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LESSONS FROM A GLOBAL PERSPECTIVE ON TREE HEALTH

Michael J. Wingfield

**Institute of Chartered Foresters
National Conference
Cardiff 22-23 April 2015**



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NEW PATHOGEN/PEST INTRODUCTIONS AND NEW EPIDEMICS WILL CONTINUE TO EMERGE



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27 October 2012 Last updated at 14:01 GMT

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Ash tree import ban to halt disease

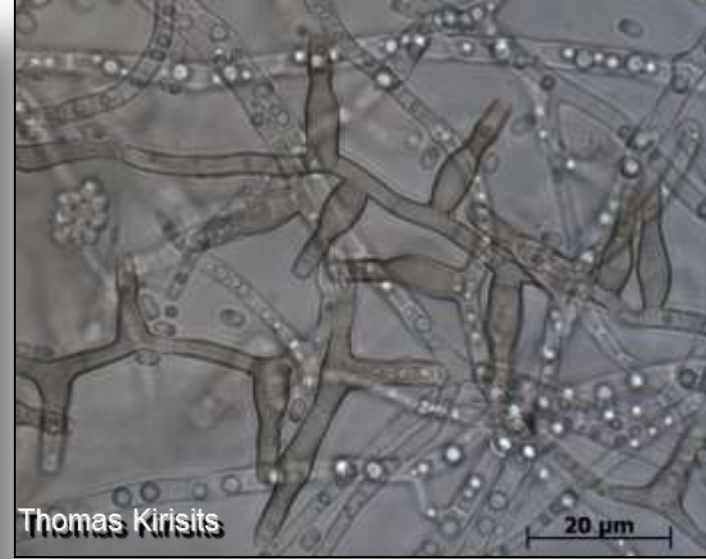
A ban on the import of ash trees will come into force on Monday in an attempt to halt the spread of a deadly disease, the environment secretary has said.

Owen Paterson has denied ministers were slow to react to the outbreak.

The Chalara fraxinea fungus, which causes Chalara dieback, has already killed 90% of ash



COLIN VARDELL



Thomas Kirsits



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Ash dieback: Government faces possible legal action

A nursery forced to destroy 50,000 ash trees after a fungal disease was found is considering taking legal action against the government for failing to block imports sooner.



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Thomas Kirsits





Plant Pathology (2008) 57, 715–727

Doi: 10.1111/j.1365-3059.2008.01893.x

***Phytophthora pinifolia* sp. nov. associated with a serious needle disease of *Pinus radiata* in Chile**

A. Durán^{a,c*}, M. Gryzenhout^a, B. Slippers^b, R. Ahumada^{a,c}, A. Rotella^c, F. Flores^c,
B. D. Wingfield^b and M. J. Wingfield^b

^aDepartment of Microbiology and Plant Pathology and ^bDepartment of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa; and ^cBioforest S.A., Casilla 70-C, Concepción, Chile



British Mycological
Society promoting fungal science

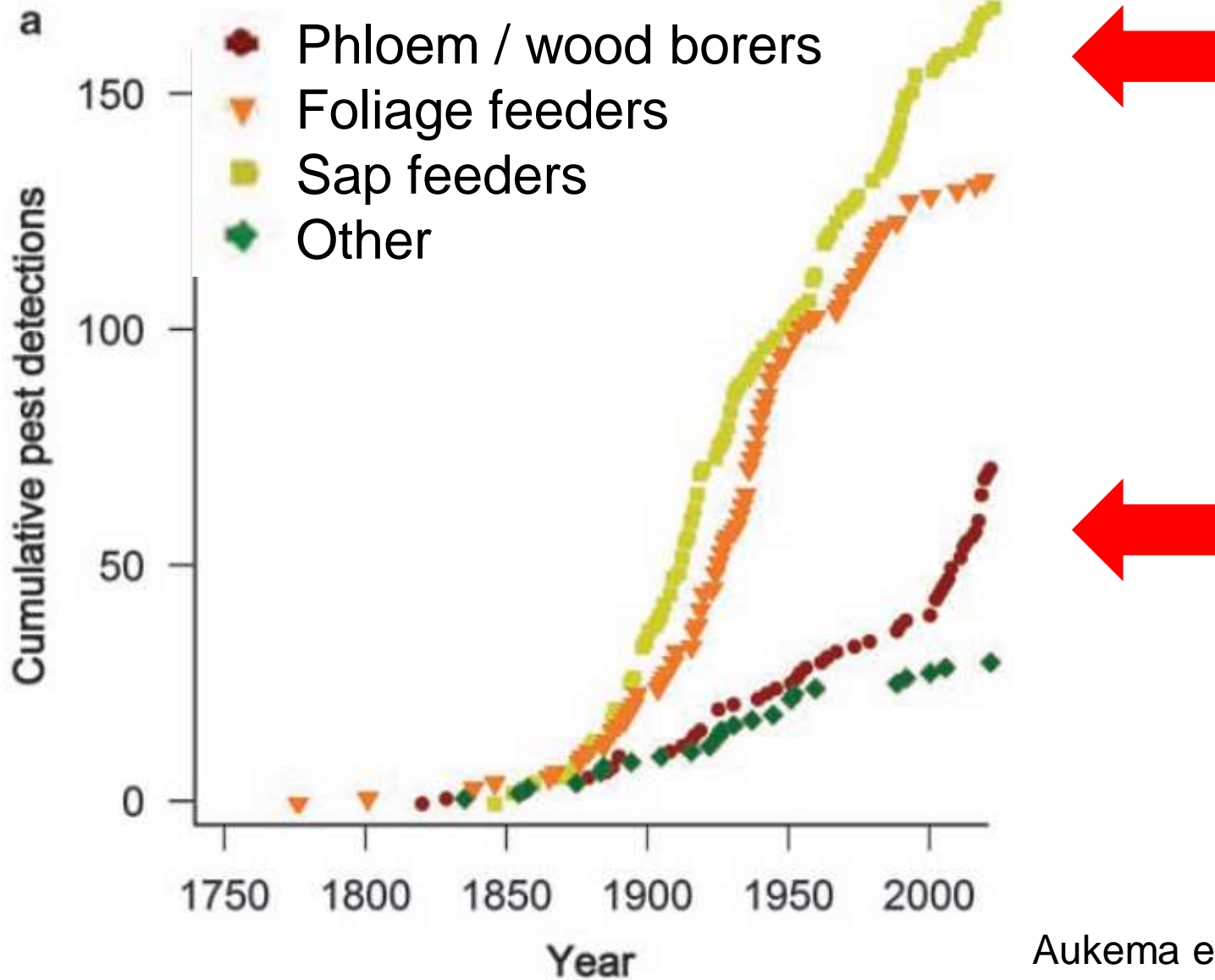
journal homepage: www.elsevier.com/locate/funbio



