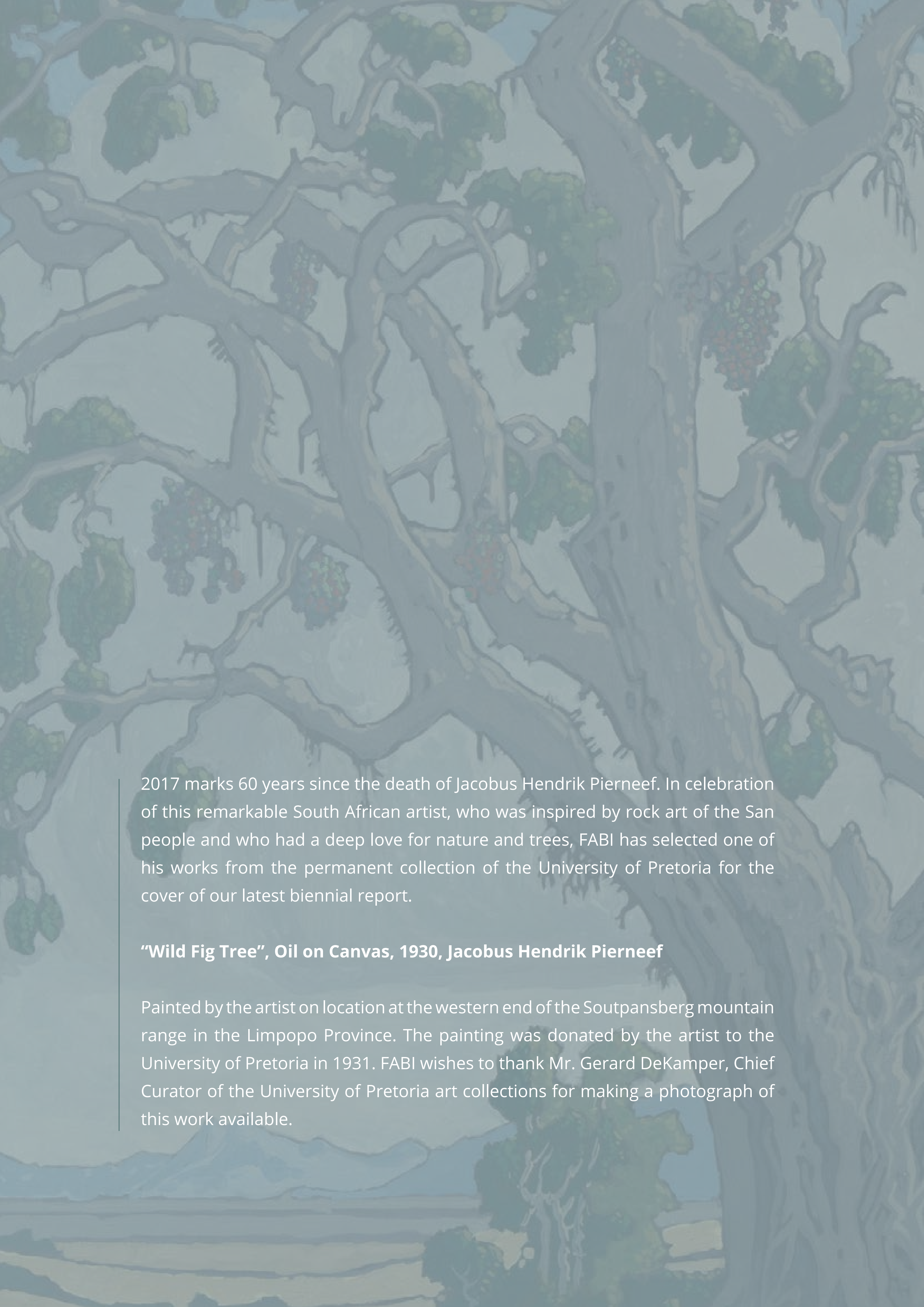
Forestry and Agricultural Biotechnology Institute

BIENNIAL REPORT

MAY 2015–MAY 2017

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

FABI



2017 marks 60 years since the death of Jacobus Hendrik Pierneef. In celebration of this remarkable South African artist, who was inspired by rock art of the San people and who had a deep love for nature and trees, FABI has selected one of his works from the permanent collection of the University of Pretoria for the cover of our latest biennial report.

“Wild Fig Tree”, Oil on Canvas, 1930, Jacobus Hendrik Pierneef

Painted by the artist on location at the western end of the Soutpansberg mountain range in the Limpopo Province. The painting was donated by the artist to the University of Pretoria in 1931. FABI wishes to thank Mr. Gerard DeKamper, Chief Curator of the University of Pretoria art collections for making a photograph of this work available.

FABI

Forestry and Agricultural Biotechnology Institute

BIENNIAL REPORT

MAY 2015–MAY 2017

The Forestry and Agricultural Biotechnology Institute (FABI) is located on the Hatfield campus of the University of Pretoria. The primary objectives of the Institute are to:

- Promote the broad field of plant biotechnology through an interdisciplinary approach and with close linkage to a wide range of academic departments.
- Undertake research of the highest possible calibre, while at the same time providing short and longer term benefits to the forestry and agricultural sectors of South Africa.
- Establish partnerships with industries linked to agriculture and forestry, both nationally and internationally.
- To produce new and improved products and thus to promote competitiveness in trading.
- Promote the education, particularly of South Africans, in the fields of forestry and agriculture.

The association of FABI with the University of Pretoria, the largest residential University in South Africa, provides access to a wide range of human and technological resources. Currently, academic staff and postgraduate students from research programmes in the Departments of Biochemistry, Genetics, Microbiology, Plant and Soil Science, and Zoology and Entomology are associated with FABI. This affords FABI the opportunity to build future resources in biotechnology which will be crucial to the future of forestry and agriculture in South Africa.

FABI, in every way, represents an amalgamation of a tremendous base of expertise in forestry and agriculture from different universities and research organisations in South Africa and other countries through our collaborations. The Institute has been operational since 1998. This document represents the sixth FABI biennial report covering the period from May 2015 to May 2017.

Forestry and Agricultural Biotechnology Institute (FABI)

University of Pretoria
Pretoria
0002

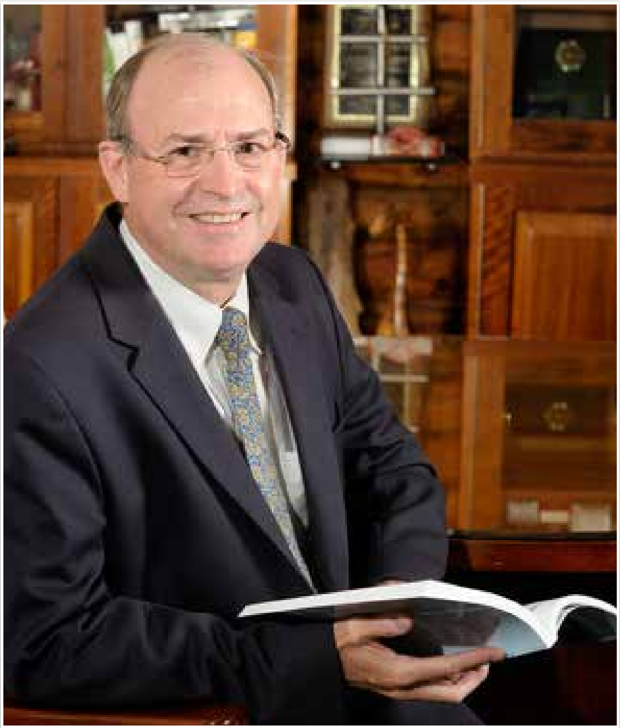
Tel: +27-12-420 3938
Fax: +27-12-420 3960
Email: mike.wingfield@fabi.up.ac.za
Website: http://fabinet.up.ac.za/

Compiled by TA Coutinho

Forestry and Agricultural
Biotechnology Institute
FUTURE FORESTS and FOOD

CONTENTS

DIRECTOR'S REPORT



Sincere greetings to friends of FABI in South Africa and globally! It is always a great pleasure for me to be able to prepare an introductory statement for our Biennial Report. Especially to be able to share with you some of our accomplishments and experiences during the past two years. This is also always a challenge as so much happens in FABI. Those of you that see our weekly news items on the FABI website (www.fabinet.up.ac.za) will understand what I mean by suggesting that even a very brief summary of key accomplishments would demand more space than this welcome note should occupy.

In 2017 FABI reaches a remarkable milestone in having entered its 20th year! It is hard to believe that 20 years ago the main FABI building was a parking lot, FABI Square (completed in 2005) stands on a site where two old University houses stood, and the new Plant Sciences Complex that encompasses many FABI activities had not been dreamed of. In 20 years, FABI has assumed a very significant national and international footprint as a leading research institute focused on education and research in the broad domain of plant improvement. While our base remains in South Africa with strong local relevance, FABI's 'reach' is increasingly global and significant.

I believe that it is relevant to understand that from its inception, FABI has been an experiment. There was a clear motive and direction when FABI was established. This was to bring together academics from a wide range of disciplines and, at postgraduate level, to promote outstanding, cross-cutting and collaborative research. This was also at a time that recombinant DNA technologies were emerging as highly relevant across the broader biological sciences. It is remarkable how FABI has grown over 20 years. Free from the constraints of an academic department, FABI has been able to experiment with new ideas and novel approaches to promote collaboration across disciplines, student engagement and mentoring and in so doing, research excellence. Lifting the bar has been a core goal and this will surely continue to be the case in the future.

At the start of the 2015 academic year and during our annual welcoming event, I launched a new FABI T-shirt with a theme of "connecting the dots". The image on this shirt is a simplified haplotype network that illustrates the global population diversity of an important tree-killing fungus. BUT it is the idiom of "connecting the dots" that I hoped to share and this is what I believe illustrates the success of FABI. I shall not go into details here save to make the point that there are so many important issues that define success in science. And that the key to this success is not only to identify the issues (dots), but to connect them effectively. FABI pursues this goal actively and I believe we are succeeding very well.

In this FABI Biennial Report, we once again share with you a summarised version of the activities of FABI. Clearly the science, as evidenced by publication outputs, and the educational achievements, reflected by students graduating, are most relevant. Yet it is the team effort that underpins our ability to reach the highest possible goals of accomplishment. Behind this, it should also be very obvious that FABI is a fun place to be and that the social element of our activities play a substantial role in what we are able to achieve. In this regard, I especially thank the members of the FABI Social Club for their voluntary contributions to this possibly less well appreciated, but incredibly important part of our operation.

How does one succinctly summarise the recent accomplishments of FABI? This is a challenge that I face at our year-end celebration each year. Members of the remarkable FABI team regularly receive many awards and accolades. Outstanding publications appear as is clear from the list in this report. And for the mycologists in our team, the recent rating of the University of Pretoria as second in the top ten universities globally to study fungi provided exciting recognition of FABI accomplishments.

FABI's outstanding research outputs rely heavily on funding from many sources. These include our primary benefactor, the University of Pretoria, but many other institutions both public and private in South Africa and globally. I take this opportunity to thank all the funding organisations that have supported FABI activities during the past two years. I am sure that this report will adequately reflect the value of your contributions to research that is resolving global challenges in the short and long term. But most importantly, your contributions are also strongly geared to education of the youth on whom we will rely increasingly in the future.

As we rapidly move towards the end of FABI's 20th year, I am mindful of the fact that this milestone deserves celebration. And indeed we will mark this important event with a Scientific Symposium from 24-25 January 2018. I hope that many of our past students and 'stakeholders' will be able to join us to celebrate excellence in science and education. And on the topic of marking milestones, I have also decided that the 20-year mark would also be an appropriate time for me to step down as FABI's Director. I have given this a great deal of thought and sincerely believe that the time has come for FABI to benefit from new leadership. I am lost for sufficient words to say what a huge privilege and honour it has been for me to be the founding Director of FABI. Few academics have the opportunity to embark on an equivalent 'journey' and this has been an amazing privilege and pleasure for me. Every one of the many successes of FABI has been due to an incredible team effort of which I have merely been part. All credit goes to them! FABI is set on a trajectory for a fabulous future. It will be one that I will continue to support and will enjoy celebrating, albeit in a somewhat different role.

Mike Wingfield

Ph.D. (Minnesota), FRSSA, ASSAf, FAAS
Mondi Professor of Forest Pathology
Director of FABI, the Tree Protection Co-operative
Programme (TPCP) & The DST-NRF Centre of
Excellence in Tree Health Biotechnology (CTHB)

FABI TEAM

This photograph includes those members of the team available on 23 January 2017.
Our apologies to those not included and who could not be captured photographically.

Front to back, left to right

Row 1: Heidi Fysh; Martha Mahlangu; Angel Maduke; Emeldah Rikhotso; Joey Hulbert; Tanay Bose; Zimbili Mlunjwa; Onke Gayiya; Zander Myburg; Valentina Nkosi; Terry Aveling; Mmatshepho Phasha; FeiFei Liu; Wilhelm de Beer; Treena Burgess; Fahimeh Jami; Puseletso Manyaka; Dineo Mailula; Thapelo Maboko.

Row 2: Sophie Nyoni; Sandisiwe Jali; Eshchar Mizrachi; Osmond Mlonyeni; Mohamed Seedat; David Nsibo; Zandile Mngadi; Firehiwot Eshetu; Bernard Slippers; Mike Wingfield; Anton Ströh; Celani Nkosi; Pritty Khumalo; Lydia Twala; Ntombi Nkomo; Collins Tanui; Sarah Stanton; Irene Barnes; Robert Backer.

Row 3: Vou Shutt; Rachel Mkandawire; Khumbuzile Bophela; Magriet van der Nest; Sophie Makua; Darryl Herron; Izette Greyling; Elsie Cruywagen; Gudrun Dittrich-Schröder; Alisa Postma; Seonju Marincowitz; Mkhululi Maphosa; Lazarus Takawira; Josephine Queffelec; Katrin Fitza; Smeetha Singh; Mandy Messal; Lucy Moleleki; Almuth Hammerbacher; Gerda Fourie; Stephanie van Wyk.

Row 4: Awelani Mutshembele; Yolanda Musasira; Namhla Tshisela; Mesfin Gossa; Sanushka Naidoo; Junior Tii-kuzu; Vicki Maloney; Donovin Coles; Thandeka Ngondo; Patience Motaung; Christy Marais; Matt Laubscher; Redzuan Rauf; Madelein van Heerden; Helen Doman; Estie van Rensburg; Melissa Simpson; Tamanique Kampman; Grieta Mahlangu; Aysha Ndou; Teresa Coutinho; Vuyiswa Bushula-Njah.

Row 5: Andisiwe Tyani; Ruth Guilande; Tersia Maabela; L'zanne Jansen van Rensburg; Tsakani Miyambo; Steven Hussey; Brigitte Langenhoven; Velushka Swart; Mamadile Kgaphu; Zander Human; Isaiah Nthenga; RunLei Chang; Jolanda Roux; Felix Fru; Emma Steenkamp; Alec Mtuyedwa; Joseph Khadile; Fanus Venter; Chrizelle Beukes; Marike Palmer; Esther Muema.

Row 6: Noelani van den Berg; Juanita Hanneman; Benedicta Swalarsk-Parry; Sonali Ranade; Melissa Joubert; Shannon Flemington; Seamus Morgan; Maria Vivas; Ginna Granados; Ximena Silva; Esna du Plessis; Tanya Welgemoed; Julanie Stapelberg; Daniel Harty; Tuan Duong; Juanita Avontuur; Markus Wilken; Alessandro Gricia; Gina Shin; Gabrielle Carstensen; Louise Shuey; Ariska van der Nest; Rianie van der Linde; Tayo Adenigba.

Row 7: Stephan Engelbrecht; Katrien Brown; Trudy Paap; Shaina Facey; Gerhard Pietersen; Catherine Tatham; Bianca Jardim; Robyn Smith; Angelique du Preez; Ludwig Eksteen; Riaan Swanepoel; Kershney Naidoo; Quentin Santana; Lizel Potgieter; Aquillah Kanzi; Buyani Ndlovu; Michael Bufe; Ashok Prabhu; Dave Berger; Michel Tchotet; Sydney Sithole; Juanita Engelbrecht.

Row 8: Duccio Migliorini; Quentin Guignard; Stuart Fraser; Morné Booij-Liewes; Caitlin Gevers; Samantha Bush; Brett Hurley; Maureen Tladi; James Mehl; Alistair McTaggart; Marc Bouwer; Albé van der Merwe; Martin Wierzbicki; Conrad Trollip; Andi Wilson; Danielle Roodt; Wilma Nel; Martin Coetzee; Mario Rajchenberg; Edohan Clasen; Phophi Nesengani; Livhuwani Mukwevho.

RESEARCH REPORTS

Avocado Research Programme

Research Leader: Prof. Noëlani van den Berg

Team Members:
Prof. Dave Berger
Prof. Teresa Coutinho
Dr. Bridget Crampton
Dr. Sanushka Naidoo
Dr. Nicolette Taylor
Dr. Zelda van Rooyen (Westfalia Technological Services)

The Avocado Research Programme (formerly the Fruit Tree Biotechnology Programme (FTBP)) was established in 2008 as a collaborative initiative between the Hans Merensky Foundation (HMF) and the University of Pretoria. Our programme is supported by the HMF, the Technology and Human Resource for Industry (THRIP) Programme of the National Research Foundation (NRF) and the Genomics Research Institute (GRI) at the University of Pretoria.

Objectives of the Research Programme:

Avocado is an important agricultural crop that has gained popularity throughout the world. *Phytophthora cinnamomi* is regarded as one of the most serious pathogens of the fruit and has a large financial impact on the South African and world-wide avocado industry. Undoubtedly the most significant problem is the lack of total resistance against the disease and severe crop losses are reported in South Africa, Latin America, California and Australia. This oomycete is notoriously difficult to control and strategies in avocado rely on an integrated approach of tolerant plant material, the use of phosphites, mulching and managing irrigation and soil moisture.

Our research objectives are:

- To elucidate mechanisms of avocado defence responses to *P. cinnamomi*, the causal agent of Phytophthora root rot.
- To identify the pathways induced when avocado is subjected to hypoxia due to flooding.
- To identify pathogenicity/virulence genes in the pathogen, *P. cinnamomi*.
- To use the genome and transcriptome of avocado and *P. cinnamomi*, respectively to identify genes involved in host defence and pathogen infection and invasion strategies.

Highlights of the Research:

Avocado Defence Responses

- The isolation and characterisation of four *NPR1* genes from avocado. These genes have been shown to play a key role in salicylic acid-mediated defence in other plant species.
- We designed an Agilent microarray that has been used to profile the defence response of both a tolerant and susceptible avocado rootstock to *P. cinnamomi* as well as the response to flooding.
- In a collaborative study with researchers from Spain we also profiled the avocado response to *Rosellinia necatrix*, the causal agent of white root rot in Spain.

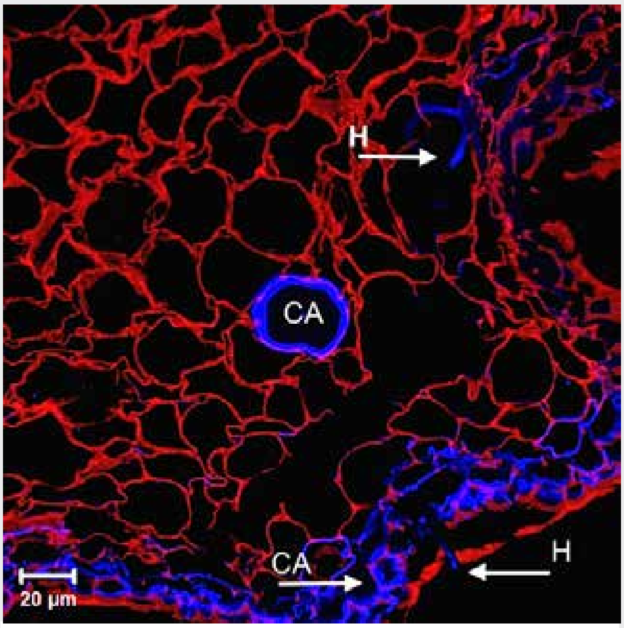
Pathogenicity/Virulence of *P. cinnamomi*

- Research of the hemibiotroph *P. cinnamomi* has focused on the identification of genes associated with pathogenicity. We have identified more than a 100 putative *RxLR* genes, Crinkler genes and genes coding for polygalacturonases important during infection and invasion.
- To facilitate the functional characterisation of genes we have established a *Nicotiana benthamiana-P. cinnamomi* system. This will allow us to evaluate the effect of both pathogen and host genes involved in either pathogenicity or defence.
- We have also developed a set of polymorphic SSR markers for *P. cinnamomi* population analysis.

Future prospects include sequencing the genome of three avocado rootstocks as part of the Avocado Genome Consortium established in 2016 with members from South Africa, Spain and the USA.

Students from the Avocado Research Programme on a field trip to the Westfalia Fruit Estate.

Avocado rootstock trees are produced by Westfalia Technological Services for inoculation trials with *Phytophthora cinnamomi* to study the host-pathogen interaction.



A tolerant avocado responds with the production of callose (CA) to *P. cinnamomi* (H) infection.

Bacterial Genomics and Tree Health

Research Leader: Prof. Fanus Venter

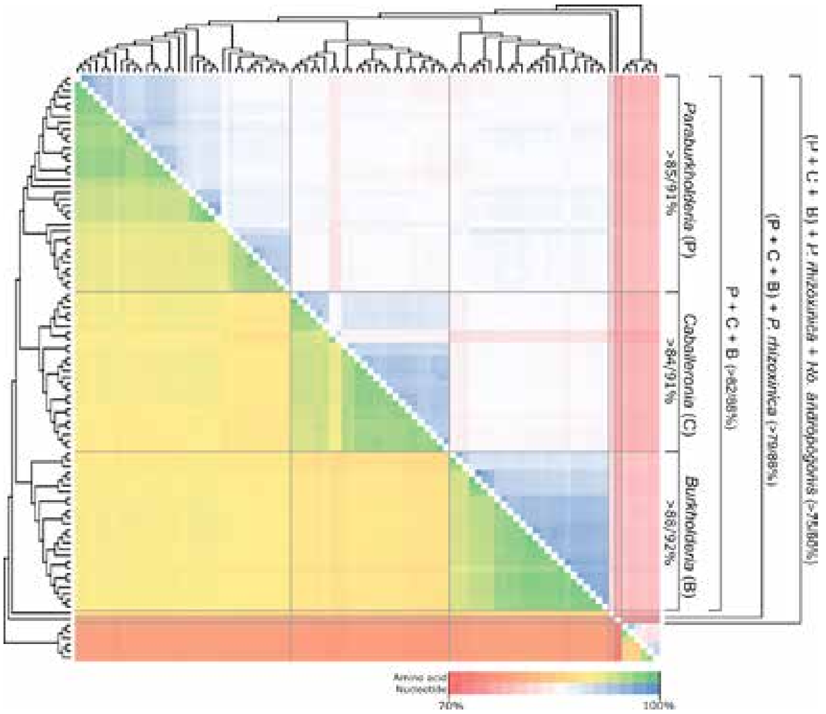
Research Team: Dr. Martin Coetzee
Prof. Teresa Coutinho
Prof. Emma Steenkamp

Objectives of the Research Programme:

- To use phylogenomics to reconstruct the evolution of plant associated genera such as *Pantoea* and *Burkholderia sensu lato* in order to understand how members of these genera have evolved.
- To use the genomes of strains representing the different species of *Pantoea* and *Paraburkholderia* to validate genomic approaches for the delineation of bacterial species.
- To use comparative genomics to study the evolution of nitrogen fixation in *Burkholderia* species nodulating trees such as *Virgilia*, and other plant hosts endemic to the Cape Floristic Region.

Highlights of the Research:

- We examined the evolutionary relationships among the closely related genera *Erwinia*, *Tatumella* and *Pantoea*. To accomplish this, we used the whole genome sequence data for 34 different species belonging to these three genera, as well as nine outgroup taxa. The trees indicated that *Pantoea, Tatumella* and *Erwinia* could be recovered as monophyletic groups and *Pantoea* and *Tatumella* grouped as sister clades to each other. The robust and well-supported evolutionary hypothesis for the three genera which confidently resolved these inter- and intrageneric relationships, represents a valuable resource for future studies.
- We were able to demonstrate in a step-wise process how genealogical concordance can be used to delimit a bacterial species. This approach to species recognition and description is straightforward and applicable to bacterial species especially in the post-genomic era, with increased availability of whole genome sequences. In fact, our results indicated that a combined genome-based comparative and evolutionary approach would be the preferred alternative for delineating coherent bacterial taxa.
- Although the taxonomy of the genus *Burkholderia sensu lato* has been extensively scrutinised, significant uncertainty remains regarding the generic boundaries and composition of this large and heterogeneous taxon. We used the amino acid and nucleotide sequences of 106 conserved proteins (see Figure) obtained from the genomes of 92 species to infer robust maximum likelihood phylogenies. These data unambiguously supported five distinct lineages, of which four correspond to *Burkholderia sensu stricto* and the newly introduced genera *Paraburkholderia*, *Caballeronia* and *Robbsia*. The fifth lineage was represented by *P. rhizoxinica*. Our findings therefore constitute a solid framework, not only for supporting current and future taxonomic decisions, but also for studying the evolution of this assemblage of medically, industrially and agriculturally important species.



Heat map depicting the broad sequence similarity of members of the genus *Burkholderia sensu stricto* based on 106 conserved genes. Nucleotide similarity values are indicated in the upper triangle of the map, with amino acid similarity values indicated in the lower triangle of the map.

CERC-FABI Tree Protection Programme (CFTPP)

Research Leader:	Dr. ShuaiFei Chen (CERC, China & FABI)
Research Team:	Prof. Wilhelm de Beer Prof. Jolanda Roux Prof. Mike Wingfield Prof. YaoJian Xie (CERC, China) Dr. Roger Arnold (CERC, China) Dr. Irene Barnes Mr. GuoQing Li (CERC, China) Ms. QianLi Liu (CERC, China)

Objectives of the Research Programme:

The China Eucalypt Research Centre (CERC) and the Forestry and Agricultural Biotechnology Institute (FABI) have a long-standing relationship promoting research collaboration and education in all aspects of tree health. This resides within the CFTPP, a formal structure first established in 2006 and revised in 2015. The overall objectives are to:

- Study the distribution, genetic diversity and biology of pathogens and pests threatening plantation forestry in southern China.
- Understand the interactions between pathogens/insects and their hosts and provide support towards breeding and selection of pest-tolerant planting stock.
- Provide education for tree health specialists and facilitate research collaboration between researchers at CERC and FABI.

CFTPP in one *Eucalyptus* experimental plantation.

Ceremony at which an MOU was signed to establish the CFTPP in Zhanjiang City, China (October 2015).

Highlights of the Research:

Eucalypt Diseases

The CFTPP has a primary focus of understanding the distribution, genetic diversity, biology and pathogenicity of the important pathogens of eucalypt trees. This includes studies on several important eucalypt plantation diseases, including leaf blight and seedling rot caused by species of *Calonectria* (conducted by Ms. JieQiong Li and Ms. QianLi Liu), stem canker disease caused by Botryosphaeriaceae (conducted by Mr. GuoQing Li) and wilt caused by species of *Ceratocystis* (conducted by Ms. FeiFei Liu). The CFTPP continues to screen eucalypt hybrids for tolerance to these and other important diseases.

Eucalypt Pests

Important insect pests causing significant damage to *Eucalyptus* plantations in China include the defoliator *Buzura suppressaria*, the Eucalyptus gall wasp *Leptocybe invasa* and the wood borer *Endoclita signifier*. The CFTPP has conducted extensive surveys to assess levels of damage and the geographic distribution of these insect pests. This knowledge is contributing to management strategies for these insect pests.

Bark Beetle-Fungus Interactions

Fungi in the Ophiostomatales are widely distributed in natural and planted forests in different regions of China. The CFTPP has conducted research to understand the taxonomy and biology of these fungi; most specifically the associates of conifer-infesting bark beetles. The work focused on beetle species in the genera of *Ips* and *Tomicus* and their fungal associates in the genera *Ophiostoma*, *Grosmannia*, and *Leptographium.* A large number of conifer-infesting bark beetles and their galleries from JiangXi, YunNan, QingHai and HeiLongJiang Provinces have been studied (research conducted by Dr. MingLiang Yin and Mr. RunLei Chang).

CFTPP Team visit to the CERC laboratory (October 2015).

Members of the CFTPP team attending the IUFRO Regional Congress for Asia and Oceania 2016 in Beijing, China (October 2016).

DST-NRF Centre of Excellence in Tree Heath Biotechnology (CTHB)

Director: Prof. Mike Wingfield

Deputy Director and Programme Manager: Prof. Emma Steenkamp

Project Leaders:
Prof. Nigel Barker (UP)
Prof. Teresa Coutinho (UP)
Prof. Pedro Crous (UP & CBS (renamed the Westerdijk Fungal Diversity Institute), the Netherlands)
Prof. Jo Dames (RU)
Prof. Wilhelm de Beer (UP)
Prof. Deanne Drake (Wits)
Prof. Leanne Dreyer (US)
Prof. Gerhard Pietersen (UP & ARC)
Prof. Jolanda Roux (UP)
Prof. Bernard Slippers (UP)
Prof. Fanus Venter (UP)
Prof. Brenda Wingfield (UP)
Prof. Edward Witkowski (WITS)
Dr. Irene Barnes (UP)
Dr. Martin Coetzee (UP)
Dr. Jeff Garnas (UP)
Dr. Marieka Gryzenhout (UFS)
Dr. Eastonce Gwata (UV)
Dr. Brett Hurley (UP)
Dr. Ednah Kunjeku (UV)
Dr. Francois Roets (US)
Dr. Alex Valentine (US)
Dr. Albé van der Merwe (UP)

Objectives of the Research Programme:

The primary goal of the CTHB is to promote the health of South Africa's woody resource through the application of biotechnology tools. To achieve this goal, the CTHB team typically studies the pathogens and pests that are associated with trees and other woody plants. Members of the Centre also explore the possible effects that factors such as climate change, fire, genetic diversity and human activity may have on the health of native woody resources and ecosystems.

The CTHB is hosted by the Forestry and Agricultural Biotechnology Institute (FABI) at the University of Pretoria. It is structured as a virtual Centre of Excellence that conducts research via a collaborative network of scientists, with the central node of the network represented by researchers at UP. In addition to the UP group, the network includes researchers and their postgraduate students at many other institutions in South Africa. Since 2011, these included the Agricultural Research Council (ARC), Rhodes University (RU), and the Universities of Stellenbosch (US), the Witwatersrand (Wits), the Free State (UFS) and Venda (UV).

The research projects of the CTHB are typically focused on the following:

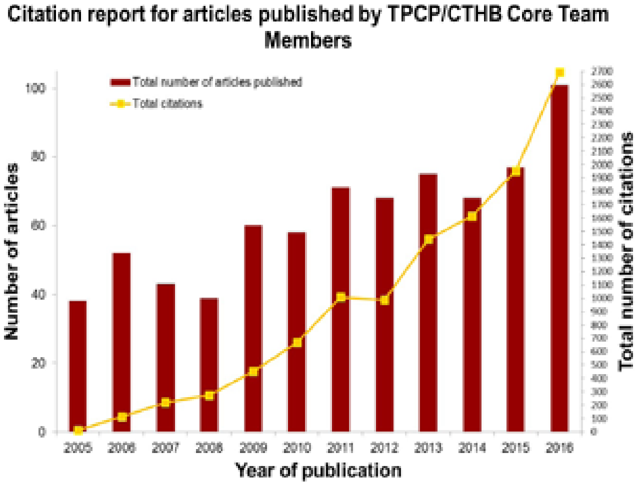
- The biology, ecology, genetics, population biology and systematics of insects and microbes associated with native woody plants.
- The biology and ecology of specific tree species, as well as the effect that human practices might have on these species, the ecosystems in which they occur and the conservation of natural habitats.
- The possible impacts of soil properties and nutrients, microbial symbioses and climatic factors on the health of woody plants in diverse landscapes.
- The effects of drought, frost, fire and human activity on the sustainable use of indigenous woody resources.

Highlights of the Research:

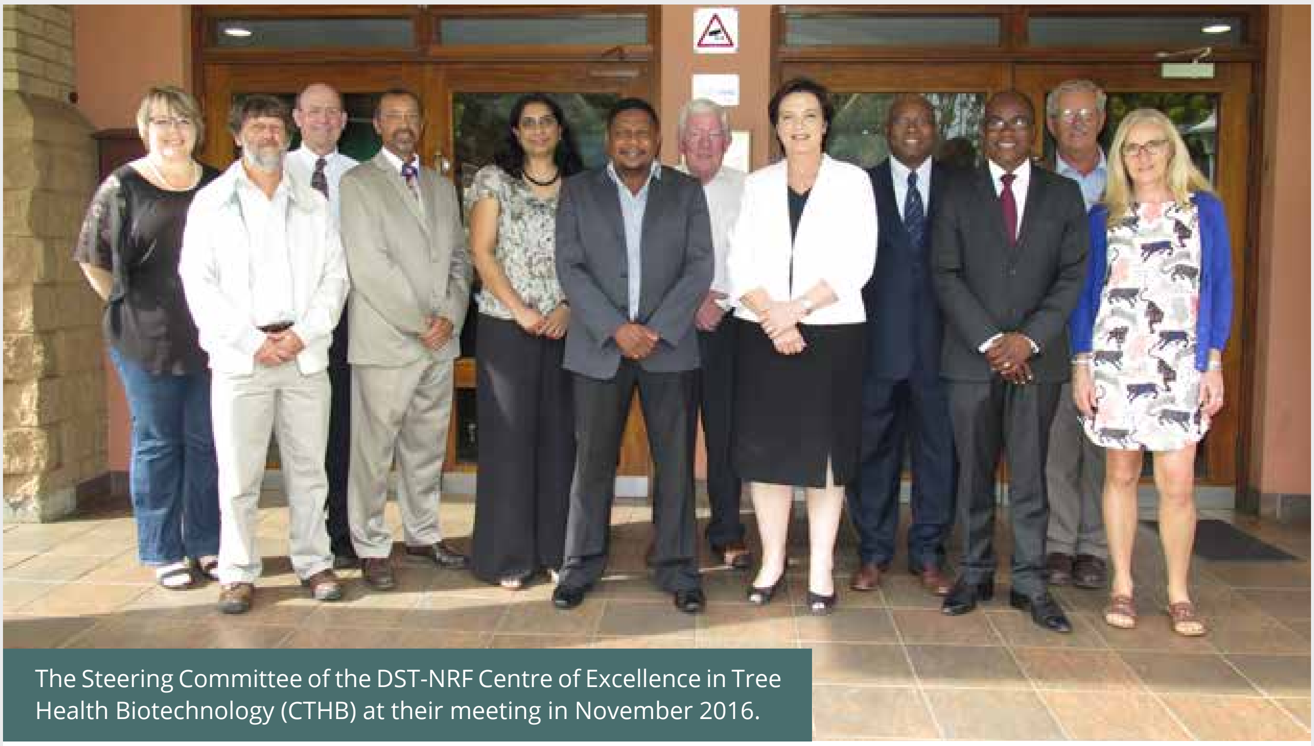
Most of the work focusing on insects and microbes associated with woody plants is conducted at the University of Pretoria. Most projects studying the effects of environmental and anthropogenic factors on the health of native woody hosts and natural habitats are conducted at the other institutions. The CTHB annually produces a large number of research papers (see Figure) of which more than 40 typically deal specifically with health issues of indigenous trees.

As a successful Centre of Excellence, the CTHB is involved in various activities that either informs its research or that emanate from the previous research of the Centre. For example, the CTHB routinely conducts surveys and field experiments in various parts of South Africa and elsewhere on the continent. Together with its partner programme, the Tree Protection Co-operative Programme (TPCP), the CTHB also maintains a world-class disease and insect pest Diagnostic Clinic. To facilitate and enhance the research and extension activities of the CTHB, the Centre has developed and implemented a number of ancillary processes. These include various databases and collections to manage and store information, data and biological material used in projects.

The CTHB is also actively involved in outreach initiatives aimed at promoting a robust and skilled South African human resource base. For this purpose a formal mentorship programme is used to specifically target undergraduate students. The CTHB is also involved in a number of initiatives aimed at improving the public's understanding of science and providing high school learners with information about post-secondary education opportunities in the natural sciences.



Citation report for articles published in international peer-review journals by researchers of the CTHB from 2005 to 2016. The data for this report were obtained using the Thomson Reuters Web of Knowledge^{SM} (accessed 4 April, 2017), which was also used to generate the citation statistics. Note that these data only include the papers produced by the members of the CTHB at the University of Pretoria, and not those produced by members of the extended programme at other Universities and at the ARC. During this analysis, the value for the H-index of Centre's publications was 48 (according to Thomson Reuters Web of Knowledge^{SM} - 4 April, 2017).



The Steering Committee of the DST-NRF Centre of Excellence in Tree Health Biotechnology (CTHB) at their meeting in November 2016.

From left to right: Prof. Emma Steenkamp (Deputy Director and Programme Manager: CTHB), Dr. Wessel Vermeulen (South African National Parks, Knysna), Prof. Mike Wingfield (Director: CTHB), Mr. Nathan Sassman (NRF Director of the Centres of Excellence), Prof. Urmilla Bob (Environmental Sciences, University of KwaZulu-Natal), Dr. Makobetsa Khati (Executive Director of the Research Chairs and Centres of Excellence), Mr. Mike Edwards (former Managing Director: Forestry South Africa), Prof. Stephanie Burton Vice-Principal: University of Pretoria), Prof. Jean Lubuma (Dean: Faculty of Natural and Agricultural Sciences, University of Pretoria), Prof. Edias Mwenje (Vice Chancellor: Bindura University of Science Education, Zimbabwe), Prof. Coert Geldenhuys (Extraordinary Professor - Forest Ecology, University of Stellenbosch), Prof. Diana Six (College of Forestry and Conservation, University of Montana, USA).

DST-NRF SARChI Chair in Fungal Genomics

Research Chair: Prof. Brenda Wingfield

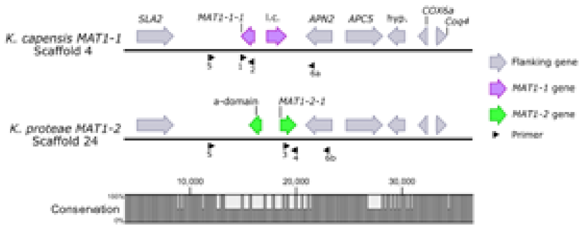
Collaborators:
Prof. Emma Steenkamp
Prof. Mike Wingfield
Dr. Irene Barnes
Dr. Martin Coetzee
Dr. Kershney Naidoo

The DST-NRF Chair in Fungal Genomics was awarded in 2016 to Prof. Brenda Wingfield. The focus of the Research Chair will be on the application of genome technologies to understand, and exploit for national benefit, the genomic resources available in the genomes of economically important fungi. The field of Genomics has become a central, if not dominant, element of the global research in the Life Sciences during the course of the past decade. "Genomics" essentially represents a new approach to the study of biological systems. It incorporates a wide range of technologies, which together provide the key to innovation and to new routes to address old problems. The core of this field lies in the acquisition and manipulation of genomic sequence data. The current high rate of development in genome sequence technologies is rapidly expanding the scope of the field, very much in the same way that the development of PCR revolutionised molecular biology in the 1980s. For example, it is envisaged that within two to five years, it will be feasible to sequence a complete human genome for as little as $1,000, opening entirely new fields such as population genomics and "personal" genomics. Equally important, "post-genomics" fields such as transcriptomics, proteomics, metabolomics and population genomics have the capacity to unlock the answers to questions underpinning the biological functions encoded in genomes. Together with genomics, these will form a strong basis for innovative research and biotechnological applications in agriculture and the health sciences. It is envisaged that the new Research Chair will provide a major contribution within UP to boost research in Genomics in general but with specific focus on tree-infecting fungi. While bringing answers to important economic problems, a key output lies in human capacity development in a growing and crucially important component of the biological sciences.

Research Rationale and Questions:

The field of molecular genetics of fungi is expanding rapidly now that we have access to hundreds of fungal genomes on which to base our research questions. This field is now firmly established in the genomics domain and many questions which would have been impossible to address are now largely within our grasp.

- In terms of phylogenetics we are no longer limited to single gene trees and we are able to follow the evolutionary histories of organisms. We now have sufficient whole genome sequences of fungal tree pathogens available to conduct phylogenomic studies. This will enable us to study the evolution of these organisms at the genome level.
- We have been able to identify Qualitative Trait Loci (QTLs) linked to growth in *Fusarium circinatum,* and plan to identify QTLs linked to pathogenicity in this pathogen. Very little characterisation of genes relating to pathogenicity has yet been achieved. Unravelling the basis of pathogenesis is likely to take us a long way towards understanding how fungi are able to move from one host to another, and in the process, evolve as separate species.
- Biological systems are highly dynamic and new tree pathogens are being recognised every year. Together with a superb group of students and various collaborators nationally and internationally, we have the critical mass of human capacity to deal with these new challenges. We are able to rapidly identify new pathogens and to then apply the ever-increasing number of technologies, which we have both developed and implemented, to ascertain the threat of the pathogens to forests and forestry.
- We are also able to establish whether a newly discovered pathogen is closely related to other known species, what the population diversity of the fungus is and potentially to determine whether the pathogen has been introduced or has jumped from a native host. Answering questions such as these allows us to determine if various pathogens have moved around the world and how some pathogens seem to be able to infect new hosts, while others do not have this capacity.
- Single nuclear genes do not provide sufficient variation to allow us to resolve species boundaries. Now that we have whole genomes available to use we will be able to use mitochondrial genes and genomes to help us better understand relationships between some of the most closely related species. Here, our hope is that the rate of change in these genes will be sufficiently rapid to allow better species resolution.



The *MAT1* mating type locus identified from the genomes of *Knoxdavesia capensis* and *K. proteae*. The graph indicates nucleotide sequence conservation between the two loci of the two fungi. Open reading frames are indicated by blocked arrows. The lack of conservation in the *APC5* gene is due to missing sequence data in the *K. proteae* genome sequence. l.c. = low complexity region protein, hyp = hypothetical protein.

Cereal Foliar Pathogens Research Programme

Research Leader:	Dr. Bridget Crampton
Research Team/Collaborators:	Prof. Dave Berger Dr. Irene Barnes Dr. Maryke Craven (ARC Grain Crops Institute) Dr. Shane Murray (University of Cape Town) Dr. Stoyan Stoychev (CSIR Biosciences) Prof. Burton Bluhm (University of Arkansas)

Objectives of the Research Programme:

Maize is an economically important cereal crop in South Africa, and is a staple diet for many people in Africa. During periods of drought, or in areas where maize does not reliably produce yields, many small scale farmers rely on sorghum as a staple food source. However, both of these crops are susceptible to pathogen attack, which can significantly reduce crop yields. The Cereal Foliar Pathogen Research (CFPR) Programme currently focusses its research on two maize fungal pathogens. *Cercospora zeina* causes grey leaf spot (GLS) of maize in South Africa, and *Exserohilum turcicum* is the causal agent of northern corn leaf blight (NCLB) in maize, sorghum and closely related grass species. We are interested in identifying and characterising pathogenicity factors in these Dothideomycete fungi, as well as understanding the hosts' responses to the fungal pathogens.

