Copyright is owned by the Author of the thesis. Permission is given for a copy to be downloaded by an individual for the purpose of research and private study only. The thesis may not be reproduced elsewhere without the permission of the Author.

Companion biota associated with Leptospermum scoparium (mānuka; Myrtaceae)

A thesis presented in partial fulfilment of the requirements for the degree of

Doctor of Philosophy

in

Ecology

at Massey University, Manawatū,

New Zealand

Julia Bohórquez Rodríguez de Medina

2018

Abstract

Leptospermum scoparium (mānuka; Myrtaceae) is involved in three crucial ecological interactions that might affect nectar production, and the New Zealand honey industry. First, these plants can be affected by scale insect infestation which have the potential to affect plant health, second, they provide nectar for honey bees (mānuka honey), and third, they are hosts for, and may receive benefits from, dual mycorrhizal fungal associations (both ecto- and endo-). The understanding of these interactions is very important for the honey industry as well as for New Zealand ecosystems. However, there is limited knowledge about the influence of scale insects and mycorrhizal fungi on plant growth and nectar production, and the influence of honey bee visitation on the honey making-process. To better understand the significance of these interactions, a variety of methods, including behavioural observations, histological, molecular, and taxonomic techniques, were used in this thesis.

Findings showed that the eriococcids *Acanthococcus campbelli* and *Acanthococcus leptospermi* are now the main species on *L. scoparium*, rather than *Acanthococcus orariensis*, which was the main causative agent of the mānuka blight in the 1940's and 1960's. Whereas the distribution of *A. leptospermi* was previously reported, the distribution of *A. campbelli* across New Zealand's islands was illustrated for the first time in this thesis. Other scale insect species classified within the families Coelostomidiidae, Diaspididae, and Pseudococcidae were also found, but their incidence and abundance was typically lower in comparison to the family Eriococcidae.

The number of eriococcids was reduced by the application of an Insect Growth Regulator (IGR) on six different cultivars in a split plot designed experiment, but cultivars differed in response to the insecticide treatment. Using the same common garden design, but just the unsprayed plants, honey bees showed a preference for the cultivar with the highest nectar sugar content and nectar DHA content. However, sugar, rather than DHA, was the best predictor of visitation pattern. The number of honey bee visits increased at midday as the day warmed up. The overall number of flowers estimated per plant was included in the model, but did not drive the visit number as, for example, it was found that the cultivar with the highest estimated number of flowers was less visited.

Bioinformatics analysis revealed the association of L. scoparium with at least 25 fungal classes, including 16 ectomycorrhizal (EcM) fungal lineages and eight arbuscular mycorrhizal (AM) families. The majority of mycorrhizal fungal lineages were shared among cultivated and wild plants at the three studied sites, which suggests that cultivated plants are naturally colonised by mycorrhizal fungi. The EcM fungal lineages /cortinarius, the AM /tomentella-thelephora, and families Glomeraceae /laccaria, Claroideoglomeraceae were the most abundant. Among the EcM fungal species, Laccaria glabripes and the endemic EcM fungal species Clavulina subrugosa, Cortinarius waiporianus and Dermocybe indotata were revealed as the most abundant. The presence of the exotic EcM fungal species Amanita muscaria was limited and mainly found in cultivated plants, that had established on a site previously with *Pinus radiata*. The cosmopolitan AM fungal species Rhizophagus irregularis and Claroideoglomus lamellosum were the dominant species found in both cultivated and wild plants.

Among cultivated and wild plants, wild plants appeared to be colonised by a more diverse mycorrhizal fungal community. For instance, the lineage /russula-lactarius was more abundant in wild plants than in cultivated plants. The presence of /russula-lactarius and other lineages and species could be improving host performance (seed establishment, drought tolerance, pathogen resistance, and plant growth) on wild plants. However, the absence of some of the mycorrhizal fungal species from cultivated plants, which could be present on wild plants, could limit the potential yield of *L. scoparium* plantation. Finding suitable combinations of mycorrhizal fungal inoculum could help optimise the development of *L. scoparium*, nectar production, and subsequently the New Zealand mānuka honey industry.

Acknowledgments

Alastair Robertson and James Millner, incommensurable thanks for giving me the opportunity to be involved in this research; encouraging me to identify scale insects and look for arbuscules, being patient, listening and believing in me. Along with you, Jonathan Stephens, Richard Archer, Patrick Biggs, Bronwyn Douglas, Georgie Hamilton, Maggie Olsen, Massey University, PGP Mānuka Research Partnership Limited and Comvita Limited have strongly supported this research.

I would like to thank to my parents, who encouraged me to study and follow my dreams. My father has always suggested that I should leave records of my experiences, which had hitherto never undertaken. Dad, in the next few pages I reveal the main experiences that shaped my PhD life. In short, I laughed and socialised, but most importantly, I learnt – what you like most. Beside my father, my mother encouraged me to follow my dream in spite of the distance that it ultimately put between me and her. Thank you both for supporting my initiatives wherever I am going, and for inculcating in me your principles of life.