AFLP analysis reveals a clonal population of *Phytophthora pinifolia* in Chile

Alvaro DURÁN^{a,d,*}, Mariëka GRYZENHOUT^a, André DRENTH^c, Bernard SLIPPERS^b,
Rodrigo AHUMADA^{a,d}, Brenda D. WINGFIELD^b, Michael J. WINGFIELD^a

Forest insects by feeding guild – USA



Aukema et al. 2010,
BioScience 60: 886-897



NOVEL PATHOGEN, PEST AND TREE ASSOCIATIONS ARE GIVING RISE TO NEW AND UNEXPECTED CHALLENGES

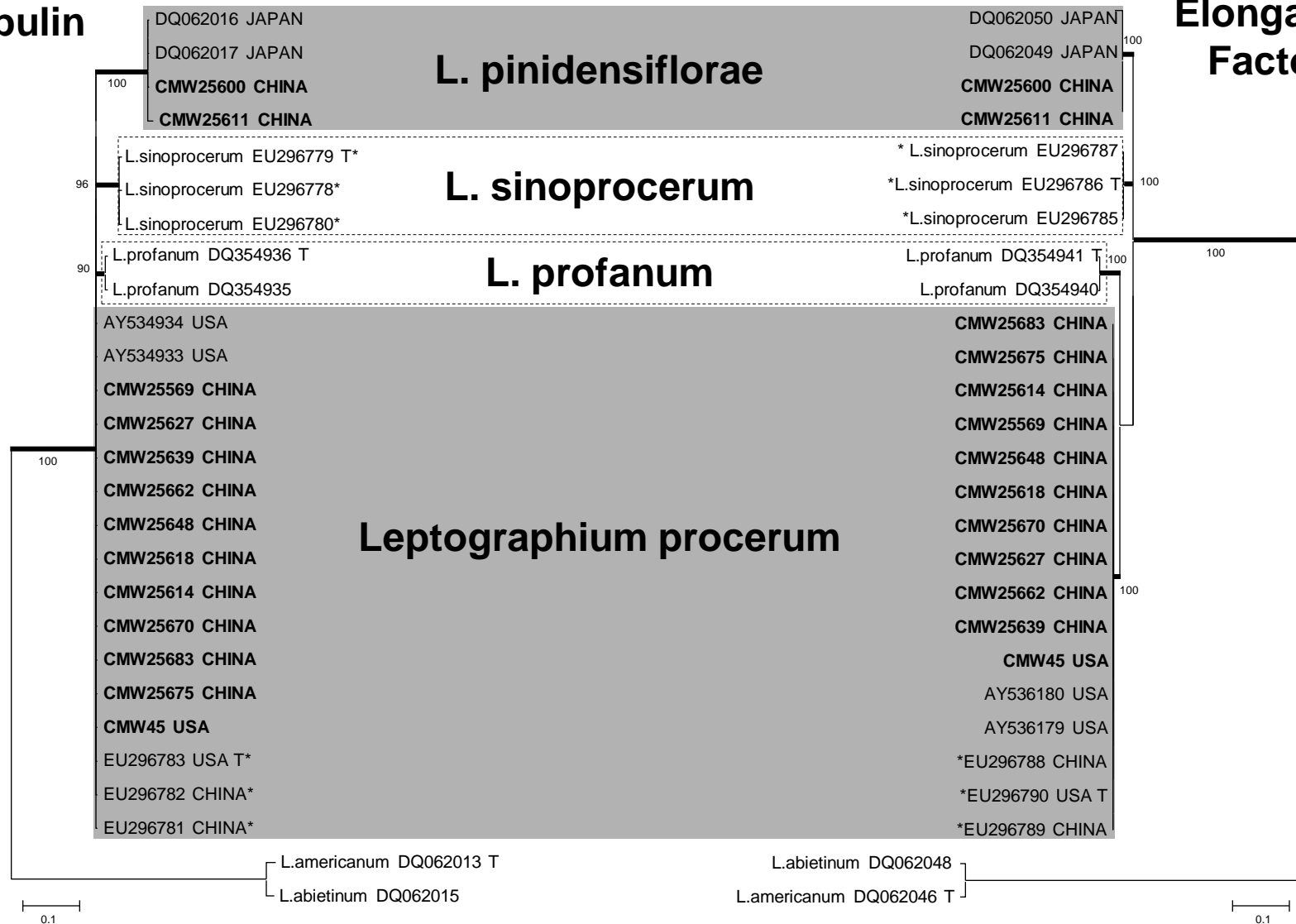






β -tubulin

Elongation
Factor-1 α



Min Lu, X.D. Zhou, Z.W. De Beer, M.J. Wingfield and J.-H. Sun. (2009). Ophiostomatoid fungi associated with the invasive pine-infesting bark beetle, *Dendroctonus valens*, in China. *Fungal Diversity* 38: 133-145

Destructive Tree Diseases Associated with Ambrosia and Bark Beetles: Black Swan Events in Tree Pathology?