Highlights of the Research:

Population Studies of *E. turcicum* in South Africa

Northern corn leaf blight (NCLB) is a destructive foliar disease of maize and sorghum that results in yield losses worldwide. In South Africa, typical yield losses range between 15-30%. As a step towards controlling this disease, we undertook research to understand the population structure of *E. turcicum* in South African maize and sorghum fields. Lesions were collected from diseased maize and sorghum leaves, where after the fungus was isolated and haplotyped using microsatellite markers developed within the research group. Results suggested that population genetic structure of *E. turcicum* in maize is likely due to the direct movement and spread of isolates undergoing a mixed reproductive lifecycle. Additional population studies showed that there was evidence for a low level of genetic separation between *E. turcicum* from maize and sorghum.

Unravelling the Maize-*E. turcicum* Molecular Interaction

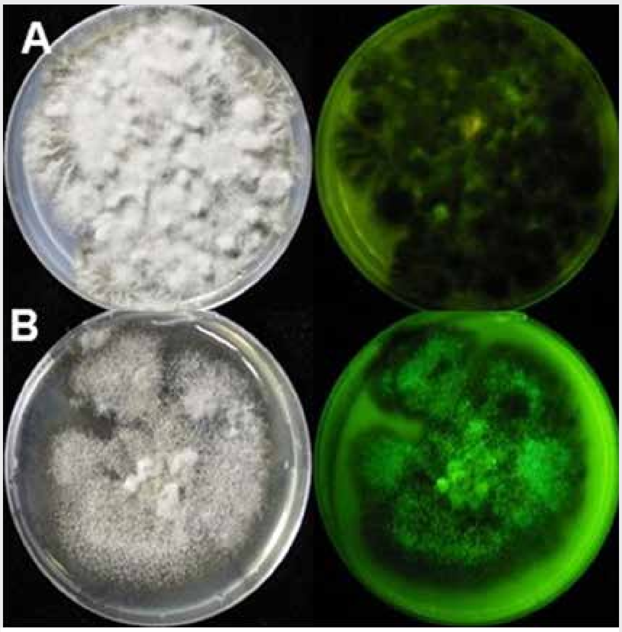
The *E. turcicum*-maize transcriptome was sequenced in order to identify pathogenicity factors in *E. turcicum*, as well as to characterise maize's molecular response to the fungus. Assembled fungal reads were subjected to a bioinformatics pipeline in order to identify secreted small peptides and effector proteins that could play a role in pathogenicity. Interestingly, effector proteins were identified that were specific to either Race 1 or Race 2 of *E. turcicum*. These proteins will form the basis of functional characterisation studies to assess their role in race specific pathogenicity. In this regard, we have developed an efficient *Agrobacterium tumefaciens* mediated transformation platform for *E. turcicum*, and are currently applying CRISPR-Cas9 technology developed within the research group to knock out selected effector genes.

Evaluation of maize genes responding to *E. turcicum* infection indicated that there was a significant upregulation of genes involved in innate immunity, and response to stress and biotic stimulus. Evaluation of a selection of salicylic acid responsive genes showed that they were significantly more upregulated at an earlier time point in a resistant maize hybrid compared with a NCLB susceptible maize line. This possibly has applications in using salicyclic acid derivatives to control NCLB in the field.

Characterisation of *Cercospora zeina* and *E. turcicum* Circadian Clock Components

Gene knockouts of the blue light photoreceptor, White Collar 1 (WC-1) in *C. zeina* suggested that this protein plays a role in fungal stomatal perception and appressorium formation, and the production of conidia and melanin. These are all important processes to establish *E. turcicum* infection in the plant with subsequent spread of the pathogen. We further expanded this study to *E. turcicum* and used bioinformatics tools to identify the circadian clock genes in the genome sequence, and to evaluate their expression under dark and light conditions. Expression of circadian clock component genes was found to be different to that observed in model fungi, and we are therefore in the process of making gene knockouts of selected circadian clock components to evaluate how this affects pathogenicity of *E. turcicum*. Selected circadian clock genes are being targeted in Host Induced Gene-Silencing (HIGS) studies as a method to control pathogen spread.

Dr. Bridget Crampton examining northern corn leaf blight symptoms in a maize field.



An untransformed *E. turcicum* isolate (A) and the same isolate transformed with the green fluorescent protein gene (B).

A maize leaf infected with both grey leaf spot disease (rectangular lesions) and northern corn leaf blight (elliptical lesions).

Diversity and Evolution of Rhizobia Associated With Native Woody Legumes

Research Leader: Prof. Emma Steenkamp

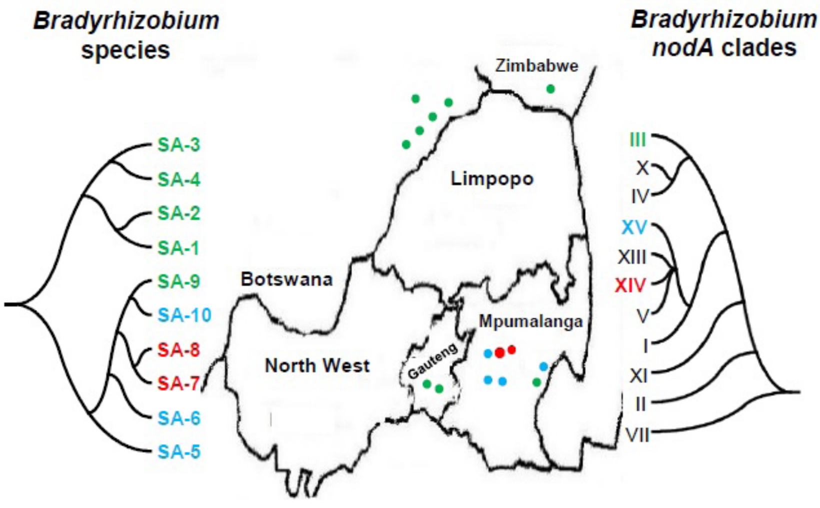
Research Team: Prof. Fanus Venter
Dr. Elritha van Zyl

Research Rationale and Questions:

South Africa is remarkably rich in legumes that, through their symbiosis with rhizobia (i.e., root nodule bacteria), contribute significantly to biological N_2-fixation and ultimately ecosystem health. Although the rhizobia associated with non-native agricultural legumes are relatively well-studied, very little is known about the rhizobia associated with the vast majority of native South African leguminous woody plants. The overall goal of our research is therefore to (i) characterise and describe the rhizobia associated with native legume species, as well as to (ii) reconstruct the evolutionary history (iii) and infer the phylo- and biogeography of these to bacteria. Ultimately, comparisons with the findings of similar studies on legumes from other parts of the world and with those conducted on non-native agricultural crops will provide valuable insight into the possible forces determining the biogeography and ecology of these bacteria.

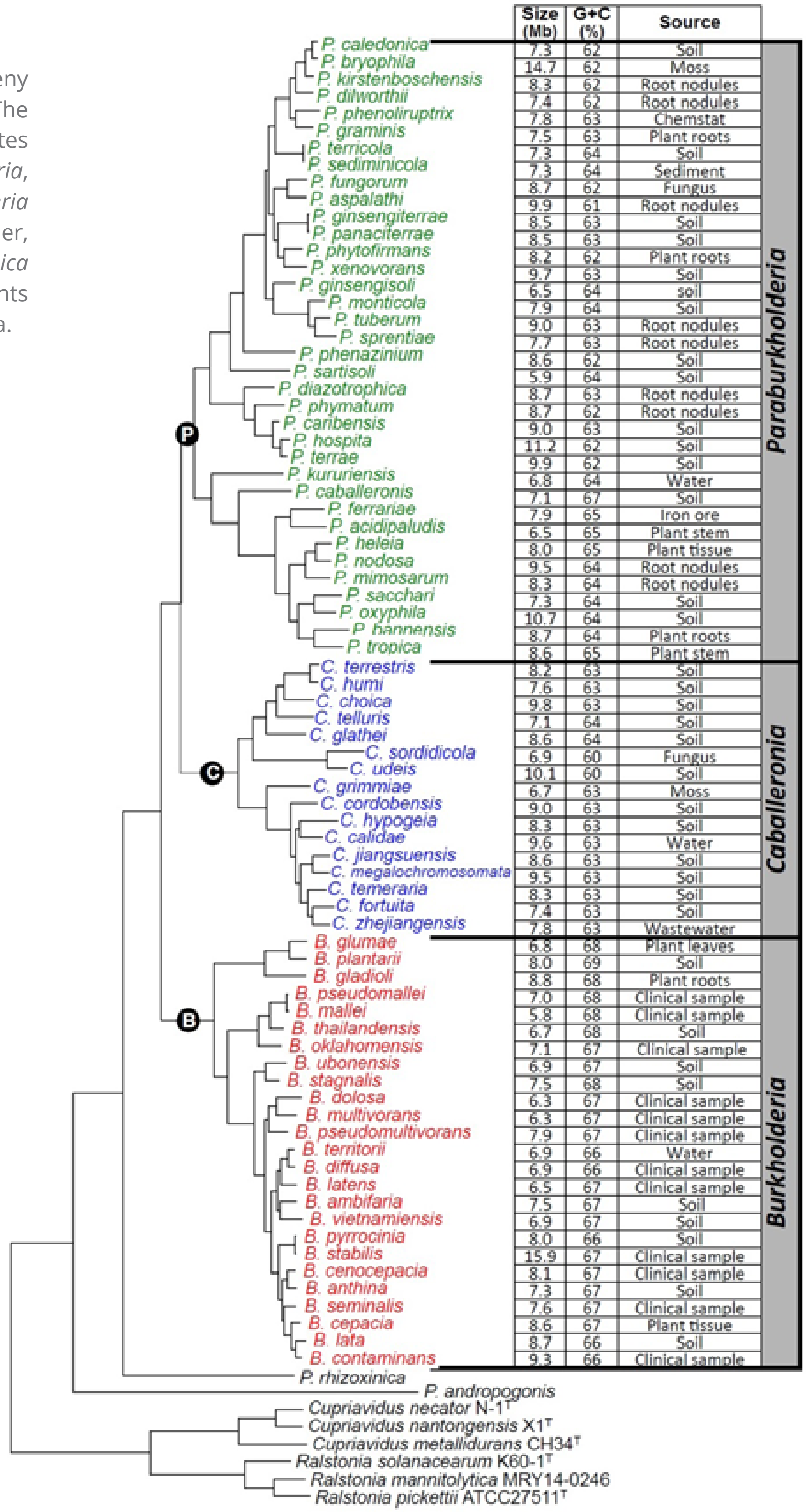
Highlights of the Research:

- The diversity of the rhizobia native to South Africa appears to match those of their legume hosts. Much of our previous research efforts thus have gone into formally describing South African rhizobia. *Paraburkholderia kirstenboschensis* was formally described towards the end of 2015 and the combination was validated later that year. The descriptions for a number of additional species are currently in review.
- Genomics research is significantly impacting bacterial systematics, especially for those groups capable of establishing N_2-fixing symbioses with legumes. Through our collaborations with local groups and with the Joint Genome Institute of the US Department of Energy, the genomes of a large number of species have been sequenced or are in the process of being sequenced. The data generated so far already has been invaluable for addressing critical taxonomic problems. One of these pertains to the generic status of the assemblage widely referred to as *Burkholderia sensu lato*, which includes numerous pathogens of animals, humans and plants. Phylogenomic data unambiguously split this taxon into clades that largely correspond to existing and newly proposed genera. Our data showed that pathogen species seem to be limited to *Burkholderia sensu stricto.* Such information is crucial for future use of local N_2-fixing species for agricultural purposes.
- A hypothesis that emerged from previous work is that indigenous legumes may be nodulated by various rhizobial species, but that their symbiotic abilities likely originate from other species occurring in the same niche. During the



Evolution and distribution of *Bradyrhizobium* species isolated from the root nodules of legumes indigenous to the Great Escarpment and other regions of South Africa. Phylogeographic information for the symbiotic loci of these species is depicted by the *nodA* clustering pattern (*nodA* encodes a protein needed for nodulation).

last two years we addressed this hypothesis by using *Bradyrhizobium* from legumes indigenous to the Great Escarpment in the Mpumalanga Province of South Africa. Our findings showed that these legumes are nodulated by diverse *Bradyrhizobium* species with unique symbiotic loci. In fact, this region appeared to represent distinct centres of diversity for *Bradyrhizobium*. The largely unexplored diversity of indigenous African rhizobia is thus associated with unique evolutionary trajectories that likely correspond to the distribution of their hosts and the environmental factors responsible for their emergence and persistence.



	Size (Mb)	G+C (%)	Source
P. caledonica	7.3	62	Soil
P. bryophila	14.7	62	Moss
P. kirstenboschensis	8.3	62	Root nodules
P. dilworthii	7.4	62	Root nodules
P. phenoliruptrix	7.8	63	Chemstat
P. graminis	7.5	63	Plant roots
P. terricola	7.3	64	Soil
P. sediminicola	7.3	64	Sediment
P. fungorum	8.7	62	Fungus
P. aspalathi	9.9	61	Root nodules
P. ginsengiterrae	8.5	63	Soil
P. panaciterrae	8.5	63	Soil
P. phytofirmans	8.2	62	Plant roots
P. xenovorans	9.7	63	Soil
P. ginsengisoli	6.5	64	soil
P. monticola	7.9	64	Soil
P. tuberum	9.0	63	Root nodules
P. sprentiae	7.7	63	Root nodules
P. phenazinium	8.6	62	Soil
P. sartisoli	5.9	64	Soil
P. diazotrophica	8.7	63	Root nodules
P. phymatum	8.7	62	Root nodules
P. caribensis	9.0	63	Soil
P. hospita	11.2	62	Soil
P. terrae	9.9	62	Soil
P. kururiensis	6.8	64	Water
P. caballeronis	7.1	67	Soil
P. ferrariae	7.9	65	Iron ore
P. acidipaludis	6.5	65	Plant stem
P. heleia	8.0	65	Plant tissue
P. nodosa	9.5	64	Root nodules
P. mimosarum	8.3	64	Root nodules
P. sacchari	7.3	64	Soil
P. oxyphila	10.7	64	Soil
P. bannensis	8.7	64	Plant roots
P. tropica	8.6	65	Plant stem
C. terrestris	8.2	63	Soil
C. humi	7.6	63	Soil
C. choica	9.8	63	Soil
C. telluris	7.1	64	Soil
C. glathei	8.6	64	Soil
C. sordidicola	6.9	60	Fungus
C. udeis	10.1	60	Soil
C. grimmiae	6.7	63	Moss
C. cordobensis	9.0	63	Soil
C. hypogeia	8.3	63	Soil
C. calidae	9.6	63	Water
C. jiangsuensis	8.6	63	Soil
C. megalochromosomata	9.5	63	Soil
C. temeraria	8.3	63	Soil
C. fortuita	7.4	63	Soil
C. zhejiangensis	7.8	63	Wastewater
B. glumae	6.8	68	Plant leaves
B. plantarii	8.0	69	Soil
B. gladioli	8.8	68	Plant roots
B. pseudomallei	7.0	68	Clinical sample
B. mallei	5.8	68	Clinical sample
B. thailandensis	6.7	68	Soil
B. oklahomensis	7.1	67	Clinical sample
B. ubonensis	6.9	67	Soil
B. stagnalis	7.5	68	Soil
B. dolosa	6.3	67	Clinical sample
B. multivorans	6.3	67	Clinical sample
B. pseudomultivorans	7.9	67	Clinical sample
B. territorii	6.9	66	Water
B. diffusa	6.9	66	Clinical sample
B. latens	6.5	67	Clinical sample
B. ambifaria	7.5	67	Soil
B. vietnamiensis	6.9	67	Soil
B. pyrrocinia	8.0	66	Soil
B. stabilis	15.9	67	Clinical sample
B. cenocepacia	8.1	67	Clinical sample
B. anthina	7.3	67	Soil
B. seminalis	7.6	67	Clinical sample
B. cepacia	8.6	67	Plant tissue
B. lata	8.7	66	Soil
B. contaminans	9.3	66	Clinical sample

A genome-based phylogeny for *Burkholderia sensu lato*. The tree unambiguously separates the genera *Paraburkholderia*, *Caballeronia* and *Burkholderia sensu stricto* from one another, and shows that *P. rhizoxinica* and *P. andropogonis* represents members of their own genera.

Eucalyptus and Pine Pathogen Interactions (EPPI)

Research Leader: Dr. Sanushka Naidoo

Collaborators: Prof. Dave Berger
Prof. Lucy Moleleki
Prof. Zander Myburg
Prof. Bernard Slippers
Prof. Emma Steenkamp
Dr. Nanette Christie
Dr. Albé van der Merwe

Objectives of the Research Programme:

The overarching aim of the research programme is to understand the molecular basis of defence responses of *Eucalyptus* and pine to pests and pathogens. Specifically, defence mechanisms against *Leptocybe invasa* (Eucalyptus gall wasp), fungal pathogens *Chrysoporthe austroafricana* and *Fusarium circinatum*, the root rot pathogen *Phytophthora cinnamomi* and Myrtle rust (*Austropuccinia psidii*) are studied.

Highlights of the Research:

Eucalyptus Defence Responses Against Fungi

We have recently focused on induced systemic responses of *Eucalyptus* following inoculation with a fungal pathogen, *Chrysoporthe austroafricana*. Stem inoculations resulted in large changes in gene expression patterns and secondary metabolites in the leaves. We are investigating if the induced responses provide protection against a secondary biotic challenge (Ms. Shannon Flemington, MSc student). This research is especially important for long-lived forest tree species which would encounter several pathogens over their life-time.

Light microscopy of the disease progression of *Chrysoporthe austroafricana* infection (Ms. Lizahn Zwart, PhD candidate) helped to determine the mode of invasion and to identify important infection stages for molecular investigation. Dr. Ronishree Mangwanda successfully identified genes encoding effectors, cell wall degrading enzymes and possible toxins expressed *in planta*. The manuscript detailing these findings was published in *Frontiers in Microbiology* (2016). We subsequently used quantitative proteomics, and coupled with previous transcriptomic and phytohormone data, provided support for salicylic acid defence signalling in the resistant genotype. This evidence supports the hypothesis that *C. austroafricana* has a hemibiotrophic lifestyle rather than necrotrophic; which is important to know when forming a control strategy for this disease.

Based on progress made in 2015, Dr. Louise Shuey (postdoctoral researcher) extended the investigation of the *Eucalyptus* defence responses to *A. psidii* by analysing additional time points after pathogen inoculation in resistant and susceptible seedlings. Her initial observation of sugar signalling as an important over-represented gene ontology pertaining to the resistant interaction was supported by the additional data. To provide further insight into the pathogen transcripts expressed during the infection, Dr. Shuey has embarked on sequencing the *A. psidii* genome in a collaborative effort with the TPCP. The availability of genomes for both host and pathogen allows for a dual-RNA sequencing approach to identify plant and pathogen responses simultaneously. Our review in *Current Issues in Molecular Biology* (2017) details this approach for the plant-pathogens interaction community.

Eucalyptus Defence Against the Insect Pest, *Leptocybe invasa*

After completing her initial analysis on the effect of the tissue pooling sampling strategy used, Ms. Caryn Oates (PhD candidate) focused on a transcriptional time-course of the responses of the host after oviposition by the insect pest. She has made interesting observations of hormone manipulation such as auxin and gibberellin signalling that may play a role in the gall development at the later time points. Ms. Oates completed a review paper describing the use of systems biology as a tool to gain more insight into plant-galling insect interactions. We have completed a Genome-Wide Association Study (GWAS) of genetic markers with resistance to *L. invasa* in a *Eucalyptus grandis* half-sibling population and have identified a set of SNPs. This work was conducted by Ms. Lorraine Mhoswa (PhD candidate) and holds the potential to provide a valuable tool for selection of genotypes carrying resistance to the pest.

Combined *Eucalyptus* Defence Research

The large amount of data that was generated for the different *Eucalyptus*-biotic stress interactions necessitated the development of a comparative tool to identify core defence pathways and tailored defence mechanisms to insect, fungus and oomycete challenge. For this purpose, Mr. Yves du Toit (MSc

The EPPI team.

student) has developed both a Venn Plot tool, and a hierarchical clustering tool, to extract commonly expressed genes for further interrogation.

International Collaborations for *Eucalyptus* Defence

We collaborated with researchers at the Australian National University and the University of Sydney to characterise the resistance (R) gene and chitinase gene family repertoire of *Eucalyptus*. This provides a basis for the selection of novel defence genes to deploy in future improvement of *E. grandis* material.

Pine Defence Responses

We have extended the competence developed in *Eucalyptus* genomics to pine species and have generated the first genomic resources for the tropical pines *Pinus patula* and *Pinus tecunumanii*. The transcriptomes for these economically important tree species provide the information needed to unpack the molecular mechanisms governing defence responses against the devastating pitch canker disease caused by *Fusarium circinatum*. Mr. Erik Visser (PhD candidate) is collaborating with Prof. Jill Wegrzyn (University of Connecticut) to lead this initiative and Ms. Tamanique Kampman (MSc student) is extending the study to include other tropical pine species. Ms. Robyn Smith (MSc student) is focusing on the defence signalling pathways active in resistant *P. tecunumanii* that are absent in *P. patula* in response to *F. circinatum*.

Programme Summary

Taken together, we are building a knowledge base on the defence response of forest trees. We are also developing capacity in new technologies by adopting the "2015 Science Breakthrough of the Year" CRISPR-cas9 genome editing technology for functional genetics characterisation (Mr. Donovin Coles, MSc student). As our knowledge in this area grows, the DNA markers and mechanisms identified in our projects will become the focus of translational research into field conditions to improve tree defences against forest pests and pathogens.

Forest Molecular Genetics (FMG) Programme:Genomics and Biotechnology for Superior Wood and Fibre

Research Leader: Prof. Zander Myburg (Population genomics and molecular breeding)

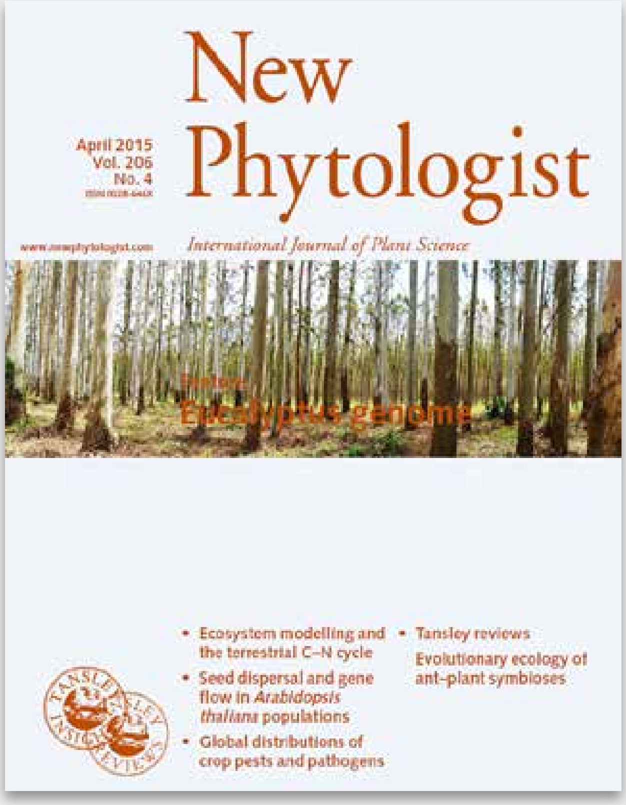
Research Team: Dr. Nanette Christie (Statistical genomics and bioinformatics)
Dr. Steven Hussey (Transcriptional and epigenetic control)
Dr. Eshchar Mizrachi (Systems and evolutionary biology)
Dr. Sanushka Naidoo (Defence genomics)

Objectives of the Research Programme:

The Forest Molecular Genetics (FMG) Programme focuses on the genetic control of growth and development in fast-growing plantation trees with a view to develop biotechnology applications to enhance biomass production and improve wood properties for timber, pulp, paper, and other bio-based products. Concomitant with this, we aim to understand molecular mechanisms involved in pest and disease resistance in trees for woody biomass protection (see *Eucalyptus* Pine Pathogen Interactions - EPPI Group pages elsewhere in this report). We work in close collaboration with South African forestry companies through the FMG Consortium to develop human capacity and resources for the application of biotechnology in tree improvement programmes.

Highlights of the Research:

Following on the publication of the *Eucalyptus* genome (Myburg *et al*. 2014, *Nature*), FMG researchers and students, together with our international collaborators, contributed eight articles in a special issue of the journal *New Phytologist* covering diverse topics such as genome diversity, comparative genomics, protein evolution, carbon allocation, reproductive biology and woody biomass production in *Eucalyptus* trees. Together with the completed genome of *Populus*, the *E. grandis* genome resource is serving as a model and reference for the study of fast-growing woody plants that are used as renewable feedstocks for a growing number of bio-based products.


New Phytologist

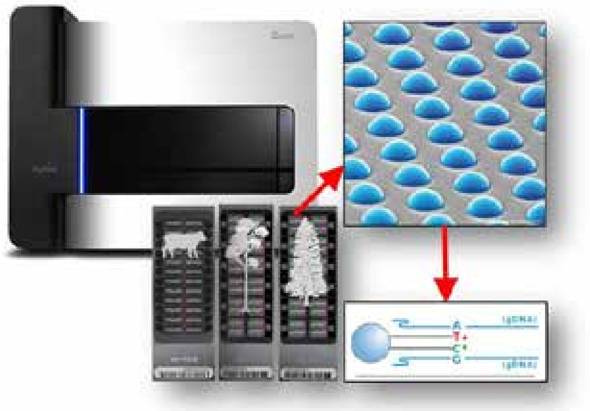
April 2015
Vol. 206
No. 4

www.newphytologist.com

International Journal of Plant Science

Feature
Eucalyptus genome

- Ecosystem modelling and the terrestrial C–N cycle
- Seed dispersal and gene flow in *Arabidopsis thaliana* populations
- Global distributions of crop pests and pathogens
- Tansley reviews
  Evolutionary ecology of ant–plant symbioses


DNA marker chips for *Eucalyptus* and pine species.

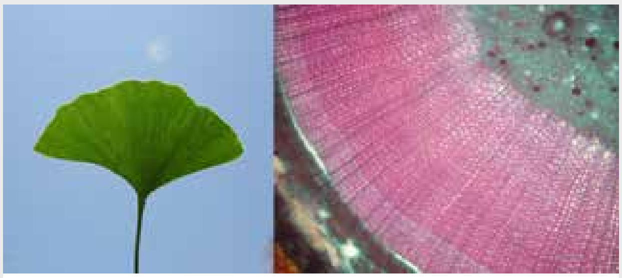
The genome sequence has also served as a reference for the development of a genome-wide DNA marker resource for *Eucalyptus*, which we have deployed for genomic breeding and selection in two large pilot projects in *E. grandis* and *E. dunnii* initiated with our industrial partners. Another major genomic resource generated in the past two years is whole-transcriptome assemblies for *Pinus patula* and *P. tecunumanii* (see EPPI Group pages), which will allow us to develop similar genomic breeding resources for tropical pine species and hybrids grown in South Africa.

Investing in Synthetic Biology Innovation:

Synthetic biology is an emerging field which combines modern molecular biology and systems engineering concepts to develop innovative solutions such as cancer-targeting viruses, novel biosensors or even DIY biological 3D printers. To promote the development of scarce skills among undergraduates in synthetic biology, an important future facet of the Bioeconomy Strategy, FMG has invested over the past two years, with a major sponsorship from Sappi, in mentoring undergraduate student teams to compete in the 2015 and 2016 International Genetically Engineered Machines (iGEM) Competition in the USA.

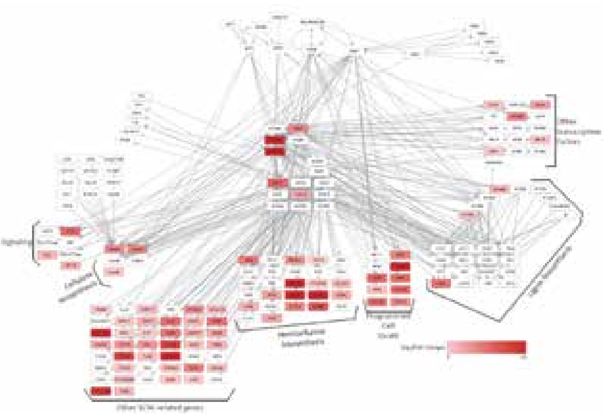
Systems and Evolutionary Biology of Wood:

Wood development involves a series of programmes - encoded for by the genome of the tree - that are meticulously coordinated, and respond consistently to the availability of sugars and nutrients that the tree absorbs from its environment, or in most cases produces itself. These programmes have been evolving for over 400 million years in different plant lineages, and account for a significant amount of the world's sequestered carbon, mainly in the form of polysaccharides (such as cellulose and hemicelluloses) and lignin. Industrially, these biopolymers are of high value in renewable energy and materials. Our group models the formation of wood, from the determination of cell identities to their development, to the allocation and processing of carbon and other small molecules inside to form these valuable biopolymers in the secondary cell walls. This is achieved by measuring and analysing different 'layers' of biology (that is, how genes are expressed, how proteins are expressed, and how small molecules like sugars and phenolics are made). The integration of this knowledge across various tissues or states of wood formation is called Systems Biology − a holistic approach that provides a top-level view of the organisation of these small molecules during wood development. Since the variation in the genome of trees contributes in part to variation in how genes are expressed, an exciting dimension to this research is modelling this process across related individuals in a population, referred to as Systems Genetics. Here, we integrate measurements of thousands of expressed genes, hundreds of metabolites, and dozens of industrially important traits across several hundred trees. This has led to the reconstruction of a model that shows which parts of the system have an impact on (and in some cases control) aspects such as carbon availability, growth, density, and the formation of important biopolymers.



Leaf and a stem cross-section from *Ginkgo biloba*, a missing link in the evolution of wood.

With this new insight and a rich model as a framework, we focus mainly on two important aspects. First, how is carbon used during wood formation and allocated to form these different biopolymers, particularly in the metabolically active organelles (specialised compartments within the cells) such as plastids and mitochondria? Second, since this process is fundamentally common to most land plants, how has it evolved? From an evolutionary point of view, we have performed strategic genomic comparisons, including sequencing gene catalogues from lineages representing "missing links" in the evolution of vasculature such as ferns and non-coniferous gymnosperms. This has resulted in new insight into genes and gene interactions that may be considered essential, auxiliary or redundant in wood development. Testing these genes using synthetic approaches biology can lead to new biotechnology strategies for the beneficiation of biomass.

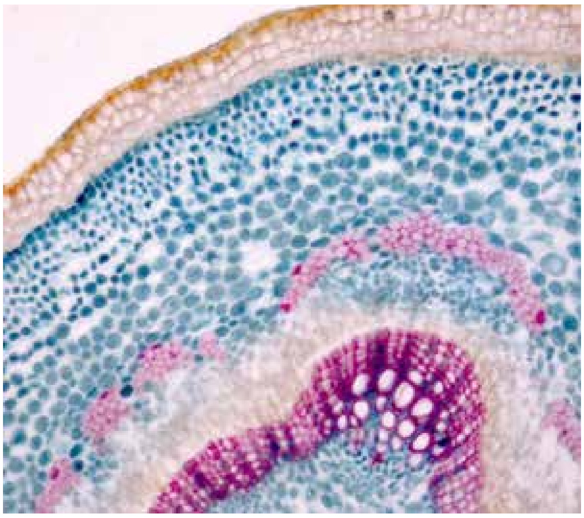


Transcriptional network induced by a *Eucalyptus* secondary cell wall-related transcription factor.

Transcriptional and Epigenetic Regulation of Wood Development:

Complex transcriptional networks underlie secondary cell wall biosynthesis of different cell types such as fibres and vessels in secondary xylem, as studied in the model organisms *Arabidopsis* (herbaceous dicot) and *Populus* (woody dicot). Studies have shown that woody traits can be manipulated through transcriptional network re-engineering. However, our knowledge of transcriptional control of wood development (xylogenesis) is in its infancy. Our research uses cutting-edge genomics approaches such as chromatin immunoprecipitation sequencing (ChIP-seq), DNA affinity purification sequencing (DAP-seq), RNA-seq analysis and transgenic approaches to unravel the functions of transcription factors and modified histones involved in wood development in *Eucalyptus*. We use transgenic *Populus* trees as a reverse genetics model to study the long-term phenotypic effects of overexpression and dominant repression of *Eucalyptus* transcription factor candidates and analysis of their expression patterns, with emphasis on wood chemistry and microscopy analysis of xylem development. We have also explored the short-term impact of transcriptional network perturbation through transient transfection of protoplast cells with *Eucalyptus* transcription factor gene constructs.

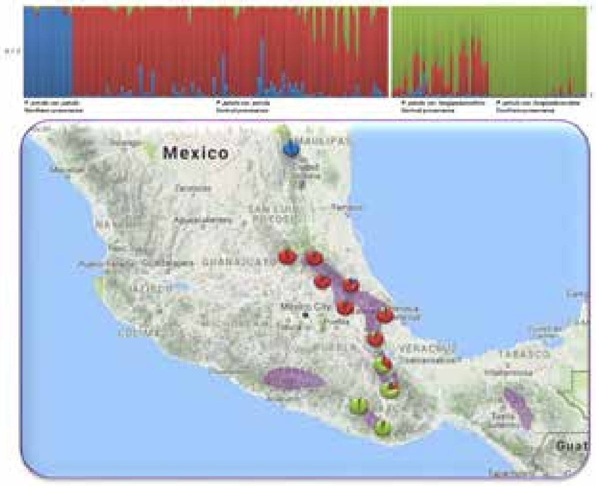
In addition to exploring the regulatory roles of secondary cell wall-associated *Eucalyptus* transcription factors, we have also successfully generated high-quality genome-wide profiles of modified histones in *Eucalyptus* developing xylem (H3K4me3 and H3K27me3), and we are currently reconstructing a chromatin state "atlas" for woody and non-woody tissues using DNase-seq, in order to understand the regulatory function of the noncoding genome. Furthermore, we are exploring the tissue- and cell-specific expression patterns of secondary cell wall-related transcription factors as a function of their promoter cis-regulation.



GUS reporter gene expression (blue) driven by the *Cellulose synthase7* gene promoter in poplar.

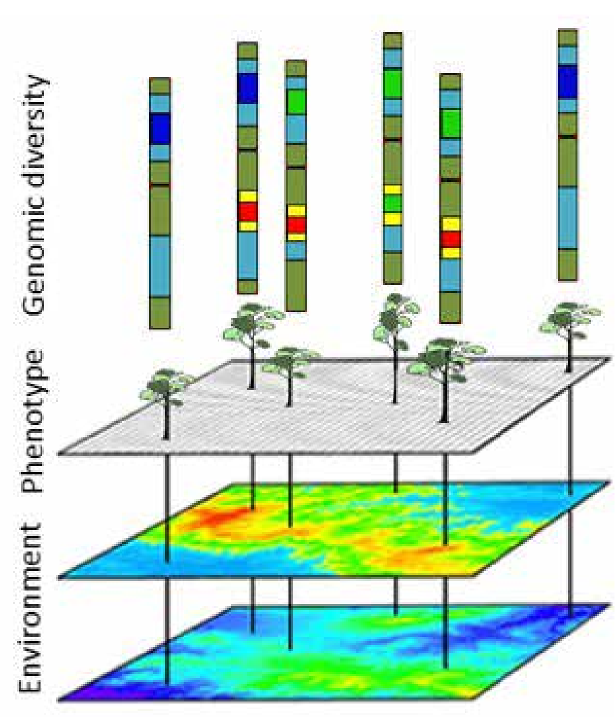
Population Genomics and Molecular Breeding:

Here our research interest is the genetic control of growth and development in trees with a focus on wood formation in fast-growing *Eucalyptus* and tropical pine species and their hybrids. Most commercially important phenotypes are quantitative in nature and affected by hundreds to thousands of genes throughout the genome. DNA marker technology (such as genome-wide SNP chips) has proven to be a powerful tool to tag this genetic variation and develop predictive models of the breeding values of individual trees. By adding molecular traits such as gene expression and metabolite variation, we can gain further biological insight into the molecular basis of quantitative traits. This forms the basis of *systems genetics* approaches combining the power of population genetics and systems biology (multi-level 'omics) analyses to understand the nature of genetic variation affecting wood formation in tree breeding populations. Our group has successfully used this approach in an interspecific backcross population of *E. grandis* x *E. urophylla* to map key genomic regions affecting gene expression and metabolic profiles associated with variation in growth and wood chemistry (Mizrachi *et al*. 2017, *PNAS*). The systems genetics data is a rich source for identifying individual genes and pathways to engineer wood chemistry traits and we have embarked on an effort to use gene editing (CRISPR-Cas9) for precision breeding of cell wall traits such as xylan content and structure affecting pulp yield in trees.

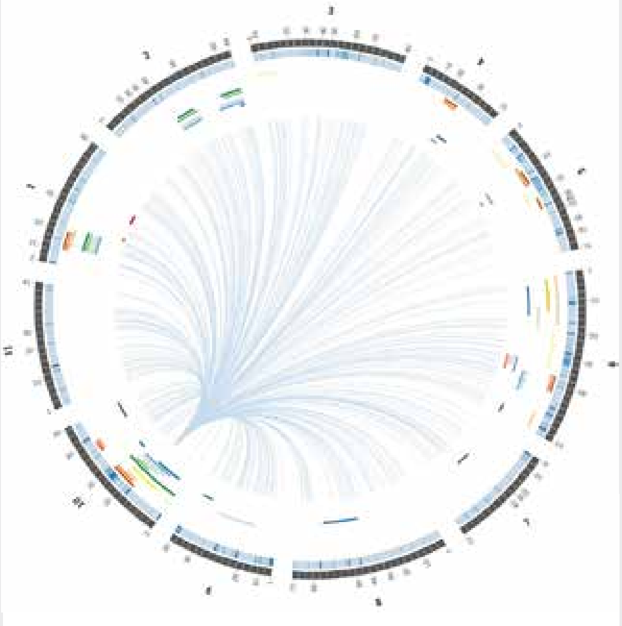


Genome diversity atlas for *Pinus patula.*

Over the past three years we have successfully used a Single Nucleotide Polymorphism (SNP) marker chip with 60,000 DNA markers to genotype over 3,000 *Eucalyptus* trees from *E. grandis*, *E. dunnii* and *E. grandis* x *E. urophylla* hybrids. This has provided us with unprecedented resolution to rapidly dissect complex traits in *Eucalyptus* and develop predictive models for genomic selection of growth and wood properties in tree breeding populations. With support from the Forestry Sector Innovation Fund (FSIF) we are expanding this to other *Eucalyptus* and pine tree species and constructing a Genome Diversity Atlas for *Eucalyptus* and pine species grown in South Africa. Together with an international consortium of pine genomics researchers, we will generate a multi-species SNP genotyping chip for tropical pines, on par with what is available for *Eucalyptus.* These resources will be useful for genetic resource management and molecular breeding of pines. The project will lay the foundation for the emerging field of *landscape genomics,* which combines population genomics with analysis of interactions with biotic and abiotic stresses such as cold, drought and disease to predict tree genotypes that are best adapted to such environments, or that can be deployed to combat new biotic challenges such as pests and diseases.



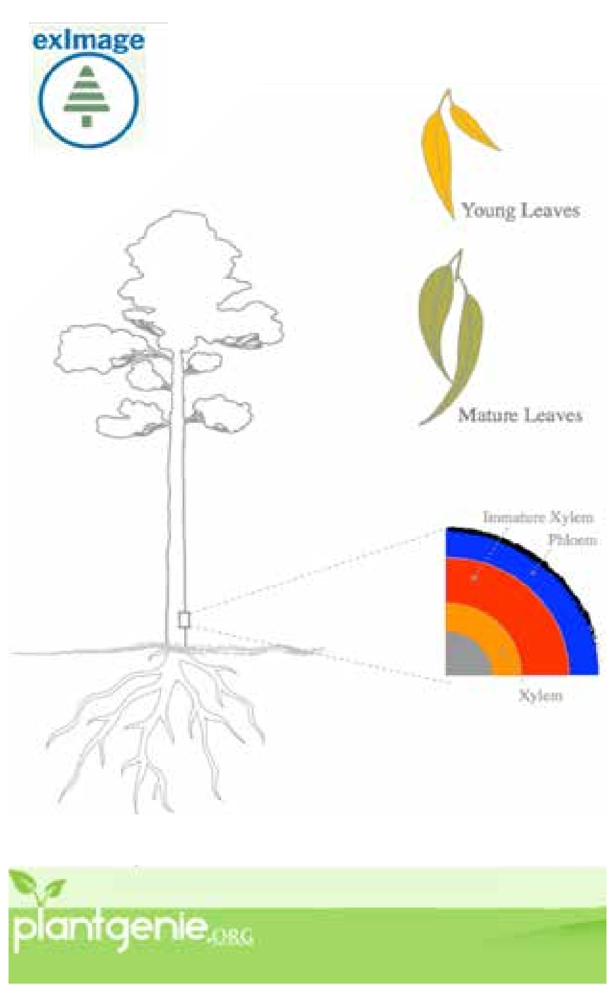
Landscape genomics approach for tree species.



Genome map of gene expression and trait variation.

Bioinformatics and Statistical Genomics:

Understanding the regulatory gene networks underlying traits in *Eucalyptus* trees will enable molecular breeding and genetic engineering to improve wood quality and disease resistance in the long term. Achieving this goal involves the application and development of advanced data analysis tools for large genomics datasets across many individuals in breeding populations.



Visualising gene expression in *Eucalyptus.*

A major branch of our research includes the development of systems genetics data analysis pipelines for *Eucalyptus* data from our breeding populations. This involves the identification of Quantitative Trait Loci (QTLs), i.e. genomic regions containing genetic variation, for phenotypic, gene expression (eQTLs) and metabolite (mQTLs) traits, as well as the visualisation and co-localisation of the different types of QTLs. This platform, together with gene co-expression and correlation analysis, provides an excellent basis for the study of molecular networks underlying our phenotypic traits of interest.

The Plant Genome Integrative Explorer (PlantGenIE) is a web resource for searching, visualising and analysing genomics and transcriptomics data from model forest tree species, including spruce, poplar and recently also *Eucalyptus*. Together with integrating EucGenIE into PlantGenIE, we are developing a suite of online population genomics tools. By considering entire populations, we have the statistical power to identify correlations between genotype and phenotype, via QTL or GWAS studies. We are working on two tools: (i) qtlXplorer to browse QTL data and (ii) qtlNet to visualise QTL networks.

Transgenic poplar trees growing in a greenhouse trial.

Functional Genetic Testing Wood Formation Genes:

Over the past five years, we have established capacity for genetic transformation and gene testing in *Arabidopsis* and *Populus* plants. In the last two years, we have conducted greenhouse trials of seven gene constructs in hybrid poplar to study gene and promoter function. We have also developed capacity for tissue culture and *in vitro* propagation of different *Eucalyptus* genotypes. We have set up collaborations with Prof. Steve Strauss at Oregon State University (OSU) and the Biotechnology company FuturaGene towards developing a *Eucalyptus* transgenic platform at the University of Pretoria.

Technology Platforms:

Besides the Bioinformatics Platform and Tissue Culture and Transformation Platforms mentioned above, we have further expanded our Wood Chemistry Platform to include Klason lignin and HPLC cell wall sugar analys, as well as α-cellulose and S:G lignin monomer composition. Our DNA Marker Analysis Platform offers DNA fingerprintig, parentage analysis and species identification of *Eucalyptus* and pine trees accessible to members of the FMG Consortium and other forestry companies in South Africa.