Incommensurable thanks to the multicultural companion biota at the office 1.42: *Jerry singapurinus*, *Lizzy zelandicus var. palmerstonian*, *Chau vietnaminus*, *David hispanicus*, *Miriam germanicus*, *Ackim zambinus*, *Yen vietnaminus*, *Agneta indinus*, *Dimitrius grekus* and *Martin caledonius*. Your support, worries, happiness, reviews, food and patience gave me the strength to work in the most challenging and happiest moments of the past years.

Challenging moments have been significantly influenced by DNA, being remarkably complex and demanding. Renee Johansen, you mostly introduced me into the Next Generation Sequencing and the mycorrhizal fungi world. Thanks for enthusiastically sharing your knowledge, your time and your advices. Beside you, Trish McLenachan, who made me feel as Cinderella in the lab, has been my fairy mother and Miss Amplicon of the year. Thanks Trish for arriving to the lab with your magic wand and with your terrific DNA passion. Many thanks also to Mike Gemmell, Rosie Bradshaw, Pranav Chettri, Andre Sim, Simon Hills, Gillian Gibb, Jerry Cooper, Peter Johnston and the root sampling team, for helping me during the mycorrhizal fungal study.

Eriococcids have been my 'lovers' during this PhD, a love that has been transferred from passionate coccidologists. Discovering the limited number of coccidologists and the interest of scale insects, engage me not only to remember them, but most importantly to seek them. Thank you Penny Gullan and Danièle Matile-Ferrero for your advices, time and knowledge. Many thanks also to Cleland and Nikki for your time and your help. Thanks also to Landcare Research and specially Grace Hall for facilitating microscope slides from the New Zealand Arthropod Collection.

Importantly, all this research would have not been feasible without the support of the Ecology group, with whom I have felt at home; which may explain why I spent that much time working. Thanks to all staff members and students for giving me the opportunity to belong to this group; a group that embraces the richness of academic researchers who are involved in unique and interesting studies. Within this group, I thank the crucial team of Cleland Wallace, Paul Barrett, Sharon Wright, Shaun Nielsen and Tracy Harris for being patient and support us with everything that we need.

Thanks to the international kiwi family, it has been a pleasure to meet you all. This multicultural family is characterised by a wide range of skills. Including people such as Ermanno with his amazing drone, Pablo with his super Linux knowledge, Marta with her Ukulele, Marie with her knitting, Stefi with her GIS and Kelly with her energy. Additionally, I will remember Tessa and her patience while I looked for my eriococcids on holidays, and Clemens and Rolland for sharing the memorable and amazing hiking walk (we got there!). Invaluable thanks to Ivana, Patricia, Layla, Angela and the Dutch girls Aniek and Flo. Thanks for being there while I spent too much time in my mānuka world. Thank you Layla, as chopping roots can be harsh, but with you it seemed much easier. And with you Eric, who showed faith for our family. I will not forget that dinner at Massey to avoid falling asleep while the roots dried – thanks Eric! Overall, invaluable thanks to the family, for your time, talks, laughs, worries and potlucks. All of you have been the driving forces of my PhD life.

Many thanks to Marta Delmás and Reyes Alejano, your advices guided me to the present point. Both of you have helped me to create my career's path.

Finally, I wish to thank my siblings, Maria, Patricio and Cristina, for your support in my decisions and for taking care of me. Thanks Cristina for being *la pulga* and for your sense

of humour. Along with my siblings, Catana, Cristina, Chari and Fatima, have always been very supportive, thank you deeply.

Many thanks also to all my Spanish friends. Anything that I needed has always being provided by having you there.

Kilometres do not make the distance, people make the distance.



Illustration: Ester Gámez Blánquez

Contents

Abstract	i
Acknowledgments	iii
Glossary of abbreviations	xi
Chapter 1. General introduction	1
1.1. Introduction	
1.1.1. General background	3
1.1.2. From the natural source to the final product	3
1.2. Literature review	8
1.2.1. Taxonomy and biology of Leptospermum scoparium	8
1.2.2. Companion biota associated with Leptospermum scoparium	11
1.3. Research objectives and thesis outline	21
1.4. References	23
Chapter 2. An update of eriococcids on Leptospermum scoparium in New	Zealand
2.1. Introduction	
2.2. Material and methods	
2.2.1. Survey of eriococcid infestation in Central North Island	
2.2.2. Statistical analysis	
2.2.3. Survey of eriococcid species associated with <i>Leptospermum scopar</i>	
2.3. Results	
2.3.1. Survey of eriococcid infestation in Central North Island2.3.2. Survey of eriococcid species associated with <i>Leptospermum scopar</i>	
2.4. Discussion	
2.4.1. Survey of eriococcid infestation in Central North Island	
2.4.2. Survey of eriococcid species associated with <i>Leptospermum scopar</i>	
2.5. References	
2.6. Appendices	
Chapter 3. Scale insect presence, honey bee visitation and nectar	
Leptospermum scoparium cultivars	-
3.1. Introduction	77
3.2. Material and methods	81
3.2.1. Study area and plant material	81
3.2.2. Estimation of flower density through basal area	83
3.2.3. Application of insecticide	
3.2.4. Nectar quality and quantity	
3.2.5. Recording honey bees' visitation	
3.2.6. Description of statistical analysis	
3.3. Results	
3.3.1. Flower density estimation through basal area	94