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University of Florida, Tropical Research & Education Center,
Homestead, FL 33031

Jiri Hulcr

University of Florida, School of Conservation
and Forest Resources, and USDA Forest Service, Gainesville, FL 32611

Michael J. Wingfield and Z. Wilhelm de Beer

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Forest & Agricultural Biotechnology Institute, Pretoria, South Africa

Diseases that are associated with ambrosia and bark beetles comprise some of the most significant problems that have emerged in trees in the last century. They are caused by fungi in the Ophiotomatales, Microascales, and Hypocreales, and have vectors in the Scolytinae (ambrosia and bark beetles) and Platypodinae (ambrosia beetles) subfamilies of the Curculionidae (Coleoptera) (1,2,3,4). Some of the most significant destructive diseases

In a recent book, Taleb (155) developed Black Swan Theory (BST). Unlike the “black swan” to which Mill referred (68), Taleb focuses on unexpected events of large magnitude and consequence (155). Taleb (155) recognized such events in diverse fields including finance, history, science, and technology. He suggests that black swan events:





GROWING PLANTATION FORESTRY CAN NEGATIVELY INFLUENCE GLOBAL TREE HEALTH



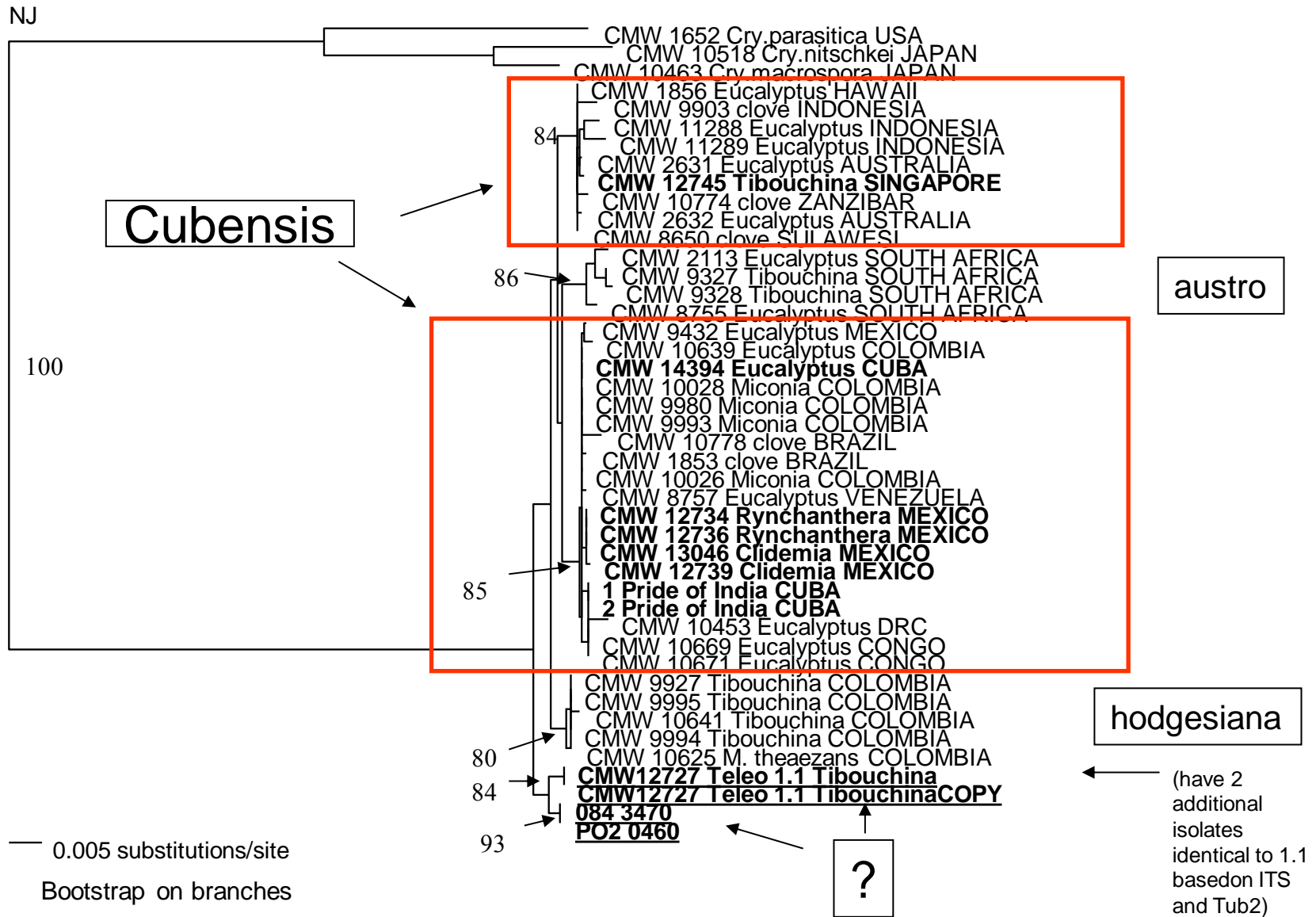
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Melastoma (Sumatra) in Asia