The Forest Molecular Genetics team.

Fusarium Research at FABI

Research Leader: Prof. Emma Steenkamp

Research Team: Prof. Jolanda Roux
Prof. Brenda Wingfield
Prof. Mike Wingfield
Dr. Martin Coetzee
Dr. Sanushka Naidoo
Dr. Albé van der Merwe

Objectives of the Research Programme:

The *Fusarium fujikuroi* complex (FFC) represents a monophyletic assemblage of medically, veterinary and agriculturally important species. *Fusarium* species are excellent subjects for studying a range of fundamental biological phenomena, ranging from issues pertaining to their genetics and evolution through to those of a more practical or applied nature. For the latter, we focus primarily on the pine pitch canker pathogen *Fusarium circinatum*, which is also a member of this complex. In fact, most of our questions during the last two years involved the genomics and population biology of this pathogen.

Some Research Highlights:

- Genomics is a major field of research that already has and that will continue to impact all fundamental and applied fields of research, regardless of the focal organism(s). This is also true for *Fusarium* species in the FFC. During the last two years, we have demonstrated the use of comparative genomics for identifying regions that can potentially be exploited for diagnostic purposes. We focused on protein-coding genes with products that are likely secreted into the environment. Therefore, these *F. circinatum*-specific markers can likely be used for future development of rapid, in-the-field diagnostic assays using PCR methodologies, as well as those based on enzyme-linked immunosorbent assay (ELISA) methodologies.
- The value of whole genome sequences and comparative genomics also extend into the biosafety arena. Biosecurity risks are almost always assessed based on the taxonomy of particular organisms. In other words, decisions regarding the perceived risks are made based on the specific plant, insect or microorganism associated with a particular sample. This approach is, however, often not adequate (e.g. many microbial pathogens are still not known to science while others evolve rapidly, making it almost impossible to realistically assess the risks they pose). In 2016 we argued for a paradigm shift away from a taxonomy-based system towards a gene-based system. This is because comparative genomics work during the last decade clearly showed that the presence of certain gene or genomic signatures are highly accurate predictors of lifestyle and evolvability, as well as virulence and pathogenicity in the case of microbial pathogens. We emphasised that the incorporation of such information would be crucial for food security and protecting the natural biological resources.
- Because of *F. circinatum*-associated root disease, the pathogen has been a significant problem in seedling production nurseries and when new plantations are established. In recent years, the presence of the pathogen is also increasingly being reported in established plantations, where it causes pitch canker (see the images below). Our research has shown that the population biology of the pathogen is markedly different when above- and below-ground symptoms are compared, which in turn dictates disease management practices specific to the two situations. Nevertheless, our data shows that human activity remains the most important risk associated with the pathogen, and that the picture will probably become even more dynamic given global and climate change.

Symptoms of infection with *Fusarium circinatum*. Left: resinous cankers on the main stem of a pine tree in an established plantation. Right: root disease in the pine seedling from a commercial plant nursery.

Macademia Protection Programme (MPP)

Research Leader: Dr. Gerda Fourie

Collaborators:
Prof. Bernard Slippers
Prof. Noëlani van den Berg
Prof. Brenda Wingfield
Prof. Mike Wingfield
Dr. Brett Hurley

Objectives of the Research Programme:

The overall goal of the Macadamia Protection Programme (MPP) is to provide biological information required to control pests and diseases of importance to the South African Macadamia industry. Currently, the industry relies heavily on the use of commercially available pesticides and chemicals. There is however growing concern regarding continuous build-up of resistance, and the long-term sustainability of the industry is dependent on the use of alternative control options and management strategies. The research conducted in the MPP aims to assist the industry in the development of commercially viable biological control options, as well as in the implementation of effective and environmentally acceptable management strategies. More specifically, the MPP focus is on:

- The biology and ecology of important pests and pathogens and to improve integrated pest management systems.
- The generation of biologically relevant knowledge that will support the development of biological and natural control agents.
- Research to support the selection of pest tolerant or resistant cultivars.

Highlights of the Research:

The MPP is a collaborative research partnership between the Southern African Macadamia Growers' Association (SAMAC), the University of Pretoria and the Forestry and Agricultural Biotechnology Institute (FABI). The programme was officially launched on 22 February 2017 with a ceremonial signing of a certificate by SAMAC Chairman, Walter Giuricich, Dean of the University of Pretoria's Faculty of Natural and Agricultural Sciences, Prof. Jean Lubuma and FABI Director, Prof. Mike Wingfield. This day also marked the first official research meeting of the MPP where specific research objectives were discussed with industry partners (summarised below).

The macadamia industry is severely affected by two groups of insects. One of these is a complex of indigenous stink bugs (Heteroptera, Pentatomidae), of which the two-spotted (*Bathycoelia natalicola*), the yellow-edged (*Nezara pallidoconspersa*) and the small green stink bug (*Nezara prunasis*) are most dominant. The other is the nut borer complex that includes tortricid moths, most notably the Litchi moth (*Cryptophlebia illepida*), the False codling moth (*Thaumatotibia leucotreta*), and the Macadamia nut borer (*Thaumatotibia batrachopa*). Both of these insect groups most likely also include unidentified species. MPP research projects focus on the biology and life cycle of these insects, their population biology, structure and diversity and the identification of new species.

Macadamia husk rot, a fungal disease of the pericarp, has been considered a minor disease in South Africa. However, during the last few seasons, this disease has become more prevalent. The causal agent of macadamia husk rot in South Africa is currently unknown. Both *Colletotrichum gloeosporioides sensu lato* (Anthracnose husk rot), as well as *Diaporthe* spp. (*Phomopsis*) have been isolated from nuts with characteristic husk rot symptoms. A detailed investigation of the primary causal agent of this disease is currently being undertaken.

Other than research that focuses on pests and diseases of immediate concern to the macadamia industry, the MPP will conduct surveys and monitoring for new pests and diseases that could potentially cause damage in the future. The programme offers a disease diagnostic service to all SAMAC members. This diagnostic service will ensure early discovery of disease and pest problems. Knowledge accumulated over time will also ensure the maintenance of historical records that will inform long-term strategic planning regarding macadamia health issues.

Dr. Gerda Fourie collecting stink bugs (Heteroptera, Pentatomidae) during a Macadamia Protection Programme field trip in March 2017 in the Mpumalanga Province.

Signing of a certificate by Southern African Macadamia Growers' Association (SAMAC) Chairman, Walter Giuricich, Dean of the University of Pretoria's Faculty of Natural and Agricultural Sciences, Prof. Jean Lubuma and FABI Director Prof. Mike Wingfield at the Macadamia Protection Programme (MPP) launch on 22 February 2017.

Molecular Plant Pathogen Interactions (MPPI)

Research Leader: Prof. Dave Berger

Research Team: Prof. Terry Aveling
Prof. Zander Myburg
Dr. Irene Barnes
Dr. Bridget Crampton

Objectives of the Research Programme:

The MPPI Research Group aims to gain a molecular understanding of host-pathogen interactions, using grey leaf spot (GLS) disease of maize as a model system. GLS is a foliar disease of global importance, caused by the fungus *Cercospora zeina* in Africa. This pathogen infects maize in wetter environments from KwaZulu-Natal to East Africa.

Two aspects of the project will be highlighted in this report, namely (i) a transcriptomics study of GLS resistance and susceptibility in a segregating maize population; and (ii) a population genetics analysis of *C. zeina* in South Africa. Bioinformatics support was provided by the Centre for Bioinformatics and Computational Biology (CBCB) at the University of Pretoria.

Research Highlights:

Systems Genetics of Maize Responses to *C. zeina*

Previously, the MPPI research group identified Quantitative Trait Loci (QTL) for GLS resistance in a sub-tropical maize Recombination Inbred Line (RIL) population. The next step was to explore the molecular basis for the observed quantitative resistance using transcriptomics. We hypothesised that regulation of gene expression was an important contributor to the trait.

The maize population was planted in the field in KwaZulu-Natal under high GLS disease pressure, and exhibited the expected range of GLS resistance and susceptibility due to segregation of the resistance QTL. GLS disease was scored and leaf samples were collected from 100 RILs for transcriptome analysis using microarrays.

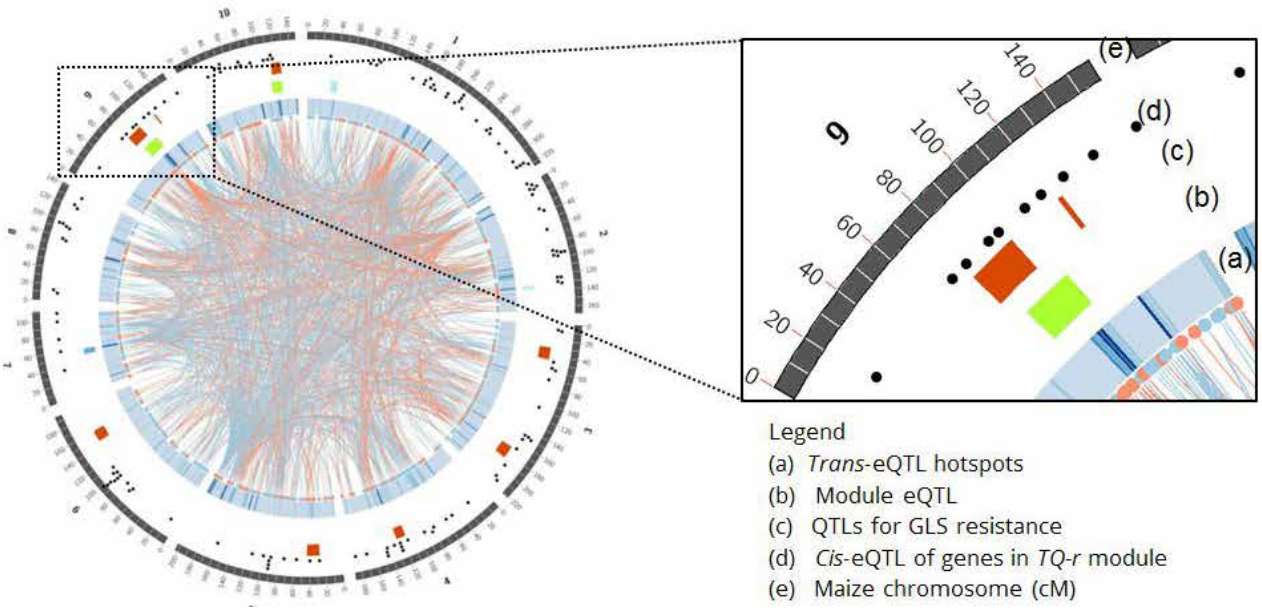
Systems genetics is a framework for understanding complex traits (such as disease resistance) by applying bioinformatics and statistical analysis to component traits such as transcripts, proteins or metabolites in a population segregating for the trait of interest. Our systems genetics strategy was to analyse the transcript data for ~19,000 genes across each of the 100 maize RILs using two bioinformatics methods: co-expression analysis and expression QTL (eQTL) analysis (Christie *et al*., 2016). The results were then integrated with trait data (GLS disease scores) and genetic data (QTL for GLS resistance).

The major finding of the study was that we identified two sets of genes, one that was expressed higher in susceptible plants (co-expression module S1), and another correlated with resistant plants (module R1). Importantly, integration of the data showed that module S1 was subject to genetic control that corresponded to QTL on chromosome 9 and 10. Similarly, module R1 coincided with GLS resistance QTL on chromosome 9 (see Figure).

A transcriptional network was built for module S1, and revealed two novel aspects:

- First, the up-regulation of lipid metabolism and the glyoxylate pathway, which may represent manipulation of the host by the pathogen to release energy rich fats into sugars. Second, key enzymes in an anti-fungal secondary metabolite pathway were expressed together with pathogenesis-related protein genes, which we interpret as fruitless attempts by susceptible plants to battle the pathogen after it has colonised the leaf tissue.
- We followed up these results with a RNAseq transcriptional profile of the GLS susceptible maize line B73, and remarkably found 55% of the module S1 genes induced by the pathogen. These results point to a conserved response to GLS in unrelated temperate and sub-tropical maize lines.

An interesting candidate gene in the GLS resistance module R1 was the receptor (named COI-1) for jasmonate, a plant hormone known to be important for disease resistance in many pathosystems. Furthermore, a suite of ubiquitination genes were co-expressed which is consistent with the role of this type of protein modification in jasmonate defence signalling. Finally, a callose synthase was found in module R1, pointing to the role of callose as a physical barrier to fungal entry, a strategy employed by plants resistant to other fungi. Ongoing MPPI research is aimed at validating candidate maize genes and processes using functional genomics.



Genome view of R1 co-expression module (1,498 genes), showing overlap of trans-eQTL hotspots, module eQTL and GLS resistance QTL on maize chromosome 9.

Genetic Diversity of *C. zeina* in South Africa

GLS disease of maize was first reported from South African maize fields in the 1980s, however its origin and spread was not known. The MPPI group addressed these questions by collecting isolates and applying population genetics analyses (Muller *et al*., 2016). A total of 369 single-spore isolates were made from commercial maize fields in KwaZulu-Natal, Mpumalanga and North-West Provinces. No DNA markers were available for *C. zeina*, therefore the genome was sequenced and mined for microsatellite markers, and a panel of 16 polymorphic markers was developed.

The microsatellite data showed that there was high genetic diversity with 66% of the *C. zeina* isolates with unique multi-locus haplotypes. Mating-type gene analysis showed that both MAT types were present in all fields, and they were predominantly present in a ratio of 1:1. Only the asexual form of the fungus has been seen, however these results indicate that cryptic sex may contribute to the high genetic diversity. Interestingly, the South African population did not split into regional sub-populations, and the data showed high levels of gene flow between Provinces with some haplotypes present in two Provinces. These results indicate widespread dispersal of fungal spores across South Africa, possibly on wind currents, and alert breeders to diversify resistance breeding to counter the high diversity. Current MPPI research involves expanding the focus to small-holder farms in Africa, and tracing the global origin of the pathogen.

Ncobile Kunene was awarded an MSc Biotechnology degree for the *C. zeina MAT* gene analysis.

Molecular Plant Physiology Programme

Research Leaders: Dr. Juan Vorster
Prof. Karl Kunert

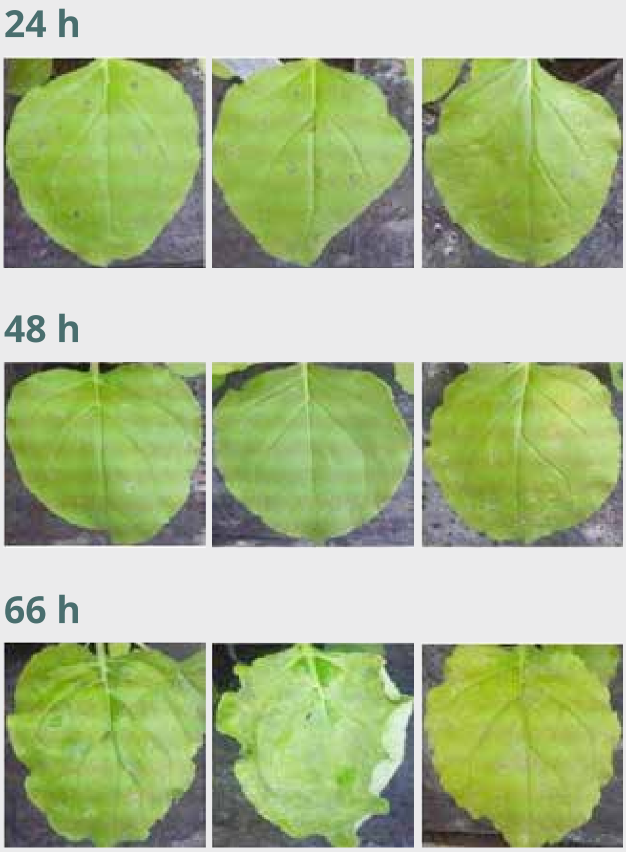
Research Team: Dr. Eugene Makgopa

Objectives of the Research Programme:

Our research group studies proteases, which help to process and recycle plant proteins, and protease inhibitors that regulate protease activity. A particular focus is on cysteine proteases and cysteine protease inhibitors, also called cystatins, with the objective to explore their roles in proteolytic events either induced during natural plant development or due to stress-induced senescence. A first research focus to address the objective is to explore their roles in soybean root nodules. Root nodules are specialised root organs that host symbiotic rhizobium bacteria. The bacteria, which in turn for carbohydrates from the plant, bind and supply the plant with Nitrogen reducing reliance on synthetic Nitrogen fertilisers and thereby improving sustainable farming. Nodules are, however, sensitive to environmental stress such as drought. Stress-induced premature senescence leads to Nitrogen limitations in the plant which is associated with reduced yield. An advanced understanding of the role of cysteine proteases and cystatins in natural and stress-induced proteolytic events in nodules might ultimately allow us to apply native or engineered proteases and their inhibitors for improvement of Nitrogen fixation to limit yield losses under stress. A second research topic to address our set objective relates to studying protease expression with the aim to ultimately improve plant-based recombinant-protein production by avoiding in-plant degradation of expressed commercially interesting recombinant proteins. We explore protease expression in agro-infiltrated *Nicotiana benthamiana* leaves with the help of RNAseq libraries to identify proteases specifically induced upon the induction of recombinant expressed proteins. We intend to target identified proteases with protease inhibitors using inhibitor engineered transgenic plants to limit their proteolytic activity and improve recombinant protein yield. In all our activities we also include training of the next generation of researchers with an understanding of the practical as well as research challenges faced in Agricultural Sciences in Africa.

Highlights of the Research:

The Molecular Plant Physiology Group collaborates with partners in Canada, USA and UK which also involves participating in the World University Network and the Australia-Africa Universities Network. Over the past decade we have built up extensive experience and knowledge not only in protease-protease inhibitor expression and function in plants but also in soybean root and nodule biology by applying a combination of whole-plant physiology, biochemistry and functional genomics. By using RNAseq, we have also produced various gene expression catalogues of developing and prematurely senescing root nodules and we identified specific stress-induced cysteine proteases by comparing their expression under stress- and non-stress conditions. These identified proteases form the basis of our current and future research which further includes as a vital component the research work by Dr. Makgopa on studying the effect of expressed recombinant cysteine protease inhibitors in soybean nodules, nodule development and nodule stress tolerance.



Transient expression of recombinant proteins in tobacco leaves.

Potato Soft Rot Research Programme

Research Leader: Prof. Lucy Moleleki

Research Team: Prof. Teresa Coutinho
Prof. Jacques Theron

Objectives of the Research Programme:

To investigate the interactions between *Pectobacterium carotovorum* subsp. *brasiliense* and its host potato using a transcriptomic approach.

Highlights of the Research:

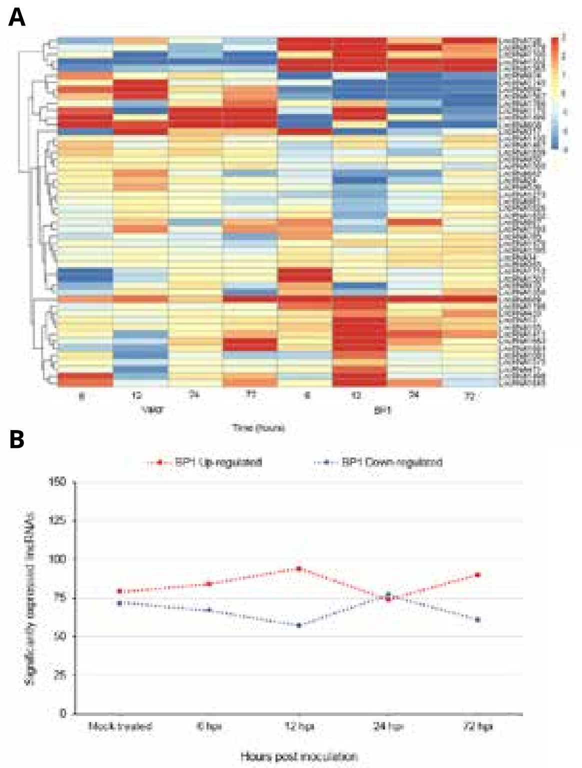
Amongst the different soft rot Enterobacteriaceae, *Pectobacterium carotovorum* subsp. *brasiliense* (*Pcb*) was identified as the most important pathogen of potatoes not only in South Africa but also in East Africa. Because *Pcb* is such an important potato pathogen regionally, much of the current research focuses on virulence mechanisms that *Pcb* utilises to infect potato stems and tubers as well as studying cognate defence responses in the host plant potato.

Identification of Pcb Tolerant Cultivars and Associated Defence Mechanisms

Resistance to soft rot pathogens in potatoes is generally rare. Often partial resistance, based on stems or tubers, has been identified. In this project we screened different potato cultivars against *Pcb* infection. While most commercially available cultivars tested were highly susceptible to *Pcb* and developed excessive blackleg symptoms, one of the cultivars that appeared to be highly tolerant to *Pcb* subsequently did not develop visible blackleg symptoms. A time course RNASeq study revealed key differences in the transcriptomes of the susceptible compared to the tolerant cultivar. These differences include MAPK signalling cascade, transcription factors such as the WRKY transcription factor and secondary cell wall biosynthesis as well as genes involved in the ethylene-signalling pathway. Furthermore, using strand specific RNASeq, we identified a pool of 1,113 long non-coding RNAs (lincRNA) in potato, and of these, 559 were found to be induced by *Pcb* challenge.

Pcb Weaponry Used to Colonise Potato Stems

To understand *Pcb* mechanisms, we used confocal and transmission electron microscopy to follow *Pcb* colonisation of a susceptible vs. a tolerant cultivar. We observed development of an intricate network of cellulose matrix and ultimate encapsulation of *Pcb* cells with an extracellular polysaccharide (EPS) that protects bacteria from the onslaught of host defences. We were interested in genes involved in formation of this EPS matrix and used a random mutagenesis approach. Screening of this library identified at least 19 genes that are important for EPS and biofilm formation. We used starvation media to study genes involved in the ability of *Pcb* to adapt and cope with hostile nutrient deficient conditions (starvation) typical of xylem tissue. In this respect, using ssRNASeq, we identified a number of sRNAs that play an important role in adaptation and survival under nutrient limited condition. Quorum sensing, a density dependent form of communication in bacteria, is a global regulator of many virulence genes for most *Pectobacterium* spp. We evaluated the role of quorum sensing in the ability of *Pcb* to colonise potato stems. In this respect, we generated a mutant defective in the ability to synthesise Acyl Homoserine Lactones (AHL), a key molecule that mediates density dependent communication in bacteria. From our results, quorum sensing did not seem to regulate the ability of *Pcb* to form aggregates in vascular tissues on stems of a susceptible potato cultivar. Currently, the transcriptome of *Pcb* during colonisation of potato tubers at two time points is being evaluated. Furthermore, we are interested in establishing quorum sensing regulation both *in planta* and *in vitro.*



LincRNAs significantly expressed over time between Valor and BP1 following infection with Pcb1692.

(A) Heatmap showing 20 most differentially expressed lincRNAs. Red represent significantly up-regulated and blue represent significantly down-regulated.

(B) Expression patterns of lincRNAs through the time-course. Red dotted-line, lincRNAs up-regulated in BP1 compared to Valor. Blue dotted-line, lincRNAs down-regulated in BP1 compared to Valor.

Phytobacteriology Programme

Research Leader:	Prof. Teresa Coutinho
Research Team:	Prof. Lucy Moleleki Prof. Jolanda Roux Prof. Fanus Venter Prof. Mike Wingfield Dr. Pieter de Maayer (WITS) Dr. Teresa Goszczynska (ARC-PPRI) Dr. Yolanda Petersen (ARC-Infruitec)

Objectives of the Research Programme:

- Characterise and type isolates of pathogenic bacteria responsible for economically important diseases of *Eucalyptus* and selected agricultural crops.
- Study the epidemiology, ecology and biology of selected emerging plant pathogenic bacteria.
- Identify pathogenicity factors of selected plant pathogenic bacteria using a genomic approach.

Highlights of our Research:

Bacterial Diseases of *Eucalyptus*

Bacterial wilt is one of the world's most destructive plant diseases. The causal agents, a complex of *Ralstonia* species, infect plants in over 50 families including *Eucalyptus*. The most susceptible species are *E. pellita* and *E. urophylla* that are mainly grown in the tropical and sub-tropical regions of the world. Recently, the causal agents of bacterial wilt were reclassified. Based on this new system, strains isolated from *Eucalyptus* displaying typical symptoms of wilt in South Africa, the Democratic Republic of the Congo (DRC), Ivory Coast, China and Indonesia, were characterised as *R. pseudosolanacearum*. Strains collected in Brazil and Colombia were *R. solanacearum*. Proving Koch's Postulates is difficult – stress factors caused by biotic and/or abiotic agents appear to play a key role in disease outbreaks. Unlike the situation in herbaceous crops where these bacteria are the primary pathogen, their interaction with *Eucalyptus* is considered to be opportunistic.

Pantoea ananatis has a wide host range including *Eucalyptus* where it causes bacterial blight and die-back. The genomes of a number of strains have now been sequenced, including a strain from this host. Analyses of these genomes led to the discovery of a number of putative pathogenicity genes including motility, Type VI secretion system and quorum sensing systems. In one study which focused on quorum sensing, mutagenesis of the genes for the two LuxI/R quorum sensing systems, i.e. EanI/R and RhlI/R, in the type strain of this species was achieved. Functional analysis of these mutants showed that the two quorum sensing systems are essential for pathogenicity and biofilm formation in *P. ananatis.*

Symptoms of bacterial canker on a branch of a cherry tree.

Plum tree orchard infected with the ring nematode.

Bacterial Canker of Stone Fruit Trees

A survey to determine the presence of bacterial canker was conducted in the major stone fruit tree growing areas of the Western Cape Province. Apricot, cherry and plum trees were most severely affected with branch cankers being the most conspicuous symptom. A number of strains of *Pseudomonas* were isolated from these hosts. Based on a multilocus sequence analysis (MLSA), strains were identified as *Pseudomonas syringae* pv. *syringae*. *Ps. viridiflava* was also isolated from plum trees. The next step in these studies is to determine the role of biotic (ring nematodes and *Phytophthora*) and abiotic (drought) factors in the expression of bacterial symptoms in plum trees.

Bacterial Diseases of Agricultural Crops

Our focus over the last two years has been on identifying bacterial pathogens of onion and tomato plants. We identified a new pathovar of *Ps. syringae* (pv. *allii*) on onion and confirmed the presence of *Xanthomonas euvesicatoria, X. vesicatoria, X. perforans, X. gardneri, R. pseudosolanacearum* and *Clavibacter michiganesis* subsp. *michiganesis* on tomato plants in South Africa. We have also undertaken an extensive population study of *X. campestris* pv. *musacearum*, causal agent of banana Xanthomonas wilt, in east and central Africa.

Plant Virology Research Programme

Research Leader:	Prof. Gerhard Pietersen
Collaborators/Team Members:	Dr. Vaughn Bell (University of West Victoria) Dr. Lindy Esterhuizen (University of Johannesburg) Dr. Elize Jooste (ARC-PPRI) Dr. Sherrie-Anne New (University of Johannesburg) Dr. Hong Lin (United States Department of Agriculture (USDA)) Dr. Beatriz Stein (EAOCC, Argentina) Dr. Schalk van Heerden (Sakata)

Objectives of the Research Programme

The research programme of the Plant Virology Group focuses on viruses and virus-like diseases of primarily agricultural importance. Focus until the recent past has been mainly on grapevine leafroll disease of wine grapes, the citrus disease caused by citrus tristeza virus (CTV), soybean blotchy mosaic virus and the maize lethal necrosis disease complex. The group also studies citrus greening disease, associated with a fastidious bacterium *Candidatus* Liberibacter africanus (Laf), which has an epidemiology not unlike that of plant viruses.

Highlights of the Research

- The control strategy developed for grapevine leafroll disease based on planting certified planting material, rouging of infected vines, control of mealybug numbers and preventing mealybug dispersal has been implemented widely within the South African Wine Grape Certification Scheme. Amongst 335 foundation vineyard blocks, representing 572,000 grapevines monitored in 2015, 290 contained no leafroll infected grapevines. Within the remaining 45 foundation vineyards a total of 168 infected grapevines were observed in 2015, with the majority of these (n=82) occurring in just three vineyards where clear deviations from the control strategy were implemented. In 119 commercial vineyards of various ages (2-16 years old) in various districts, utilised as mother blocks in the South African Wine Grape Certification Scheme, 38 had no leafroll infected grapevines in 2015 and none of the remaining vineyards exceeded a 1% level of infected grapevines. A very high correlation between disease symptoms and ELISA to GLRaV-1, 2 and 3 were found in red wine cultivars, suggesting that within the certification scheme ELISA need no longer be conducted on red cultivars and visual assessment of material can be utilised. This will allow the greater deployment of resources to testing for the virus in white cultivars. At the same time methods to replace laboratory tests of white cultivars is also being assessed with a field trial to test the efficiency of red "sentinel" canes being initiated. Studies have also shown that poor detection of GLRaV-3 in rootstocks is not due to the presence of PCR inhibiting substances in the rootstocks, or to the selection of GLRaV-3 strains not detected by the PCR tests used but is rather due to low virus titers and erratic distribution of the virus in rootstocks.

Symptomless sucker from rootstock (in red) sprouting from a grapevine leafroll infected vine. Studies to improve detection of grapevine leafroll associated virus 3 in such rootstocks are being conducted in the Plant Virology Research Group.

- An analysis pipeline has been developed for a high throughput detection method based on polyvalent PCRs and next generation sequencing for the South African Wine Grape Certification Scheme.
- A new subspecies of *Candidatus* Liberibacter africanus (Laf), for which the name *Candidatus* Liberibacter africanus spp. Teclae is proposed was detected in a single specimen of *Teclea gerrardii* an indigenous tree member of the Rutaceae (citrus-family).
- In studies to determine the persistence of soybean blotchy mosaic virus (SoyBMV) between soybean growing seasons it was shown that the virus is not seed transmitted but that a number of alternative hosts to soybean exist. We are actively continuing studies on this issue.

Seed Science and Pathology of Flowers, Trees and Agronomic Crops

Research Leader: Prof. Terry Aveling

Research Team:
Prof. Paxie Chirwa
Prof. Bradley Flett (ARC-GRI)
Dr. Riana Jacobs (ARC-PPRI)
Dr. Quenton Kritzinger
Dr. Mariette Truter (ARC-VOPI)

Objectives of the Research Programme:

To research and solve seed problems for emerging and commercial farmers on a range of plants including seed pathology, seed vigour and seed treatments.

Highlights of the Research:

Seed-borne *Alternaria* spp. of Sunflower

Alternaria species have been associated with sunflower seeds and grain and have been reported to affect seed quality. This research determined (i) if mycoflora associated with sunflower grain had an effect on seed vigour and seed health and (ii) determined the geographical location of the sunflower grain with the most *Alternaria* species inoculum. Standard germination and seed health (agar plate method) tests were conducted on 19 sunflower grain seed - lots collected from various parts of South Africa. Standard germination tests were done on "paper dolls" according to the International Seed Testing Association (ISTA) regulations. The agar plate method was used for the detection of mycoflora on the grain seeds. Germination percentages ranged from 70-91%. Germination was found to be influenced by the severity of seed infection, but the correlation was relatively weak (56%). Five genera were isolated from the grain seeds, namely *Trichoderma*, *Stemphylium*, *Rhizopus*, *Fusarium* and *Alternaria* species which were there most predominant having a disease incidence ranging from 28 -82% between the various grain seed-lots. Germination tests showed that the germinated seedlings of the various grain seed-lots had seedling blight. Seed component tests will be done to determine the location of infection using agar plate method, qPCR and digital droplet PCR.

Alternative Seed Treatment Methods for the Control of *Alternaria brassicicola* on *Brassica* spp.

Alternaria leaf spot, caused by the seed-borne pathogen *Alternaria brassicicola,* is responsible for yield reduction in smallholder brassica vegetable production. Seed treatments are often used to eradicate or reduce this pathogen. In this study the efficacy of plant extracts, commercial biocontrol agents (BCAs) and hot water were evaluated against *A. brassicicola* artificially inoculated on rape seeds and on germination *in vitro*. Furthermore, selected alternative seed treatments were evaluated for the control of the disease under greenhouse conditions. Water extracts of *Agapanthus caulescens* and *Lavandula anguistifolia* significantly reduced the incidence of *A. brassicicola* on rape seeds *in vitro* by 39.3% and 35.7%, respectively, compared to the untreated inoculated control. *Bacillus* sp., effectively reduced *A. brassicicola* incidence to 8.3% when compared to untreated inoculated control (52.3%) and also enhanced seed germination by 29%. Hot water treatment at 53ºC for 10 minutes was the most effective treatment as it significantly reduced *A. brassicicola* incidence on seeds to 1.5% and it increased seed germination by 27%. In the greenhouse this treatment increased rape seedling emergence and it recorded the highest reduction of Alternaria leaf spot disease incidence and severity, which was comparable to the fungicide Captab. The BCA, *Trichoderma* sp., also increased rape seedling emergence and reduced the Alternaria leaf spot disease, recording a disease incidence of 4.1% and severity of 0.8%. The findings of this study show that potential exists for use of alternative seed treatments for control of *A. brassicicola* in brassicas.

Fungi Associated With Mesembs of the Namaqua National Park

The Aizoaceae, commonly known as mesembs or "ice plants" is a plant family endemic to Namaqualand, an area inside the Succulent Karoo biodiversity hotspot in South Africa. Here biome-specifc factors drive germination success with more than 1,800 unique species contributing in making this the most diverse arid ecoregion in the world. Several fruit construction types occur within this family although complex, hygrochastic capsules with high structural diversity (including differences in funicles, covering membranes and closing bodies) are the norm. Several seeds exhibit physical dormancy, often requiring gradual scarification by fungi to germinate over time in favourable conditions such as after prolonged rain. The relationships of plants co-inhabiting with microbial life that may confer thermotolerance, drought resistance and other important survival strategies has only recently received attention, e.g. fungi are known to play a role in establishment of cacti. We found that even in propagative material as specialised as the seed capsules of Aizoaceae microbes exist. We isolated fungi from seed within these sealed capsules harvested during the dry and flowering seasons in Namaqualand. The fungi were identified using morphology and molecular tools. Fungi in the orders Capnodiales, Eurotiales, Hypocreales and Pleosporales were represented, with those in the genus *Alternaria* being the most common. In addition we investigated differences in the fungal population between the two seasons. This work represents a first contribution to the study of fungal diversity associated with seeds of Aizoaceae in the Succulent Karoo biome.

Godfrey Kgatle (PhD candidate) visiting sunflower farmers with *Alternaria* problems in the Free State Province.

Severe *Alternaria* symptoms on sunflower.

Tree Protection Co-operative Programme (TPCP)

Research Leader: Prof. Mike Wingfield

Research Team:
Prof. Wilhelm de Beer
Prof. Jolanda Roux
Prof. Bernard Slippers
Prof. Emma Steenkamp
Prof. Fanus Venter
Prof. Brenda Wingfield
Dr. Irene Barnes
Dr. ShuaiFei Chen
Dr. Martin Coetzee
Dr. Jeff Garnas
Dr. Brett Hurley
Dr. Kershney Naidoo
Dr. Albé van der Merwe

Objectives of the Research Programme:

- Development of field monitoring techniques to recognise the appearance of new pests and diseases as well as to monitor the spread and impact of those already established in South Africa.
- Identify new and important tree pests and pathogens and evaluate their genetic structure so that they can be more effectively controlled.
- Develop methods to screen trees for tolerance to the most important diseases present in the country.
- Establish and evaluate contemporary breeding strategies in order to produce disease and pest tolerant species, clones and hybrids.
- Establish an understanding of the biology of tree pests and pathogens to promote their better management.
- Study and evaluate novel strategies for disease and pest control, particularly biological control.

Highlights of our Research:

Pests and diseases pose one of the greatest threats to plantation forestry worldwide and this is certainly true in the case of South Africa. Some forestry companies that participate in the activities of the TPCP would argue that pests and diseases have begun to have a more important place in terms of threats than fire damage. Here, amongst the many issues associated with pest and disease damage is the fact that losses can be gradual, but incremental. It is seldom that a pest will rapidly wipe out a species, provenance or clone. But experience over the past 30 years has taught us that entire species can be lost from the planting mix. *Pinus patula* damaged by the pitch canker fungus and *Eucalyptus grandis* by a number of pest and disease problems, but most noticeably *Leptocybe invasa* provide apt and worrying examples. Thus, the huge investments that are made in the genetic improvement, the silviculture, management and marketing of specific species can be lost over time.

The TPCP provides the bulk of core research on pests and pathogens required by the South African forestry industry. This research work represents a balance between short-term needs of the industry and longer-term positioning research that will ensure the sustainability of the industry into the future. It is important to recognise that the disease management (integrated pest management) and extension services of the TPCP are very closely linked to, and informed by, the research being undertaken by the TPCP. As an example, fundamental research on *Eucalyptus* leaf diseases by team members made it possible to rapidly and accurately identify the pathogen (*Teratosphaeria destructans*) responsible for the first outbreak of Destructans leaf blight on the KwaZulu-Natal coast during 2015, as well as a second “type” of *L. invasa* to name but two of many examples. This would not have been possible if the TPCP had not maintained a core capacity to deal with *Eucalyptus* leaf pests and diseases. There are many other examples of TPCP projects that might be considered somewhat distant from the problems being experienced at any one time, but that have been crucially important in dealing with newly emerging problems. It is thus clear that maintaining a broad capacity to deal with the most important categories of pests and pathogens affecting tree species of importance to the South African forestry industry represents a strategic necessity.

The strategic focus of the TPCP research has always been on the most important pests and pathogens affecting forestry in South Africa. Numerous student projects are maintained for these problems in a manner that ensures a continuity of knowledge and experience. Pathology and entomology are very specialised disciplines requiring unique skill sets that are learned over long periods of time. This is equally true for forest entomology and pathology where specialists with an understanding of the particular problems are required to provide informed and useful knowledge. Globally, specialists in these fields concentrate on particular crops and where generalists are involved, results are typically peripheral and disappointing. The strength and worldwide reputation of the TPCP lie precisely in the fact that the team members have specialised in pests and pathogens of trees and more specifically on those affecting forest plantation trees of interest to South Africa. The research team thus represents a valuable and perhaps under-appreciated resource, which the South African forestry industry needs to protect for its own long-term security.

Managing tree pest problems is very similar to dealing with animal diseases and there is much that forestry can learn from the human health domain. As with animals, diseases originate in particular areas and begin to spread mainly due to human (anthropogenic) influences. There are a number of major issues that need to be understood. These include (i) the areas of origin of the insect pests or causal agents of disease; (ii) the manner in which they spread; (iii) knowledge of their biology. These factors together with an understanding of the interactions between the environment, the pest and the host plants must then be understood as efforts are made to reduce their impact. A key factor that underpins the past successes of the TPCP lies in the fact that team members have established global collaborations enabling them to be aware of growing pest threats, where they occur, how they are moving and where opportunities might lie to control these problems.

A first line of defence in ensuring the security of South African plantations against the ravages of pests must be to avoid, as far as possible, new introductions. This goal is underpinned by quarantine, a process that dates back to the 14th century when ships were kept at bay for 40 days to prevent introductions of human diseases. The word “quarantine” originates from the Italian word “*quaranta giorni*” or 40 days. While this is a simple concept, it is one that is extremely difficult to manage as was vividly illustrated by the recent and dramatic Ebola virus outbreak in Africa. In terms of forestry, South Africa has porous boundaries to the north and any pest or pathogen entering, for example from Mozambique, will eventually (and probably rapidly) move to South Africa. It is ironic then that some of the most serious pests of forest trees in South Africa have apparently entered this country first and they have now moved northwards into our neighbouring countries. But both directions of movement will be important in the future and our challenge is to try and manage this threat as best we possibly can.

One of the key reasons why South African forestry has been spared catastrophic losses due to pest problems lies in the fact that the industry is based on plantings of different tree genera and species. This is underpinned by the very different climatic conditions found in different parts of the country where plantation forestry is practiced. This broad genetic diversity, together with the diversity that has emerged more recently with the deployment of hybrids (particularly *Eucalyptus*) has allowed for substantial pest avoidance. Avoidance is one of the most powerful strategies available in forest protection and this will likely continue to be true in years to come. It is, however, important to recognise that the avoidance strategy, at least in terms of *Eucalyptus* hybrid clones is substantially less powerful for insect pests than it is for pathogens. Insect pests in this regard, tend to be more polyphagous and thus have the ability to overcome barriers to infestation that are more durable in terms of pathogen infection. For insect pests, there will logically be a greater emphasis on tools such as biological control.

Many lessons have been learned regarding the management of forest pest problems over a long period of time. This is true as much for South Africa as it is for other parts of the world. Trees are long-lived and even in the case of plantation forestry, rotations are relatively long at least in comparison to those for agronomic crops. Options to reduce the impact of tree diseases are primarily those of avoidance that is achieved by planting non-susceptible material or control, which for insects is best achieved biologically. There are minimal opportunities for chemical control, other than in nurseries, and the environmental risks will mean that this will be increasingly true in the future. Although there is always hope of a rapid solution, experience has taught us that ‘silver bullets’ are never realistic. Experience with the *Sirex* woodwasp in South Africa has illustrated this fact very clearly. What is needed, and this will always be so, is a clear understanding of the cause of the problem and solutions that are carefully considered.

Long periods of time are typical to achieve reasonable levels of control for forest insect pests and diseases. This strongly emphasises the need to manage risk. A warning ‘clarion’ here is a tendency in various parts of the world to believe that genetic modification will solve all pest and disease problems. While this technology will clearly be increasingly valuable as one of the tools to help combat pest damage, it should not be seen as replacing disease screening and biological control approaches. In this regard, GMO technology will in time enhance our ability to manage pest problems, but it should be seen as but one of many tools to achieve this goal. And most importantly, accurate diagnoses of the causal agents and an understanding of their biology and genetic structure will continue to be crucially important elements of any success that might be achieved.

Examples of Pest and Disease Problems:

Sirex Woodwasp

The woodwasp *Sirex noctilio* is one of the most important pests affecting South African forestry. In this regard, its management remains an important focus for the TPCP. This is likely to remain the case for numerous years to come. Yet it must also be said that losses due to *Sirex* have been significantly reduced since the establishment of the Sirex Steering Committee. The TPCP has played an important role in supporting the programme to reduce losses but this has been a national effort with considerable inputs from various sources including forestry companies (TPCP members) and the Institute for Commercial Forestry Research (ICFR).

The role of the TPCP is to provide research support for the Sirex Control Programme. This is also underpinned by the key role that the TPCP has in developing monitoring tools, producing biological control nematodes (*Deladenus siricidicola*) and to assist in evaluating the efficacy of the biological control program by dissecting thousands of *Sirex* wasps each year to assess parasitism by the nematode. These efforts have continued in 2016.

From a research perspective, it is fundamentally important to recognise that the success of the biological control programme will rest on knowledge of the genetic diversity of the target pest (*Sirex*), as well as ensuring that the primary biological control agent *D. siricidicola* does not lose its virulence, as has happened elsewhere. Thus, important aspects of TPCP research on *Sirex* is to understand the genetics of the wasp and to continue to develop and select nematode strains that will be effective as biological control agents in the future. Markers to undertake such studies have been developed and improved through analysis of the genomes of these organisms. A global collection of nematode strains has been assembled and characterised to determine their diversity and relationship. This includes the description of a new species from Japan. Ongoing work is now assessing their ability to interbreed with each other, as well as to characterise key traits such as virulence, parasitism levels in the field and ability to feed on different fungal strains.

