1), 161.
- Zhou, J., Wang, M., Sun, Y., Gu, Z., Wang, R., Saydin, A., & Guo, S. (2017). Nitrate increased cucumber tolerance to *Fusarium* wilt by regulating fungal toxin production and distribution. *Toxins*, 9(3), 100.
- Zhu, C., Ling, N., Guo, J., Wang, M., Guo, S., & Shen, Q. (2016). Impacts of fertilization regimes on arbuscular mycorrhizal fungal (AMF) community composition were correlated with organic matter composition in maize rhizosphere soil. *Frontiers in microbiology*, 7, 1840.