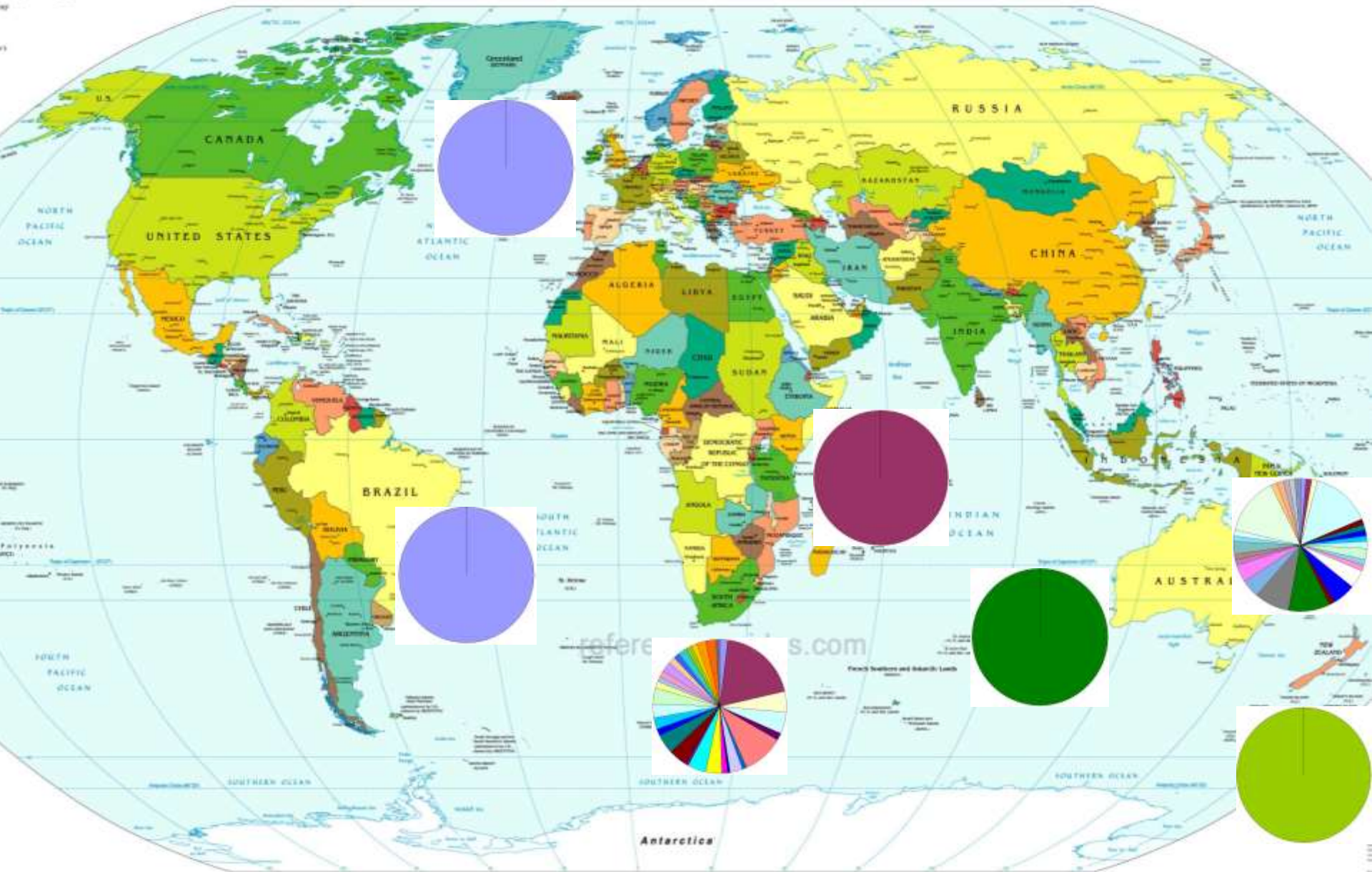


Gryzenhout M, C.A. Rodas, J. Mena Portales, P. Clegg, B.D. Wingfield and M.J. Wingfield. (2006). Mycological Research 110: 833-845





Brazil and Uruguay 2007 (*T. nubilosa*)