An important aspect of TPCP research on *Sirex* is to bring to South Africa additional biological control agents for it. Substantial effort has been made in the last year to introduce the parasitoid *Megarhyssa nortoni*. In this regard, we have imported these parasitoids into our quarantine facility, where efforts to rear the insects are underway. There are also many other opportunities to ensure long-term management of *S. noctilio*. As facilities and appropriate support becomes available, these are being considered and investigated.

In addition, a range of ongoing studies is looking at the future of *Sirex* management. Information stemming from the analysis of the genomes of these organisms (for example with relation to their sex determination mechanisms) could in future be used in biotechnological approaches to management. Ongoing work is also assessing both visual and chemical attractants of the wasp to improve attraction for trapping and monitoring.

Woodwasp, *Sirex noctilio.*

Eucalyptus Gall Wasp (*Leptocybe invasa*)

The Eucalyptus gall wasp, *Leptocybe invasa* remains one of the most important threats to South African plantations. In a relatively short period of time, the pest spread throughout the forestry plantations of the country, and indeed the world and it has also had a hugely negative impact on plantations of *E. grandis* and particularly clones incuding *E. grandis* x *E. camaldulensis*. The TPCP has conducted a substantial amount of research towards managing this pest. Past focus areas have been on understanding resistance in the hosts and in developing a biological control agent for *L. invasa*. A major advance has been the development and release of the parasitoid *Seletrichodes neseri* that appears to already be having a positive impact on the pest.

From 2016 a National Leptocybe Monitoring project was launched, which involves industry and research institutes, specifically the ICFR and TPCP. The objectives of this project are to monitor infestation levels of *L. invasa* over space and time, as well as that of its biological control agent *S. neseri*. Interestingly, previous surveys have shown that other wasps are also associated with the *Leptocybe* galls, including two *Megastigmus* species and *Quadristichus mendeli* - a known biological control agent of *L. invasa* that is suspected to have been unintentionally introduced into South Africa. The role of the TPCP in the monitoring project is to assess the establishment of *S. neseri*, but also the other wasps associated with this complex gall community. In addition, the role of these gall wasps and the distribution of the two *Leptocybe* lineages will also be investigated.

Myrtle (Eucalyptus) Rust (*Austropuccinia psidii*)

The discovery of the myrtle rust pathogen in South Africa was expected, but also raised considerable concern for our industry. This followed a long period where the TPCP had been aware of the problem and had included this in our intensive field monitoring programme. As part of that monitoring, another rust affecting *Eucalyptus* was discovered. This turned out to be a fungus not previously known to science and it was provided with the name *Phakopsora eucalaypti*. This rust appears not to be causing serious damage although it needs to be monitored given that it belongs to a group of serious primary pathogens.

Much as the situation in South Africa, *Austropuccinia psidii* (previously *Puccinia psidii*) is appearing in many new *Eucalyptus* plantation situations globally. These new reports are of concern as they illustrate failures in quarantine systems and new threats to *Eucalyptus* forestry globally. What is particularly significant here is that this rust pathogen needs to be considered in terms not of its name, but rather linked to the particular genotypes that are appearing in various parts of the world. For example, we now know that the *A. psidii* genotype in South Africa is different to the so-called 'pandemic strain' that has moved globally and it seem not to be a great threat to *Eucalyptus*. However, the global trends suggest that that the pandemic strain and thus one that is able to damage *Eucalyptus* is likely to eventually (probably sooner rather than later) reach South Africa. Other strains are also likely to emerge that are important on *Eucalyptus* and this will also rest on our knowledge of the ability of new strains to evolve.

Galls formed by *Leptocybe invasa.*


Root rot symptoms.


Austropuccinia psidii symptoms on *Eugenia* sp.

The TPCP research programme now has a focus on this important question.

One of the first steps taken in response to the first record of *A. psidii* in South Africa was to consider the threat of the pathogen to *Eucalyptus* species (and families of species) being grown in South Africa. This risk assessment work also considered climatic conditions in South Africa and where the pathogen might emerge as a serious threat. This initial work was undertaken in Australia and showed that the strain of the rust in Australia could impart serious damage in South Africa in the future.

Phytophthora Diseases

The TPCP has had a focus on *Phytophthora* diseases and the broad root disease complex for many years. This has changed over time depending on problems emerging in plantations. Over the years, these have included problems such as replant diseases in pines, eucalypts and acacias and more specifically *Phytophthora* root disease on cold-tolerant gums. Against this background, the research team is also acutely aware of the fact that very serious *Phytophthora* diseases are emerging globally. Worryingly, many of these are not root diseases, but diseases of the above-ground parts of trees including canker, shoot and leaf diseases. For this reason, broad surveys have been initiated to determine which *Phytophthora* spp. occur in South Africa and thus to establish a base line of understanding regarding new introductions and long-term threats. These studies are ongoing and have been intensified during the last few years due to a growing number of reports of root disease particularly on young *Eucalyptus* including the important *E. nitens* in various parts of the major forestry regions of South Africa.

The emergence of what appears to be a new wave of root disease problems, particularly in the first year of growth of *Eucalyptus* is of great concern. Particularly important is the fact that *E. nitens*, a species that has previously not been considered at high risk is severely affected in some areas. In response to this problem, the industry arranged a workshop to interrogate the issue in early 2017 and this will lead to a more comprehensive research strategy during the coming year.

An interesting but serious concern going forward is the fact that the *Phytophthora* spp. being found on the roots of diseased *Eucalyptus* spp. are different to those found previously. Going back 30 years, the most important and obvious species present was the well-known pathogen *P. cinnamomi*. Recent studies have yielded various other species. Our impression is that *P. cinnnamomi* has been replaced by these organisms and this is probably linked to repeated rotations of trees on the same sites. In effect we appear to be driving sites to a state usually found with agronomic crops where soils become relatively sterile and where the populations of root pathogens build up over time. This is not only of *Phytophthora* spp. but other root pathogens including species of *Fusarium, Calonectria, Pythium* and *Rhizotonia*, etc.

SABBATICAL VISITS

Dr. Sanushka Naidoo

Plant secondary metabolites such as the terpenes and the conjugated terpenes are often associated with defence against insect pests and herbivory. Dr. Sanushka Naidoo undertook a research sabbatical to the Research School of Biology at the Australian National University in Canberra, from October 2015 to January 2016 and February to March 2016 to work with Prof. William Foley and Dr. Carsten Külheim. The purpose of the visit was to conduct a detailed analysis of the terpene profiles of over 500 individual *Eucalyptus grandis* leaf samples. These plants had been subjected to infestation by the Eucalyptus gall wasp, *Leptocybe invasa* in field and samples had been collected in the summer of 2014 in a Mondi second and third generation *E. grandis* hybrid population that was planted on three sites in KwaZulu-Natal. The leaves were sampled based on infestation scores of 0, 1, 2 and 3; where 0 represented no evidence of oviposition, 1 displayed signs of infestation but no galls were apparent, 2 had the appearance of galls while 3 was highly infested by *L. invasa* showing stunting and death.

During the sabbatical, Dr. Naidoo conducted near-infra-red (NIR) analysis on the samples and calculated the terpene concentrations of the samples based on the Gas Chromatography-Mass Spectroscopy data and the dry weights of each sample. The identities of the terpenes were determined based on the available library of standards. The results indicated that the samples could not be separated into specific chemotypes with distinct terpenes, rather, there was a large variation in the amount of specific terpenes within the samples. The collaboration was extended to include Prof. Juan José Acosta from North Carolina State University and Dr. Nanette Christie, Department of Genetics to model the terpenes with the NIR data and the *Leptocybe* scores. Based on an association test, there are four terpenes which seem to be associated with the resistance to *L. invasa*. This is the subject of further investigation by Dr. Naidoo and Dr. Külheim.

During her sabbatical, Dr. Naidoo had the opportunity to survey a *E. polybractea* population in West Wyalong. This species is used for *Eucalyptus* essential oil production. Insect damage was evident in the population. In addition, root, stem and leaf samples showing signs of infection were obtained. Several interesting fungal species were identified as present in the population and are currently being described.

SERVICES

Tree Health Extension

Responsible Researchers: Prof. Jolanda Roux (Extension, monitoring, diagnostic clinic)
Prof. Wilhelm de Beer (Treehealthnet and FABI website)
Prof. Mike Wingfield
Dr. Brett Hurley (Pest monitoring and extension)
Ms. Izette Greyling (Extension and diagnostic clinic)
Mr. Darryl Herron (Diagnostic clinic)

Objectives:

Extension activities form an important component of the Tree Protection Co-operative Programme (TPCP) and DST-NRF Centre of Excellence in Tree Health Biotechnology (CTHB). These activities are divided into a number of components. They include all activities linked to the monitoring of pests and diseases of native and plantation trees. Furthermore, they form an important component in the training of postgraduate students and the creation of tree health awareness amongst the general public, foresters, farmers and conservation staff. Monitoring includes efforts to detect new pathogens and pests in a timely fashion and the evaluation of the change in status of pathogens and pests, which have been present for many years. One of the key components of the monitoring programme is the diagnostic clinic that provides one means of rapid detection of new diseases and pests. Data from the clinic and field extension/monitoring activities also form part of a longer-term historical record of pests and diseases in South Africa and many other countries where the teams work.

Extension Activities 2015/2016:

The TPCP expends considerable effort on its extension responsibilities. In terms of pest and pathogen advice at the field level, this represents the bulk of the support available to the South African forestry industry. While requiring substantial effort, this provides the group with close contact with the stakeholders of the programme. In turn it makes it possible to educate foresters and forest managers as to the new problems being experienced in the field and to provide the newest and most relevant information relating to management options. Here, Ms. Izette Greyling is responsible for the bulk of the team's in-field extension activities, covering both entomology and pathology consulting visits and assistance with field trial evaluations. She is joined at regular intervals by other TPCP management team members and senior students in presenting at field days and industry arranged workshops for company staff.


Dr. Casper Crous giving a lecture to foresters at a field day.

Extension services of the TPCP include a wide range of activities such as lectures presented at field days, mainly those organised by the Institute for Commercial Forestry Research (ICFR), reports in magazines and newspapers, radio and TV interviews, newsletters such as Tree Health News and also via routine field visits. The extension services of the TPCP are closely linked to the pest and disease diagnostic clinic that receives samples and is able to provide advice based on high quality studies at the laboratory level. The results of diagnoses made by

TPCP team members examining eucalypt seedlings at a nursery.

the clinic form a crucially important component of the monitoring function of the TPCP, which is further extended by field visits linked to enquiries sent to the clinic.

The e-mail list server TreeHealthNet forms a crucially important part of the extension services of the TPCP. This list server is now connected to more than 800 foresters and forest managers in South Africa and important news is disseminated regularly. The list server also provides and important feed-back mechanism where forests can report new sightings of pest and disease problems to the TPCP. Furthermore, field days and other field extension activities are advertised on TreeHealthNet and in this way maximum benefit from field visits can be assured. We encourage all foresters in South Africa to join TreeHealthNet. This is achieved by writing a note to Prof. Wilhelm de Beer (wilhelm.debeer@fabi.up.ac.za) and being listed on TreeHealthNet@kendy.up.ac.za. Once listed, it is possible for any member to write a note and this will rapidly reach all other members.

Like TreeHealthNet, the TPCP web pages form an extremely important part of the portal of communication between the Programme and its members. All newsletters of the TPCP are posted on the website and all disease diagnostic aids can also be found there. This is a major source of information for members. The TPCP site can be accessed via the FABI website at www.fabinet.up.ac.za.

Prof. Jolanda Roux giving a lecture to staff and visitors to the TPCP.

TPCP team members examing acacia seedlings infected with a rust fungus.

World Class Facilities and Capacity in the FABI Biocontrol Centre

FABI's Biocontrol Centre at the Univeristy of Pretoria's Research Precinct.

The movement of insects and pathogens around the world has been steadily increasing over the last century, largely as a consequence of globalised trade. Once established, such organisms can and do colonise native trees, often with devastating effects on native forests and woody ecosystems. The South African forestry industry is no different, and has suffered from a number of recent introductions of serious pests, the resurgence of pests introduced decades ago and host shifts from native pests onto plantation tree species.

Industries and governments the world over are grappling with ways to deal with this rapidly increasing number and rate of emerging pests. The vast geographic scales under consideration together with the high cost of chemical or cultural control leaves few options for management. One of the most effective options for the management of forest insect pests is biological control. Here, organisms are imported (or sometimes sourced locally) to colonise and hopefully suppress invasive pest populations. Building a successful biological control programme is a substantial and often difficult undertaking. There is a realisation worldwide that the capacity, speed and efficiency of developing management programmes need to increase if the sustainability of plantation forestry is to be assured.

Fortunately, Industry-University-Government partnership through the Tree Protection Co-operative Programme (TPCP)/DST-NRF Centre of Excellence in Tree Health Biotechnology (CTHB) programmes in FABI have been building capacity for over 10 years with respect to the students, staff and equipment/facilities essential for working in this area. This includes the development of a world class and Government-approved quarantine facility, and various other laboratory, glasshouse, tunnel and outdoor netting facilities at the FABI Biocontrol Centre.

Today, the FABI Biocontrol Centre is a leader in the field of biological control of plantation forestry pests. With close connections between frontier research projects using the latest genetics, genomics, remote sensing, microscopy, chemistry and other tools, it has become a high precision and highly effective operation for the development, deployment and monitoring of biological control agents. In addition, the FABI Biocontrol Centre is placing South Africa at the centre of developing global networks to deal with forestry pests, such as the international BiCEP (Biological Control of Eucalyptus Pests) programme, which many believe is critical to the future survival of this sector.

Questions in the realm of biocontrol typically have an applied focus and address the basic biology of introduction of native pests along with that of potential candidates for control agents. Understanding origin and native status is key, as are careful risk assessments that evaluate the potential for non-target effects. These studies are complemented by molecular genetics studies, from phylogenetics to population genetics and genomics, to complement the understanding of the biology of the organisms, understand diversity, pathways and native distributions, and to develop diagnostic tools for research and monitoring.

Much of the research is focused on the use of parasitoids and parasitic nematodes, specifically *Deladenus siricidicola,* as classical biological control agents. However, recent research includes investigating the potential of native entomopathogenic nematode (EPN) species for the control of soil pests in an augmentative biological control approach. This work will help further understanding of patterns of colonisation, host use and potential movement to and from native environments and the consequences of these aspects for invasion biology and biocontrol.

Insect quarantine glasshouse.

Semi-quarantine tunnel.

At work in the lab.

Samantha Bush in the glasshouse.

Pine Pitch Canker Screening Facility

Facility Management Team:	Prof. Emma Steenkamp Prof. Mike Wingfield
Technical Manager:	Dr. Fahimeh Jami
Technical Committee:	Prof. Steve Verryn (Hans Merensky) Dr. Johan de Graaf (Hans Merensky) Dr. Kitt Payne (Mondi) Ms. Ilse Botman (PG Bison) Ms. Lizette de Waal-Mitchell (York Timbers) Mr. Pieter de Wet (PG Bison) Mr. Phillip Hlongwane (KLF) Mr. André Nel (Sappi Forests)

The Pitch Canker Screening Facility was established in 2005. It is primarily used for screening pine breeding stock for tolerance to the pitch canker fungus, *Fusarium circinatum*. This facility forms part of a collaborative project that was originally initiated by Sappi Forests, Mondi Business Paper, Komatiland Forestry (KLF) and FABI. During the 2015-2017 period, three additional companies (i.e., Hans Merensky, York Timbers and PG Bison) also participated in the project. The Pitch Canker Screening Facility is located next to the FABI Biocontrol Centre on the University of Pretoria's Experimental Farm. Dr. Fahimeh Jami is the technical manager of the facility.

Twice every year, between 25,000 and 30,000 seedlings and/or cuttings are inoculated with *F. circinatum*. For this purpose, a standardised method developed at FABI is used. After six weeks of incubation in this greenhouse facility, lesion development is measured. The various forestry companies then analyse the performance of their seedlings/cuttings to inform their pine breeding programmes.

Pine seedlings in the Pine Pitch Canker Screening Facility. Left: healthy seedlings before inoculation with *Fusarium circinatatum*. Right: seedlings, after inoculation with the pathogen (the progression of disease is clearly visible from the point of inoculation down the stem of the seedling).

FABI postgraduate students (top left and right) in the process of inoculating pine seedlings with *Fusarium circinatum* (bottom left) and recording the length of the lesions it induced (bottom right).

Ion Torrent Sequencing Facility

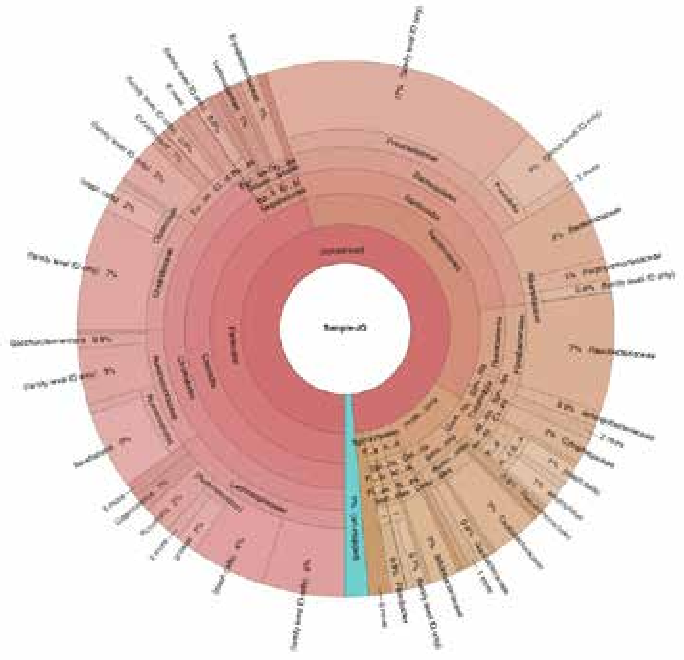
Facility Director: Prof. Brenda Wingfield

Facility Staff: Mr. Nicky Olivier
Ms. Mmatshepho Phasha (From April 2015)
Ms. Renate Zipfel

The Ion Torrent Sequencing Facility at the University of Pretoria provides high-quality high-throughput sequencing solutions to researchers in Southern Africa. The Ion Torrent Personal Genome Machine (PGM) housed in a dedicated laboratory in the Plant Sciences Complex is capable of generating up to 2GB sequence data from single or multiplexed samples. Average single-end reads of 400bp length are produced, and the data is utilised for a variety of research questions. In collaboration with the University of Stellenbosch larger scale projects are accommodated on the Ion Proton and Ion S5 instruments, yielding up to 10GB of sequence data with 200bp read lengths. The consistent quality of sequencing data relies on the expert skills of a dedicated technician. Since April 2015 Ms. Mmatshepho Phasha has created quality libraries within very consistent size selection tolerances, and has managed sequencing reactions on the PGM instrument. To date the facility has produced whole genome, targeted amplicon and metagenomic sequencing for virus, bacterial, fungal, human and veterinary samples.

The managers of the facility believe strongly in student training and capacity building in high-throughput sequencing, and students are encouraged to attend project planning sessions with their supervisors to understand the complex planning process for optimal sequencing results in their respective sequencing projects. In addition, the facility presents annual seminars on high-throughput sequencing technology and advances to interested researchers and students in the region. A contribution is also made to the Genetics, Microbiology, Biochemistry and Plant Science Honours Advanced Techniques courses. A lecture on the basics and applications of high-throughput sequencing provides the students with a background into the different platforms, as well as the information required for planning a sequencing project.

During 2016 the facility hosted a PGM 16S Metagenomic sequencing and data analysis workshop in collaboration with Thermo Fisher Scientific. Samples were submitted by researchers from the University of Pretoria (Departments of Microbiology/FABI, Genetics and Zoology), the KwaZulu-Natal Agriculture & Rural Development Department, Vaal University of Technology and Botswana International University of Science & Technology. Specific amplicons from the 16S region of each sample were sequenced and training was provided on the data analysis using the Thermo Fisher Scientific Ion Reporter software. Follow-up projects using the 16S Metagenomic kit will be accomodated for interested researchers.



Krona visualization of metagenomic sequencing results.

Microarray Service

Facility Manager: Prof. Dave Berger

Microarray Scientific Officer: Mr. Nicky Olivier

The ACGT (African Centre for Gene Technologies) Microarray Facility has a good track record in providing microarray services for researchers throughout Africa. Traditionally whole genome microarray studies were confined to model organisms for which well annotated genome information and sequences were available. Researchers were often forced to perform cross-species hybridisations and take species-specific gene composition and sequences into account, or had to rely on cDNA libraries spotted on glass slides. Due to the current dearth of genome sequence data and the relatively low cost of generating genomic or transcriptomic sequence data from any organism, the use of microarrays to perform transcriptome studies has become easier and more representative of the specific biological system under investigation.

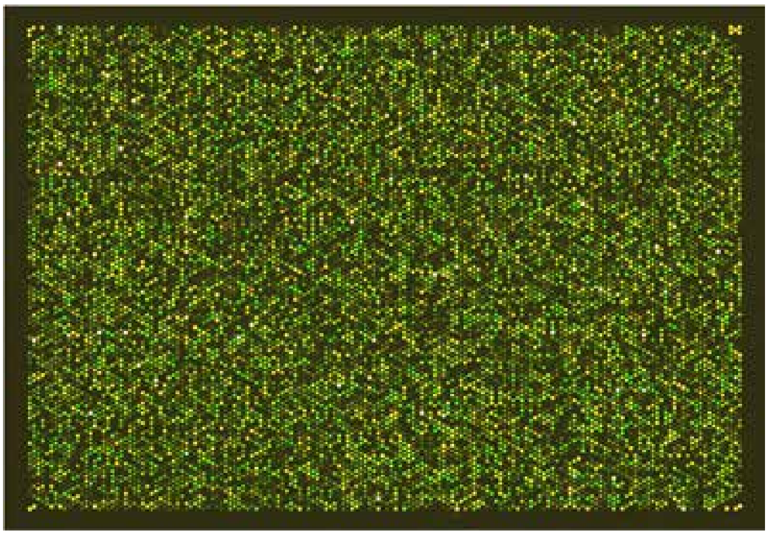
Most current users of the ACGT Microarray Facility make use of the Agilent microarray platform. This enables users to compile a catalogue of sequences to be added to their array (e.g. from genome sequence information), and the free web-based Agilent software computes the most optimal oligonucleotides (60mer) to be synthesised on their slides. Flexible configurations of arrays on the slides with scalable numbers of spots can also be selected, providing a good balance between cost and data throughput. Common formats are 4 x 44,000 or 8 x 15,000 spots per slide. Due to the highly reproducible spot diameters and spot oligonucleotide concentrations, this microarray platform produces high-quality data across multiple experiments.

The ACGT microarray facility houses all the required hardware for processing Agilent slides, along with extensive expertise in experimental design, hybridisation procedures and custom data analysis using open-source software (R and Bioconductor). In addition, the facility is housed in a building with well-appointed laboratories for RNA isolation and all the required molecular biology techniques. Researchers with limited access to such facilities at their home institutions are accommodated in these laboratories to perform the critical RNA isolations and QC to ensure that the final data is representative of the biological effect under study.

The facility has not only been of great support to researchers in the Faculty of Natural and Agricultural Sciences, but also of the Faculties of Medicine and Veterinary Sciences. In 2015-2017 microarray projects have been processed for Prof. Noëlani van den Berg's Avocado Research Group, contributing to several student postgraduate degrees and publications.

Since RNA integrity and purity is critical for downstream expression analyses (RT-qPCR, microarrays, etc.) and RNA sequencing applications, the facility's BioRad Experion automated electrophoresis system is of great importance. The cost-only use of the instrument is not limited to microarray studies, and is available to all interested researchers in the ACGT partner institutions.

For more information, please consult:
http://www.microarray.up.ac.za/



Scanned microarray image from FABI microarray.

QuantStudioTM 12K Flex Platform

The QuantStudio™ 12K Flex Real-Time PCR Facility was established in 2014 through funding obtained from the NRF National Equipment Platform (NEP) Grant. Quantitative Real-Time PCR is a valuable and extensively used analysis in molecular biology research. The aim of the platform is to provide a user-friendly real-time PCR service to researchers throughout South Africa and to promote real-time PCR-based research, techniques and analysis.

The QuantStudio™ Real-Time PCR System allows for small to large-scale functional genomics studies. The QuantStudio™ 12K Flex instrument together with high-throughput OpenArray® technology supports two important large-scale functional applications. These include the gene expression analysis of hundreds of targets under varying conditions and treatments as well as SNP genotyping of up to 960 samples for up to 256 SNPs. In the past three years, the QuantStudio™ 12K Flex Platform has encouraged collaboration and mentorship across a wide range of research groups. The instrument has already been used by researchers from various institutions such as the University of KwaZulu-Natal (UKZN), University of the Free State (UFS), University of Pretoria (UP) and ILRI, on projects ranging from human disease diagnostics to gene expression of plants under stress.

The platform was managed by Ms. Jane Bredenkamp from 2014 to 2016 but was taken over by Mr Stephan Henning in 2017. Mr. Henning (MSc student within FABI) gained experience using the platform during his honours degree and is currently responsible for the administration, technical execution and troubleshooting of experiments and maintenance of the instruments. Workshops are held each year in conjunction with ThermoScientific for training of new users. Each experiment is designed in consultation with ThermoScientific experts and technical assistance in the laboratory is provided by the platform.

AWARDS & HONOURS

FABI AWARDS FOR EXCELLENCE

Ever since its establishment in 1998, FABI has pursued excellence across its many key performance indicators. This approach has resulted in many accolades for FABI students, academic staff members and for the Institute itself. Large numbers of students have thus received prestigious bursaries from various organisations, awards for research excellence and for travel to mention but a few. Likewise academic staff members have received special awards from organisations such as the Department of Water Affairs and Forestry, the Department of Science and Technology, the National Research Foundation, the South African Association for Art and Science, the Royal Society of South Africa, the Academy of Sciences of South Africa and various others. Against this background of excellence, FABI management decided to institute a suite of awards to be made annually to exceptional FABIans and FABI stakeholders.

FABI awards were presented for the first time in 2007 and these have come to be recognised as important and highly prized. The FABI awards are as follows:

Best FABI Student Publication

Given the importance of research quality in FABI, one award recognises the best publication produced by a FABI student in the award year. The recipient in the case of this award is easily chosen based on the ISI impact factor of the paper produced.

2015	Darryl Herron
2016	Angelica Marsberg-de Villiers

Best Postdoctoral Fellow Publication

This award recognises the best publication produced by a postdoctoral Fellow in the award year. The recipient in the case of this award is chosen based on the ISI impact factor of the paper produced.

2015	Dr. Maria Vivas
2016	Dr. Alistair McTaggart

Best FABI MSc Thesis

This award is given to an MSc student who achieved the highest mark through external examination of a thesis.

2015	Danielle Roodt
2016	Andrea Wilson

FABI Award for Mentorship

MSc or PhD students who have demonstrated outstanding mentorship, in the broad sense, to other students.

2015	Chrizelle Beukes, Desre Pinard, RunLei Chang
2016	James Mehl, Katrin Fitza, Esna du Plessis, Tanay Bose, Arista Fourie, Andrea Wilson, FeiFei Liu

FABI Award for "Getting the Message to the Public"

This award goes to a student who has excelled in transferring the FABI science message to the public. Tangible evidence of transferring the accomplishments of FABI, or the science conducted by FABI or its members to the public must be demonstrated.

2015	Juanita Avontuur
2016	Darryl Herron, Joey Hulbert, Benedicta Swalarsk-Parry, Arista Fourie

FABI Award for Recognising Contributions by a Member of Staff of the University

This award is made to a member of staff of the University of Pretoria that has provided exceptional support to FABI.

2015	Prof. Anton Ströh
2016	Leanne van Zyl

FABI Award for Recognising Contributions by a Person External to the University

This award acknowledges the exceptional contributions to FABI by a stakeholder external to the University of Pretoria. Selection of the recipient is made by the FABI community.

2015	Dr. Terry Stanger, SAPPI
2016	Dr. Charlie Clark, SAPPI

FABIan of the Year

This is FABI's premium award for students and it recognises excellence across a broad range of contributions including research, mentorship, support to the maintenance of the structures of the Institute and others. The recipient is chosen by FABI students.

2015	Darryl Herron
2016	Arista Fourie

Best FABI Student Personal Website

2015 Miekie Human, Osmond Mlonyeni
2016 Joey Hulbert, Darryl Herron, Tanay Bose

Photographic Awards

Two awards will be made annually for photographs judged to be the best in their category. These categories were:

Best Photograph Illustrating a FABIan or FABIans at Work

2015 Ludwig Eksteen
2016 Prof. Jolanda Roux

Best Photograph Illustrating FABI Research

2015 Ludwig Eksteen
2016 Ginna Granados

AWARDS TO MANCOM MEMBERS

Prof. Brenda Wingfield was awarded the prestigious Harry Oppenheimer Memorial Fellowship Award by the Oppenheimer Memorial Trust (OMT). In receiving this, award she was joined by Prof. Xolela Mangcu, political commentator and leading academic at the University of Cape Town. The awards were announced by OMT Trustee, Mr. Bobby Godsell, former CEO of the De Beers Diamond Company and they were presented by Mr. Nicky Oppenheimer. The awards ceremony, held in the Brenthurst Library of the Brenthurst Estate (home of the Oppenheimer family), was attended by colleagues, family and friends of the awardees. Many distinguished guests, including former South African President Kgalema Motlanthe also attended the ceremony. The R1,5 million prize money will be used to pursue the awardees' chosen research goals during the coming year. Prof. Wingfield will extend her studies of reproduction in fungi, and specifically will provide her students with an opportunity to participate in an international project on this topic.

Former South African President Kgalema Motlanthe, Ms. Gugu Mtshali and Prof. Brenda Wingfield.

Professor Zander Myburg received the **National Science and Technology Forum (NSTF)-BHP Billiton-TW Kambule Award** for Contribution to Research and its Outcomes in South Africa (last 5-10 years) in 2015.

South African Minister of Science and Technology, Naledi Pandor, Prof. Zander Myburg and Dr. Ali Dhansay.

FELLOWSHIP AWARDS

Professor Gerhard Pietersen and **Prof. Teresa Coutinho** both received Fellowships from the Southern African Society of Plant Pathology in 2015 and 2016, respectively.

UNIVERSITY OF PRETORIA AWARDS

Chancellor's Award

Prof. Bernard Slippers (2016)

Professor Bernard Slippers receiving the Chancellor's Award from Prof. Wiseman Nkuhlu.

Exceptional Young Researcher Awards

Dr. Irene Barnes (2015)
Dr. Brett Hurley (2017)

Exceptional Achievers Awards

Prof. Teresa Coutinho (2016-2018)
Prof. Jolanda Roux (2014-2017)
Prof. Fanus Venter (2017-2019)
Prof. Zander Myburg (2017-2019)

WORKSHOPS & CONFERENCES

Phylogenetic Workshops

The Phylogenetic Workshops presented under the auspices of the DST-NRF Centre of Excellence in Tree Health Biotechnology (CTHB) focus on the theoretical and applied aspects of contemporary methods used to infer phylogenetic relationships amongst organisms. The importance of these workshops, within the CTHB context, stems from the fact that understanding phylogenetic relationships is an essential aspect of pest and pathogen identification and management. The workshops were initiated in 2004 following the realisation that most researchers have limited experience in the practical application of evolutionary models and tree building algorithms as well as the execution of computer software used for the analyses. A major objective for the workshops has been to provide "hands-on" experience in the use of databases available on the world-wide-web and the range of software, both commercial and freeware, currently available for evolutionary biologists. These workshops - designed and presented by Dr. Martin Coetzee - are offered on a yearly basis and cater for researchers ranging from novices to those having advanced knowledge in the field.

Initially, each workshop catered for participants at all levels of experience. Sessions were paced in such a way as to ensure that the most inexperienced participants were able to keep up. It soon became evident, however, that this format allowed insufficient time for providing researchers with an in-depth knowledge regarding phylogenetic theory and hands-on experience in phylogenetic software. In 2009, the workshops were therefore split into separate introductory- and advanced-level sessions.

The introductory-level phylogenetic workshop provides a basic understanding of various phylogenetic techniques, from inspecting a sequence to constructing a tree. The instruction format is a mixture of presentations, exercises and discussions. Dr. Jane Wright, who previously was a postdoctoral Fellow in the CTHB, is contracted annually in a joint venture between the CTHB and Inqaba Biotechnical Industries to steer the workshops.

The advanced-level phylogenetic workshop focuses on advanced phylogenetic concepts and methods, and builds on the concepts introduced during the introductory-level workshops. Phylogenetic methods covered during this workshop include parsimony, maximum likelihood and Bayesian inference of phylogenies, hypothesis testing and molecular clock dating. The instruction format of this workshop is similar to the introductory-level workshop. The advanced-level phylogenetic workshop is presented biannually over five days under the leadership of Dr. Coetzee and the assistance of Dr. Wright and Ms. Marika Palmer.

Since the introduction of the phylogenetic workshops until 2016, 301 researchers have been trained. Of these, 153 participants were students and academic staff associated with FABI. The remainder were from other research programmes at the University of Pretoria and elsewhere in South Africa, as well as countries in Africa, Europe, Australia, South America, North America and Asia.

Phylogenomics Workshops

Phylogenomics is a relatively new field in biological sciences that combines genome data and evolutionary reconstruction. In a phylogenenomic study, phylogenetic trees are constructed based on comparisons between entire genomes or large portions of genomes. Different to phylogenetics, phylogenomics does not only consider the evolutionary relationships of an organism, but also the evolutionary pathways of genomes. With the increasing number of fungal genomes being sequenced at FABI and interest in using these genomes for phylogenetic studies, a phylogenomics workshop was introduced in 2014.

The workshop is coordinated by Dr. Martin Coetzee, and presented by Ms. Marike Palmer (CTHB, UP). Ms. Palmer deals with hands-on tools to conduct phylogenomic studies. The workshop is attended by a selection of postdoctoral Fellows and PhD students, all conducting their research at FABI.

Mycology Workshop

In June 2016, 15 TPCP/CTHB students in FABI participated in a mycology workshop. The workshop was presented by a team of mycological experts from the Biosystematics Division of the Plant Protection Research Institute (PPRI) at the Agricultural Research Council (ARC) and academic staff members at FABI.

The presenters included Drs Riana Jacobs, Mariëtte Truter and Elna van der Linde, together with Dr. Irene Barnes and Prof. Wilhelm de Beer.

The purpose of the workshop was to train postgraduate students who did not have mycology as part of their undergradute training, in the basics of working with fungi in the laboratory. They got hands-on experience working with isolates from all the major groups of fungi in the laboratory, from the isolation and purification thereof to microscopy. Other topics treated during the course included taxonomy, nomenclature, typifications, sporogenesis and spore types of different groups, species concepts and how to do and interpret BLAST results obtained with fungal sequences. The participants all received a certificate at the end of the course.

Dr. Elna van der Linde, Dr. Irene Barnes, Prof. Wilhelm de Beer, Dr. Riana Jacobs and Dr. Mariette Truter.

Participants in the Mycology Workshop.

The International *Fusarium* Laboratory Workshop

The 17th International *Fusarium* Laboratory Workshop was hosted by FABI from 30 May to 3 June 2016. This annual event brings together some of the world's leading authorities on this fungal genus which includes many species that are important pathogens of plants, animals and humans. The workshop comprised various lectures on a wide range of topics such as laboratory strain identification, molecular identification, mycotoxins, VCG analysis, mating types as well as species concepts, phylogenetics, population genetics and genomics. The hands on laboratory sessions taught participants how to culture, isolate and store strains and how to PCR, sequence and BLAST barcoding genes for molecular identification. The participants were also given the unique opportunity to observe and compare the various morphological characters of more than 80 *Fusarium* species in one week.

The first International *Fusarium* Laboratory Workshop was initiated by Prof. John Leslie from the Kansas State University and Dr. Brett Summerell from the Royal Botanic Gardens, Sydney. It is held bi-annually at its home base at Kansas State University, USA and then at Universities elsewhere in the world. Thirty delegates from 11 countries including South Africa, Zimbabwe, Nigeria, Philippines, New Zealand, Australia, the Netherlands and Norway attended the 2016 workshop. Whilst the 2016 workshop was more southern hemisphere focused in terms of delegates, it allowed researchers from the northern and southern hemispheres to interact and foster new collaborative efforts to further research on this important genus. All the participants were awarded a certificate for completing the course while the instructors were thanked for sharing their vast wealth of knowledge on *Fusarium* with the group.

The 17th International *Fusarium* Laboratory Workshop instructors:

Prof. John Leslie (Kansas State University), Prof. David Geiser (Pennsylvania State University), Dr. Brett Summerell (Royal Botanic Gardens, Sydney), Prof. Emma Steenkamp (FABI, University of Pretoria), Prof. Mike Wingfield (FABI, University of Pretoria), Prof. Brenda Wingfield (FABI, University of Pretoria), Dr. Gerda Fourie (FABI, University of Pretoria), Dr. Lieschen de Vos (FABI, University of Pretoria), Dr. Sandra Lamprecht (Agricultural Research Council, PPRI), Dr. Gordon Shephard (Institute of Biomedical and Microbial Biotechnology, Cape Peninsula University of Technology), Dr. Lorenzo Lombard (CBS (now renamed the Westerdijk Fungal Biodiversity Institute), the Netherlands) and Prof. Pedro Crous (CBS (now renamed the Westerdijk Fungal Biodiversity Institute), the Netherlands).

The 17th International *Fusarium* Laboratory Workshop participants.

PUBLICATIONS 2015–2017

These lists include only publications that had appeared by the end of May 2017. Manuscripts in press and submitted for publication are not included.

In Refereed Journals

Abate BA, Malan AP, Tiedt LR, Wingfield MJ, Slippers B, Hurley BP. (2016). *Steinernema fabii* n. sp. (Rhabditida: Steinernematidae), a new entomopathogenic nematode from South Africa. *Nematology* 18: 235-255.

Andjic V, Maxwell A, Hardy GES, Burgess TI. (2016). New cryptic species of *Teratosphaeria* on *Eucalyptus* in Australia. *IMA Fungus* 7: 253-263.

Apetorgbor MM, Roux J. (2015). Diseases of plantation forestry trees in Southern Ghana. *International Journal of Phytopathology* 4: 5-13.

Aylward J, Dreyer LL, Steenkamp ET, Wingfield MJ, Roets F. (2015). *Knoxdaviesia proteae* is not the only *Knoxdaviesia*-symbiont of *Protea repens*. *IMA Fungus* 6: 471-476.

Aylward J, Dreyer LL, Steenkamp ET, Wingfield MJ, Roets F. (2015). Long-distance dispersal and recolonization of a fire-destroyed niche by a mite-associated fungus. *Fungal Biology* 119: 245-256.

Aylward J, Steenkamp ET, Dreyer LL, Roets F, Wingfield BD, Wingfield MJ. (2016). Genome sequences of *Knoxdaviesia capensis* and *K. proteae* (Fungi: Ascomycota) from *Protea* trees in South Africa. *Standards in Genomic Sciences* 11: 1-7.

Aylward J, Steenkamp ET, Dreyer LL, Roets F, Wingfield BD, Wingfield MJ. (2017). A plant pathology perspective of fungal genome sequencing. *IMA Fungus* 8: 1-15.

Aylward J, Steenkamp ET, Dreyer LL, Roets F, Wingfield MJ, Wingfield BD. (2016). Genetic basis for high population diversity in *Protea*-associated *Knoxdaviesia*. *Fungal Genetics and Biology* 96: 47-57.

Backer R, Mahomed W, Reeksting B, Engelbrecht J, Ibarra-Laclette E, van den Berg N. (2015). Phylogenetic and expression analysis of the NPR1-like gene family from *Persea americana* (Mill.). *Frontiers in Plant Science* 6: 300.

Barnes I, van der Nest A, Mullett MS, Crous PW, Drenkhan R, Musolin DL, Wingfield MJ. (2016). Neotypification of *Dothistroma septosporum* and epitypification of *D. pini*, causal agents of Dothistroma needle blight of pine. *Forest Pathology* 46: 388-407.

Baron S, van der Merwe NA, Madder M, Maritz-Olivier C. (2015). SNP analysis infers that recombination is involved in the evolution of Amitraz resistance in *Rhipicephalus microplus*. *PLoS ONE* 10: e0131341.

Beukes CW, Stepkowski T, Venter SN, Clapa T, Phalane FL, le Roux MM, Steenkamp ET. (2016). Crotalarieae and Genisteae of the South African Great Escarpment are nodulated by novel *Bradyrhizobium* species with unique and diverse symbiotic loci. *Molecular Phylogenetics and Evolution* 100: 206-218.

Bible AN, Fletcher SJ, Pelletier DA, Schadt CW, Jawdy SS, Weston DJ, Engle NL, Tschaplinski T, Masyuko R, Bohn PW, Coutinho TA, Doktycz MJ & Morrell-Falvey JL. (2016). A carotenoid-deficient mutant in *Pantoea* sp. YR343, a bacteria isolated from the rhizosphere of *Populus deltoides*, is defective in root colonization. *Frontiers in Microbiology* 7: 491.

Bihon W, Cloete M, Gerrano AS, Oelofse D, Adebola P. (2016). Draft genome sequence of *Alternaria alternata* isolated from onion leaves in South Africa. *Genome Announcements* 4: e01022-16.

Bouwer MC, Slippers B, Degefu D, Wingfield MJ, Lawson S, Rohwer ER. (2015). Identification of the sex pheromone of the tree infesting Cossid moth *Coryphodema tristis* (Lepidoptera: Cossidae). *PLoS ONE* 10: e0118575.

Brawner J, Japarudin Y, Lapammu M, Rauf R, Boden D, Wingfield MJ. (2015). Evaluating the inheritance of *Ceratocystis acaciivora* symptom expression in a diverse *Acacia mangium* breeding population. *Southern Forests* 77: 83-90.

Bulman LS, Bradshaw RE, Fraser S, Martín-García J, Barnes I, Musolin DL, La Porta N, Woods A, Diez JJ, Koltay A, Drenkhan R, Ahumada R, Poljakovic-Pajnik L, Queloz V, Piškur B, Doğmuş-Lehtijärvi HT, Chira D, Tomešová-Haataja V, Georgieva M, Jankovský L, Anselmi N, Markovskaja S, Papazova-Anakieva I, Sotirovski K, Lazarević J, Adamčíková K, Boroń P, Bragança H, Vettraino AM, Selikhovkin AV,

Bulgakov TS, Tubby K. (2016). A worldwide perspective on the management and control of Dothistroma needle blight. *Forest Pathology* 46: 472-488.

Burgess T, White D, McDougall K, Garnas J, Dunstan W, Catalã S, Carnegie A, Worboys S, Cahill D, Vettraino AM, Stukely M, Liew E, Paap T, Bose T, Migliorini D, Williams B, Brigg F, Crane C, Rudman T, Hardy G. (2017). *Phytophthora* distribution and diversity across Australia. *Pacific Conservation Biology* 23.