3.3.2. Influence of an insecticide treatment on scale insects	97
3.3.3. Nectar quality and quantity	. 101
3.3.4. Relative visitation rates of honey bees and other insects	. 107
3.4. Discussion	.113
3.4.1. Influence of an insecticide treatment on scale insect	. 113
3.4.2. Nectar quality and quantity	. 115
3.4.3. Relative visitation rates of honey bees and other insects	. 117
3.5. References	.121
3.6. Appendices	.132
Chapter 4. Mycorrhizal fungal communities associated with Leptosperi	mum
scoparium	.151
4.1. Introduction	. 153
4.2. Material and methods	.157
4.2.1. Study area	. 157
4.2.2. Sample collection	. 158
4.2.3. Root staining	. 158
4.2.4. DNA extraction	
4.2.5. Bioinformatics analysis	. 163
4.2.6. Statistical analysis	
4.3. Results	
4.3.1. Root staining	
4.3.2. ITS region	
4.3.3. SSU region	
4.4. Discussion	
4.4.1. Fungal communities associated with <i>Leptospermum scoparium</i>	
4.4.2. Diversity and distribution of fungal communities among <i>Leptospermum</i>	
scoparium provenances	
4.4.3. Mycorrhizal fungal species associated with Leptospermum scoparium	
4.5. References	
4.6. Appendices	.218
Chapter 5. Soil inoculation trial on Leptospermum scoparium seedlings	.241
5.1. Introduction	.243
5.2. Material and methods	. 245
5.3. Results	.248
5.4. Discussion	.252
5.5. References	.254
5.6. Appendices	.256
Chapter 6. General discussion	. 259
6.1. Synthesis.	
6.2. Challenges and limitations	
6.3. Future research	
6.4. References	.272

Glossary of abbreviations

Abbreviation	Full name
AAs	Amino acids
acc. no.	Accession number
ACN	Acetonitrile
AGRF	Australian Genomic Research Facility
AK	Auckland
AM	Arbuscular mycorrhizal
am	Ante meridiem
ANOVA	Analysis of Variance
В	Blue (cultivar)
BA	Basal area
BIOM	Biological Observation Matrix
BLAST	Basic Local Alignment Search Tool
bp	Base Pairs
BP	Bay of Plenty
CL	Coromandel
Dev	Deviance
d.f.	Degrees of freedom
DHA	Dihydroxyacetone
DSE	Dark-septate endophyte
E	East
EcM	Ectomycorrhizal
GIS	Geographic Information System
GLM	Generalized Linear Model
GPS	Global Positioning System
Н	Height
HA	Hydroxyacetone
НВ	Hawkes Bay
HCl	Hydrochloric acid
HPLC	High Performance Liquid Chromatography
IGR	Insect Growth Regulator
ITS	Internal Transcribed Spacer
KA	Kaikoura
KOH	Potassium hydroxide
LC	Lethal concentration
LG	Lime green (cultivar)
LOD	Limit of detection
LSU	Large Subunit
M	Molar
MG	Mint green (cultivar)
MGO	Methylglyoxal
N	North
NaOH	Sodium hydroxide
NC	North Canterbury
NCBI	National Center for Biotechnology Information
ND	Northland
NGS	Next Generation Sequencing

NIWA National Institute of Water and Atmospheric

NMDS Nonmetric Multidimensional Scaling

NN Nelson

NPA Nonperoxide activity

NZAC New Zealand Arthropod Collection NZGL New Zealand Genomics Limited

O Orange (cultivar)

OTU Operational Taxonomic Unit

P Pink (cultivar)

PCR Polymerase Chain Reaction PCRU Pasture & Crop Research Unit

PermANOVA Permutational multivariate analysis of variance PFBHA O-(2,3,4,5,6-Pentafluorobenzyl) hydroxylamine

PGP Primary Growth Partnership

pH Potential of hydrogen
Ph. As. Phylum Ascomycota
Ph. Ba. Phylum Basidiomycota
Ph. Ch. Phylum Chytrydiomycota
Ph. Mu. Phylum Mucoromycota

pm Post meridiem

QIIME Quantitative Insights into Microbial Ecology

Ra Rangitatau
RI Rangitikei
RI Refractive Index

Ru Ruatiti

rRNA Ribosomal Nuclear A

S South

SE Standard error sec Seconds

SH Species hypothesis
SI Stewart Island
SSU Small Subunit

Tut Tutira

UMF Unique Mānuka Factor

UV Ultraviolet VT Virtual Taxa

W West
WA Wairarapa
WD Westland
WI Wanganui

Y Yellow (cultivar)