**INTERNATIONAL
COLLABORATION BETWEEN
TREE HEALTH SPECIALISTS IS
BECOMING INCREASINGLY
MORE IMPORANT**

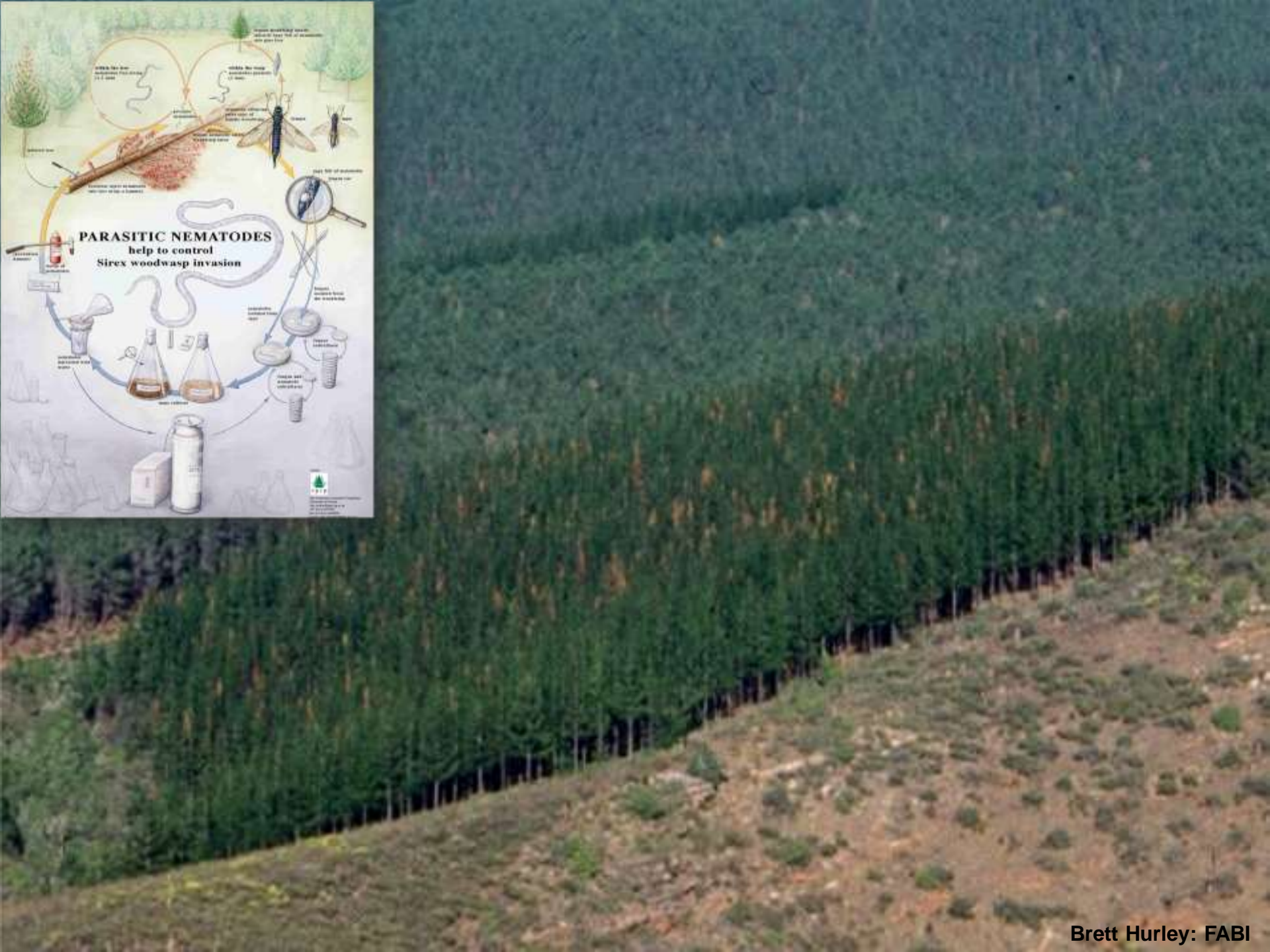
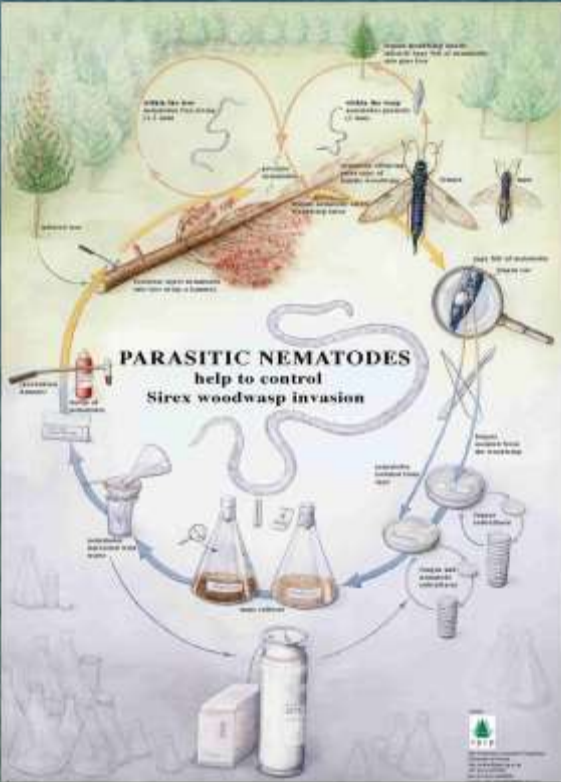