Bush SJ, Slippers B, Neser S, Harney M, Dittrich-Schröder G, Hurley BP. (2016). Six recently recorded Australian insects associated with *Eucalyptus* in South Africa. *African Entomology* 24: 539-544.

Carocha V, Soler M, Hefer CA, Cassan-Wang H, Fevereiro P, Myburg AA, Paiva JAP, Grima-Pettenati J. (2015). Genome-wide analysis of the lignin toolbox of *Eucalyptus grandis*. *New Phytologist* 206: 1297-1313.

Carstensen GD, Venter SN, Wingfield MJ, Coutinho TA. (2017). Two *Ralstonia* species associated with bacterial wilt of *Eucalyptus. Plant Pathology* 66, 395-403.

Chen SF, Li GQ, Liu FF, Michailides TJ. (2015). Novel species of Botryosphaeriaceae associated with shoot blight of pistachio. *Mycologia* 107: 780-792.

Chen SF, van der Merwe NA, Wingfield MJ, Roux J. (2016). Population structure of *Holocryphia capensis* (Cryphonectriaceae) from *Metrosideros angustifolia* and its pathogenicity to *Eucalyptus* species. *Australasian Plant Pathology* 45: 201-207.

Chen SF, Wingfield MJ, Li GQ, Liu FF. (2016). *Corticimorbus sinomyrti* gen. et sp. nov. (Cryphonectriaceae) pathogenic to native *Rhodomyrtus tomentosa* (Myrtaceae) in South China. *Plant Pathology* 65(8): 1254-1266.

Christie N, Myburg AA, Joubert F, Murray SL, Carstens M, Lin YC, Meyer J, Crampton BG, Christensen SA, Ntuli JF, Wighard SS, van de Peer Y, Berger DK. (2017). Systems genetics reveals a transcriptional network associated with susceptibility in the maize-gray leaf spot pathosystem. *The Plant Journal* 89: 746-763.

Coetzee MPA, Marincowitz S, Muthelo VG, Wingfield MJ. (2015). *Ganoderma* species, including new taxa associated with root rot of the iconic *Jacaranda mimosifolia* in Pretoria, South Africa. *IMA Fungus* 6: 249-256.

Coetzee MPA, Wingfield BD, Zhao J, van Coller SJ, Wingfield MJ. (2015). Phylogenetic relationships among biological species of *Armillaria* from China. *Mycoscience* 56: 530-541.

Conlon BH, de Beer ZW, de Fine Licht HK, Aanen DK, Poulsen M. (2016). Phylogeneticanalyses of diverse *Podaxis* specimens from Southern Africa reveal hidden diversity and new insights into associations with termites. *Fungal Biology* 120: 1065-1076.

Conlon BH, Mitchell J, de Beer ZW, Carøe C, Gilbert MTP, Eilenberg J, Poulsen M, de Fine Licht HH. (2017). Draft genome of the fungus-growing termite pathogenic fungus *Ophiocordyceps bispora* (Ophiocordycipitaceae, Hypocreales, Ascomycota). *Data in Brief* 11: 537–542.

Coutinho TA, van der Westhuizen L, Roux J, McFarlane SA, Venter SN. (2015). Significant host jump of *Xanthomonas vasicola* from sugarcane to a *Eucalyptus grandis* clone in South Africa. *Plant Pathology* 64: 576-581.

Coutinho TA, Wingfield MJ. (2017). *Ralstonia solanacearum* and *R. pseudosolanacearum* on *Eucalyptus*: opportunists or primary pathogens? *Frontiers in Plant Science* 8: 761.

Crous CJ, Malan FS, Wingfield MJ. (2016). Securing African forests for future drier climates: applying ecophysiology in tree improvement. *Southern Forests* 78: 241-254.

Crous PW, Groenewald JZ, Slippers B, Wingfield MJ. (2016). Global food and fibre security threatened by current inefficiencies in fungal identification. *Philosophical Transactions of the Royal Society B* 371, 20160024.

Crous PW, Hawksworth DL, Wingfield MJ. (2015). Identifying and naming plant-pathogenic fungi: Past, present, and future. *Annual Review of Phytopathology* 53: 247-267.

Crous PW, Schumacher RK, Wingfield MJ, Lombard L, Giraldo A, Christensen M, Gardiennet A, Nakashima C, Pereira OL, Smith AJ, Groenewald JZ. (2015). Fungal Systematics and Evolution: FUSE 1. *Sydowia* 67: 81-118.

Crous PW, Slippers B, Groenewald JZ, Wingfield MJ. (2017). Botryosphaeriaceae: Systematics, pathology, and genetics. *Fungal Biology* 121: 305-306.

Crous PW, Wingfield MJ, Burgess TI, Hardy G, Crane C, Barrett S, Cano-Lira JF, Le Roux JJ, Thangavel R, Guarro J, Stchigel AM, Martín MP, Alfredo DS, Barber PA, Barreto RW, Baseia IG, Cano-Canals J, Cheewangkoon R, Ferreira RJ, Gené J, Lechat C, Moreno G, Roets F, Shivas RG, Sousa JO, Tan YP, Wiederhold NP, Abell SE, Accioly T, Albizu JL, Alves JL, Antoniolli ZI, Aplin N, Araújo J, Arzanlou M, Bezerra JDP, Bouchara JP, Carlavilla JR, Castillo A, Castroagudín VL, Ceresini PC, Claridge GF, Coelho G, Coimbra VRM, Costa LA, Da Cunha KC, Da Silva SS, Daniel R, De Beer ZW, Dueñas M, Edwards J, Enwistle P, Fiuza PO, Fournier J, García D, Gibertoni TB, Giraud S, Guevara-Suarez M, Gusmão LFP, Haituk S, Heykoop M, Hirooka Y, Hofmann TA, Houbraken J, Hughes DP, Kautmanová I, Koppel O, Koukol O, Larsson E, Latha KPD, Lee DH, Lisboa DO, Lisboa WS, López-Villalba Á, Maciel JLN, Manimohan P, Manjón JL, Marincowitz S, Marney TS, Meijer M, Miller AN, Olariaga I, Paiva LM, Piepenbring M, Poveda-Molero JC, Raj KNA, Raja HA, Rougeron A, Salcedo I, Samadi R, Santos TAB, Scarlett K, Seifert KA, Shuttleworth LA, Silva GA, Silva M, Siqueira JPZ, Souza-Motta CM, Stephenson SL, Sutton DA, Tamakeaw N, Telleria MT, Valenzuela-Lopez N, Viljoen A, Visagie CM, Vizzini A, Wartchow F, Wingfield BD, Yurchenko E, Zamora JC, Groenewald JZ. (2016). Fungal Planet description sheets: 469-557. *Persoonia* 37: 218-403.

Crous PW, Wingfield MJ, Guarro J, Hernandez-Restrepo M, Sutton DA, Acharya K, Barber PA, Boekhout T, Dimitrov RA, Duenas M, Dutta AK, Gene J, Gouliamova DE, Groenewald M, Lombard L, Morozova OV, Sarkar J, Smith M, Stchigel AM, Wiederhold NP, Alexandrova AV, Antelmi I, Armengol J, Barnes I, Cano-Lira JF, Castaneda Ruiz RF, Contu M, Courtecuisse Pr R, Da Silveira AL, Decock CA, de Goes A, Edathodu J, Ercole E, Firmino AC, Fourie A, Fournier J, Furtado EL, Geering ADW, Gershenzon J, Giraldo A, Gramaje D, Hammerbacher A, He XL, Haryadi D, Khemmuk W, Kovalenko AE, Krawczynski R, Laich F, Lechat C, Lopes UP, Madrid H, Malysheva EF, Marin-Felix Y, Martin MP, Mostert L, Nigro F, Pereira OL, Picillo B, Pinho DB, Popov ES, Rodas Pelaez CA, Rooney-Latham S, Sandoval-Denis M, Shivas RG, Silva V, Stoilova-Disheva MM, Telleria MT, Ullah C, Unsicker SB, Van der Merwe NA, Vizzini A, Wagner HG, Wong PTW, Wood AR, Groenewald JZ. (2015). Fungal Planet description sheets: 320-370. *Persoonia* 34: 167-266.

Crous PW, Wingfield MJ, Le Roux JJ, Richardson DM, Strasberg D, Shivas RG, Alvarado P, Edwards J, Moreno G, Sharma R, Sonawane MS, Tan YP, Altés A, Barasubiye T, Barnes CW, Blanchette RA, Boertmann D, Bogo A, Carlavilla JR, Cheewangkoon R, Daniel R, de Beer ZW, de Jesús Yáñez-Morales M, Duong TA, Fernández-Vicente J, Geering ADW, Guest DI, Held BW, Heykoop M, Hubka V, Ismail AM, Kajale SC, Khemmuk W, Kolařík M, Kurli R, Lebeuf R, Lévesque CA, Lombard L, Magista D, Manjón JL, Marincowitz S, Mohedano JM, Novakova A, Oberlies NH, Otto EC, Paguigan ND, Pascoe IG, Perez-Butron JL, Perrone G, Rahi P, Raja HA, Rintoul T, Sanhueza RMV, Scarlett K, Shouche YS, Shuttleworth LA, Taylor PWJ, Thorn RG, Vawdrey LL, Solano-Vial R, Wong PTW, Wood AR, Zamora JC, Groenewald JZ. (2015). Fungal Planet description sheets: 371-399. *Persoonia* 35: 264-327.

Cruywagen EM, Crous PW, Roux J, Slippers B, Wingfield MJ. (2015). Fungi associated with black mould on baobab trees in southern Africa. *Antonie van Leeuwenhoek* 108: 85-95.

Cruywagen EM, Slippers B, Roux J, Wingfield MJ. (2017). Phylogenetic species recognition and hybridisation in *Lasiodiplodia*: A case study on species from baobabs. *Fungal Biology* 121(4): 420-436.

Cullis C, Kunert KJ. (2017). Unlocking the potential of orphan legumes. *Journal of Experimental Botany* 68(8): 1895-1903.

Daru B, Berger DK, van Wyk AE. (2016). Opportunities for unlocking the potential of genomics for African trees. *New Phytologist* 210: 772-778.

Davin N, Edger PP, Hefer CA, Mizrachi E, Schuetz M, Smets E, Myburg AA, Douglas CJ, Schranz ME, Lens F. (2016). Functional network analysis of genes differentially expressed during xylogenesis in soc1ful woody *Arabidopsis* plants. *The Plant Journal* 86: 376-390.

de Beer ZW, Duong TA, Wingfield MJ. (2016). The divorce of *Sporothrix* and *Ophiostoma*: solution to a problematic relationship. *Studies in Mycology* 83: 165-191.

de Beer ZW, Marincowitz S, Duong TA, Kim JJ, Rodrigues A, Wingfield MJ. (2016). *Hawksworthiomyces* gen. nov. (Ophiostomatales), illustrates the urgency for a decision on how to name novel taxa known only from environmental nucleic acid sequences (ENAS). *Fungal Biology* 120: 1323-1340.

de Errasti A, de Beer ZW, Coetzee MPA, Roux J, Rajchenberg M, Wingfield MJ. (2016). Three new species of Ophiostomatales from *Nothofagus* in Patagonia. *Mycological Progress* 15: 17.

de Errasti A, de Beer ZW, Rajchenberg M, Coetzee MPA, Wingfield MJ, Roux J. (2015). *Huntiella decorticans* sp. nov. (Ceratocystidaceae) associated with dying *Nothofagus* in Patagonia. *Mycologia* 107: 512-521.

de Maayer P, Chan WY, Martin DAJ, Blom J, Venter SN, Duffy B, Cowan DA, Smits THM, Coutinho TA. (2015). Integrative conjugative elements of the ICEPan family play a potential role in *Pantoea ananatis* ecological diversification and antibiosis. *Frontiers in Microbiology* 6: 576.

Denman S, Barrett G, Kirk SA, McDonald JE, Coetzee MPA. (2017). Identification of *Armillaria* species on declined oak in Britain: implications for oak health. *Forestry* 90, 148-161.

Doilom M, Shuttleworth LA, Roux J, Chukeatirote E, Hyde KD. (2015). Botryosphaeriaceae associated with *Tectona grandis* (teak) in Northern Thailand. *Phytotaxa* 233: 1-26.

Drenkhan R, Tomešová-Haataja V, Fraser S, Bradshaw RE, Vahalík P, Mullett MS, Martín-García J, Bulman LS, Wingfield MJ, Kirisits T, Cech TL, Schmitz S, Baden R, Tubby K, Brown A, Georgieva M, Woods A, Ahumada R, Jankovský L, Thomsen IM, Adamson K, Marçais B, Vuorinen M, Tsopelas P, Koltay A, Halasz A, La Porta N, Anselmi N, Kiesnere R, Markovskaja S, Kačergius A, Papazova-Anakieva I, Risteski M, Sotirovski K, Lazarević J, Solheim H, Boroń P, Bragança H, Chira D, Musolin DL, Selikhovkin AV, Bulgakov TS, Keča N, Karadžić D, Galovic V, Pap P, Markovic M, Poljakovic Pajnik L, Vasic V, Ondrušková E, Piškur B, Sadiković D, Diez JJ, Solla A, Millberg H, Stenlid J, Angst A, Queloz V, Lehtijärvi A, Doğmuş-Lehtijärvi HT, Oskay F, Davydenko K, Meshkova V, Craig D, Woodward S, Barnes I. (2016). Global geographic distribution and host range of *Dothistroma* species: a comprehensive review. *Forest Pathology* 46: 408-442.

du Raan S, Coutinho TA, van der Waals JE. (2015). Cardinal temperature differences, determined *in vitro*, between closely related species and subspecies of pectinolytic bacteria responsible for blackleg and soft rot on potatoes. *European Journal of Plant Pathology* 144: 361-369.

Duong TA, de Beer ZW, Wingfield BD, Eckhardt LG, Wingfield MJ. (2015). Microsatellite and mating type markers reveal unexpected patterns of genetic diversity in the pine root-infecting fungus *Grosmannia alacris*. *Plant Pathology* 64: 235-242.

Duong TA, de Beer ZW, Wingfield BD, Wingfield MJ. (2016). Mating type markers reveal high levels of heterothallism in *Leptographium sensu lato*. *Fungal Biology* 120: 538-546.

Faulkner KT, Hurley B, Robertson MP, Rouget M, Wilson JRU. (2017). The balance of trade in alien species between South Africa and the rest of Africa. *Bothalia* 47: a2157.

Fitza KNE, Tabata M, Kanzaki N, Kimura K, Garnas J, Slippers B. (2016). Host specificity and diversity of *Amylostereum* associated with Japanese siricids. *Fungal Ecology* 24: 76-81.

Fourie A, Wingfield MJ, Wingfield BD, Barnes I. (2015). Molecular markers delimit cryptic species in *Ceratocystis sensu stricto*. *Mycological Progress* 14: 1-18.

Fourie A, Wingfield MJ, Wingfield BD, Thu PQ, Barnes I. (2016). A possible centre of diversity in South East Asia for the tree pathogen, *Ceratocystis manginecans*. *Infection, Genetics and Evolution* 41, 73-83.

Foyer CH, Lam HM, Nguyen HT, Siddique KHM, Varshney RK, Colmer TD, Cowling W, Bramley H, Mori TA, Hodgson JM, Cooper JW, Miller AJ, Kunert K, Vorster J, Cullis C, Ozga JA, Wahlqvist ML, Liang Y, Shou H, Shi K, Yu J, Fodor N, Kaiser BN, Wong FL, Valliyodan B, Considine MJ. (2016). Neglecting legumes has compromised human health and sustainable food production. *Nature Plants* 2: 16112.

Fraser S, Martin-Garcia J, Perry A, Kabir MS, Owen T, Solla A, Brown AV, Bulman L, Barnes I, Hale MD, Vasconcelos MW, Lewis K, Doğmuş-Lehtijarvi HT, Markovskaja S, Woodward S, Bradshaw RE. (2016). A review of Pinaceae resistance mechanisms against needle and shoot pathogens with a focus on the *Dothistroma-Pinus* interaction. *Forest Pathology* 46: 453-471.

Fru FF, Steenkamp ET, Wingfield JW, Santana QC, Roux J. (2017). Unique clones of the pitch canker fungus, *Fusarium circinatum*, associated with a new disease outbreak in South Africa. *European Journal of Plant Pathology* 148(1): 97-107.

Garnas J, Auger-Rozenberg M, Roques A, Bertelsmeier C, Wingfield MJ, Saccaggi DL, Roy HE, Slippers B. (2016). Complex patterns of global spread in invasive insects: Eco-evolutionary and management consequences. *Biological Invasions* 18: 935-952.

Gordon TR, Swett CL, Wingfield MJ. (2015). Management of *Fusarium* diseases affecting conifers. *Crop Protection* 73: 28-39.

Gorshkov V, Kwenda S, Petrova O, Osipova E, Gogolev Y, Moleleki LN. (2017). Global Gene Expression Analysis of Cross-Protected Phenotype of *Pectobacterium atrosepticum*. *PLoS ONE* 12.

Govinden-Soulange J, Lobine D, Frederich M, Kodj H, Coetzee MPA, Ranghoo-Sanmukhiya VM. (2016). Metabolomic and molecular signatures of Mascarene Aloes using a multidisciplinary approach. *South African Journal of Botany* 108: 137-143.

Greyling I, Wingfield MJ, Coetzee MP, Marincowitz S, Roux J. (2016). The *Eucalyptus* shoot and leaf pathogen *Teratosphaeria destructans* recorded in South Africa. *Southern Forests* 78: 123-129.

Haavik LJ, Dodds KJ, Allison JD. (2015). Do native insects and associated fungi limit non-native woodwasp, *Sirex noctilio*, survival in a newly invaded environment? *PLoS ONE* 10: e0138516.

Hajek AE, Hurley BP, Kenis M, Garnas J, Bush SJ, Wingfield MJ, Lenteren JCV, Cock MJW. (2016). Exotic biological control agents: a solution or contribution to arthropod invasions? *Biological Invasions* 18: 953-969.

Harrison Jdu G, Wingfield MJ. (2016). A taxonomic review of white grubs and leaf chafers (Coleoptera: Scarabaeidae: Melolonthinae) recorded from forestry and agricultural crops in Sub-Saharan

Africa. Bulletin of Entomological Research 2: 141-153.

Hefer CA, Mizrachi E, Myburg AA, Douglas CJ, Mansfield SD. (2015). Comparative interrogation of the developing xylem transcriptomes of two wood-forming species: *Populus trichocarpa* and *Eucalyptus grandis. New Phytologist* 204: 1391-1405.

Hernández-Restrepo M, Groenewald JZ, Crous PW. (2015). *Neocordana* gen. nov., the causal organism of Cordana leaf spot on banana. *Phyotaxa* 205: 229-238.

Hernández-Restrepo M, Schumacher RK, Wingfield MJ, Ahmad I, Cai L, Duong TA, Edwards J, Gené J, Groenewald JZ, Jabeen S, Khalid AN, Lombard L, Madrid H, Marin-Felix Y, Marincowitz S, Miller AN, Rajeshkumar KC, Rashid A, Sarwar S, Stchigel AM, Taylor PWJ, Zhou N, Crous PW. (2016). Fungal Systematics and Evolution: FUSE 2. *Sydowia* 68: 193-230.

Herron DA, Wingfield MJ, Wingfield BD, Rodas CA, Marincowitz S, Steenkamp ET. (2015). Novel taxa in the *Fusarium fujikuroi* species complex from *Pinus* spp. *Studies in Mycology* 80: 131-150.

Hill MP, Bertelsmeier C, Clusella-Trullas S, Garnas J, Robertson MP, Terblanche JS. (2016). Predicted decrease in global climate suitability masks regional complexity of invasive fruit fly species response to climate change. *Biological Invasions* 18: 1105-1119.

Hudson CJ, Freeman JS, Myburg AA, Potts BM, Vaillancourt RE. (2015). Genomic patterns of species diversity and divergence in *Eucalyptus*. *New Phytologist* 204: 1378-1390.

Hui C, Richardson DM, Landi P, Minoarivelo HO, Garnas J, Roy HE. (2016). Defining invasiveness and invasibility in ecological networks. *Biological Invasions* 18: 971-983.

Human MP, Barnes I, Craven M, Crampton BG. (2016). Lack of population structure and mixed reproduction modes in *Exserohilum turcicum* from South Africa. *Phytopathology* 106: 1386-1392.

Human ZR, Moon K, Bae M, de Beer ZW, Cha S, Wingfield MJ, Slippers B, Oh DC, Venter SN. (2016). Antifungal *Streptomyces* spp. associated with the infructescences of *Protea* spp. in South Africa. *Frontiers in Microbiology* 7: 1657.

Human ZR, Slippers B, de Beer ZW, Wingfield MJ, Venter SN. (2017). Antifungal actinomycetes associated with the pine bark beetle, *Orthotomicus erosus*, in South Africa. *South African Journal of Science* 113: 2016-0215.

Hurley BP, Garnas J, Cooperband MF. (2015). Assessing trap and lure effectiveness for the monitoring of *Sirex noctilio. Agricultural and Forest Entomology* 17: 64-70.

Hurley BP, Garnas J, Wingfield MJ, Branco M, Richardson DM, Slippers B. (2016). Increasing numbers and intercontinental spread of invasive insects on eucalypts. *Biological Invasions* 18: 921-933.

Hussey SG, Mizrachi E, Groover A, Berger DK, Myburg AA. (2015). Genome-wide mapping of histone H3 lysine 4 trimethylation in *Eucalyptus grandis* developing xylem. *BMC Plant Biology* 15: 117.

Jami F, Slippers B, Wingfield MJ, Loots MT, Gryzenhout M. (2015). Temporal and spatial variation of Botryosphaeriaceae associated with *Acacia karroo* in South Africa. *Fungal Ecology* 15: 51-62.

Janousek J, Wingfield MJ, Marmolejo Monsivais JG, Jankovský L, Stauffer C, Konečný A, Barnes I. (2016). Genetic analyses suggest separate introductions of the pine pathogen *Lecanorticta acicola* into Europe. *Phytopathology* 106: 1413-1425.

Jimu L, Chen SF, Wingfield MJ, Mwenje E, Roux J. (2016). The *Eucalyptus* stem canker pathogen *Teratosphaeria gauchensis* represents distinct genetic groups in Africa and South America. *Forest Pathology* 46(3): 229-239.

Jimu L, Chen SF, Wingfield MJ, Mwenje E, Roux J. (2016). Three genetic groups of the *Eucalyptus* stem canker pathogen *Teratosphaeria zuluensis* introduced into Africa from an unknown source. *Antonie van Leeuwenhoek* 109: 21-33.

Jimu L, Kemler M, Wingfield MJ, Mwenje E, Roux J. (2016). The *Eucalyptus* stem canker pathogen *Teratosphaeria zuluensis* detected in seed samples. *Forestry* 89: 316-324.

Jimu L, Wingfield MJ, Mwenje E, Roux J. (2015). Diseases on *Eucalyptus* species in Zimbabwean plantations and woodlots. *Southern Forests* 77: 221-230.

Kandasamy D, Gershenzon J, Hammerbacher A. (2016). Volatile organic compounds emitted by fungal associates of conifer bark beetles and their potential in bark beetle control. *Journal of Chemical Ecology* 42(9): 952-969.

Kandolo SD, Thompson AH, Calitz FJ, Laurie SM, Truter M, van Der Waals JE, Aveling TAS. (2016). Field tolerance of selected varieties to and fungicide efficacy against *Alternaria* blight of sweet potato. *African Crop Science Journal* 24: 331-339.

Kanzaki N, Tanaka SE, Fitza KNE, Kosaka H, Slippers B, Kimura K, Tsuchiya S, Tabata M. (2016). *Deladenus nitobei* n. sp. (Tylenchomorpha: Allantonematidae) isolated from *Sirex nitobei* (Hymenoptera: Siricidae) from Aomori, Japan, a new member of the siricidicola superspecies. *Nematology* 18: 1199-1217.

Kanzi AM, Wingfield BD, Steenkamp ET, Naidoo S, van der Merwe NA. (2016). Intron derived size polymorphism in the mitochondrial genomes of closely related *Chrysoporthe* species. *PLOS ONE* 11: e0156104.

Kenis M, Hurley BP, Hajek A, Cock MJW. (2017). Classical biological control of insect pests of trees: facts and figures. *Biological Invasions* 1-17.

Klein H, Hoffmann JH, Neser S, Dittrich-Schroder G. (2015). Evidence that *Quadrastichodella nova* (Hymenoptera: Eulophidae) is the only gall inducer among four hymenopteran species associated with seed capsules of *Eucalyptus camaldulensis* (Myrtaceae) in South Africa. *African Entomology* 23: 207-223.

Kleynhans J, Pietersen G. (2016). Comparison of multiple viral population characterization methods on a candidate cross-protection Citrus tristeza virus (CTV) source. *Journal of Virological Methods* 237: 92-100.

Kunert K, Vorster BJ, Fenta BA, Kibido T, Dionisio G and Foyer CH. (2016). Soybean roots and nodules: A drought stress target. *Frontiers in Plant Science* 7: 1015.

Kunert KJ, van Wyk SG, Cullis CA, Vorster BJ, Foyer CH. (2015). Potential use of phytocystatins in crop improvement, with a particular focus on legumes. *Journal of Experimental Botany* 66: 3559-3570.

Kwenda S, Birch PRJ, Moleleki LN. (2016). Genome-wide identification of potato long intergenic noncoding RNAs responsive to *Pectobacterium carotovorum* subspecies *brasiliense* infection. *BMC Genomics* 17: 614.

Kwenda S, Gorshkov V, Ramesh AM, Naidoo S, Rubagotti E, Birch PRJ, Moleleki LN. (2016). Discovery and profiling of small RNAs responsive to stress conditions in the plant pathogen *Pectobacterium atrosepticum*. *BMC Genomics* 17: 47.

Kwenda S, Motlolometsi TV, Birch PRJ, Moleleki LN. (2016). RNA-seq profiling reveals defense responses in a tolerant potato cultivar to stem infection by *Pectobacterium carotovorum* ssp. *brasiliense*. *Frontiers in Plant Science* 7: 1905.

Lee DH, Roux J, Wingfield BD, Barnes I, Mostert L, Wingfield MJ. (2016). The genetic landscape of *Ceratocystis albifundus* populations in South Africa reveals a recent fungal introduction event. *Fungal Biology* 120: 690-700.

Lee DH, Roux J, Wingfield BD, Barnes I, Wingfield MJ. (2016). New host range and distribution of *Ceratocystis pirilliformis* in South Africa. *European Journal of Plant Pathology* 146: 483-496.

Lee DH, Roux J, Wingfield BD, Wingfield MJ. (2015). Variation in growth rates and aggressiveness of naturally occurring self-fertile and self-sterile isolates of the wilt pathogen *Ceratocystis albifundus*. *Plant Pathology* 64: 1103-1109.

Li GQ, Arnold RJ, Liu FF, Li JQ, Chen SF. (2015). Identification and pathogenicity of *Lasiodiplodia* species from *Eucalyptus urophylla* x *grandis, Polyscias balfouriana* and *Bougainvillea spectabilis* in southern China. *Journal of Phytopathology* 163: 956-967.

Li Q, Yu H, Cao PB, Fawal N, Mathe C, Azar S, Wang H, Myburg AA, Grima-Pettenati J, Marque C, Tiulieres C, Dunand C. (2015). Explosive tandem and segmental duplications of multigenic families in *Eucalyptus grandis*. *Genome Biology and Evolution* 7: 1068-1081.

Lin H, Pietersen G, Han C, Read DA, Lou B, Gupta G, Civerolo EL. (2015). Complete genome sequence of "*Candidatus* Liberibacter africanus," a bacterium associated with Citrus Huanglongbing. *Genome Announcements* 3: e00733-00715.

Linnakoski R, Jankowiak R, Villari C, Kirisits T, Solheim H, de Beer ZW, Wingfield MJ. (2016). The *Ophiostoma clavatum* species complex: a newly defined group in the Ophiostomatales including three novel taxa. *Antonie van Leeuwenhoek* 109: 987-1018.

Linnakoski R, Mahilainen S, Harrington A, Vanhanen H, Eriksson M, Mehtätalo L, Pappinen A, Wingfield MJ. (2016). Seasonal succession of fungi associated with *Ips typographus* beetles and their phoretic mites in an outbreak region of Finland. *PLOS ONE* 11: e0155622.

Liu FF, Mbenoun M, Barnes I, Roux J, Wingfield MJ, Li GQ, Li JQ, Chen SF. (2015). New *Ceratocystis* species from *Eucalyptus* and *Cunninghamia* in South China. *Antonie van Leeuwenhoek* 107: 1451–1473.

Liu QL, Li GQ, Li JQ, Chen SF. (2016). *Botrytis eucalypti*, a novel species isolated from diseased *Eucalyptus* seedlings in South China. *Mycological Progress* 15: 1057.

Lombard L, Chen SF, Mou X, Zhou XD, Crous PW, Wingfield MJ. (2015). New species, hyper-diversity and potential importance of *Calonectria* spp. from *Eucalyptus* in South China. *Studies in Mycology* 80: 151-188.

Lombard L, van der Merwe NA, Groenewald JZ, Crous PW. (2015). Generic concepts in Nectriaceae. *Studies in Mycology* 80: 189-245.

Lombardero MJ, Ayres MP, Krivak-Tetley FE, Fitza KNE. (2016). Population biology of the European woodwasp, *Sirex noctilio*, in Galicia, Spain. *Bulletin of Entomological Research* 106: 569-580.

Machingambi NM, Dreyer LL, Oberlander KC, Roux J, Roets F. (2015). Death of endemic *Virgilia oroboides* trees in South Africa caused by *Diaporthe virgiliae* sp. nov. *Plant Pathology* 64: 1149-1156.

Machua J, Jimu L, Njuguna J, Wingfield MJ, Mwenje E, Roux J. (2016). First report of *Teratosphaeria gauchensis* causing stem canker of *Eucalyptus* in Kenya. *Forest Pathology* 46: 168-170.

Magadlela A, Vardien W, Kleinert A, Steenkamp ET, Valentine AJ. (2016). Variable P supply affects N metabolism in a legume tree, *Virgilia divaricata*, from nutrient-poor Mediterranean-type ecosystems. *Functional Plant Biology* 43: 287-297.

Maier W, McTaggart AR, Roux J, Wingfield MJ. (2015). *Phakopsora myrtacearum* sp. nov., a newly described rust (Pucciniales) on eucalypts in eastern and southern Africa. *Plant Pathology* 65: 189-195.

Mandiriza-Mukwirimba G, Kritzinger Q, Aveling TAS. (2016). A survey of brassica vegetable smallholder farmers in the Gauteng and Limpopo provinces of South Africa. *Journal of Agriculture and Rural Development in the Tropics and Subtropics* 117: 35-44.

Mangwanda R, Myburg AA, Naidoo S. (2015). Transcriptome and hormone profiling reveals *Eucalyptus grandis* defence responses against *Chrysoporthe austroafricana*. *BMC Genomics* 16: 319.

Mangwanda R, Zwart Z, van der Merwe NA, Moleleki L, Berger DK, Myburg AA, Naidoo S. (2016). Localization and transcriptional responses of *Chrysoporthe austroafricana* in *Eucalyptus grandis* identify putative pathogenicity factors. *Frontiers in Microbiology* 7: 1953.

Mangwenda E, Kabengele JBK, Truter M, Aveling TAS. (2015). First report of white rust of rocket (*Eruca sativa*) caused by *Albugo candida* in South Africa. *Plant Disease* 99: 290.

Maphosa MN, Steenkamp ET, Wingfield BD, (2016). Genome-based selection and characterization of *Fusarium circinatum*-specific sequences. *G3: Genes|Genomes|Genetics* 6: 631-639.

Marincowitz S, Coetzee MPA, Wilken PM, Wingfield BD, Wingfield MJ. (2015). Phylogenetic placement of Itajahya: An unusual Jacaranda fungal associate. *IMA Fungus* 6: 257-262.

Marincowitz S, Duong TA, de Beer ZW, Wingfield MJ. (2015). *Cornuvesica*: A little known mycophilic genus with a unique biology and unexpected new species. *Fungal Biology* 119: 615-630.

Marsberg A, Kemler M, Jami F, Nagel JH, Postma-Smidt A, Naidoo S, Wingfield MJ, Crous PW, Spatafora J, Hesse CN, Robbertse B, Slippers B. (2017). *Botryosphaeria dothidea*: A latent pathogen of global importance to woody plant health. *Molecular Plant Pathology* 18(4): 477-488.

Marzano M, Dandy N, Papazova-Anakieva I, Avtzis D, Connolly T, Eschen R, Glavendekić M, Hurley BP, Lindelöw Å, Matošević D, Tomov R, Vettraino AM. (2016). Assessing awareness of tree pests and pathogens amongst tree professionals: A pan-European perspective. *Forest Policy and Economics* 70: 164-171.

Masangwa J, Kritzinger Q, Aveling TAS. (2017). Germination and seedling emergence responses of common bean and cowpea to plant extract seed treatments. *The Journal of Agricultural Science* 155: 18-31.

Mausse-Sitoe SND, Chen SF, Wingfield MJ, Roux J. (2016). Diseases of eucalypts in the central and northern provinces of Mozambique. *Southern Forests* 78: 169-183.

Mausse-Sitoe SND, Rodas C, Wingfield MJ, Chen SF, Roux J. (2016). Endophytic Cryphonectriaceae on native Myrtales: possible origin of Chrysoporthe canker on plantation-grown *Eucalyptus*. *Fungal Biology* 120: 827-835.

May TW, de Beer ZW, Crous PW, Hawksworth DL, Liu X, Norvell LL, Pennycook SR, Redhead SA, Seifert KA. (2016). (362–363) Proposals to amend the Code to modify its governance with respect to names of organisms treated as fungi. *Taxon* 65: 918-920.

Mbenoun M, Wingfield BD, Nyassé S, Dibog L, Mfegue CV, ten Hoopen GM, Petchayo Tigang S, Nsouga Amougou F, Begoude Boyogueno AD, Wingfield MJ, Roux J. (2016). Diversity and pathogenicity of the Ceratocystidaceae associated with cacao agroforests in Cameroon. *Plant Pathology* 65: 64-78.

Mbenoun M, Wingfield MJ, Letsoalo T, Bihon W, Wingfield BD, Roux J. (2015). Independent origins and incipient speciation among host-associated populations of *Thielaviopsis ethacetica* in Cameroon. *Fungal Biology* 119: 957-972.

McTaggart AR, Doungsa-ard C, Wingfield MJ, Roux J. (2015). *Uromycladium acaciae*, the cause of a sudden, severe disease epidemic on *Acacia mearnsii* in South Africa. *Australasian Plant Pathology* 44: 637-645.

McTaggart AR, Roux J, Granados GM, Gafur A, Tarrigan M, Santhakumar P, Wingfield MJ. (2016). Rust (*Puccinia psidii*) recorded in Indonesia poses a threat to forests and forestry in South-East Asia. *Australasian Plant Pathology* 45: 83-89.

McTaggart AR, Shivas RG, Boekhout T, Oberwinkler F, Vánky K, Pennycook SR, Begerow D. (2016). *Mycosarcoma* (Ustilaginaceae), a resurrected generic name for corn smut (*Ustilago maydis*) and its close relatives with hypertrophied, tubular sori. *IMA Fungus* 7: 309-315.

McTaggart AR, Shivas RG, van der Nest MA, Roux J, Wingfield BD, Wingfield MJ. (2016). Host jumps shaped the diversity of extant rust fungi (Pucciniales). *New Phytologist* 209: 1149-1158.

McTaggart AR, van der Nest MA, Steenkamp ET, Roux J, Slippers B, Shuey LS, Wingfield MJ, Drenth A. (2016). Fungal genomics challenges the dogma of name-based biosecurity. *PLoS Pathogens* 12: e1005475.

Mehl JWM, Slippers B, Roux J, Wingfield MJ. (2017). Overlap of latent pathogens in the Botryosphaeriaceae on a native and agricultural host. *Fungal Biology* 121: 405-419.

Mewalal R, Mizrachi E, Coetzee B, Mansfield SD, Myburg AA. (2016). The Arabidopsis domain of unknown function 1218 (DUF1218) containing proteins, modifying wall lignin-1 and 2 (At1g31720/MWL-1 and At4g19370/MWL-2) function redundantly to alter secondary cell wall lignin content. *PLOS ONE* 11: e0150254.

Meyer FE, Shuey LS, Ramsuchit S, Mamni T, Berger DK, van den Berg N, Myburg AA, Naidoo S. (2016). Dual RNA-sequencing of *Eucalyptus nitens* during *Phytophthora cinnamomi* challenge reveals pathogen and host factors influencing compatibility. *Frontiers in Plant Science* 7: 191.

Meyer J, Murray SL, Berger DK. (2016). Signals that stop the rot: Regulation of secondary metabolite defences in cereals. *Physiological and Molecular Plant Pathology* 94: 156-166.

Misse AC, Barnes I, Roets F, Mbenoun M, Wingfield MJ, Roux J. (2017). Ecology and population structure of a tree wound-infecting fungus in a native South African forest environment. *Fungal Biology* 121: 69-81.

Mizrachi E, Myburg AA. (2016). Systems genetics of wood formation. *Current Opinion in Plant Biology* 30: 94-100.

Mizrachi E, Verbeke L, Christie N, Fierro AC, Mansfield SD, Davis MF, Gjersing E, Tuskan GA, Van Montagu M, van de Peer Y, Marchal K, Myburg AA. (2017). Network-based integration of systems genetics data reveals pathways associated with lignocellulosic biomass accumulation and processing. *PNAS*.

Moleleki LN, Pretorius RG, Tanui CK, Mosina G, Theron J. (2016). A quorum sensing-defective mutant of *Pectobacterium carotovorum* subsp. *brasiliense* 1692 is attenuated in virulence and unable to occlude xylem tissue of susceptible potato plant stems. *Molecular Plant Pathology* 18: 32-44.

Moloto V, Goszczynska T, du Toit L, Coutinho TA. (2016). A new pathovar of *Pseudomonas syringae*, pathovar *allii*, isolated from onion plants exhibiting symptoms of blight. *European Journal of Plant Pathology* 146: 591-603.

Mongae A, Moleleki L. (2015). The effect of β-aminobutyric acid (BABA) on root knot nematode and soft rot pathogen disease complexes in *Solanum tuberosum* plants. *European Journal of Plant Pathology* 142: 117-124.

Muller MF, Barnes I, Kunene NT, Crampton BG, Bluhm B, Phillips S, Olivier NA, Berger DK. (2016). *Cercospora zeina* from maize in South Africa exhibits high genetic diversity and lack of regional population differentiation. *Phytopathology* 106: 1194-1205.

Mullett MS, Brown AV, Barnes I. (2015). Population structure and reproductive mode of *Dothistroma septosporum* in the Brittany peninsula of France. *European Journal of Plant Pathology* 143: 261-275.

Musvuugwa T, de Beer ZW, Duong T, Dreyer L, Oberlander K, Roets F. (2015). New species of Ophiostomatales from Scolytinae and Platypodinae beetles in the Cape Floristic Region, including the discovery of the sexual state of *Raffaelea*. *Antonie van Leeuwenhoek* 108: 933-950.

Musvuugwa T, de Beer ZW, Duong TA, Dreyer LL, Oberlander K, Roets F. (2016). Wounds on *Rapanea melanophloeos* provide habitat for a large diversity of Ophiostomatales including four new species. *Antonie van Leeuwenhoek* 109: 877-894.

Nadel RL, Wingfield MJ, Scholes MC, Garnas JR, Lawson SA, Slippers B. (2015). Population dynamics of *Thaumastocoris peregrinus* in *Eucalyptus* plantations of South Africa. *Journal of Pest Science* 88: 97-106.

Nagel JH, Slippers B, Wingfield MJ, Gryzenhout M. (2015). Multiple *Phytophthora* species associated with a single riparian ecosystem in South Africa. *Mycologia* 107: 915–925.

Naidoo SIM, Laurie SM, Odeny DA, Vorster BJ, Mphela WM, Greyling MM, Crampton BG. (2016). Genetic analysis of yield and flesh colour in sweetpotato. *African Crop Science Journal* 24: 61-73.

Ndunguru J, Ascencio-Ibáñez JT, Aveling TAS, Tohme J, Thompson G, Legg JP, Plata G, Sseruwagi P, Doyle CD, De León L, Hanley-Bowdoin L. (2016). Two novel DNAs that enhance symptoms and overcome CMD2 resistance to cassava mosaic disease. *Journal of Virology* 90: 4160-4173.

Ndunguru J, de Leon L, Doyle CDm Sseruwagi, Plata G, Legg JP, Thompson G, Tohme J, Aveling TAS Ascensio-Ibanez JT, Hanley-Bowdoin L. (2016). Two novel DNAs that enhance symptoms and overcome CMD2 resistance to cassava mosaic disease. *Journal of Virology* 90: 4160-4173

Nemesio-Gorriz M, Hammerbacher A, Ihrmark K, Källman T, Olsen A, Lascoux M, Stenlid J, Gershenzon J, Elfstrand M. (2016). Different alleles of a gene encoding leucoanthocyanidin reductase (PaLAR3) influence resistance against the fungus *Heterobasidion parviporum* in *Picea abies*. *Plant Physiology* 171(4): 2671-2681.

Nesamari R, Coutinho TA, Roux J. (2017). Investigations into *Encephalartos* insect pests and diseases in South Africa identifies *Phytophthora cinnamomi* as a pathogen of the Modjadji cycad. *Plant Pathology* 66: 612-622.

Nesamari R, Millar IM, Coutinho TA, Roux J. (2015). South African cycads at risk: *Aulacaspis yasumatsui* (Hemiptera: Coccoidea: Diaspididae) in South Africa. *African Entomology* 23: 198-206.

New SA, van Heerden SW, Pietersen G, Esterhuizen LL. (2016). First report of a Turnip Yellows virus in association with the Brassica Stunting Disorder in South Africa. *Plant Disease* 100: 2341.

Nüsslein K, Parkash Dhankher O, Xing B, Smith-Doerr L, Sacco T, Maathuis F, Pareek Jawaharlal A, Vara Prasad PV, Botha A-M, Foyer CH, Kunert K, Cullis C, Dumont MG, Chen B and Zhejiang LL. (2016). Project management: Food security needs social-science input. Nature 535(7610): 37.

Oates CN, Denby KJ, Myburg AA, Slippers B, Naidoo S. (2016). Insect gallers and their plant hosts: From omics data to systems biology. *International Journal of Molecular Sciences* 17: 1891.

Oates CN, Külheim C, Myburg AA, Slippers B, Naidoo S. (2015). The transcriptome and terpene profile of *Eucalyptus grandis* reveals mechanisms of defence against the insect pest, *Leptocybe invasa*. *Plant & Cell Physiology* 56: 1418-1428.

Oelofse D, Gazendam I, Veale A, Djami-Tchatchou A, Berger D, Dubery I. (2016). Functional characterization of a defense-related class-III chitinase promoter from *Lupinus albus*, active in legume and monocot tissues. *European Journal of Plant Pathology* 146: 923-936.

Ohse B, Hammerbacher A, Seele C, Meldau S, Reichelt M, Ortmann S, Wirth C. (2016). Salivary cues: Simulated roe deer browsing induces systemic changes in phytohormones and defense chemistry in wild-grown maple and beech saplings. *Functional Ecology* 31(2): 340-349.

Olivier-Espejel S, Hurley BP, Garnas J. (2017). Assessment of beetle diversity, community composition and potential threats to forestry using kairomone-baited traps. *Bulletin of Entomological Research* 107: 106-117.

Oloka BM, Lamo J, Rubaihayo P, Gibson P and Vorster J. (2015) The use of multiplexed simple sequence repeat (SSR) markers for analysis of genetic diversity in African rice genotypes. *African Journal of Biotechnology* 14: 1533-1542.

Onkendi EM, Ramesh AM, Kwenda S, Naidoo S, Moleleki LN. (2016). Draft genome sequence of a virulent *Pectobacterium carotovorum* subsp. *brasiliense* isolate causing soft rot of cucumber. *Genome Announcements* 4: e01530-15.

Osorio JA, Crous CJ, de Beer ZW, Wingfield MJ, Roux J. (2017). Endophytic Botryosphaeriaceae, including five new species, associated with mangrove trees in South Africa. *Fungal Biology* 121(4): 361-393.

Osorio JA, Crous CJ, Wingfield MJ, de Beer ZW, Roux J. (2017). An assessment of mangrove diseases and pests in South Africa. *Forestry* 90(3): 343-358.

Osorio JA, de Beer ZW, Wingfield MJ, Roux J. (2016). Ophiostomatoid fungi associated with mangroves in South Africa, including *Ophiostoma palustre* sp. nov. *Antonie van Leeuwenhoek* 109: 1555-1571.

Osorio JA, Wingfield MJ, de Beer ZW, Roux J. (2015). *Pseudocercospora mapelanensis* sp. nov., associated with a fruit and leaf disease of *Barringtonia racemosa* in South Africa. *Australasian Plant Pathology* 44: 349-359.

Osorio JA, Wingfield MJ, Roux J. (2016). A review of factors associated with decline and death of mangroves, with particular reference to fungal pathogens. *South African Journal of Botany* 103: 295-301.

Palmer M, de Maayer P, Poulsen M, Steenkamp ET, van Zyl E, Coutinho TA, Venter SN. (2016). Draft genome sequences of *Pantoea agglomerans* and *Pantoea vagans* isolates associated with termites. *Standards in Genomic Sciences* 11: 23.

Palmer M, Steenkamp ET, Coetzee MPA, Chan WY, van Zyl E, de Maayer P, Coutinho TA, Blom J, Smits THM, Duffy B, Venter SN. (2017). Phylogenomic resolution of the bacterial genus *Pantoea* and its relationship with *Erwinia* and *Tatumella*. *Antonie van Leeuwenhoek*.

Pavlic-Zupanc D, Piskur B, Slippers B, Wingfield MJ, Jurc D. (2015). Molecular and morphological characterization of *Dothiorella* species associated with dieback of *Ostrya carpinifolia* in Slovenia and Italy. *Phytopathologia Mediterranea* 54: 222-231.

Payn T, Silva LN, Rodriguez L, Orazio C, Liu S, Kollert W, Kimberley M, Freer-Smith P, Camus JM, Wingfield MJ. (2015). Changes in planted forests and future global implications. *Forest Ecology and Management* 352: 57-67.

Pillay P, Kunert KJ, van Wyk S, Makgopa ME, Cullis CA, Vorster BJ. (2016). Agroinfiltration contributes to VP1 recombinant protein degradation. *Bioengineered* 7: 459-477.

Pinard DS, Mizrachi E, Hefer C, Kersting AR, Joubert F, Douglas C, Mansfield SD, Myburg AA. (2015). Comparative analysis of plant carbohydrate active enZymes and their role in xylogenesis. *BMC Genomics* 16: 402.

Pratt RB, MacKinnon ED, Venturas MD, Crous CJ, Jacobsen AL. (2015). Root resistance to cavitation is accurately measured using a centrifuge technique. *Tree Physiology* 35: 185-196.

Quain MD, Makgopa ME, Cooper JW, Kunert KJ and Foyer, CH. (2015). Ectopic phytocystatin expression increases nodule numbers and influences the responses of soybean (*Glycine max*) to nitrogen deficiency. *Phytochemistry* 112: 179-187.

Ramusi TM, van Der Waals JE, Labuschagne N, Aveling TAS. (2017). Evaluation of mefenoxam and fludioxonil for control of *Rhizoctonia solani, Pythium ultimum* and *Fusarium solani* on cowpea. *South African Journal of Plant and Soil* 34: 27-33.

Read DA, Pietersen G. (2015). Genotypic diversity of Citrus tristeza virus within red grapefruit, in a field trial site in South Africa. *European Journal of Plant Pathology* 142: 531-545.

Read DA, Pietersen G. (2016). PCR bias associated with conserved primer binding sites, used to determine genotype diversity within Citrus tristeza virus populations. *Journal of Virological Methods* 237: 107-113.

Reblova M, Ju YM, Judith C, Maharachchikumbura SSN, Pang KL, Petrini LE, Raja HA, Romreo AI, Shearer C, Senanayake IC, Voglmayr H, Weir BS, Jones EBG, Jaklitsch W, Jayawardena R, Miller AN, Rossman AY, Seifert KA, Crous PW, Hawksworth DL, Abdel-Wahab MA, Cannon PF, Daranagama DA, de Beer ZW, Huang SK, Hyde KD, Wijayawarden NN. (2016). Recommendations for competing sexual-asexually typified generic names in Sordariomycetes (except Diaporthales, Hypocreales, and Magnaporthales). *IMA Fungus* 7: 131-153.

Reeksting B, van den Berg N. (2016). Transcriptome responses of avocado (*Persea americana*) to multiple stresses: flooding and *Phytophthora cinnamomi*. *BMC Plant Biology* 16: 205.

Reitmann A, Berger DK, van den Berg N. (2017). Putative pathogenicity genes of *Phytophthora cinnamomi* identified via RNA-Seq analysis of pre-infection structures. *European Journal of Plant Pathology* 147: 211-228.

Riess K, Bauer R, Kellner R, Kemler M, Piatek M, Vánky K, Begerow D. (2015). Identification of a new order of root-colonising fungi in the Entorrhizomycota: Talbotiomycetales ord. nov. on eudicotyledons. *IMA Fungus* 6: 129-133.

Roberts R, Pietersen G. (2016). A novel subspecies of '*Candidatus* Liberibacter africanus' found on native *Teclea gerrardii* (Family: Rutaceae) from South Africa. *Antonie van Leeuwenhoek* 110(3): 437-444.

Roberts R, Steenkamp ET, Pietersen G. (2015). Three novel lineages of '*Candidatus* Liberibacter africanus' associated with native rutaceous hosts of *Trioza erytreae* in South Africa. *International Journal of Systematic and Evolutionary Microbiology* 65: 723-731.

Rodas CA, Roux J, Maier W, Granados GM, Bolaños MD, McTaggart AR, Wingfield MJ. (2015). First report of *Puccinia psidii* on *Corymbia citriodora* and *Eucalyptus* in Colombia. *Forest Pathology* 45: 534-536.

Rodas CA, Serna R, Bolaños MD, Granados GM, Wingfield MJ, Hurley BP. (2015). Biology, incidence and host susceptibility of *Pineus boerneri* (Hemiptera: Adelgidae) in Colombian pine plantations. *Southern Forests* 77: 165-171.

Rodas CA, Wingfield MJ, Granados GM, Barnes I. (2016). Dothistroma needle blight: an emerging epidemic caused by *Dothistroma septosporum* in Colombia. *Plant Pathology* 65: 53-63.

Roques A, Auger-Rozenberg M, Blackburn TM, Garnas J, Pyšek P, Rabitsch W, Richardson DM, Wingfield MJ, Liebhold AM, Duncan RP. (2016). Temporal and interspecific variation in rates of spread for insect species invading Europe during the last 200 years. *Biological Invasions* 18: 907-920.

Rossman AY, Crous PW, Hyde KD, Hawksworth DL, Aptroot A, Bezerra JL, Bhat JD, Boehm E, Braun U, Boonmee S, Camporesi E, Chomnunti P, Dai DQ, D'Souza MJ, Dissanayake A, Jones EBG, Groenewald JZ, Hernández-Restrepo M, Hongsanan S, Jaklitsch WM, Jayawardena R, Jing LW, Kirk PM, Lawrey JD, Mapook A, McKenzie EHC, Monkai J, Phillips AJL, Phookamsak R, Raja HA, Seifert KA, Senanayake I, Slippers B, Suetrong S, Taylor JE, Thambugala KM, Tian Q, Tibpromma S, Wanasinge DN, Wijayawardene NN, Wikee S, Woudenberg JH, Wu HX, Yan J, Zhang Y. (2015). Recommended names for pleomorphic genera in Dothideomycetes. *IMA Fungus* 6: 507-523.

Roux J, Germishuizen I, Nadel R, Lee DJ, Wingfield MJ, Pegg GS. (2015). Risk assessment for *Puccinia psidii* becoming established in South Africa. *Plant Pathology* 64: 1326-1335.

Roux J, Granados GM, Shuey L, Barnes I, Wingfield MJ, McTaggart AR. (2016). A unique genotype of the rust pathogen, *Puccinia psidii*, on Myrtaceae in South Africa. *Australasian Plant Pathology* 45: 645-652.

Rudolph N, Aveling TAS, Labuschagne N. (2015). The effect of plant growth promoting rhizobacteria on seed germination, vigour and seedling growth of maize. *Seed Science and Technology* 43: 507-518.

Sainsbury F, Jutras PV, Vorster J, Goulet MC, Michaud D. (2016). A chimeric affinity tag for efficient expression and chromatographic purification of heterologous proteins from plants. *Frontiers in Plant Science* 7: 141.

Santana QC, Coetzee MPA, Wingfield BD, Wingfield MJ, Steenkamp ET. (2016). Nursery linked plantation outbreaks and evidence for multiple introductions of the pitch canker pathogen *Fusarium circinatum* into South Africa. *Plant Pathology* 65: 357-368.

Sapountzis P, de Verges L, Rousk K, Cilliers M, Vorster BJ, Poulsen M. (2016) Potential for nitrogen fixation in the fungus-growing termite symbiosis. *Frontiers in Microbiology* 7: 1993.

Selochnik NN, Pashenova NV, Sidorov E, Wingfield MJ, Linnakoski R. (2015). Ophiostomatoid fungi and their roles in *Quercus robur* die-back in Tellermann forest, Russia. *Silva Fennica* 49: 1328.

Shyntum D, Theron J, Moleleki L, Toth I, Venter SN, Coutinho TA. (2015). *Pantoea ananatis* utilizes a type VI secretion system for pathogenesis and bacterial competition. *Molecular Plant-Microbe Interactions* 28: 420-431.

Sibanda S, Theron J, Shyntum DY, Moleleki LN, Coutinho TA. (2016). Characterization of two LuxI/R homologs in *Pantoea ananatis* LMG 2665 T. *Canadian Journal of Microbiology* 62: 893-903.

Simmons DR, de Beer ZW, Huang YT, Bateman CC, Campbell A, Dreaden TJ, Li Y, Ploetz RC, Black A, Li HF, Chen CY, Wingfield MJ, Hulcr J. (2016). New *Raffaelea* species (Ophiostomatales) from the USA and Taiwan associated with ambrosia beetles and plant hosts. *IMA Fungus* 7: 265-273.

Siziba VI, Wingfield MJ, Sadikovic D, Mullett MS, Piskur B, Barnes I. (2016). Development of microsatellite markers for the pine needle blight pathogen, *Dothistroma pini*. *Forest Pathology* 46: 497-506.

Slippers B, Crous PW, Jami F, Groenewald JZ, Wingfield MJ. (2017). Diversity in the Botryosphaeriales: Looking back, looking forward. *Fungal Biology* 121: 307-322.

Slippers B, Hurley BP, Wingfield MJ. (2015). *Sirex* woodwasp: A model for evolving management paradigms of invasive forest pests. *Annual Review of Entomology* 60: 601-619.

Soler M, Myburg AA, Paiva JAP, Hefer CA, Savelli B, Clemente HS, Cassan-Wang H, Carocha V, Camargo ELO, Grima-Pettenati J. (2015). The *Eucalyptus grandis* R2R3-MYB transcription factor family: evidence for woody growth-related evolution and function. *New Phytologist* 206: 1364-1377.

Steenkamp ET, van Zyl E, Beukes CW, Avontuur J, Chan WY, Palmer M, Mthombeni LS, Phalane FL, Sereme TK, Venter SN. (2015). *Burkholderia kirstenboschensis* sp. nov. nodulates papilionoid legumes indigenous to South Africa. *Systematic and Applied Microbiology* 38: 545-554.

Stielow JB, Lévesque CA, Seifert KA, Meyer W, Irinyi L, Smits D, Renfurm R, Verkley GJM, Groenewald M, Chaduli D, Lomascolo A, Welti S, Lesage-Meessen L, Favel A, Al-Hatmi AMS, Damm U, Yilmaz N, Houbraken J, Lombard L, Quaedvlieg W, Binder M, Vaas LAI, Vu D, Yurkov A, Begerow D, Roehl O, Guerreiro M, Fonseca A, Samerpitak K, Van Diepeningen AD, Dolatabadi S, Moreno LF, Casaregola S, Mallet S, Jacques N, Roscini L, Egidi E, Bizet C, Garcia-Hermoso D, Martín MP, Deng S, Groenewald JZ, Boekhout T, de Beer ZW, Barnes I, Duong TA, Wingfield MJ, de Hoog GS, Crous PW, Lewis CT, Hambleton S, Moussa TAA, Al-Zahrani HS, Almaghrabi OA, Louis-Seize G, Assabgui R, McCormick W, Omer G, Dukik K, Cardinali G, Eberhardt U, de Vries M, Robert V. (2015). One fungus, which genes? Development and assessment of universal primers for potential secondary fungal DNA barcodes. *Persoonia* 35: 242-263.

Taerum SJ, Hoareau TB, Duong TA, de Beer ZW, Jankowiak R, Wingfield MJ. (2017). Putative origins of the fungus *Leptographium procerum*. *Fungal Biology* 121: 82-94.

Taerum SJ, Konečný A, de Beer ZW, Cibrian-Tovar D, Wingfield MJ. (2016). Population genetics and symbiont assemblages support different invasion scenarios for the red turpentine beetle (*Dendroctonus valens*). *Biological Journal of the Linnean Society* 118: 486-502.

Taole M, Bihon W, Wingfield BD, Wingfield MJ, Burgess TI. (2015). Multiple introductions from multiple sources: invasion patterns for an important *Eucalyptus* leaf pathogen. *Ecology and Evolution* 5: 4210-4220.

Tsopelas P, Santini A, Wingfield MJ, de Beer ZW. (2017). Canker stain: A lethal disease destroying iconic plane trees. *Plant Disease* 101(5): 645-658.

van der Linde JA, Six DL, de Beer ZW, Wingfield MJ, Roux J. (2016). Novel ophiostomatalean fungi from galleries of *Cyrtogenius africus* (Scolytinae) infesting dying *Euphorbia ingens*. *Antonie van Leeuwenhoek* 109: 589-601.

van der Nest MA, Wingfield MJ, Wilken PM, Coetzee MPA, Naidoo K, Roodt D, Sauerman E, Godlonton T, Trollip C, McTaggart AR, Steenkamp ET, Wingfield BD. (2015). Saprophytic and pathogenic fungi in the Ceratocystidaceae differ in their ability to metabolize plant-derived sucrose. *BMC Evolutionary Biology* 15: 273.

van Wyk SG, Kunert KJ, Cullis CA, Pillay P, Makgopa ME, Schluter U, Vorster BJ. (2016). The future of cystatin engineering. *Plant Science* 246: 119-127.

Vanneste K, Sterck L, Myburg AA, van de Peer Y, Mizrachi E. (2015). Horsetails are ancient polyploids: Evidence from *Equisetum giganteum*. *The Plant Cell* 27: 1567-1578.

Vardien W, Steenkamp ET, Valentine AJ. (2016). Legume nodules from nutrient-poor soils exhibit high plasticity of cellular phosphorus recycling and conservation during variable phosphorus supply. *Journal of Plant Physiology* 191: 73-81.

Vining KJ, Myburg AA, Jaiswal P, Solomon L, Wesley-Smith J, Ranik M, Naithani S, Dharmawardhana P, Amarasinghe V, Hefer CA, Alves-Ferreira M, Klocko A, Jones RC, Romanel E, Strauss SH. (2015). The floral transcriptome of *Eucalyptus grandis*. *New Phytologist* 204: 1406–1422.

Visser EA, Mangwanda R, Becker JVW, Külheim C, Foley WJ, Myburg AA, Naidoo S. (2015). Foliar terpenoid levels and corresponding gene expression are systemically and differentially induced in *Eucalyptus grandis* clonal genotypes in response to *Chrysoporthe austroafricana* challenge. *Plant Pathology* 64: 1320-1325.

Visser EA, Wegrzyn JL, Steenkamp ET, Myburg AA, Naidoo S. (2015). Combined *de novo* and genome guided assembly and annotation of the *Pinus patula* juvenile shoot transcriptome. *BMC Genomics* 16: 1057.

Vivas M, Kemler M, Slippers B. (2015). Maternal effects on tree phenotypes: considering the microbiome. *Trends in Plant Science* 20: 541-544.

Vorster J, Rasoolizadeh A, Goulet MC, Cloutier C, Sainsbury F and Michaud D. (2015) Positive selection of digestive Cys proteases in herbivorous Coleoptera. *Insect Biochemistry and Molecular Biology* 65:10-19.

Wadke N, Kandasamy D, Vogel H, Lah L, Wingfield BD, Paetz C, Wright LP, Gershenzon J, Hammerbacher A. (2016). Catechol dioxygenases catalyzing the first step in Norway spruce phenolic degradation are key virulence factors in the bark beetle-vectored fungus *Endoconidiophora polonica*. *Plant Physiology* 171: 914-931.

Weller-Stuart T, de Maayer P, Coutinho T. (2017). *Pantoea ananatis*: genomic insights into a versatile pathogen. *Molecular Plant Pathology*.

Weller-Stuart T, Toth I, de Maayer P, Coutinho T. (2017). Swimming and twitching motility are essential for attachment and virulence of *Pantoea ananatis* in onion seedlings. *Molecular Plant Pathology*.

Wilson AM, Godlonton T, van der Nest MA, Wilken PM, Wingfield MJ, Wingfield BD. (2015). Unisexual Reproduction in *Huntiella moniliformis*. *Fungal Genetics and Biology* 80: 1-9.

Wilson AM, Wilken PM, van der Nest MA, Steenkamp ET, Wingfield MJ, Wingfield BD. (2015). Homothallism: An umbrella term for describing diverse sexual behaviours. *IMA Fungus* 6: 207-214.

Wingfield BD, Ades PK, Al-Naemi FA, Beirn LA, Bihon W, Crouch JA, de Beer ZW, de Vos L, Duong TA, Fields CJ, Fourie G, Kanzi AM, Malapi-Wight M, Pethybridge SJ, Radwan O, Rendon G, Slippers B, Santana QC, Steenkamp ET, Taylor PWJ, Vaghefi N, van der Merwe NA, Veltri D, Wingfield MJ. (2015). IMA Genome-F4. Draft genome sequences of *Chrysoporthe austroafricana, Diplodia scrobiculata, Fusarium nygamai, Leptographium lundbergii, Limonomyces culmigenus, Stagonosporopsis tanaceti*, and *Thielaviopsis punctulata*. *IMA Fungus* 6: 233-248.

Wingfield BD, Ambler JM, Coetzee MPA, de Beer ZW, Duong TA, Joubert F, Hammerbacher A, McTaggart AR, Naidoo K, Nguyen HDT, Ponomareva E, Santana QS, Seifert KA, Steenkamp ET, Trollip C, van der Nest MA, Visagie CM, Wilken PM, Wingfield MJ, Yilmaz N. (2016). IMA Genome-F 6: Draft genome sequences of *Armillaria fuscipes, Ceratocystiopsis minuta, Ceratocystis adiposa, Endoconidiophora laricicola, E. polonica* and *Penicillium freii* DAOMC 242723. *IMA Fungus* 7: 217-227.

Wingfield BD, Barnes I, de Beer ZW, de Vos L, Duong TA, Kanzi AM, Naidoo K, Nguyen HDT, Santana QC, Sayari M, Seifert KA, Steenkamp ET, Trollip C, van der Merwe N, van der Nest MA, Wilken PM, Wingfield MJ. (2015). Draft genome sequences of *Ceratocystis eucalypticola, Chrysoporthe cubensis, C. deuterocubensis, Davidsoniella virescens, Fusarium temperatum, Graphilbum fragrans, Penicillium nordicum*, and *Thielaviopsis musarum*. *IMA Fungus* 6: 493-506.

Wingfield BD, Duong TA, Hammerbacher A, van der Nest MA, Wilson A, Chang R, de Beer ZW, Steenkamp ET, Wilken PM, Naidoo K, Wingfield MJ. (2016). IMA Genome-F 7 Draft genome sequences for *Ceratocystis fagacearum, C. harringtonii, Grosmannia penicillata*, and *Huntiella bhutanensis*. *IMA Fungus* 7: 317-323.

Wingfield MJ, Brockerhoff EG, Wingfield BD, Slippers B. (2015). Planted forest health: The need for a global strategy. *Science* 349: 832-836.

Wingfield MJ, Garnas JR, Hajek A, Hurley BP, de Beer ZW, Taerum SJ. (2016). Novel and co-evolved associations between insects and microorganisms as drivers of forest pestilence. *Biological Invasions* 18: 1045-1056.

Wondafrash M, Slippers B, Garnas J, Roux G, Foit J, Langor DW, Hurley BP. (2016). Identification and genetic diversity of two invasive *Pissodes* spp. Germar (Coleoptera: Curculionidae) in their introduced range in the southern hemisphere. *Biological Invasions* 18: 2283.

Woudenberg JC, van der Merwe NA, Jurjević Z, Groenewald JZ, Crous PW. (2015). Diversity and movement of indoor *Alternaria alternata* across the mainland USA. *Fungal Genetics and Biology* 81: 62-72.

Yang T, Groenewald Z, Cheewangkoon R, Jami F, Abdollahzadeh J, Lombard L, Crous PW. (2016). Families, genera and species of Botryosphaeriales. *Fungal Biology* 121(4): 322-346.

Yin M, Duong TA, Wingfield MJ, Zhou X, de Beer ZW. (2015). Taxonomy and phylogeny of the *Leptographium procerum* complex, including *L. sinense* sp. nov. and *L. longiconidiophorum* sp. nov. *Antonie van Leeuwenhoek* 107: 547-563.

Yin M, Wingfield MJ, Zhou X, de Beer ZW. (2016). Multigene phylogenies and morphological characterization of five new *Ophiostoma* spp. associated with spruce-infesting bark beetles in China. *Fungal Biology* 120: 454-470.

Yu H, Soler M, Clemente HS, Mila I, Paiva JAP, Myburg AA, Bouzayen M, Grima-Pettenati J, Cassan-Wang H. (2015). Comprehensive genome-wide analysis of the Aux/IAA gene family in *Eucalyptus*: evidence for the role of EgrIAA4 in wood formation. *Plant Cell Physiology* 56: 700-714.

Zlatković M, Keca N, Wingfield MJ, Jami F, Slippers B. (2016). Botryosphaeriaceae associated with the die-back of ornamental trees in the Western Balkans. *Antonie van Leeuwenhoek* 109: 543-564.

Zlatković M, Keča N, Wingfield MJ, Jami F, Slippers B. (2016). Shot hole disease on *Prunus laurocerasus* caused by *Neofusicoccum parvum* in Serbia. *Forest Pathology* 46: 666-669.

Commentaries and Editorials

Crous CJ. 2015. Develop energy from shale with local ecosystems in mind. *South African Journal of Science* 111: 3-4.

Hulbert JM. 2016. Citizen science tools available for ecological research in South Africa. *South African Journal of Science* 112: 1-2.

Kemler M, 2015. Education: Botanists still need to tell plants apart. *Nature* 521: 32.

Slippers B. 2016. ASSAf and young scientists: Transforming the future of science in South Africa. *South African Journal of Science* 112, a0189.

Slippers B, Alisic E. 2015. Leadership training for African scientists. *Nature* 519: 414.

Slippers B, Vogel C. Fioramonti L, 2015. Global trends and opportunities for development of African research universities. *South African Journal of Science* 111: 1-2.

Slippers B, Vogel C, Fioramonti L. 2015. Opportunities for African research institutions. *Chemical Technology* March, 3.

Strauss SH, Myburg AA. 2015. Plant scientists celebrate new woody plant genome. *New Phytologist* 206: 1185-1187.

Wingfield BD, 2017. What "decolonised education" should and shouldn't mean. *The Conversation*.

Wingfield BD. (2016) Breast cancer: When do you stop reading the literature? *South African Journal of Science* 112: 1-2.

Book Chapters

Carstens M, Berger DK, 2016. Biotechnology and crop disease resistance in South Africa, *Biotechnology for Plant Disease Control*. Wiley, New York and London, p.16 (Chapter).

Coutinho TA & Walcott R, 2016. Chapter 21: Detection of *Pantoea* species in onion seed. APS Manual on detection of plant pathogenic bacteria in seed and planting material. (Ed. By Schaad N, Barek F, Walcott R), APS Press, St. Paul.

Garnas JR, Hurley BP, Slippers B, Wingfield MJ, Roux J, 2016. Insects and diseases of mediterranean forests: A South African perspective, *Insects and Diseases of Mediterranean Forest Systems*. Springer International Publishing, Switzerland, pp. 397-430.

Hussey SG, Wegrzyn JL, Vasquez-Gross HA, 2017. Evolutionary histories of gene families in angiosperm trees, *Comparative and Evolutionary Genomics of Angiosperm Trees*. Springer International Publishing, Cham, pp. 1-17.

Moleleki LN, 2015, Root knot nematodes and soft rot enterobacteriaceae, two emerging problems of potatoes. Ed Low J, Nyongesa M, Quinn S and Parker M. Potato and sweet potato in Africa. *Value Chain for Food and Nutrition Security*. CABI, UK.

Roux J, Coetzee MPA, 2016. Armillaria root rot of *Theobroma cacao*, *Cacao Diseases: A History of Old Enemies and New Encounters*. Springer International Publishing, Cham, pp. 429-447.

Papers/Posters Delivered at International Conferences

Backer B, Mahomed W, Reeksting BJ, Engelbrecht J, Ibarra-Laclette E & van den Berg N. (2015). Insighs into the phylogeny and expression of the *Persea americana* (Mill) NPR1-like gene family. VIII World Avocado Conference, Lima, Peru.

Balkwill CG, Myburg AA & Mizrachi E. (2015). Functional annotation of the central circadian clock components in *Eucalyptus* and *Populus*. Plant & Animal Genome XXIII Conference P937, January 10-14. San Diego, California.

Behrens D, Myburg AA & Mizrachi E. (2016). Discovery and transcriptional dynamics of small noncoding RNAs in source, transport and woody sink tissues in *Eucalyptus grandis*. Plant & Animal Genome XXIV Conference W318, January 9-13. San Diego, CA.

Bell VA, Chooi KM, Blouin AG, Cohen D, Pietersen G & MacDiamid RM. (2015). Timing of the symptoms influences the management strategies of grapevine leafroll-associated virus 3 in New Zealand. 18th Congress of ICVG, Ankara, Turkey, 7-11 September.

Berger DK, Christie N & Myburg AA. (2015). Systems genetics analysis of the maize-grey leaf spot disease pathosystem. NextGen Genomics, Biology, Bioinformatics and Technologies (NGBT) Conference, October, Hyderabad International Conference Centre, Hyderabad, India.

Berger DK, Christie N & Myburg AA. (2015). Transcriptional regulation in a maize population segregating for susceptibility to grey leaf spot disease. 20th Biennial Conference of the Australasian Plant Pathology Society, September, Freemantle, Western Australia.

Berger DK, Christie N & Myburg AA. (2016). Integration of resistance QTL, expression QTL and co-expression modules reveals molecular responses of maize to the fungal pathogen *Cercospora zeina*. XVII International Congress on Molecular Plant-Microbe Interactions. July, Portland, Oregon, USA.

Berger DK, Christie N & Myburg AA. (2016). Systems genetics of maize leaf responses to *Cercospora zeina*, the causal agent of gray leaf spot disease. 3rd Biennial Genetics of Maize-Microbe Interactions Workshop, April, Texas A&M University, College Station, USA.

Berger DK, Muller MF, Kunene NT, Crampton BG, Bluhm BH, Phillips S, Olivier NA & Barnes I. (2016). High genetic diversity of the grey leaf spot pathogen, *Cercospora zeina,* observed in commercial maize in South Africa. XVII International Congress on Molecular Plant-Microbe Interactions, July, Portland, Oregon, USA.

Botha J, Mizrachi E, Myburg AA & Cowan D. (2015). Hyperthermophiles: A source of CAZymes for industrial lignocellulosic degradation. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Chan WY, Steenkamp ET, Vorster J, Riva O & Venter SN. (2015). Genome comparisons reveal the evolution of nitrogen fixation in *Burkholderia*. 6th Congress of European Microbiologists, Maastricht, the Netherlands, 7-11 June.

Christie N, Mbanjo G, Calvert M, Pinard D, Verbeke L, Marchal K, van de Peer Y, Mizrachi E & Myburg AA. (2015). Interspecific differentiation of gene expression regulation affecting growth and wood development in *Eucalyptus*. Plant Genome Evolution 2015 Conference, Amsterdam, The Netherlands, 6-8 September.

Cilliers M, van Wyk SG, van Heerden RDP & Vorster BJ. (2015). Transcriptional analysis of cysteine proteases in soybean root nodules experiencing premature senescence due to water deficit. Plant Biology, July, Minnesota, USA.

Coutinho TA. (2015). Plant pathology in South Africa (and opportunistic plant pathogenic bacteria). British Society of Plant Pathology (BSPP) Molecular Plant Pathogens Congress, UWE, Bristol UK, 8-9 April.

de Beer ZW, Duong T & Wingfield MJ. (2015). Taxonomy of the genus *Sporothrix* and *S. schenckii* in South Africa. 19th ISHAM (International Society for Human and Animal Mycology) Congress, 4-8 May, Melbourne, Australia.

de Beer ZW, Duong TA, Wingfield BD & Wingfield MJ. (2015). Current taxonomic status of the Ophiostomatales and Microascales. The Second International Workshop on Ascomycete Systematics, CBS Symposium Week, 22-24 April, Royal Netherlands Academy of Arts and Sciences, Amsterdam.

Duong TA, de Beer ZW, Wingfield MJ & Wingfield BD. (2015). Genome analyses reveals evolution towards homothallism in *Leptographium sensu lato*. 28th Fungal Genetics Conference, 17-22 March, Pacific Grove, California.

Fouche S, Wingfield BD, Coetzee MPA, Slinski S & Steenkamp ET. (2015). Characterization of a dispensable chromosome in *Fusarium circinatum*. 28th Fungal Genetics Conference, 17-22 March, Pacific Grove, California.

Fourie G, de Vos L, Wingfield BD, van der Merwe NA, Wingfield MJ & Wingfield BD. (2015). Segregation distortion in the progeny of an interspecific cross between *Fusarium circinatum* and *F. temperatum*: nuclear-cytoplasmic incompatibility and hybrid breakdown. 28th Fungal Genetics Conference, 17-22 March, Pacific Grove, California.

Harris M & Pietersen G. (2015). Detection of grapevine leafroll associated virus-3, Viti- and Foveaviruses in Vitis rootstocks. Virology Africa 2015, Cape Town, 30 November - 3 December.

Human MP, Berger DK & Crampton BG. (2016). Effector identification and transcriptional profiling of the *Exserohilum turcicum-Zea mays* interaction. XVII International Congress on Molecular Plant-Microbe Interactions, Portland, Oregon, USA.

Hurley BP, Dittrich-Schröder G, Baffoe KO, Slippers B & Wingfield MJ. (2015). The biology, host specificity and in-field establishment of *Selitrichodes neseri* (Eulophidae), a biological control agent of *Leptocybe invasa* (Eulophidae). IOBC Benefits and Risks of Biological Control Agents meeting, 12-15 May, Bornholm, Denmark.

Hussey SG, Loots MT, Mizrachi E, Myburg AA. (2016). Modelling transcript abundance from chromatin immunoprecipitation data in plants: lessons from *Eucalyptus grandis*. American Society of Plant Biology Conference, Austin, TX, USA, 9-13 July.

Hussey SG, Mizrachi E, Berger DK & Myburg AA. (2015). ChIP-seq analysis of histone modifications and transcription factors regulating wood formation in *Eucalyptus*. Front Lines of Plant Cell Wall Research Symposium, 20-21 March, Nara, Japan.

Hussey SG, Mizrachi E & Myburg AA. (2015). Epigenomic profiles of two antagonistic histone modifications, H3K4me3 and H3K27me3, in *Eucalyptus grandis* developing xylem. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Hussey SG & Myburg AA. (2015). Gene expression regulation and duplication is associated with H3K4me3 and H3K27me3 histone modifications during wood development in *Eucalyptus grandis*. 11th International Congress of Plant Molecular Biology, Iguazú Falls, Brazil.

Krüger KK, Pietersen G, Smit N & Carstens R. (2015). Epidemiology of aster yellows phytoplasma: alternate host plants and the vector *Mgenia fuscovaria* (Hemiptera: Cicadellidae) in South Africa. 18th Congress of ICVG, Ankara, Turkey, 7-11 September.

Kwenda S, Rubagotti E, Birch P & Moleleki LN. (2016). Genome wide identification and characterization of long noncoding RNAs in potato responsive to *Pectobacterium carotovorum* subspecies *brasiliense* infection. MPMI, 17-21 July, Portland, USA.

Liversage J, Berger DK & Crampton BG. (2015). Functional characterisation of the *Cercospora zeina crp1* gene as a putative pathogenesis regulation factor: Cell biology at the plant-microbe interface. 36th New Phytologist Symposium, Munich, Germany.

Lombard L, Chaverri P, Miller AN, Jaklitsch WM, Voglmayr H, de Beer ZW, Duong TA, Wingfield BD, Wingfield MJ, Hirooka Y, Schoch CL, Thrane U, Cai L, Summerbell RC, Restrepo MIH, Réblová M, Põldmaa K, Spatafora JW, Groenewald JZ & Crous PW. (2015). Hypocreomycetidae. The Second International Workshop on Ascomycete Systematics, CBS Symposium Week, 22-24 April, Royal Netherlands Academy of Arts and Sciences, Amsterdam.

Mangwanda R, van der Merwe NA, Myburg AA & Naidoo S. (2015). Transcriptional profiling of *Eucalyptus grandis* and *Chrysoporthe austroafricana* elucidates host defence mechanisms and putative pathogenicity strategies. IUFRO Conference on Genetics of Tree-Parasite Interactions, Orléans, France, 23-23 August.

Mewalal R, Mizrachi E, Mansfield SD & Myburg AA. (2015). *Arabidopsis* proteins, Modifying Wall Lignin (MWL) -1 and 2 containing the domain of unknown function 1218 (DUF1218) function redundantly to alter secondary cell wall lignin content. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Meyer FE, Shuey LS, Berger DK & van den Berg N, Myburg AA, Naidoo S. (2015). Two sides of the coin: Investigating defence responses against *Phytophthora cinnamomi* in *Eucalyptus nitens* using dual RNA-Sequencing. APPS Pathogen Bioinformatics Symposium. Esplanade Hotel Fremantle, Western Australia. 14-16 September.

Miller AN, Nguyen N-P, Warnow T, Schoch C, Réblová M, Jones EBG, de Beer ZW, BoonyueN N, Crous PW, Duong TA, Ferrer A, Hashimoto A, Hernández-Restrepo M, Huhndorf SM, Hyde KD, Kruys Å, Lombard L, Luo J, Maharachchikumbura S, Marin-Felix Y, Matsumura M, Pang K-L, Raja HA, Sakayaroj J, Stchigel AM, Sueterong S, Tanaka K, Abdel-Wahab MA, Wingfield BD, Wingfield MJ, Zelski S & Zhang N. (2015). Overview of Sordariomycetes. The Second International Workshop on Ascomycete Systematics, CBS Symposium Week, 22-24 April Royal Netherlands Academy of Arts and Sciences, Amsterdam.

Mitchell B, Engelbrect J, Reeksting B & van den Berg N. (2015). Integrated analysis of early *Phytophthora cinnamomi* infection in tolerant and susceptible avocado rootstocks. VIII World Avocado Conference, Lima, Peru.

Mizrachi E, Marchal K, van de Peer Y & Myburg AA. (2015). Modeling xylogenesis and its evolution. Plant Genome Evolution 2015 Conference, Amsterdam, The Netherlands, 6-8 September.

Mizrachi E, Pinard D, Gutierrez ACF, Verbeke L, Balkwill CG, Behrens D, Ekoka E, Hussey SG, van de Peer Y, Marchal K & Myburg AA. (2016). Multilevel modelling of lignocellulosic biomass accumulation in *Eucalyptus*. Plant & Animal Genome XXIV Conference W339, January 9-13. San Diego, CA.

Mizrachi E, Verbeke L, Fierro AC, Christie N, Pinard D, Balkwill C, Mansfield SD, Tschaplinski, Tuskan GA, Marchal K, van de Peer Y & Myburg AA. (2015). Systems genetics dissection of lignocellulosic biomass and bioenergy related traits in *Eucalyptus*. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Moleleki LN, Shyntum D & Tanui C. (2016). Competitive fitness: An important survival strategy for *Pcb1692*? Euphresco III Meeting, 10-11 November, Helsinki, Finland.

Moleleki LN, Pretorius R, Tanui C, Mosina G & Theron J. (2016). Quorum sensing defective mutants of Pcb are hyperpilliated but unable to infect potato tubers and stems. MPMI, 17-21 July, Portland, USA.

Mphahlele MM, van Deventer F, Reynolds SM, O'Neill MM, Hodge GR, Isik F & Myburg AA. (2015). Genotyping and phenotyping of a *Eucalyptus grandis* training population towards the development of genomic selection models. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Myburg AA, Christie N, Wierzbicki M, Mbanjo G, Calvert M, Pinard D, Verbeke L, Tschaplinski TJ, Tuskan GA, Mansfield SD, Marchal K, van de Peer Y & Mizrachi E. (2015). Beyond the *Eucalyptus* genome: Systems genetics reveals novel woody plant biology. International Plant Molecular Biology (IPMB) 2015 Conference, Iguazu Falls, Brazil, 25-30 October.

Naidoo S, du Toit Y & Coetzee N. (2015). Comparative transcriptomics of *Eucalyptus grandis* clones under various biotic stress challenges disclose common elements of defence. International Plant Molecular Biology (IPMB) 2015 Conference, Iguazu Falls, Brazil, 25-30 October.

Naidoo S, Wilken FE, Shuey L, Berger DK, van den Berg N & Myburg AA. (2015). Two sides of the coin: Investigating defence responses against *Phytophthora cinnamomi* in *Eucalyptus nitens* using dual RNA-sequencing. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Oates C, Kulheim C, Myburg AA & Naidoo S. (2015). A preliminary view of *Leptocybe*-induced gall development and host transcriptional responses in *Eucalyptus*. IUFRO Conference on Genetics of Tree - Parasite Interactions, Orléans, France, 23-23 August.

Oates C, Myburg AA, Slippers B, Naidoo S & Denby K. (2015). A preliminary view of *Leptocybe invasa*-induced gall development and host transcriptional responses in a susceptible *Eucalyptus grandis* hybrid clone. IUFRO Conference on Genetics of Tree-Parasite Interactions, Orléans, France, 23-23 August.

Palmer M, Steenkamp ET, Coetzee MPA, Coutinho TA & Venter SN. (2016). Genome based phylogenetic analysis to investigate relationships between the genera *Erwinia*, *Pantoea* and *Tatumella*. Oral presentation at the 3rd Meeting of the Bergey's International Society for Microbial Systematics, Pune, India, 12-15 September.

Pietersen, G. (2015). Leafroll disease: the end is nigh. Romeo Bragato Conference 2015, 26-28 August. Napier, New Zealand.

Pietersen G. (2015). Eliminating Leafroll disease: What about white cultivars? Romeo Bragato Conference 2015, 26-28 August. Napier, New Zealand.

Pietersen G, Louw M, Krüger KK, Faure B & van Rensburg, H. (2015). Grapevine leafroll disease spread from old to replacement vineyards. 18th Congress of ICVG, Ankara, Turkey, 7-11 September.

Pietersen G, Zim N, Barendsen V, Claassens R, Ind A, Makwela M, Msimango T, Querl B, Mizarchi E, Myburg AA & Hussey S. (2015). Switch-coli: synchronized, conditional, genetic chemotaxis programming. International Genetically Engineered Machine (iGEM) Competition. Boston, USA, 24-28 September.

Pinard D, Fierro Gutiérre AC, van de Peer Y, Marchal K, Myburg AA & Mizrachi E. (2015). Transcriptional networks of plastid targeted genes affecting carbon metabolism in *Eucalyptus* xylem. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Seale T, Steenkamp ET, Brözel VS & Venter SN. (2016). Unique environmental *E.coli* strains isolated from aquatic environments. Poster presentation at the American Society for Microbiology's Microbe 2016, Boston, United States of America, 16-20 June.

Seedat M, Reitmann A. Naidoo S & van den Berg N. (2015) Identification of Crinkler (CRN) genes in *Phytophthora cinnamomi*. VIII World Avocado Conference, Lima, Peru.

Shuey L, Pegg G & Naidoo S. (2015). Defence responses to *Puccinia psidii* in *Eucalyptus grandis*. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Shuey L, Pegg G & Naidoo S. (2015). *Eucalyptus grandis* defence responses against the myrtle rust pathogen, *Puccinia psidii*: insights from transcriptome profiling. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Shuey LS, Pegg GS & Naidoo S. (2015). *Eucalyptus grandis* defence response against the myrtle rust pathogen, *Puccinia psidii* insights from RNA-Seq transcriptome profiling. Australasian Plant Pathology Conference. Esplanade Hotel, Fremantle, Western Australia from 14-16 September.

Swart V, Crampton BG, Bluhm BH & Berger DK. (2015). *Cercospora zeina CTB* gene expression profiles suggests an early role for cercosporin in grey leaf spot disease development in maize: Cell biology at the plant-microbe interface. 36th New Phytologist Symposium, 29 November - 1 December, Munich, Germany.

Swart V, Crampton BG, Bluhm BH & Berger DK. (2016). Gray leaf spot of maize: annotation and expression of the cercosporin biosynthesis pathway in *Cercospora zeina*. 3rd Biennial Genetics of Maize-Microbe Interactions Workshop, 30 March - 2 April, Texas A&M University, College Station, USA.

van den Berg N, Mahomed W, Crampton B & Olivier N. (2016) Global gene expression of tolerant avocado infected with *Phytophthora cinnamomi*. Plant

Biology Europe EPSO/FESPB, Praque, Czech Republic.

van Wyk S, Wingfield BD, de Vos L, van der Merwe NA & Steenkamp ET. (2015). Diverse origins of genes associated with a growth QTL in *Fusarium circinatum*. 28th Fungal Genetics Conference, 17-22 March, Pacific Grove, California.

Venter SN, Chan WY, Palmer, M, Shin G, Beukes CW, van Zyl E, Coutinho TA & Steenkamp ET. (2016). Genealogical concordance and other lines of evidence for the recognition and description of bacterial species. Oral presentation at the 3rd Meeting of the Bergey's International Society for Microbial Systematics, Pune, India, 12-15 September.