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Brett Hurley: FABI

Brett Hurley: FABI



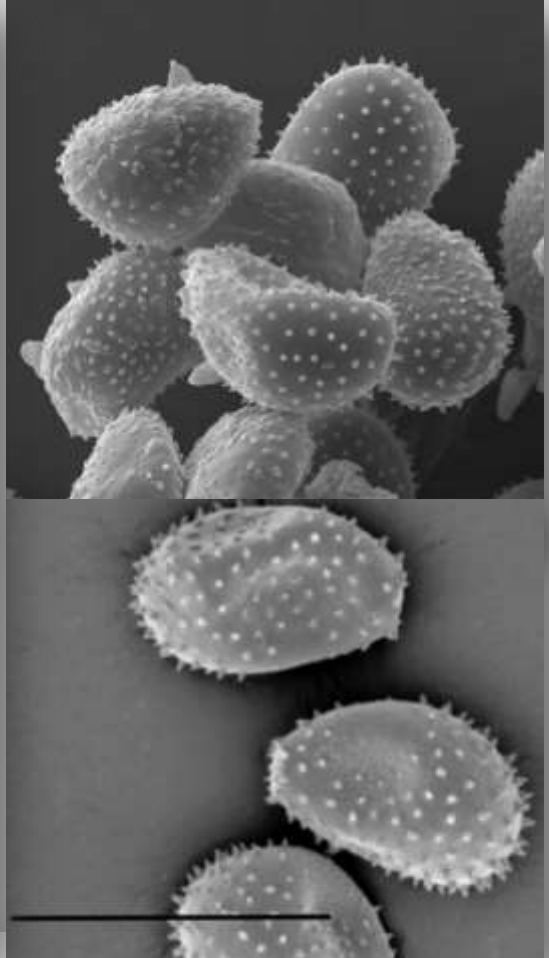
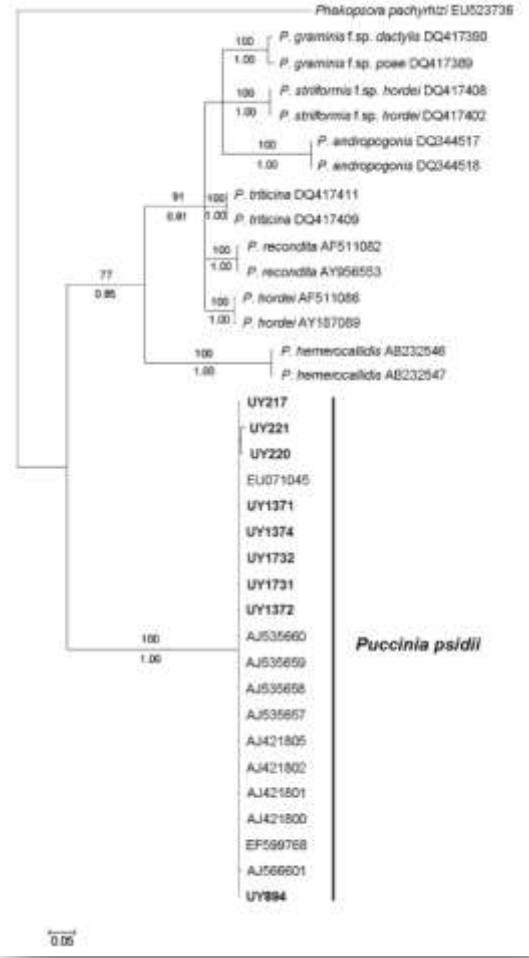
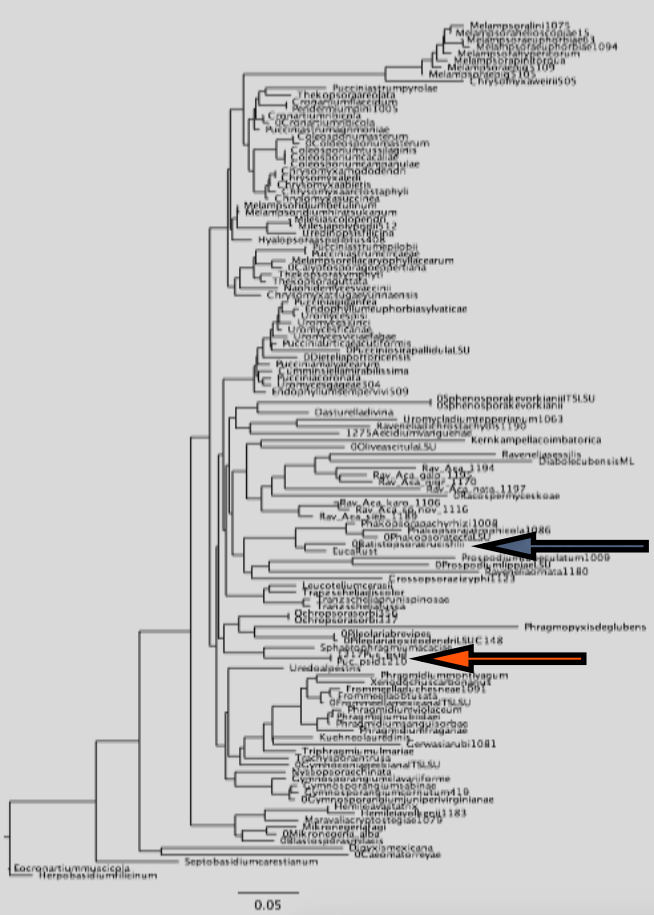


INVESTMENT IN TREE HEALTH ISSUES IS INADEQUATE AND FAILS TO CAPTURE OPPORTUNITIES OFFERED BY NEW TECHNOLOGIES



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Mycol Progress (2011) 10:273–282
 DOI 10.1007/s11557-010-0698-x

ORIGINAL ARTICLE

Puccinia psidii infecting cultivated *Eucalyptus* and native myrtaceae in Uruguay

Carlos A. Pérez · Michael J. Wingfield · Nora A. Altier ·
 Sofia Simeto · Robert A. Blanchette



Ultrafast X-rays probe supercooled water on the brink of crystallization

PAGE 381 & 381

WATER COOLED

FIGHTING PSEUDOSCIENCE

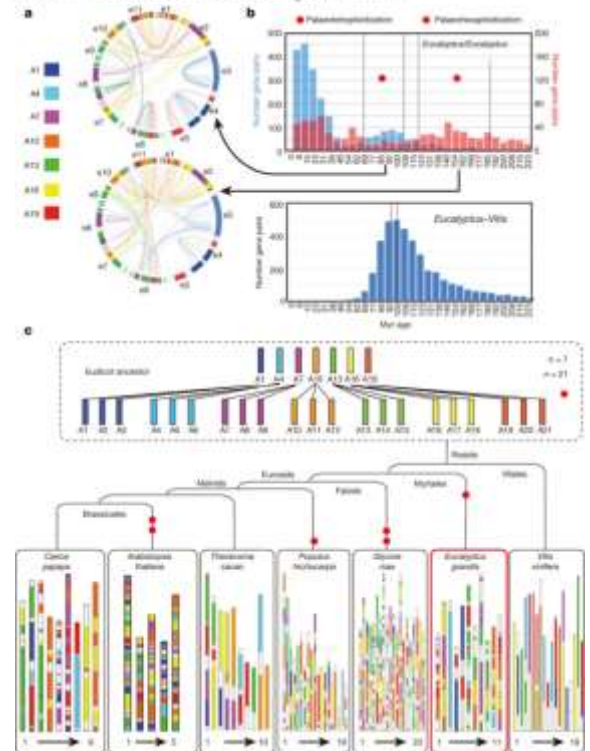
WATER, WATER EVERYWHERE...
Dissolution in oil: how cool? — see article below