Venter SN, du Plessis M, Coetzee MPA, Coutinho TA & Steenkamp ET. (2015). Applying an evolution-based species concept for the delineation of bacterial species: the *Pantoea* example. FEMS, Maastricht, the Netherlands, 8-11 June.

Venter SN, Palmer M, Coetzee MPA, Coutinho TA & Steenkamp ET. (2015). Applying an evolution based species concept for delineation of bacterial species: The *Pantoea* example. Invited speaker at the 6th Congress of European Microbiologists, Maastricht, the Netherlands, 7-11 June.

Visser E, Wegrzyn J, Steenkamp E, Myburg AA & Naidoo S. (2015). Sequencing of the *Pinus patula* shoot transcriptome and identification of antifungal defence genes. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June, 2015.

Wayland J, Jooste AEC & Pietersen G. (2015). The optimisation of a High-Throughput Sequencing-based diagnostic system for the detection of viruses of grapevines. Virology Africa 2015, Cape Town, 30 November - 3 December.

Wierzbicki MP, Mansfield SD, Christie N, Mizrachi E & Myburg AA. (2016). Systems genetics of xylan modification in *Eucalyptus* hybrid populations. American Society of Plant Biology Conference, Austin, TX, USA, 9-13 July.

Wilken FE, Shuey LS, Berger DK, Myburg AA, van den Berg N & Naidoo S. (2015). Two sides of the coin: Investigating defence responses against *Phytophthora cinnamomi* in *Eucalyptus nitens* using dual RNA-sequencing. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Zwart L, Mangwanda R, Myburg AA & Naidoo S. (2015). Using induced resistance in *Eucalyptus grandis* to identify broad spectrum defence mechanisms. IUFRO Tree Biotechnology Conference, Florence, Italy, 8-12 June.

Papers/Posters Delivered at National Conferences

Adenigba OO, Wingfield BD, Duong TA, van der Merwe NA, Wingfield MJ & Steenkamp ET. (2015). Generation of a mating pheromone deletion mutant in Fusarium circinatum. 49th Congress of the Southern African Society for Plant Pathology, Bloemfontein, 19-21 January.

Appelgryn E, Pietersen G. (2017). Alternative hosts and seed transmissibility of Soybean blotchy mosaic virus. 50th Anniversary Congress of the Southern African Society for Plant Pathology, Champagne Sports Resort, Drakensburg, 15-18 January.

Avontuur JR, Steenkamp ET, van Zyl E, Beukes CW, Boshoff FS & Venter SN. (2016). Delineation and characterization of novel *Bradyrhizobium* species associated with South African legumes. 12th meeting of the Southern African Society for Systematic Biology, Bloemfontein, 10-13 January.

Backer R, Joubert M & van den Berg N. (2016) Developing a novel pathosystem for the study of *Phytophthora cinnamomi* using *Nicotiana benthamiana*. 4th Joint Congress of the South African Society for Bioinformatics and the South African Genetics Society, Durban, South Africa, 20-23 September.

Berger DK. (2015). Genomics of grey leaf spot disease: from the field to the lab. 11th Regional Plant Biotechnology Forum, University of Johannesburg, 13 April.

Berger DK. (2016). Systems genetics - exploring stress responses in plant. 3rd DuPont Plant Sciences Symposium, North West University, Potchefstroom, 18 October.

Berger DK. (2017). Grey leaf spot disease of maize and food security research. 43rd Annual Conference of the South African Association of Botanists (SAAB), Milnerton, 8-11 January.

Berger DK, Muller MF, Kunene NT, Crampton BG, Bluhm B, Phillips S, Olivier NA & Barnes I. (2017). High genetic diversity of the grey leaf spot pathogen, *Cercospora zeina,* observed in commercial maize in South Africa. 50th Congress of the Southern African Society for Plant Pathology, Champagne Castle Sports Resort, Drakensberg, 15-18 January.

Beukes CW, Steenkamp ET, Van Zyl E, Avontuur JR, Chan WY, du Plessis M, Mthombeni L, Phalane FL, Sereme TK & Venter SN. (2015). *Burkholderia kirstenboshi* sp. nov., *B. steynii* sp. nov, *B. sophoroidus* sp. nov., *B. hypocalyptii* sp. nov. and *B. coluteoidii* sp. nov., indigenous rhizobial species which nodulate members of the Hypocalypteae and Podalyrieae. 41st Annual Conference of the South African Association of Botanists, January.

Beukes CW, Venter SN, Stępkowski T, Boshoff, SF, le Roux MM & Steenkamp ET. (2016). Investigation of the invasion strategy used by *Lotus* and *Acacia* species in South Africa. 12th meeting of the

Southern African Society for Systematic Biology, Bloemfontein, 10-13 January.

Carstensen GD, Venter SN, Wingfield MJ & Coutinho TA. (2015). Identification of two *Ralstonia* species associated with bacterial wilt of *Eucalyptus*. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Crampton BG, Murray SL, Lombard B, Meyer J & Berger DK. (2015). Pathogenesis related proteins play an important role in the maize defence response to *Cercospora zeina*. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Christie N, Mizrachi E & Myburg AA. (2016). Genome-wide dissection of regulatory gene networks and metabolite variation underlying wood property traits in *Eucalyptus*. South African Society for Bioinformatics and South African Genetics Society Conference, Durban, 20-23 September.

Christie N, Myburg AA, Joubert F, Murray SL, Carstens M, Lin YC, Meyer J, Crampton BG, Christensen SA, Ntuli JF, Wighard SS, van de Peer Y & Berger DK. (2017). A maize transcriptional network associated with susceptibility to the grey leaf spot pathogen *Cercospora zeina*. 50th Congress of the Southern African Society for Plant Pathology, Champagne Castle Sports Resort, Drakensberg, 15-18 January.

Cilliers M, van Heerden RDP & Vorster BJ. (2016). Soybean's ability to recover after the onset of premature senescense caused by water deficit conditions. Combined Congress of the South African Society for Crop Production, South African Soil Science Society, Horticulture Society of South Africa and the South African Weed Science Society, January, Bloemfontein, South Africa.

de Beer ZW. (2015). Diseases, diagostics and DNA. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

du Preez A, de Maayer P & Coutinho TA. (2015). A comparative analysis of the flagellin glycosylation island in stains of *Pantoea ananatis* from different ecological niches. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

du Raan S, Coutinho TA & van der Waals J. (2015). Cardinal temperature differences between closely related species and subspecies of pectinolytic bacteria responsible for blackleg and soft rot of potatoes. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

de Ridder K, Berger DK & Aveling TAS. (2017). A survey of pre-harvest ear rot diseases of maize in selected small-holder maize plots in KwaZulu-Natal and the Eastern Cape in SA. 50th Congress of the Southern African Society for Plant Pathology, Champagne Castle Sports Resort, Drakensberg, 15-18 January.

du Toit Y, Christie N, Myburg AA & Naidoo S. (2016). A meta-analysis approach to understand defence response patterns in *Eucalyptus*. South African Society for Bioinformatics and South African Genetics Society Conference, Durban, 20-23 September.

Engelbrecht S, Christie N & Myburg AA. (2016). Towards a robust genome-wide allele-specific expression analysis pipeline for outbred plants based on RNA-seq data. Society for Bioinformatics and South African Genetics Society Conference, Durban, 20-23 September.

Engelbrecht S, Henning S, Reynolds SM, Marais C & Myburg AA. (2016). High-throughput SNP-based fingerprinting of *Eucalyptus* species and hybrids for routine breeding applications. Society for Bioinformatics and South African Genetics Society Conference, Durban, 20-23 September.

Fourie G, de Vos L, van der Merwe NA, Wingfield BD, Wingfield MJ & Steenkamp ET. (2015). Understanding nuclear-cytoplasmic incompatibility between *Fusarium circinatum* and *F. temperatum*. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Goszczynska T, Moloto VM, Coutinho TA, Botha WJ & Jacobs A. (2015). A new disease of banana, scaly black spot of fruit, caused by a *Xanthomonas* sp. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Haasbroek M, Barnes I, Craven M & Crampton B. (2015). Evidence for multiple introductions, migration and clonal spread of *Exserohilum turcicum* in South Africa. 49th Congress of the Southern African Society for Plant Pathology, Bloemfontein, 19-21 January.

Harris M & Pietersen G. (2017). Detection of grapevine leafroll associated virus 3, Viti- and Foveaviruses in Vitis rootstocks. 50th Anniversary Congress of the Southern African Society for Plant Pathology, Champagne Sports Resort, Drakensburg, 15-18 January.

Human M, Berger DK & Crampton BG. (2016). Transcriptional profiling and effector identification of the *Exserohilum turcicum-Zea mays* interaction. 3rd DuPont Plant Sciences Symposium, North West University, Potchefstroom, 18 October.

Jami F, Wingfield MJ, Hudler GW & Slippers B. (2015). The Botryosphaeriaceae associated with *Ribes* spp. in New York, USA. 49th Congress of the Southern

African Society for Plant Pathology, Bains Lodge, Bloemfontein, South Africa, 19-21 January.

Kibido TR, Vorster BJ & Makgopa ME. (2017). Selection of osmotolerant and effective rhizobial strains on symbiotic nitrogen fixation efficiency in soybean under water deficit stress. Combined Congress of the South African Society for Crop Production, South African Soil Science Society, Horticulture Society of South Africa and the South African Weed Science Society, Klein Kariba, South Africa, 23-27 January.

Laubscher M, Mizrachi E, Myburg AA & Hussey SG. (2016). Dissecting *Eucalyptus grandis* secondary cell wall master regulators through heterologous induction in *Arabidopsis* protoplasts. South African Society for Bioinformatics and South African Genetics Society Conference, Durban, 20-23 September.

Liversage R, Berger DK & Crampton BG. (2015). Functional characterisation of the *Cercospora zeina crp1* gene as a putative pathogenesis regulation factor. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Liversage J, Berger DK & Crampton BG. (2016). Functional characterisation of the *Cercospora zeina crp1* gene, as a putative pathogenesis regulation factor. 3rd DuPont Plant Sciences Symposium, North West University, Potchefstroom, 18 October.

Lombard B, Berger D, Crampton B. (2015). Insight into three putative *Cercospora zeina* effector genes and the role they play in virulence. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Malefo MBL, Berger D & Crampton B. (2015). Functional characterisation of the putative pathogenicity factor, CZK3 in *Cercospora zeina*. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Maluleke N & Moleleki LN (2015) Impact of soft rot Enterobacteriaceae on food crops in South Africa. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Mbedzi PP & Vorster BJ. (2016). Genetic diversity and herbicide tolerance in *Conyza bonariensis*. Combined Congress of the South African Society for Crop Production, South African Soil Science Society, Horticulture Society of South Africa and the South African Weed Science Society, January, Bloemfontein, South Africa.

Mbedzi PP & Vorster BJ (2016) Genetic diversity and herbicide tolerance in *Conyza bonariensis*. 3rd DuPont Plant Science Symposium, October, Potchefstroom, South Africa.

Mbedzi PP, van der Waals JE & Vorster BJ. (2017). Initial screening of soybean for microsatellite markers conferring resistance to Sclerotinia stem rot. Combined Congress of the South African Society for Crop Production, South African Soil Science Society, Horticulture Society of South Africa and the South African Weed Science Society, January, Bloemfontein, South Africa.

McTaggart AR, Maier W, Roux J & Wingfield MJ. (2015). A new species of rust on *Eucalyptus* in South Africa. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

Mhoswa L, O'Neill MM, Mphahlele MM, Slippers B, Myburg AA & Naidoo S. (2016). Genome Wide Association Study (GWAS) of *Leptocybe invasa* resistance in *Eucalyptus grandis*. South African Society for Bioinformatics and South African Genetics Society Conference, Durban, 20-23 September.

Mitchell B, Engelbrecht J & van den Berg N. (2015). Scanning electron microscopy and quantification of *Phytophthora cinnamomi* infection in tolerant and susceptible avocado rootstocks. South African Society for Plant Pathology (SASPP) Conference, January, South Africa.

Moloto VM, Coutinho TA & Goszczynska T. (2015). Characterisation and identification of *Agrobacterium* species from South Africa. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein 19-21 January.

Moloto VM, Goszczynska T & Coutinho TA. (2015). Bacterial pathogens in onion seed. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein 19-21 January.

Moloto VM, Goszczynska T & Coutinho TA. (2015). New pathovar of *Pseudomonas syringae* from onion plants. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein 19-21 January.

Mosina GKE & Moleleki LN. (2015). Plant defence against pathogenic bacteria: A focus on Pectobacterium-potato interactions. South African Association of Botanists, University of Venda, South Africa, 11-15 January.

Ndlovu B, Prabhu A, Duong TA, van den Berg N. (2016) Transient expression and effect-evaluation of putative *Phytophthora cinnamomi* RxLRs on *Nicotiana benthamiana* leaves. 4th Joint Congress of the South African Society for Bioinformatics and the South African Genetics Society in Durban, South Africa, 20-23 September.

New SA, van Heerden SW, Pietersen G & Esterhuizen LL. (2015). Investigation of the "Brassica-stunting disorder" affecting various *Brassica* crops in South Africa. 49th Congress of the Southern African Society for Plant Pathology, Bloemfontein 18-21 January.

Nxumalo KM, Boshoff FS, Beukes CW, Steenkamp ET & Venter SN. (2016). Novel root-nodule bacteria associated with *Vachellia karroo*. 12th meeting of the Southern African Society for Systematic Biology, Bloemfontein, 10-13 January.

Pavlic-Zupanc D, Piškur B, Slippers B, Wingfield MJ & Jurc D. (2015). Molecular and morphological characterisation of *Dothiorella* species associated with dieback of *Ostrya carpinifolia* in Slovenia and Italy, and a host and geographic range extension for *D. parva*. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, South Africa, 18-21 January.

Phasha MM, de Vos L, Coetzee MPA, Wingfield BD, Wingfield MJ & Steenkamp ET. (2015). Heritability of pathogenicity towards *Pinus patula* in a back-crossed population of *Fusarium circinatum*. 49th Annual Congress of the Southern African Society for Plant Pathology, Bloemfontein, 19-21 January.

Pietersen G. (2017). Control of grapevine leafroll disease in white grapevine cultivars. 50th Anniversary Congress of the Southern African Society for Plant Pathology, Champagne Sports Resort, Drakensburg, 15-18 January.

Roberts R, Cook G, Grout TG, Rwomushana I, Nderitu P, Seguni Z, Materu C, Steyn C, Pietersen G & le Roux H. (2016). Detection of '*Candidatus* Liberibacter species' from citrus in Uganda, Kenya and Tanzania. 9th Citrus Research Symposium Champagne Sports Resort, Drakensberg, 21-25 August.

Roberts R & Pietersen G. (2017). Variability amongst '*Candidatus* Liberibacter africanus' populations of citrus in South Africa. 50th Anniversary Congress of the Southern African Society for Plant Pathology, Champagne Sports Resort, Drakensburg, 15-18 January.

Roodt D, Li Z, van de Peer Y & Mizrachi E. (2016). The evolution of xylogenesis in dicots and its loss in monocots. South African Society for Bioinformatics and South African Genetics Society Conference, Durban, 20-23 September.

Roux J, McTaggart A, Herron D, Greyling I, Fouche S, Chan J, Norris C, Mbatha T, Wingfield BD & Wingfield MJ. (2015). A devastating new rust disease of *Acacia mearnsii* in South Africa. 49th Congress of the Southern African Society for Plant Pathology, Bloemfontein, South Africa, 19-21 January.

Roux J & Wingfield MJ. (2015). Heading for an unknown future: We must do more to protect our native plants from attack by invasive pests and pathogens. Congress of the Southern African Association of Botanists, January, Tshipise, Limpopo Province.

Schulze A & Pietersen G. (2017). The detection, identification, genome sequencing and characterisation of members of the *Potyvirus* genus that are novel to South Africa. 50th Anniversary Congress of the Southern African Society for Plant Pathology, Champagne Sports Resort, Drakensburg, 15th-18th January.

Tanui CK & Moleleki LN. (2015). Charaterisation of the *Pectobacterium carotovorum* subsp. *brasiliense (Pcb)* expl gene during infection of potato tubers and stems. Southern African Society for Plant Pathology, Bloemfontein, South Africa, 19-21 January.

van der Linde JA, Six DL, Wingfield MJ & Roux J. (2015). *Cyrtogenius africus* (Scolytinae), its phoretic mites and novel ophiostomatoid partners: the final blow leading to the *Euphorbia ingens* die-off. 49th Congress of the Southern African Society for Plant Pathology, Bloemfontein, South Africa, 19-21 January.

van Wyk S, Wingfield BD, de Vos L, van der Merwe NA & Steenkamp ET. (2015). Diverse origins of genes associated with growth QTL in *Fusarium circinatum*. 49th Annual Congress of the Southern African Society for Plant Pathology, Bloemfontein, 19-21 January.

Weller-Stewart T, Toth I, Theron J, P de Maayer & Coutinho TA. (2015). Mutations of flagella (*flgK* and *motA*) and type IV pili (*pilA* and *pilT*) genes of *Pantoea ananatis* LMG20103 reduces motility, attachment and virulence in onion seedlings. 49th Congress of the Southern African Society for Plant Pathology, Bains Lodge, Bloemfontein, 19-21 January.

SEMINAR PRESENTATIONS

All postgraduate students linked to FABI present two seminars each year on a Thursday morning. Special seminars, presented by invited speakers, are also regularly held.

Prof. Koos Boomsma, Department of Biology, University of Copenhagen, Denmark
Commitment in social life, sex and symbiosis.
January 2015

Prof. Michael Poulsen, Department of Biology, University of Copenhagen, Denmark
30 millon years of farming and pharmacy innovation in fungus-growing termites.
February 2015

Prof. Rees Kassen, Research Chair: Expreimental Evolution, University of Ottawa, Canada
Genetics of adaptation and parallelism in an opportunistic pathogen.
June 2015

Dr. Marie-Agnes Jacques, French National Institute for Agriculture (INRA), France
Emergence of *Xylella fastidiosa* in Europe: Diversity and biology of the causal agent.
June 2015

Prof. David Collinge, Department of Plant and Environmental Science, University of Copenhagen, Denmark
From transgenic plants to endophytic fungi: Contrasting approaches to disease control in plants.
June 2015

Prof. Ian Toth, James Hutton Institute, Scotland, UK
Is GM the only solution to crop protection in Europe? Integrated pest management at the James Hutton Institute.
October 2015

Dr. Enrique Ibarra-Laclette, Instituto de Ecologia, Mexico
The avocado genome: A progress report.
October 2015

Dr. Claudia-Anahi Perez-Torres, Instituto de Ecologia, Mexico
Phosphorus uptake in plants.
October 2015

Prof. Richard Goodman, Department of Food Science and Technology, University of Nebraska - Lincoln, USA
Biosafety: Evaluation and regulation of GM crops in the US.
October 2015

Prof. Tobin Peever, Washington State University, USA
Speciation of plant-pathogenic fungi: does host specificity matter?
November 2015

Prof. Louis Bernier, Université Laval, Quebec City, Canada
Analysis of the yeast-mycelium dimorphism in the Dutch elm disease fungi. From old tricks to omics.
November 2015

Prof. Jeremy McNiel, Western University, Ontario, Canada
The role of host plant volatiles and sex pheromones in the reproductive biology of the potato aphid *Macrosiphum euphorbiae* and its parasitoid *Aphidius nigripes*.
April 2016

Prof. Everett Hansen, Department of Botany and Plant Pathology, Oregon State University, USA
Two “new” needle cast diseases of Douglas fir in Oregon. On the watch for the next “big” thing.
May 2016

Prof. Wei He, Chinese Academy of Forestry, Peoples Republic of China
Pathogen, pathogenicity and epidemic of Poplar canker.
May 2016

Prof. Ying Zhang, Institute of Microbiology at the Beijing Forestry University, Peoples Republic of China
Summary of Botryosphaeriaceous fungi in China.
May 2016

Prof. John Leslie, Kansas State University, USA
Mycotoxins in Afghanistan.
May 2016

Prof. Peter Thrall, Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
Coevolutionary interactions in the *Linum-Melampsora* host-pathogen system.
June 2016

Prof. David Geiser, Pennsylavania State University, USA
Two *Fusarium* stories.
June 2016

Prof. Panos Tsopelas, Institute of Mediterranean Forest Ecosystems, Athens, Greece
Canker stain disease: a major threat to natural stands of *Platanus orientalis* in the Balkan Peninsula.
August 2016

Prof. Frits Rijkenberg, University of KwaZulu-Natal (retired)
Rusts and their early penetration.
September 2016

Dr. Marc Kenis, Centre for Agriculture and Biosciences International (CABI), UK
Drosophila suzukii, a worldwide invasive pest.
October 2016

Prof. Joerg Bohlmann, University of British Colombia, Vancouver, Canada
Fragrance biosynthesis in tropical sandalwood: function genomics and the definition of heartwood.
November 2016

Prof. Roy Halling, New York Botanical Gardens, USA
Fungi down under: sand, gum trees and porcini.
November 2016

Prof. Mary Barbercheck, Pennsylvania State University, USA
Effect of soil characteristics and management on *Metarhizium*, a bifunctional fungus, in organic cropping systems.
January 2017

Prof. Mario Rajchenberg, CIEFAP, Uruguay
Pinotage...Malbec...Eucalypts and wood-rots.
January 2017

Dr. Robert Waterhouse, University of Lausanne, Switzerland
Genome biology and evolution of harmful and helpful arthropods.
March 2017

Dr. Frederique van Gijsegem, INRA, France
The soft rot enterobacteria *Dickeya* genus: regulatory networks and comparative genomics of potato pathogens.
March 2017

FABI TEAM 2015–2017

FULL TIME ACADEMIC & RESEARCH STAFF

Prof. Dave Berger
Prof. Teresa Coutinho
Prof. Pedro Crous
Prof. Karl Kunert, Emeritus Professor
Prof. Zander Myburg
Prof. Jolanda Roux
Prof. Bernard Slippers
Prof. Emma Steenkamp
Prof. Fanus Venter
Prof. Brenda Wingfield
Prof. Michael Wingfield
Extraordinary Prof. Gerhard Pietersen
Assoc. Prof. Terry Aveling
Assoc. Prof. Wilhelm de Beer
Assoc. Prof. Lucy Moleleki
Assoc. Prof. Noëlani van den Berg
Dr. Irene Barnes
Dr. Martin Coetzee
Dr. Bridget Crampton
Dr. Jeff Garnas
Dr. Brett Hurley
Dr. Steven Hussey
Dr. Eshchar Mizrachi
Dr. Sanushka Naidoo
Dr. Albé van der Merwe
Dr. Juan Vorster

TECHNICAL STAFF

Ms. Dirkie Boshoff (until January 2015)
Ms. Jane Bredenkamp (until September 2016)
Ms. Samantha Bush
Ms. Elna Cowley (until January 2017)
Ms. Juanita Engelbrecht
Dr. Gerda Fourie
Ms. Onke Gayiya
Ms. Izette Greyling
Ms. Sandisiwe Jali
Ms. L'Zanne Jansen van Rensburg
Mr. Joseph Khadile
Ms. Pritty Khumalo
Ms. Mamadile Kgaphu
Ms. Grieta Mahlangu
Ms. Christy Marais
Dr. Seonju Marincowitz
Ms. Sharon Masipa (until January 2016)
Mr. Guelor Mayonde
Ms. Zandile Mngadi
Ms. Tersia Moabelo
Ms. Patience Motaung
Ms. Eva Müller
Ms. Aysha Ndou
Mr. Celani Nkosi
Ms. Valentina Nkosi
Ms. Sophie Nyoni
Mr. Nicky Olivier
Ms. Marja O'Neill
Ms. Melissa Reynolds
Ms. Maleshoane Selaocoe (until December 2015)
Ms. Maureen Tladi
Ms. Lydia Twala
Ms. Andisiwe Tyani
Ms. Karen van der Merwe
Ms. Adri Veale

ADMINISTRATIVE STAFF

Mr. Morné Booij-Liewes
Ms. Helen Doman
Ms. Heidi Fysh
Ms. Martha Mahlangu
Ms. Resego Moje (until June 2015)
Ms. Lauren Moonsamy (until December 2015)
Ms. Thandeka Ngondo
Ms. Namhla Tshisela
Ms. Madelein van Heerden
Ms. Estie van Rensburg

INFORMATION SPECIALIST

Ms. Rianie van der Linde

HONORARY PROFESSORS

Prof. Jeremy Allison
Prof. Paul Birch
Prof. Treena Burgess
Prof. Brion Duffy
Prof. Stefan Neser
Prof. Ian Toth
Prof. Steve Verryn
Prof. XuDong Zhou

SABBATICAL VISITORS

Dr. Clara Pliego Pietro, IFAPA, Malaga, Spain.

UP RESEARCH FELLOWS

Dr. Casper Crous
Future-proofing African forests for drier climates.

Dr. Tuan Duong
Molecular characterisation of *Leprographium serpens.*

Dr. Almuth Hammerbacher
Chemical ecology of trees and fungal pathogens.

Dr. Fahimeh Jami
Identification, taxonomy and biology of the Botryosphaeriaceae associated with woody hosts.

Dr. Martin Kemler
Molecular ecology and evolution of Botryosphaerieaceae.

Dr. Magriet van der Nest
Ceratocystis genomics.

POSTDOCTORAL FELLOWS

Dr. Ramesh Aadi Moolam
Flagella-mediated motility in *Pectobacterium carotovorum* subsp. *Brasiliense.*

Dr. Marc Bouwer
Chemical ecology of South African forest insects.

Dr. Maryke Carstens
Genomics of quantitative disease resistance in African maize varieties.

Dr. Nanette Christie
Transcriptional control underlying wood quality and disease resistance traits in *Eucalyptus* trees.

Dr. Elsie Cruywagen
Population genetics and species diversity of prominent fungi infecting baobab.

Dr. Lieschen de Vos
Genomes of *Fusarium* species in the *Gibberella fujikuroi* complex.

Dr. Gudrun Dittrich-Schröder
Understanding and control of *Leptocybe invasa.*

Dr. Stuart Fraser
Epidemiology of *Uromycladium acaciae* on *Acacia mearnsii.*

Dr. Gerda Fourie
Evolution of species within the *Fusarium fujikuroi* species complex.

Dr. Mesfin Gossa
Diversity and distribution of eucalypt insect pests and their natural enemies in sub-Saharan Africa.

Dr. DongHyeon Lee
Invasive biology of *Ceratocystis* in South Africa.

Dr. Mark Maistry
Investigating proteins impacting organellar carbon metabolism during xylogenesis.

Dr. Victoria Maloney
Functional genetic analysis of cellulose and xylan related genes affecting woody biomass processing.

Dr. Gaby Nkouaya Mbanjo
Genome-wide dissection and molecular breeding of wood property traits in a clonal interspecific backcross population of *Eucalyptus grandis* and *E. urophylla.*

Dr. Alistair McTaggart
Rust fungi in South Africa.

Dr. Duccio Migliorini
Fungal pathogen distribution within cultivated and natural Proteaceae in South Africa and Western Australia.

Dr. Bilal Mir
Expression of recombinant hyperthermophilic enzymes in plant tissues: a novel approach for lignocellulose digestion.

Dr. Awelani Mutshembele
Evolution of the MAT locus and chromosome habouring it in *Fusarium sacchari*.

Dr. Trudy Paap
Monitoring tree health at sentinel sites: Botanic gardens and arboreta.

Dr. Sonia Phillips
Genomics of quantitative disease resistance in African maize varieties.

Dr. Ashok Prabhu
Unravellng the molecular basis of interaction between avocado-*Phytophthora cinnamoni* interaction through gene silencing.

Dr. Sonali Ranade
Population genetics of tropical pines.

Dr. Bianca Reeksting
Flooding responses in avocado.

Dr. Michelle Schröder
Local adaptation to temperature and host in the Eucalyptus snout beetle.

Dr. Louise Shuey
Defence responses against *Austropuccinia psidii* in *Eucalyptus grandis.*

Dr. Divine Shyntum
Omics of Pectobacterium carotovorum subsp. *Brasiliense.*

Dr. Stephen Taerum
Ophiostoma spp. associated with bark beetles.

Dr. Libert Brice Tonfack
Cell wall engineering to improve woody biomass feedstock degradation.

Dr. Maria Vivas
Environmental maternal effects on *Eucalyptus* microbiome and pathogen response.

Dr. Lydia Wahba
Expression profile for small RNAs for resistant/susceptible root rot in avocado.

Dr. Tania Weller-Stuart
Motility in *Pantoea ananatis.*

Dr. Markus Wilken
Understanding mating type switching in *Ceratocystis.*

POSTGRADUATE STUDENTS

CURRENT PhD STUDENTS

Omotayo Adenigba
The role of peptide pheromones in the biology of *Fusarium.*
Advisors: ET Steenkamp, NA van der Merwe, MJ Wingfield & BD Wingfield

Daniel Ali
Taxonomy and pathogenicity of Cryphonectriaceae on native Myrtales from Africa and Indonesia.
Advisors: MJ Wingfield, J Roux & A McTaggart

Teddy Amuge
Gene expression study of interactions between cassava and cassava brown streak disease.
Advisors: DK Berger, M Ferguson, J Harvey & AA Myburg
Advisors: B Slippers, S Naidoo & MJ Wingfield

Elrea Appelgryn
Characterisation and mechanisms of seasonal persistence of Soybean blotchy mosaic virus.
Advisor: G Pietersen

Juanita Avontuur
Identification and delineation of *Bradyrhizobium* supergroups based on genome data.
Advisors: ET Steenkamp & SN Venter

Robert Backer
Isolation and characterisation of non-expresser of pathogenesis related 1 (NPR1) in *Phytophthora cinnamomi* infected avocado (*Persea americana*).
Advisors: N van den Berg & S Naidoo

Kwabena Baffoe
Establishment of *Selitrichodes neseri* for the biological control of the bluegum chalcid, *Leptocybe invasa.*
Advisors: BP Hurley, B Slippers, J Garnas & MJ Wingfield

Tessa Bauman
Associations between fungi and root-infesting bark beetles in the USA and Nicaragua.
Advisors: ZW de Beer & MJ Wingfield

Chrizelle Beukes
Systematics and phylgeography of *Bradyrhizobium* in South Africa.
Advisors: ET Steenkamp & SN Venter

Khumbuzile Bophela
Abiotic and biotic factors associated with slow plum decline in the Western Cape.
Advisors: TA Coutinho, J Roux & Y Petersen

Tanay Bose
Diversity and distribution of Phytophthora species in South Africa with special reference to those causing diseases of *Eucalyptus* and *Acacia*.
Advisors: MJ Wingfield, J Roux & T Burgess (Australia)

Jonathan Botha
Chimeric enzymes for the *in planta* modification of secondary cell wall biopolymers.
Advisors: D Cowan & AA Myburg

Gabrielle Carstensen
Eucalyptus/Ralstonia interactions.
Advisors: TA Coutinho, SN Venter & MJ Wingfield

Annie Chan
Evolutionary history of the nitrogen fixation of rhizobial *Burkholderia* species associated with indigenous South African legumes.
Advisors: SN Venter & ET Steenkamp

RunLei Chang
Fungal associates of Ips bark beetles in China.
Advisors: ZW de Beer & MJ Wingfield

Magdaleen Cilliers
Soybean nodule development, nitrogen fixation and gene expression under water limiting conditions.
Advisor: BJ Vorster

Nicolene Douglas-Smith
Transmission of aster yellows to grapevine by insect vectors.
Advisors: K Kruger & G Pietersen

Marike du Plessis
Evolutionary approaches to delineate bacterial genera and species.
Advisors: SN Venter, ET Steenkamp & MPA Coetzee

Angelique du Preez
Diseases of cycads.
Advisors: J Roux & TA Coutinho

Elodie Ekoka
Investigation of putative transporters involved in carbon partition during xylogenesis.
Advisor: E Mizrachi & AA Myburg

Berhanu Fenta
Investigation of the physiological responses in soybean and common beans to water deficit.
Advisor: BJ Vorster

Katrin Fitza
The diversity and specificity of the *Deladenus siricidicola-Sirex noctilio-Amylostereum areolatum* complex.
Advisors: B Slippers & J Garnas

Arista Fourie
Genetics of host specificity.
Advisors: I Barnes, BD Wingfield & MJ Wingfield

Felix Fon Fru
Field ecology and epidemiology of the pitch canker pathogen, *Fusarium circinatum*, in South African pine plantations.
Advisors: J Roux, ET Steenkamp & MJ Wingfield

Izette Greyling
Ambrosia beetle associated diseases of *Eucalyptus* in South Africa.
Advisors: J Roux, ZW de Beer & MJ Wingfield

Quentin Guignard
Chemical and visual ecology of *Sirex noctilio.*
Advisors: B Slippers & J Allison (Natural Resources Canada)

Darryl Herron
The biodiversity of *Fusarium* spp. occurring in the commercial forestry industry.
Advisors: ET Steenkamp, BD Wingfield & MJ Wingfield

Joey Hulbert
Surveying the diversity and distribution of *Phytophthora* species in the Cape Floral Kingdom with citizen science.
Advisors: MJ Wingfield, J Roux, F Roets & T Burgess (Australia)

Miekie Human
Identification and characterisation of *Exserohilum turcicum.*
Advisors: BG Crampton & DK Berger

Zander Human
Bacterial symbionts of bark beetles.
Advisors: ZW de Beer, SN Venter & MJ Wingfield

Josephine Jere
Bacterial diseases of potatoes in Zimbabwe.
Advisors: J van der Waals & TA Coutinho

Delphin Kandolo
Altenaria spp. on a sweet potato.
Advisors: TAS Aveling, M Truter & J van der Waals

Aquillah Kanzi
Mating systems and the evolution of *Chrysoporthe* species.
Advisors: NA van der Merwe, ET Steenkamp & BD Wingfield

Godfrey Kgatle
Alternaria species associated with sunflower (*Helianthus annuus* L.) in South Africa: morphological, chemical and molecular characterisation, its implications and control.
Advisors: TAS Aveling, M Truter & B Flett

Tsholofelo Kibido
The role of *Rhizobium* strain and soybean cultivar on nitrogen fixation.
Advisor: BJ Vorster

Ilkadim Kiper
Molecular screening for interacting partners of *Phytophthora cinnamomi RxLR* effectors via yeast two-hybrid system.
Advisor: N van den Berg

Brigitte Langenhoven
Unravelling sorghum's transcriptomic response to *Exserohilum turcicum.*
Advisors: BG Crampton & SL Murray

JieQiong Li
Investigation of the taxonomy, mating types and population biology of *Calonectria* species.
Advisors: SF Chen, MJ Wingfield, I Barnes & J Roux

FeiFei Liu
Ceratocystidaceae in China.
Advisors: J Roux, MJ Wingfield & S Chen

Johan Liversage
Blue light perception in the maize foliar pathogen *Exserohilum turcicum.*
Advisors: BG Crampton & S Stoychev

Joseph Machua
Diseases of Eucalypts in Kenya.
Advisors: B Slippers, MJ Wingfield & J Roux

Molly Malefo
The role of serine protease inhibitors in maize during drought and pathogen stress.
Advisors: BG Crampton & E Makgopa

Edgar Mangwende
Seedbrone pathogens of *Eucalyptus* spp.
Advisor: TAS Aveling

Mkhululi Maphosa
Core and accessory genome of *Fusarium circinatum.*
Advisors: BD Wingfield & ET Steenkamp

Celia Martins
Characterising four cowpea (*Vigna unguiculata* (L.) Walp.) Mozambique landraces deposited in a seed bank for drought tolerance.
Advisor: J Vorster

Angelica Marsberg
Genetics of the endophyte-host interaction.
Advisors: B Slippers, S Naidoo & MJ Wingfield

Mandy Messal
Endophyte-host interactions.
Advisors: B Slippers, M Kemler & S Naidoo

Lorraine Mhoswa
Genome wide association study for *Leptocybe* resistance and associated chemotypes in *E. grandis.*
Advisors: S Naidoo & AA Myburg

Alain Misse
Ceratocystis species and their insect associates in the Tsitsikamma National Forests, South Africa.
Advisors: J Roux & MPA Coetzee

Rachel Mkandawire
Fusarium species associated with malformed inflorescences in *Syzigium cordatum*.
Advisors: ET Steenkamp, MJ Wingfield & G Fourie

Osmond Mlonyeni
Population genetics of *Deladenus siricidicola.*
Advisors: B Slippers, BP Hurley, MJ Wingfield & BD Wingfield

Valery Moloto
Bacterial diseases of onions.
Advisors: TA Coutinho, T Goszczynska & L du Toit

Mmoledi Mphahlele
Genome-wide selection for growth and wood property traits in *Eucalyptus grandis.*
Advisors: AA Myburg, F Isik & G Hodge

Jan Nagel
Causes and consequences of speciation within the *Neofusicoccum parvum/N. ribis* complex.
Advisors: B Slippers & MJ Wingfield

Valentine Nakato
Studies on the interaction between banana and *Xanthomonas campestris* pv. *Musacearum.*
Advisors: TA Coutinho, G Mahuku & J Legg

Buyani Ndlovu
Functional characterisation of putative *RxLR* effector genes from *Phytophthora cinnamomi.*
Advisor: N van den Berg

Phophi Nethononda
Biological control of Gonipterus sp. 2.
Advisors: BP Hurley & B Slippers

Sherrie-Anne New (University of Johannesburg)
Investgation of the “Brassica stunting disorder” affecting various brassica crops in South Africa.
Advisors: LL Esterhuizen & G Pietersen

Nare Ngoepe
Genome imputation and genome-wide association of fibre cell wall biosynthesis *in Eucalyptus grandis.*
Advisor: AA Myburg

Ntombi Nkomo
Pcb transcription factors and their role in adaptation to various environments.
Advisors: L Moleleki & D Shyntum

David Nsibo
Population genetics of *Cercospora zeina.*
Advisors: DK Berger & I Barnes

Isaiah Nthenga
Patterns and mechanisms of defense of entomopathogenic nematodes against white grubs (Scarabaeidae, Coleoptera).
Advisors: BP Hurley & B Slippers

Caryn Oates
A systems biology model of the interaction between *Eucalyptus* and the galling pest, *Leptocybe invasa.*
Advisors: S Naidoo, AA Myburg, B Slippers & K Denby

Marja O’Neill
Identification of the genetic basis for adaptation and selection in South African breeding populations of *Eucalyptus grandis.*
Advisor: AA Myburg

Margot Otto
Pseudomonas syringae pv. *syringae* as a pathogen of cherry trees.
Advisors: TA Coutinho, J Roux & Y Petersen

Edward Onkendi
High throughput functional analysis of *Pectobacterium.*
Advisors: L Moleleki & IK Toth

Mmatshepho Phasha
Pathogenicity factors of *Fusarium* species.
Advisors: ET Steenkamp, BD Wingfield, MJ Wingfield & MPA Coetzee

Zelda Pieterse
Fungi associated with mesembs in the Namaqua National Park in the Succulent Karoo biome.
Advisors: TAS Aveling & R Jacobs

Desre Pinard
The role of plastids and mitochondria in carbon allocation in the xylem of *Eucalyptus.*
Advisors: E Mizrachi & AA Myburg

Alisa Postma
Genomics of *Sirex-Amylostereum-Deladenus.*
Advisors: B Slippers, F Joubert & MJ Wingfield

Josephine Queffelec
Sex determination in *Sirex noctilio.*
Advisors: B Slippers, J Greeff & J Allison (Natural Resources Canada)

Danielle Roodt
Gene evolution of non-coniferous gymnosperms.
Advisors: E Mizrachi & Y van de Peer

Quentin Santana
Genome evolution and characteristics of *Fusarium circinatum.*
Advisors: MPA Coetzee, BD Wingfield, ET Steenkamp & MJ Wingfield

Mohammad Sayari
Pathogenicity factors of *Ceratocystis* species.
Advisors: BD Wingfield & ET Steenkamp

Gina Shin
Small RNAs in *Pantoea ananatis.*
Advisors: TA Coutinho, L Moleleki & D Shyntum

Vou Shutt
Bacterial diseases of potatoes in Nigeria.
Advisors: TA Coutinho & J van der Waals

Melissa Simpson
Microsatellite analysis of *Ceratocystis* species.
Advisors: BD Wingfield, MPA Coetzee, M van der Nest & MJ Wingfield

Elrea Strydom
Studies in the interseasonal persistence of soybean blotchy mosaic virus.
Advisor: G Pietersen

Lazarus Takawira
Identification of transcriptional networks regulating secondary cell wall biogenesis in *Eucalyptus grandis* through cis-element mining of key transcription factors.
Advisors: S Hussey & E Mizrachi

Collins Tanui
Transcriptome profiling of *Pectobacterium carotovorum* subsp. *brasiliense* reveals genes involved in ecological fitness and virulence mechanisms during infection.
Advisor: L Moleleki

Michel Tchotet
Woodrot fungi on native African trees.
Advisors: J Roux & MJ Wingfield

Renaan Thompson
Seedborne fungi on seeds of *Pinus* spp..
Advisor: TAS Aveling

Ariska van der Nest
Taxonomy and population studies on pine needle pathogens.
Advisors: I Barnes & MJ Wingfield

Johan van der Linde
Diseases of native tree *Euphorbia* species in southern Africa.
Advisors: J Roux, D Six & MJ Wingfield

Stefan van Wyk
Soybean nodule development and senescence: the role of cysteine proteases and inhibitors.
Advisor: BJ Vorster

Stephanie van Wyk
Characterisation of growth rate determining trait loci in *Fusarium circinatum*.
Advisors: ET Steenkamp & BD Wingfield

Erika Viljoen
Genetic diversity analysis of the *Amaranthus* genus using genomic tools.
Advisors: DK Berger, D Odeny & J Rees

Ronel Viljoen
Characterisation of *Candidatus* Liberobacter africanus subspecies from indigenous Rutaceae in South Africa.
Advisor: G Pietersen

Erik Visser
Models of defence mechanisms in *Pinus* species against *Fusarium circinatum.*
Advisors: S Naidoo, ET Steenkamp, L Wegryzn & AA Myburg

Andi Wilson
Unisexual reproduction in species of the *Huntiella* genus.
Advisors: BD Wingfield & MJ Wingfield

Lizahn Zwart
Characterising the temporo-spatial defense responses of *Eucalyptus grandis* to the fungal stem canker pathogen *Chrysoporthe austroafricanus.*
Advisors: S Naidoo, AA Myburg, D Berger, NA van der Merwe & L Moleleki

MSc STUDENTS

Daniela Arriagada Cares
The global diversity and introduction history of *Glycaspis brimblecombei* and its endosymbiont.
Advisors: B Slippers & J Garnas

Colan Balkwill
Genetic architecture and robustness of the circadian clock in a *Eucalyptus grandis* x *E. urophylla* backcross.
Advisors: E Mizrachi & AA Myburg

Andrew Behrens
Total RNA sequencing and discovery of non-coding RNAs in *Eucalyptus* xylem.
Advisors: E Mizrachi & AA Myburg

Caitlin Botha
The genetics of sexual reproduction in a Basidiomycete, *Amylostereum areolatum.*
Advisors: B Slippers, MPA Coetzee & MA van der Nest

Kirsty Botha
Characterisation of the cannabinoid biosynthetic pathway in *Helichrysum umbraculigerum.*
Advisors: BG Crampton & D Heyman

Johnathan Bredenkamp
Pheromone receptors in *Fusarium.*
Advisors: ET Steenkamp. G Fourie & BD Wingfield

Katrien Brown
The accessible chromatin landscape of *Eucalyptus grandis.*
Advisors: S Hussey & E Mizrachi

Michael Bufe
The early physiological response of avocado rootstocks to infection with *Phytophthora cinnamomi.*
Advisors: N van den Berg & N Taylor

Samantha Bush
Risk of *Glycaspis brimblecombei* to South African plantations.
Advisors: BP Hurley & B Slippers

Megan Calvert
Genome-wide dissection of secondary cell wall transcription factor variation in hybrid *Eucalyptus* species.
Advisors: AA Myburg & E Mizrachi

Edohan Clasen
Horizontal gene transfer in *Amylostereum*, *Deladenus* and *Sirex*.
Advisors: B Slippers, O Reva, R Pierneef & A Postma-Smidt

Donovin Coles
Functional characterisation of nitrate transporter 2.5 in *Arabidopsis thaliana* defense response using CRISPR-Cas9.
Advisors: S Naidoo & S Strauss

Herman de Bruin
Entomopathogens affecting tree pests in South Africa.
Advisors: B Slippers & ZW de Beer

Katrien de Ridder
Maize diseases of smallholder farmers in South Africa.
Advisors: TAS Aveling & D Berger

Claudio de Nuzzo
Fine-mapping QTL for GLS resistance.
Advisor: DK Berger

Esna du Plessis
Myrtle rust distribution, diversity and impact in South Africa.
Advisors: J Roux, A McTaggart & I Barnes

Magdeleen du Plessis
Cysteine proteases activity and gene expression in soybean nodules during development and drought stress.
Advisor: BJ Vorster

Yves du Toit
The development of a comparative transcriptomic tool to interrogate common defence mechanisms in *Eucalyptus grandis* under various biotic challenges.
Advisors: S Naidoo, N Christie & AA Myburg

Ludwig Eksteen
Host use and spatial pattern of attachment in the invasive European wood wasp, *Sirex noctilio.*
Advisor: J Garnas & BP Hurley

Stephan Engelbrecht
Genome-wide allele-specific expression analysis of *Eucalyptus* hybrids.
Advisors: AA Myburg & N Christie

Miranda Erasmus
Taxonomy and biology of the *Ophiostoma abietinum* complex.
Advisor: ZW de Beer

Shania Facey
Grapevine leafroll associated virus S in *Vitis* rootstocks.
Advisor: G Pietersen

Shannon Flemington
Systemic defence responses of *Eucalyptus grandis* to *Chrysoporthe austroafricana* and its biological significance.
Advisor: S Naidoo

Caitlin Gevers
Investigating the complex gall community of *Leptocybe invasa.*
Advisors: BP Hurley & B Slippers

Lichelle Grobler
CRISPR-Cas9 knockout of a selected protease in *Nicotiana benthamiana.*
Advisors: BG Crampton, MM O'Kennedy & P Pillay

Megan Harris
Detection of grapevine leafroll associated viruses in *Vitis* rootstocks.
Advisor: G Pietersen

Juanita Hannemann
The development of SNP markers for the diversity analysis, identification and parentage reconstruction in avocado cultivars.
Advisors: N van den Berg, AA Myburg & D Kuhm

Daniel Harty
Reconstructing the transcriptional co-regulation of early xylem differentiation in *Eucalyptus* using network theory towards biotechnological improvement of plant biomass.
Advisors: E Mizrachi, DS Pinard, D Roodt & S Hussey

Stephan Henning
Assessment of genomic introgression patterns in *Eucalyptus grandis* x *E. urophylla* natural hybrid populations using genome-wide SNP marker analysis.
Advisors: AA Myburg & M Reynolds

Bianca Jardim
CRISPR-cas9 targets on sex determination genes in *Sirex.*
Advisor: B Slippers

Melissa Joubert
Developing a novel pathosystem for the molecular study of *Phytophthora cinnamomi* using *Nicotiana benthamiana.*
Advisor: N van den Berg

Tamanique Kampman
Assembly and annotation of the transcriptomes of three pine species - *Pinus maximinoi, P. greggii* and *P. oocarpa.*
Advisors: S Naidoo & AA Myburg

Tshepang Khahlu
Regulation of photosynthesis and nitrogen fixation in soybean.
Advisor: BJ Vorster

Ncobile Kunene
Mating type gene analysis of *Cercospora zeina* populations in South Africa
Advisors: DK Berger & S Phillips

Thapelo Maboko
Botryosphaeriaceae associated with *Myrtaceae*.
Advisors: NA van der Merwe & BG Crampton

Angel Maduke
Botryosphaeriaceae on native and non-native *Myrtaceae* in eastern and southern Africa.
Advisors: J Roux & D Pavlic-Zupanc

Ntwanano Maluleke
The impact of soft rot pathogens on crop production in South Africa.
Advisor: L Moleleki

Tintswalo Maluleke
Transcriptome analysis and protease identification in the gut of *Cosmopolites sordidus.*
Advisor: BJ Vorster

Katlego Masike
Host induced gene silencing of a *Cercospora nicotianae* pathogenicity factor.
Advisors: BG Crampton & J Liversage

Lerato Maubane (University of the Freestate)
Pine needle fungal endophytes including species of *Lophodermium.*
Advisors: M Gryzenhout, B Slippers & MJ Wingfield

Lungi Mavuso
Studying the effect of salt stress on avocado tree health.
Advisors: N van den Berg & N Taylor

Tsakani Miyambo
In silico identification and characterisation of polygalacturonases in *Persea americana* during PG-PGIP interaction.
Advisors: N van den Berg & A Prabhu

Zimbili Mlunjwa
Expression of candidate maize defence genes in response to *Cercospora zeina.*
Advisor: DK Berger

Seamus Morgan
Quambalaria species from *Eucalyptus* and *Gonipterus* weevils in South Africa.
Advisors: ZW de Beer, MJ Wingfield & M Schroder

Gabolwelwe Mosina
Towards understanding induced resistance mechanisms of potato plants.
Advisor: L Moleleki

Tshepiso Motlolometsi
Cyclic-di-GMP, a small signalling molecule aiding communication SRE.
Advisor: L Moleleki

Zanelle Mufamadi
Identiying the causal agents of macadamia husk rot in South Africa.
Advisors: N van den Berg & M Schoeman

Yolanda Musasira
Population studies on *Armilaria* species in South Africa.
Advisors: MPA Coetzee & MJ Wingfield

Dora Mwangola
Population genetics of *Chrysoporthe austroafricana* in Southern Africa.
Advisors: NA van der Merwe & J Roux

Alandie Nieuwoudt
Development of a CRISPR-Cas9 gene knockout system for *Exserohilum turcicum.*
Advisors: BG Crampton & MP Human

Wilma Nel
Taxonomy and mating in the root pathogen *Thielaviopsis basicola.*
Advisors: ZW de Beer, TA Duong & MJ Wingfield

Phophi Nesengami
Rhizobium associated with indigenous legumes of the Namaqualand region.
Advisors: ET Steenkamp & SN Venter

Kayla Noeth
Biology and management of the cossid moth.
Advisors: BP Hurley & B Slippers

Mashudu Nxumalo
Diversity of nitrogen symbionts of *Lebeckia* species.
Advisors: SN Venter & ET Steenkamp

Owen Petersen
The effect of pine seed size on emergence in the nursery.
Advisors: P Chirwa & TAS Aveling

Nam Pham
Calonectria species from Vietnam.
Advisors: MJ Wingfield, J Roux, I Barnes & SF Chen

Liezl Potgieter
Armillaria polygalacturonases.
Advisors: MPA Coetzee, BD Wingfield & M van der Nest

Wilhelm Pretorius
Potato microRNA profiling.
Advisor: L Moleleki

Stefan Priem
Root knot nematodes interaction with Pcb - the role of biofilms.
Advisors: L Moleleki & TA Coutinho

Mohd Redzuan Abdul Rauf
Diseases of forestry importance to Malaysia.
Advisors: MJ Wingfield, I Barnes & J Roux

Emeldah Rikhotso
Leaf diseases of *Eucalyptus grandis* and hybrids in South Africa, with particular reference to Teratosphaeria.
Advisors: J Roux & I Greyling

Kavani Sanasi
Fungal associates of pine bark beetles in Guatemala.
Advisors: ZW de Beer & MJ Wingfield

Azille Schulze
An analysis of the maize lethal necrosis disease potyvirus components in South Africa.
Advisor: G Pietersen

Mohamed Seedat
Identification of Crinkler (CRN) effector genes in *Phytophthora cinnamomi* during avocado root infection.
Advisors: N van den Berg & S Naidoo

Karabo Sereme
Description of new *Burkholderia* species.
Advisors: SN Venter, ET Steenkamp & E Venter

Sydney Sithole
Molecular characterisation of NRPS genes in *Chrysoporthe austroafricana.*
Advisors: NA van der Merwe, S Naidoo & ET Steenkamp

Vimbai Siziba
Population genetics of the Dothistroma needle blight pathogen, *Dothiostroma pini.*
Advisors: I Barnes & MJ Wingfield

Rynhard Smit
Identification of molecular markers to assess *Moringa oleifera.*
Advisor: BJ Vorster

Robyn Smith
Targeted expression profiling of a key defence pathway in *Pinus patula, Pinus tecumumanii* and hybrid seedlings in response to *Fusarium circinatum.*
Advisors: S Naidoo & ET Steenkamp

Julanie Stapelberg
Transformation of South African microalgal species.
Advisors: BG Crampton, R Roth & MC Crampton

Riaan Swanepoel
De novo assembly and annotation of a gene catalogue from *Welwitschia mirabilis.*
Advisors: E Mizrachi & F Joubert

Benedicta Swalarsk-Parry
Characterisation of growth in *Fusarium circinatum.*
Advisors: L de Vos, ET Steenkamp & BD Wingfield

Catherine Tatham
Mat locus and population markers in *Teratosphaeria destructans*.
Advisors: BD Wingfield, MJ Wingfield & M Wilken

Yokateme Junior Tii-kuzu
Population genomics and molecular breeding in *Eucalyptus.*
Advisor: AA Myburg

Conrad Trollip
Pathogenesis of *Ceratocystis eucalypticola.*
Advisors: BD Wingfield, MA van der Nest, I Barnes & MJ Wingfield

Nadine Venter
Characterisation of T4P in Pcb.
Advisors: L Moleleki & J Theron

Bradley Vincent
The characterisation of catechol dioxygenase genes in species from the Ceratocystidaceae.
Advisors: MPA Coetzee, A Hammerbacher & BD Wingfield

Jennifer Wayland
Development of a diagnostic system for viruses of grapevines based on polyspecific PCR.
Advisor: G Pietersen

Tanya Welgemoed
Mapping and *de novo* assembly of maize transcriptomes for defence gene discovery.
Advisors: DK Berger & R Pierneef

Martin Wierzbicki
Systems genetics of xylan side chain modifications.
Advisors: AA Myburg & E Mizrachi

4TH YEAR AND HONOURS STUDENTS

Johnathan Bredenkamp (2015)
Katrien Brown (2015)
Donovin Coles (2015)
Esna du Plessis (2015)
Stephan Engelbrecht (2015)
Hanlica Erasmus (2015)
Juanita Hanneman (2015)
Robyn Kahn (2015)
Kerstin Kenchensen (2015)
Xongani Khosa (2015)
Nadine Koen (2015)
Marike Louw (2015)
Malebo Makunyane (2015)
Katlego Masike (2015)
Pfano Mbedzi (2015)
Pitsi Mokou (2015)
Wilma Nel (2015)
Alandie Nieuwoudt (2015)
Monique Otto (2015)
Shamara Polliack (2015)
Azille Schulze (2015)
Catherine Tatham (2015)
Karin van der Westhuizen (2015)
Elzette Wentzel (2015)
Catherine Wickham (2015)
Nadine Botha (2016)
Rochelle Clase (2016)
Jaco Coetzee (2016)
Claudio de Nuzzo (2016)
Shannon Flemington (2016)
Alessandro Gricia (2016)
Lichelle Grobler (2016)
Daniel Harty (2016)
Stephan Henning (2016)
Claire Jordaan (2016)
Melissa Joubert (2016)
Puseletso Manyaka (2016)
Seamus Morgan (2016)
Thabang Msimango (2016)
Brighton Ncube (2016)
Talia Pillay (2016)
Julianie Stapelberg (2016)
Bradley Vincent (2016)
Tanya Welgemoed (2016)
Rebecca Ackermann (2017)
Leandri Bezuidenhout (2017)
Julia Candotti (2017)
Ricu Claassens (2017)
Claudette Dewing (2017)
Michael du Toit (2017)
Aurona Gerber (2017)
Jess Hartley (2017)
Angelique Jacobsohn (2017)
Rochelle Janse van Rensburg (2017)
Hye Jin Lin (2017)
Eugene Kabwe (2017)
Deanah Lloyd (2017)
Lizette Loubser (2017)
Lungile Mabuza (2017)
Phinda Magagula (2017)
Kayleigh Maier (2017)
Palesa Mohale (2017)
Nicola Soal (2017)
Hannes Strydom (2017)
Francois Viljoen (2017)
Nomakula Zim (2017)

STUDENT ASSISTANTS

Walter Bronkhorst (2015)
Axel Ind (2015)
Mzuvumile Mbane (2015)
Gert Pietersen (2015)
Loandi Richter (2015)
Tanya Welgemoed (2015)
Vaughn Barendsen (2015, 2016)
Derick Classens (2015, 2016)
Rachel Makwasi (2015, 2016)
Modjadji Makwela (2015, 2016)
Mzuvumile Mbane (2015, 2016)
Thabang Msimango (2015, 2016)
Brad Querl (2015, 2016)
Nomakula Zim (2015, 2016)
Simon Badenhorst (2016)
Stephan Baggeröhr (2016)
Leandri Bezuidenhout (2016)
Peter Bredenkamp (2016)
Paige Klepper (2016)
Claire Lenahan (2016)
Kelen Pillay (2016)
Lebone Sebapu (2016)
Carol-Ann Segal (2016)
Bernard Smit (2016)
Maryn van der Laarse (2016)
Lize Elliot (2016, 2017)

CTHB MENTORSHIP STUDENTS

Thendo Budeli (2015)
Lenye Dlamini (2015)
Shannon Flemington (2015)
Keitumetse Gama (2015)
Daniel Harty (2015)
Angela Hoffman (2015)
Melissa Joubert (2015)
Frances Lane (2015)
Kubekho Makalima (2015)
Monewa Matlwa (2015)
Seamus Morgan (2015)
Lindokuhle Nkambule (2015)
Elre Sauerman (2015)
Carol-Ann Segal (2015)
Jacques Snyman (2015)
Ettiene Theron (2015)
Sarah Galichan (2015, 2016)
Doré Joubert (2015, 2016)
Smangele Malema (2015, 2016)
Claire Bekker (2016)
Riki-Lee Hartwell (2016)
Angelique Jacobsohn (2016)
Meta Leshabane (2016)
Kayleigh Maier (2016)
Reabetswe Masebe (2016)
Elizabeth Mathibela (2016)
Mary Tshiove (2016)
Anne Ankermann (2016, 2017)
Robert Jansen van Vuuren (2016, 2017)
Marin Peroski (2016, 2017)
Amber Tulloch (2016, 2017)
Anne Ankermann (2017)
Vusumuzi Chiloane (2017)
Nokukhanya Dube (2017)
Daniel Joubert (2017)
Letabo Lefoka (2017)
Sade Magabotha (2017)
Christopher Marais (2017)
Jamie Mollentze (2017)
Khanyisile Nkosi (2017)
Rochelle Rademan (2017)
Elke Roos (2017)
Kadima Tshiyoyo (2017)
Mandelie van der Walt (2017)
Palesa Zulu (2017)

FACULTY MENTORSHIP STUDENTS

Lichelle Grobler (2015)
Julanie Stapelberg (2015)
Palesa Mohale (2016)

RECENT GRADUATES

PhD

Birhan Abate (2017)
Title: Molecular characterisation and evaluation of entomopathogenic nematodes in South African forestry plantations.
Advisors: BP Hurley, B Slippers & MJ Wingfield

Janneke Aylward (2017) Stellenbosch University
Title: Comparative genomics of *Knoxdaviesia* species.
Advisors: LL Dreyer, F Roets, ET Steenkamp, MJ Wingfield & BD Wingfield

Vaughan Bell (2015) University of Victoria, Wellington, New Zealand
Title: An integrated strategy for managing *Grapevine leafroll-associated virus 3* in red berry cultivars in New Zealand.
Advisors: PJ Lester & G Pietersen

Elsie Cruywagen (2016)
Title: Diversity and taxonomy of fungi infecting species of *Adansonia* (Baobab).
Advisors: MJ Wingfield, J Roux & B Slippers

Gerda Fourie (2015)
Title: Evolution of mitochondrial genomes in the *Fusarium fujikuroi* species complex.
Advisors: ET Steenkamp, NA van der Merwe & MJ Wingfield

Mesfin Gossa (2017)
Title: Ecology and diversity of introduced *Pissodes* (Coleoptera: Curculionidea) in South Africa.
Advisors: BP Hurley, J Garnas & B Slippers

Luke Jimu (2016)
Title: Diseases and pests of *Eucalyptus* species in Zimbabwe with particular reference to Teratosphaeria stem canker.
Advisors: J Roux, MJ Wingfield & E Mwenje (University of Bindura, Zimbabwe)

Jeanne Korsman (2015)
Title: Molecular responses of maize to its foliar pathogen, *Cercospora zeina*.
Advisors: DK Berger & BG Crampton

Stanford Kwenda (2017)
Title: Transcriptome profiling of potato plant stems challenged with *Pectobacterium carotovorum* subsp. *brasiliense* and elucidation of the role of small RNAs in *Pectobacterium* survival mechanisms.
Advisors: L Moleleke & P Birch

DongHyeon Lee (2016)
Title: Biology of *Ceratocystis albifundus* and *C. pirilliformis* in South Africa.
Advisors: MJ Wingfield, J Roux & BD Wingfield

Waheed Mahomed (2016)
Title: Describing the continuum of salicylic and jasmonic acid mediated defence responses in the avocado-*Phytophtora cinnamomi* interaction.
Advisors: N van den Berg & BG Crampton

Ronishree Mangwanda (2016)
Title: Investigations into the transcriptional response of *Eucalyptus grandis* against *Chrysoporthe austroafricana.*
Advisors: S Naidoo & AA Myburg

Ritesh Mewalal (2016)
Title: Functional characterisation of cell wall-related proteins of unknown function (CW-PUFs) in *Arabidopsis thaliana*.
Advisors: AA Myburg, E Mizrachi & SD Mansfield (University of British Columbia, Canada)

James Mehl (2017)
Title: Factors influencing the distribution of selected species of the *Botryosphaeriaceae.*
Advisors: MJ Wingfield, J Roux & B Slippers

Jacqueline Meyer (2017)
Title: RNA-Seq and metabolic profiling of resistant and susceptible tropical maize lines reveals a role for kauralexins in resistance to grey leaf spot disease caused by *Cercospora zeina*.
Advisors: D Berger & S Murray (University of Cape Town) & AA Myburg

Gloria Mukwirimba (2015)
Title: Seedborne pathogens of brassica species and efficacy of alternative seed treatments as methods of control.
Advisors: TAS Aveling & Q Kritzinger

Eston Mutitu (2017)
Title: Invasion history of *Thaumastocoris peregrinus* and development of a biological control agent.
Advisors: B Slippers, J Garnas, BP Hurley & MJ Wingfield

Sarai Olivier-Espejel (2016)
Title: Patterns and drivers of insect community diversity and composition in non-native black wattle and pine plantations in South Africa.
Advisors: J Garnas & BP Hurley

Alexander Osorio (2017)
Title: Diseases of mangrove trees in South Africa.
Advisors: J Roux, ZW de Beer, B Slippers & MJ Wingfield

Priyen Pillay (2017)
Title: Characterisation of VP1 protein sensitivity against proteases and identification of agroinfiltration-induced proteases in *Nicotiana benthamiana* leaves.
Advisors: BJ Vorster

David Read (2015)
Title: Overcoming bias in citrus tristeza virus (CTV) genotype detection and a population study of CTV within southern African star ruby grapefruit orchards.
Advisor: G Pietersen

Bianca Reeksting (2015)
Title: Elucidating the early response of *Persea americana* to *Phytophthora cinnamomi* and flooding.
Advisors: N van den Berg & N Taylor

Siphathele Sibanda (2017)
Title: Functional analysis of quorum sensing in *Pantoea ananatis* LMG 2665^T.
Advisors: T Coutinho, L Moleleki & D Shyntum

Fred Ssekiwoko (2016)
Title: The mechanism of resistance to *Xanthomonas vasicola pv. musacearum* explored in *Musa balbisiana.*
Advisor: K Kunert

Gary Stevens (2015) Stellenbosch University
Title: PEPc regulation of biological nitrogen fixation in *Virgillia* during phosphate stress.
Advisors: A Valentine & ET Steenkamp

Velushka Swart (2017)
Title: Functional genomics of the cercosporin biosynthetic gene cluster in the maize pathogen, *Cercospora zeina.*
Advisors: DK Berger & BG Crampton

Stephen Taerum (2015)
Title: Origin and diversity of the invasive red turpentine beetle and its fungal symbionts.
Advisors: MJ Wingfield & ZW de Beer

Stefan van Wyk (2015)
Title: Soybean nodule development and senescence: The role of cysteine proteases and their inhibitors.
Advisors: J Vorster & C Cullis (Case Western Reserve University, USA)

Wafeeka Vardien (2015) Stellenbosch University
Title: Phosphorus acquisition strategies in *Virgillia* root systems during phosphate stress
Advisors: A Valentine & ET Steenkamp

Tania Weller-Stuart (2015)
Title: Genomic and functional characterisation in *Pantoea ananatis*.
Advisors: TA Coutinho, I Toth & P de Maayer

Markus Wilken (2015)
Title: Genetics of the mating system in *Ceratocytis fimbriata sensu stricto*, explored via whole-genome sequence analysis.
Advisors: BD Wingfield, ET Steenkamp, MJ Wingfield & ZW de Beer

MingLiang Yin (2015)
Title: Taxonomic revision of four major species complexes in the Ophiostomatales (Fungi, Ascomycota), with specific reference to associates of conifer-infesting bark beetles in China.
Advisors: ZW de Beer, XD Zhou & M Wingfield

MSc

Juanita Avontuur (2017)
Title: *Bradyrhizobium* species associated with native legumes.
Advisors: SN Venter, ET Steenkamp & E van Zyl

Johan Bestbier (2016)
Title: HPLC and colourimetric quantification of shikimic acid levels in crops after glyphosphate treatment.
Advisor: BJ Vorster

Khumbuzile Bophela (2016)
Title: Enterobacter and Xanthomonas species associated with blight and die-back of *Eucalyptus*.
Advisors: TA Coutinho & SN Venter

Francois Boshoff (2015)
Title: *Bradyrhizobium* species associated with native and non-native *Acacia* species.
Advisors: ET Steenkamp & SN Venter

Vanessa Cronje (2016)
Title: Infection and colonisation of onion seedlings by *Pantoea ananatis* and *P. allii*.
Advisors: TA Coutinho & N van den Berg

Herman de Bruin (2016) *cum laude*
Title: Characterising the diversity of Beauveria species infecting insects in South African plantations.
Advisors: B Slippers & ZW de Beer

Susan de Raan (2015) *cum laude*
Title: Management of soft rot and black leg of potatoes in South Africa.
Advisors: J van der Waals & TA Coutinho

Katrien de Ridder (2017)
Title: A survey of major foliar and ear rot diseases in selected smallholder maize farms in KwaZulu-Natal and the Eastern Cape.
Advisors: TAS Aveling & DK Berger

Angelique du Preez (2016)
Title: Flagellin glycosylation in *Pantoea ananatis*.
Advisors: P de Maayer & TA Coutinho

Simone Fouche (2015) *cum laude*
Title: Molecular characterisation of an accessory chromosome of *Fusarium circinatum.*
Advisors: ET Steenkamp, MPA Coetzee & BD Wingfield

Monique Heystek (2015)
Title: Promoter analysis of three defence gene family members from maize in response to *Cercospora zeina.*
Advisors: DK Berger & BG Crampton

Degracious Kgoale (2015)
Title: Gene expression study of candidate *Arabidopsis* defence genes in response to the bacterial wilt pathogen.
Advisors: DK Berger & S Naidoo

Matt Laubscher (2016)
Title: Functional genomic analysis of *Eucalyptus grandis* secondary cell wall-related transcription factors EgrNAC26 through heterologous induction in *Arabidopsis* mesophyll.
Advisors: S Hussey, AA Myburg & E Mizrachi

Johan Liversage (2015) *cum laude*
Title: Functional characterisation of the *Cercospora zeina crp1* gene in pathogenesis.
Advisors: BD Crampton & DK Berger

Jacolene Lubbe (2015)
Title: Molecular and biological characterisation of three citrus tristeza virus candidate cross-protection sources.
Advisor: G Pietersen

Palesa Madupe (2016)
Title: A comparative genomic study on *Xanthomonas vasicola* strains from different hosts, including an isolate from *Eucalyptus grandis*.
Advisors: TA Coutinho & SN Venter

Olga Makhari (2015)
Title: Population biology of *Fusarium circinatum* Nirenberg et O'Donnell associated with South African *Pinus radiata* D. Don plantation trees.
Advisors: ET Steenkamp, TA Coutinho & MJ Wingfield

Molly Malefo (2015)
Title: Characterisation of selected pathogenicity factors in *Cercospora zeina.*
Advisors: BG Crampton & DK Berger

Edgar Mangwende (2015)
Title: Seedborne fungi of herbs cultivated in South Africa and evaluation of non-chemical seed treatments to control *Alternaria* sp. on coriander.
Advisors: TAS Aveling & Q Kritzinger

Claire Martin (2016)
Title: Elicitation of medicinally active dicaffeoylquinic acid derivatives from *Helichrysum populifolium* (Asteraceae).
Advisors: B Crampton, I Gazendam (Agricultural Research Council); HM Heyman (Pacific Northwest National Laboratory, USA)

Mischa Muller (2015)
Title: Molecular diversity of the maize pathogen *Cercospora zeina* in South Africa.
Advisors: DK Berger, BG Crampton & I Barnes

Rofhiwa Nesamari (2016)
Title: Identification of diseases and pests of cycads in South Africa.
Advisors: J Roux & TA Coutinho

Danielle Roodt (2016)
Title: The mating genetics and core genome of *Ceratocystis albifundus.*
Advisers: BD Wingfield, MJ Wingfield & M Wilken

Gi Yoon Shin (2016) *cum laude*
Title: Investigation of the genetic diversity of *Pantoea ananatis*.
Advisors: SN Venter & TA Coutinho

Sarah Stanton (2015)
Title: Phytochemical and morphological comparison between *Pachystigma* species
Advisors: M Meyer & TA Coutinho

Thomas Schmidt (2015)
Title: Bolistic transformation in maize leaves
Advisors: DK Berger & BG Crampton

Kirsti Snyders (2016)
Title: Detection and isolation of homogeneous genotypes of citrus tristeza virus for use in virus control through cross protection.
Advisor: G. Pietersen

Collins Tanui (2016)
Title: Characterising quorum sensing regulation of virulence in *Pectobacterium carotovorum* subsp. *Brasiliensis*.
Advisor: LN Moleleki

Katie Termer (2015)
Title: Biotic and abiotic determinants of resource quality for larvae of *Sirex noctilio.*
Advisor: J Garnas

Stephanie van Wyk (2016) *cum laude*
Title: Molecular characterisation of the growth rate determining quantitative trait locus in *Fusarium circinatum.*
Advisors: ET Steenkamp, NA van der Merwe, L de Vos & BD Wingfield

Erik Visser (2015)
Title: Transcriptome based investigation of *Pinus patula* susceptibility to *Fusarium circinatum* infection.
Advisors: S Naidoo, ET Steenkamp & AA Myburg

Andrea Wilson (2016) *cum laude*
Title: Mating system in *Huntiella* species.
Advisors: BD Wingfield, MA van der Nest, PM Wilken & MJ Wingfield

PRESTIGIOUS NRF BURSARY HOLDERS

NRF SCARCE SKILLS/INNOVATION SCHOLARSHIPS

Colan Balkwill, 2014-2015
Kirsty Botha, 2014-2015
Michael Bufe, 2014-2015
Matt Laubscher, 2014-2015
Waheed Mahomed, 2014-2015
Jonathan Botha, 2014-2016
Arista Fourie, 2014-2016
Buyani Ndlovu, 2014-2016
Caryn Oates, 2014-2016
Desre Pinard, 2014-2016
Ariska van der Nest, 2014-2016
Miekie Human, 2014-2017
Andrew Behrens, 2015-2016
Lizahn Zwart, 2015-2016
Martin Wierzbicki, 2015-2016
Bianca Reeksting, 2015-2016
Robert Backer, 2015-2017
Brigitte Langenhoven, 2015-2017
Johan Liversage, 2015-2017
Molly Malefo, 2015-2017
Margot Otto, 2015-2017
Tsakani Miyambo, 2016-2017
Alandie Nieuwoudt, 2016-2017
Azille Schulze, 2016-2017
Sydney Sithole, 2016-2017
Khumbuzile Bophela, 2016-2018
Gina Shin, 2016-2018
Elrea Strydom, 2016-2019

CLAUDE LEON POSTGRADUATE FELLOWSHIPS

Dr. Gerda Fourie
Dr. Bianca Reeksting
Dr. Markus Wilken

OTHER SCHOLARSHIPS

Sonia Naidoo, Canon Collins Scholarship
Richard Kotze, Maize Trust
David Read, Citrus Research International
Ronel Roberts, Citrus Research International
Jacolene Lubbe, Citrus Research International
Kirsti Snyders, Citrus Research International
Jennifer Wayland, Winetech Industry
Megan Harris, Winetech Industry
Shania Facey, Winetech Industry

MANAGEMENT COMMITTEE

Prof. DK Berger
Prof. TA Coutinho
Prof. J Roux
Prof. K Kunert
Prof. AA Myburg
Extraordinary Prof. G Pietersen
Prof. B Slippers
Prof. ET Steenkamp
Prof. SN Venter
Prof. MJ Wingfield (Chairman)

Assoc. Prof. TAS Aveling
Assoc. Prof. ZW de Beer
Assoc. Prof. L Moleleki
Assoc. Prof. N van den Berg

Dr. I Barnes
Dr. MPA Coetzee
Dr. BG Crampton
Dr. J Garnas
Dr. BP Hurley
Dr. E Mizrachi
Dr. S Naidoo
Dr. NA van der Merwe
Dr. BJ Vorster
Dr. L Shuey (Postdoctoral representative, 2015)

ADVISORY COMMITTEE

Prof. J Lubuma (Chairman), Dean of the Faculty of Natural and Agricultural Sciences
Prof. P Bloomer, Head of the Department of Genetics
Prof. SN Venter, Head of the Department of Microbiology & Plant Pathology (2015, 2016)
Prof. L Moleleki, Acting Head of the Department of Microbiology and Plant Pathology (2016, 2017)
Prof. W Dittrich-Schubert, Acting Head of the Department of Biochemistry
Prof. N Barker, Head of the Department of Plant and Soil Science
Prof. C Allandale, Head of the Department of Plant Production
Prof. C Chimimba, Head of the Department of Zoology & Entomology
Prof. P Chirwa, Forestry School
Prof. CL Machethe, Postgraduate School of Agriculture and Rural Development
Prof. D Cowan, Genomics Research Institute
Prof. BD Wingfield, Deputy Dean of the Faculty of Natural and Agricultural Sciences
Prof. MJ Wingfield, Director of the Forestry and Agricultural Biotechnology Institute (FABI)

SOME SOCIAL HIGHLIGHTS IN FABI

ANNUAL SPOOF* MEETING 2015

**Society for the Presentation of Outrageous Findings*

Theme: If I never became a scientist... What would I be?

Mike and Brenda Wingfield.

Zander Human and Mia du Preez.

Benny Swalarsk-Parry, Angel Maduke and Dora Mwangola.

Aquillah Kanzi.

Mohammad Sayari and Alex Osorio.

Riaan Swanepoel and Mike Wingfield.

ANNUAL SPOOF MEETING 2016

Theme: Your favourite animated character is...

Nam Pham, FeiFei Liu, Emeldah Rikhotso, Daniel Ali and Angel Maduke.

Megan Harris and partner.

Bernard Slippers.

Christo van Zyl and Esna du Plessis.

Darryl Herron, Fahimeh Jami and Amin Jami.

Benny Swalarsk-Parry and Quentin Guignard.

YEAR END FUNCTION 2015

Ginna Granados, Rachel Mkandawire and Vou Shutt.

Ramesh Aadi Moolam, Buyani Ndlovu, Lydia Wahba, Ashok Prabhu and Daniel Ali.

Plant Virology Group: Jennifer Wayland, Megan Harris, Prof. Gerhard Pietersen, Elrea Strydom and Azille Schulze.

Osmond Mlonyeni and James Mehl.

Prof. Mike Wingfield and Darryl Herron.

Prof. Mike Wingfield and Juanita Avontuur.

YEAR END FUNCTION 2016

JieQiong Li, Nam Pham, Arista Fourie and Katrin Fitza.

JieQiong Li, Seonju Marincowitz and RunLei Chang.

Rachel Mkandawire, Vou Shutt, Esther Muema and Mmatshepho Phasha.

Mike Wingfield and Arista Fourie.

Mike Wingfield and Joey Hulbert.

TEAM ACHIEVEMENTS

FABI Synthetic Biology Team Wins Silver Medal at Prestigious International Competition

What do seven biologists, three engineers and a multimedia student all have in common? A passion for transdisciplinary research and excellence in scientific innovation. This eclectic group of students comprise the 2016 Pretoria_UP iGEM (international Genetically Engineered Machine) undergraduate team that developed unique synthetic biology and hardware modifications for more efficient electricity generation in plant materials-derived photo-bioelectrochemical cells. Their project, dubbed "WattsAptamer", explored the attachment of plant photosynthetic machinery to graphene electrodes using custom DNA-based linkers known as aptamers, in order to enhance the efficiency of electron harvesting from photosynthesis for electricity generation. Among other achievements, the team also developed a novel, open-source, 3D-printed photo-bioelectrochemical cell prototype that was shown to generate electricity in the presence of light. The team, which was hosted in the Forest Molecular Genetics (FMG) Programme, Department of Genetics and Forestry and Agricultural Biotechnology Institute (FABI), was mentored by their instructor Dr. Steven Hussey and additionally advised by Prof. Zander Myburg and Dr. Eshchar Mizrachi (FMG) as well as Prof. Ncholu Manyala, Dr. Tjaart Krüger and Dr. Michal Gwizdala from the Department of Physics. In October 2016, the team presented their project at the iGEM Giant Jamboree in Boston as one of over 300 teams from across the world and only two from Africa. They fulfilled the criteria for a silver medal for their project at the competition, which they documented in an extensive wiki, poster and oral presentation, and which also included an extensive human-practices portfolio focused on engagement with the energy sector, community outreach and education, local synthetic biology competency development and international collaboration. Sappi Southern Africa was the official team sponsor, with additional support from the University of Pretoria, the Department of Science and Technology, Inqaba Biotec, the National Science and Technology Forum, Whitehead Scientific, Integrated DNA Technologies and the African Centre for Gene Technologies.

The 2016 Pretoria_UP iGEM team. From L to R: Modjadji Makwela, Ricu Claassens, Maryn van der Laarse, Thabang Msimango, Simon Bezuidenhout, Nomakula Zim, Bernard Smit, Brad Querl, Vaughn Barendsen, Pieter Bredenkamp, Stephan Baggeröhr.

CONNECTING THE DOTS

The FABI "CONNECTING THE DOTS" t-shirt was launched at the at the Institute's January 2016 formal opening. The interconnected "dots" on the shirt illustrate many aspects of FABI's activities and successes. In the most simple explanation "connecting the dots" is a metaphor illustrating the ability to associate one idea with another and ultimately to find the "big picture". Many of FABI's research, community engagement and social activities aptly illustrate how this "big picture" is continuously pursued. At the 2016 FABI Opening, FABI Director Mike Wingfield spoke to the students and staff of the Institute regarding the importance of planning ahead and how this should also be achieved strategically. In this regard, he emphasised the concept of Strategic Thinking, which following the 1994 thesis of the internationally renowned business leader and academic Henry Mintzberg is about synthesis or "CONNECTING THE DOTS". This is as opposed to analysis or finding the dots. In all activities of FABI, both approaches are fundamentally important and they deeply underpin the successes achieved during the last 18 years.

The illustration on the "CONNECTING THE DOTS" t-shirt comes directly from one element of the research on tree pathogens and pests conducted in FABI. In these particular projects, students and staff seek to understand the global movement of these pests that are devastating natural and planted forests globally. The specific haplotype network on the t-shirt relates to isolates of the fungus, *Leptographium procerum*, which commonly infects pine trees, and is associated with many root-colonising beetles. Haplotype networks show the genetic relationship among different individuals - in this case of *L. procerum*. The circles represent different genotypes (or collections of alleles, which are variants of genes), while the sizes of the circles indicate the number of individuals that share that genotype (larger circles represent a greater number of individuals than smaller circles). Where a straight line links two circles, these genotypes have few genetic differences and are therefore closely related. By extension, circles that are far apart in the network indicate distantly related genotypes. Haplotype networks have allowed us to examine the inter-relationship of *L. procerum* isolates collected from China, North America and Europe. The network illustrated (and simplified) on the t-shirt supports the hypothesis that Europe is the centre of diversity for the fungus (*L. procerum*) and that the Chinese and North American isolates likely originated from Europe. This specific research was conducted by Dr. Stephen Taerum as part of his PhD project.

The "CONNECTING THE DOTS" t-shirt.

COMMUNITY INITIATIVES

Community Projects 2015 and 2016

FABI has several community outreach projects under the caring guidance of Prof. Noëlani van den Berg. These projects encompass both the well being of the community and encouraging learners to follow a career in science.

FABI continues its traditional annual Blanket Drive as its winter charity project. In 2016, 200 blankets were collected by our staff and students. These blankets, along with warm clothes were donated to the Philadelphia Congregation, one of six churches that run a feeding programme for the homeless in the Hatfield and Hillcrest suburbs surrounding the University. In 2017 this project collected 135 blankets that were donated to Akanani, an organisation under the banner of the Tshwane Leadership Foundation.

In 2016, Nelly Khumalo, a MSc student at FABI contracted cancer of the spinal column. This saw her immobilised and eventually bedridden in the ICU ward of the Steve Biko Academic Hospital. FABIans opened their hearts and purses and a total of R30,000 was collected to provide financial assistance to her parents for Nelly's expenses and needs. Sadly Nelly lost her brave fight against cancer in September 2016.

The severe drought that gripped part of the country in early 2016 prompted FABI to team up with a national drought relief campaign, Operation Hydrate, to deliver water to communities affected by water shortages. The generous spirit of FABIans shone through when they collected nearly 2,000L of bottled water during a two-week long water collection drive. FABIans delivered the water to an Operation Hydrate collection point in Centurion, Pretoria, from where it was distributed to communities in need.

FABI collected 200 blankets during the 2016 Blanket Drive.

Engaging and interacting with learners to promote science education is another pillar of FABI. The Forest Molecular Genetics (FMG) Research Group within FABI participated in the "Take a Girl Child to Work" day in 2016. Several postgraduate students within the FMG were involved in logistical planning to host the six Grade 10 learners and their teacher, from Lehlabile High School in Mamelodi and expose them to various aspects of forest biotechnology. The visit began with an introductory lecture on DNA and biotechnology applications by Dr. Sanushka Naidoo, followed by an interactive session on "Why am I interested in Science?" driven by postgraduate students. Learners visited different work stations in FABI and completed a simple bioinformatics programming exercise, prepared explants using sterile tissue culture techniques, extracted DNA and resolved the products using agarose gel electrophoresis.

FABI hosted Bianca Murray, a Grade 12 learner at Moore House Academy in Johannesburg, who spent a portion of her mid-year school holidays shadowing postgraduate students at the Institute to gain a better understanding of modern molecular techniques. Postgraduate students Esna du Plessis and Darryl Herron spent some time sharing aspects of their research with Bianca, all the while bringing her closer to her dream of becoming a forensic scientist.

Believing that it is never to early to encourage budding young scientists, FABI again hosted two Grade 7 students, Sandra Barnes and Kayla Joseph, from Irene Primary School who again conducted their annual school science projects at FABI. Their aim was to test the hypothesis that the important tree-killing fungus, *Ceratocystis manginecans*, can be found in soil samples. They used a carrot-baiting technique to screen soil samples collected from plantations where a Ceratocystis canker and wilt disease is severely affecting *Acacia mangium* trees. They won a Gold medal for this project at the regional Science Expo.

These aspiring young scientists also received a Gold Medal at the 2015 Expo for Young Scientists for their project entitled "Testing the susceptibility of different sweet potato varieties to the black rot fungus, *Ceratocystis fimbriata*", and also won the Merck Junior Microbiology prize. Their work involved testing four sweet potato varieties grown in South Africa and they found that "Blesbok" was the most susceptible. These results could then be used in the studies conducted by PhD student Arista Fourie who is now using the Blesbok variety in her studies to evaluate the host specialisation of two *Ceratocystis* species.

Akani were the recipients of the 2017 Blanket Drive initiative.

Starting young are Sandra Barnes and Kayla Joseph.

FABIans collected more than 2,000L of water for drought-striken communities.

NOTES

NOTES

NOTES

SPONSORS OF RESEARCH

Many of these commercial companies or organisations fund more than one programme in FABI

ACIAR (Australia)
Amathole Forestry
BASF
BAYER
Belgium Embassy
China/South African Governments Bilateral Agreement
Chinese Academy of Forestry
CIRAD
Citrus Growers Association
Citrus Research International
CGIAR Generation Challenge Programme
CNRS/South African Government
CSIR
DFG (Deutsche Forshungsgemeinschaft: German Research Foundation)
Department of Agriculture, Forestry and Fisheries (DAFF)
Department of Trade and Industry through THRIP initiative
Department of Science and Technology through the Innovation Fund and CTHB
Department of Science and Technology through the NRF
Department of Science and Technology
Du Roi QMS
EARO, Ethiopia
European Union 6th Framework Agreement
EU FP7 TESTA project
Forestry South Africa
Hans Merensky Holdings
Hans Merensky Foundation
International Institute of Tropical Agriculture (IITA)
Italian/South African Governments Bilateral Agreement
GRI, University of Pretoria
Japanese/South African Governments Bilateral Agreement
Loskop Irrigation Board
Maize Trust
Mellon Foundation
Ministry of Education, China
Ministry of Finance, China
Ministry of Science and Technology, China
Mondi
Mountain to Ocean (MTO) Forestry
National Natural Science Foundation, China
National Research Foundation (NRF)
NCT
Norway/South Africa Governments Bilateral Agreement
Oppenheimer Foundation
PANNAR Seed Pty (Ltd)
PG Bison
Protein Research Foundation
Rockefeller Foundation
SABI
SAFCOL/Komatiland Forestry
Sappi
SIDA/South African Governments Bilateral Agreement
South Africa/Argentina Governments Bilateral Agreement
Southern African Macadamia Growers' Association (SAMAC)
Syngenta South Africa
Tanzanian Government
Technology Innovation Agency (TIA)
Thuthuka
Tuscan Namibia/DAAD (Germany)
TWK
UP Research Development Fund
Water Research Commission
Winetech
Wheat Cereal Trust
York Timber