GHOST IN THE MACHINE
Characterizing the secret in quantum computing



The genome of *Eucalyptus grandis*

Alexander A. Myburg^{1,2}, Dario Grattapaglia^{3,4}, Gerald A. Tuskan^{5,6}, Uffe Hellsten⁵, Richard D. Hayes⁵, Jane Grimwood⁷, Jerry Jenkins⁷, Erika Lindquist⁵, Hope Tice⁵, Diane Bauer⁵, David M. Goodstein⁵, Inna Dubchak⁵, Alexandre Pollakov⁵, Eshchar Mizrahi^{1,2}, Anand R. K. Kullam^{1,2}, Steven G. Hussey^{1,2}, Desre Pinard^{1,2}, Karen van der Merwe^{1,2}, Pooja Singh^{1,2}, Ida van Jaarsveld⁸, Orzenil B. Silva-Junior⁹, Roberto C. Togawa⁹, Marília R. Pappas², Danielle A. Faria³, Carolina P. Sansaloni², Cesar D. Petrolli¹, Xiaohan Yang⁶, Priya Ranjan⁶, Timothy J. Tschaplinski⁶, Chu-Yu Ye⁶, Ting Li⁶, Lieven Sterck¹⁰, Kevin Vanneste¹⁰, Florent Murat¹¹, Marçal Soler¹², Hélène San Clemente¹², Najib Saldi¹², Hua Cassan-Wang¹², Christophe Dunand¹², Charles A. Hefer^{8,13}, Erich Bornberg-Bauer¹⁴, Anna R. Kersting^{14,15}, Kelly Vining¹⁶, Vindhya Amarasinghe¹⁶, Martin Ranik¹⁶, Sushma Naithani^{17,18}, Justin Elser¹⁷, Alexander E. Boyd¹⁸, Aaron Liston^{17,18}, Joseph W. Spatafora^{17,18}, Palitha Dharmawardhana¹⁷, Rajani Raja¹⁷, Christopher Sullivan¹⁸, Elisson Romanel^{19,20,21}, Marcio Alves-Ferreira²¹, Carsten Külheim²², William Foley²², Victor Carocha^{12,23,24}, Jorge Paiva^{23,24}, David Kudrna²⁵, Sergio H. Brommonschenkel²⁶, Giancarlo Pasquali²⁷, Margaret Byrne²⁸, Philippe Rigault²⁹, Josquin Tibbits³⁰, Antanas Spokevicius³¹, Rebecca C. Jones³², Dorothy A. Steane^{32,33}, René E. Vaillancourt³², Brad M. Potts³², Fourie Joubert^{2,8}, Kerrie Barry⁵, Georgios J. Pappas Jr³⁴, Steven H. Strauss¹⁶, Pankaj Jaiswal^{17,18}, Jacqueline Grima-Pettenati¹², Jérôme Salse¹¹, Yves Van de Peer^{2,10}, Daniel S. Rokhsar⁵ & Jeremy Schmutz^{3,5,7}



The mating type locus of *Ceratocystis fimbriata*

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¹Department of Genetics, ²Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, 0002, South Africa

Introduction

Mating type (MAT) genes are key regulators of sexual reproduction in fungi and have been studied for over a century. These genes are located at the mating (MAT1) locus, and commonly consist of two allelic versions or idiomorphs (Fig. 1). One idiomorph (MAT1-1) is characterised by the presence of the MAT1-1 gene, although the MAT1-2 and MAT1-3 genes can also be present. The other idiomorph (MAT1-2) always contains a MAT1-2-1 gene, although other genes have also been found on this idiomorph. In heterothallic (self-sterile) species, isolates carry only one of these idiomorphs, conferring a mating type to that isolate. In contrast, the MAT locus of homothallic (self-fertile) species contains both the MAT1-1 and MAT1-2-1 genes (Fig. 1).

The fungal genus *Ceratocystis* includes a range of species with diverse and intriguing mating systems. *Ceratocystis fimbriata sensu stricto* and *C. albifundus*, for example, have the ability to switch their mating type from homothallic to heterothallic, a phenomenon known as unidirectional mating-type switching. The reverse has never been observed (Harrington and McNew 1997). Little is known about unidirectional mating-type switching, but it is thought that part of the mating locus (including the MAT1-2-1 gene) is lost during the switching event (Harrington and McNew 1997; Withuho et al. 2000). Therefore, the availability of the recently sequenced genome of *C. fimbriata* s.s. as the type species of *Ceratocystis*, provides an excellent opportunity to study the MAT genes in this genus.

Aim

The aim of this study was to determine whether DNA is deleted from the genome during mating-type switching in *C. fimbriata* s.s. and thus consistent with existing hypotheses. Assuming DNA is deleted, a further aim was to determine the exact region lost during mating-type switching in the fungus.

Materials and methods

A draft genome assembly for a self-fertile isolate of *C. fimbriata* s.s. was produced using 454-pyrosequencing and the NEWBLER assembly package. The assembled contigs were screened for the presence of mating type genes using local BLASTn (i.e., search translated nucleotide databases using a protein query) analysis on the CLC Genomics Workbench software package. Gene and protein predictions from identified contigs were made using AUGUSTUS, and evaluated by BLASTp searches against the NCBI database. Primers for amplification and sequencing predicted genes and intergenic regions in switched and unswitched isolates of *C. fimbriata* s.s. were designed using Primer3.

Results

Based on the tBLASTn searches of the draft genome sequence, four contigs with significant similarity to the various MAT sequences were identified (Table 1). Analysis with AUGUSTUS identified ORFs in these contigs that encode genes similar to those predicted for MAT1-2-1, MAT1-1 and MAT1-1+2 (Table 1). Although the fourth contig harboured regions with similarity to the gene encoding MAT1-1+3, an ORF corresponding to and with similarity to known MAT1-1+3 proteins was not identified.

Primers designed from the predicted coding regions allowed the amplification and sequencing of all the genes and intergenic regions in both unswitched and switched isolates of *C. fimbriata*. The unswitched region contained three genes in the order: MAT1-1-1, MAT1-2-1 and MAT1-1+2, while the switched region only contained the MAT1-1-1 and MAT1-1+2 genes in that order. Sequence data placed the size of the unswitched MAT locus at 9208 bases, while the switched locus is 5628 bases in size (Fig. 2). No trace of the MAT1-2-1 gene could be found in the genome of a switched isolate using a PCR approach.

Discussion and conclusions

This study showed that the homothallic *C. fimbriata* MAT idiomorph consists of three mating type genes. The characteristic MAT1-1-1 and MAT1-2-1 genes were present, which most likely confer self-fertility to the homothallic individual. In addition the MAT1-1+2 gene was also present, and resembles the MAT1-1+2 gene from other fungal species. Although an HMG-box protein with similarity to MAT1-1+3 was identified, the predicted *C. fimbriata* protein did not group with known MAT1-1+3 proteins, suggesting that it does not represent a mating-type gene.

The switched MAT idiomorph contained only two genes, MAT1-1-1 and MAT1-1+2. From this analysis, it is clear that during the switching event, the MAT1-2-1 gene and flanking regions are deleted and this resulted in a loss of self-fertility. These results, combined with earlier studies that tracked a section of the MAT1-2-1 gene using Southern blotting (Withuho et al. 2000), support the view that the MAT1-2-1 gene is completely deleted during mating type switching.

Comparison of the sequence of the unswitched and switched idiomorphs, suggest that a region of 5628 bases is lost during mating-type switching (Fig. 2). In future studies, the MAT locus will be characterised in multiple isolates of *C. fimbriata* to pinpoint the deletion boundaries. This will allow us to infer the possible mechanisms involved in the process of unidirectional mating-type switching.

Table 1. Blast results from tBLASTn against the genome sequence and BLASTp of identified protein sequences against NCBI database

Protein query	tBLASTn to genome contigs/size	BLASTp to NCBI database	E-value
<i>C. fimbriata</i> MAT1-2-1 (AA953161)	3322 bases 1.58E ⁰⁸	MAT1-2 HMG box protein (<i>Ceratocystis fimbriata</i>)	3 ⁰⁰
<i>Fusarium fultum</i> MAT1-1-1 (AA672055)	26375 bases 7.52E ⁰⁹	Mating type protein 1-1-1 (<i>Fusarium sp. FE7</i>)	3E ⁰⁴
<i>F. graminearum</i> MAT1-1-2 (AB898346)	15024 bases 4.1E ⁰⁷	Mating type protein 1-1-2 (<i>Sporium obsoletum</i>)	5E ⁰⁴
<i>F. graminearum</i> MAT1-1-3 (AA842612)	54973 bases 5.4E ⁰⁷	N/A	N/A

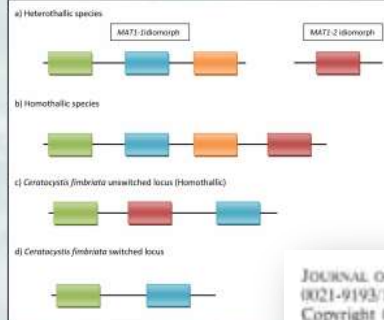


Fig. 1. Generalised structure of a heterothallic (a) and homothallic (b) idiomorph is the MAT1-1-1 (green), MAT1-2-1 (blue), MAT1-1+2 (orange) genes. Also indicated is the *C. fimbriata* MAT locus before (c) and after (d) the switch. Note the loss of the MAT1-2-1 gene (red) during the switch.

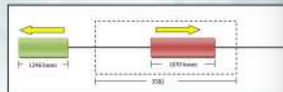


Fig. 2. Structure of the *Ceratocystis fimbriata* MAT locus indicating the gene regions involved. The MAT1-1-1 (green), MAT1-2-1 (red) and MAT1-1+2 (orange) genes are indicated (across the genes). The dotted lines indicate switching as well as the size of this region. Yellow arrows indicate the region drawn to scale.

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- Withuho R, Harrington TC, Wingfield BD, Steenkamp ET, Wingfield MJ. 2000. Cloning of a unidirectional mating-type switching in *Ceratocystis coccinea* Greville.



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Newsletter of the Mycological Society of America

— In This Issue —

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The Origin of the Term "Mycology" and Its Chinese Translation

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JOURNAL OF BACTERIOLOGY, June 2010, p. 2936-2937
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Vol. 192, No. 11

GENOME ANNOUNCEMENTS

Genome Sequence of *Pantoea ananatis* LMG20103, the Causative Agent of *Eucalyptus* Blight and Dieback[†]

Pieter De Maayer,^{1,2*} Wai Yin Chan,^{1,2} Stephanus N. Venter,^{1,2} Ian K. Toth,^{1,4} Paul R. J. Birch,^{1,4,5} Fourie Joubert,³ and Teresa A. Coutinho^{1,2}

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Received 20 January 2010/Accepted 18 March 2010

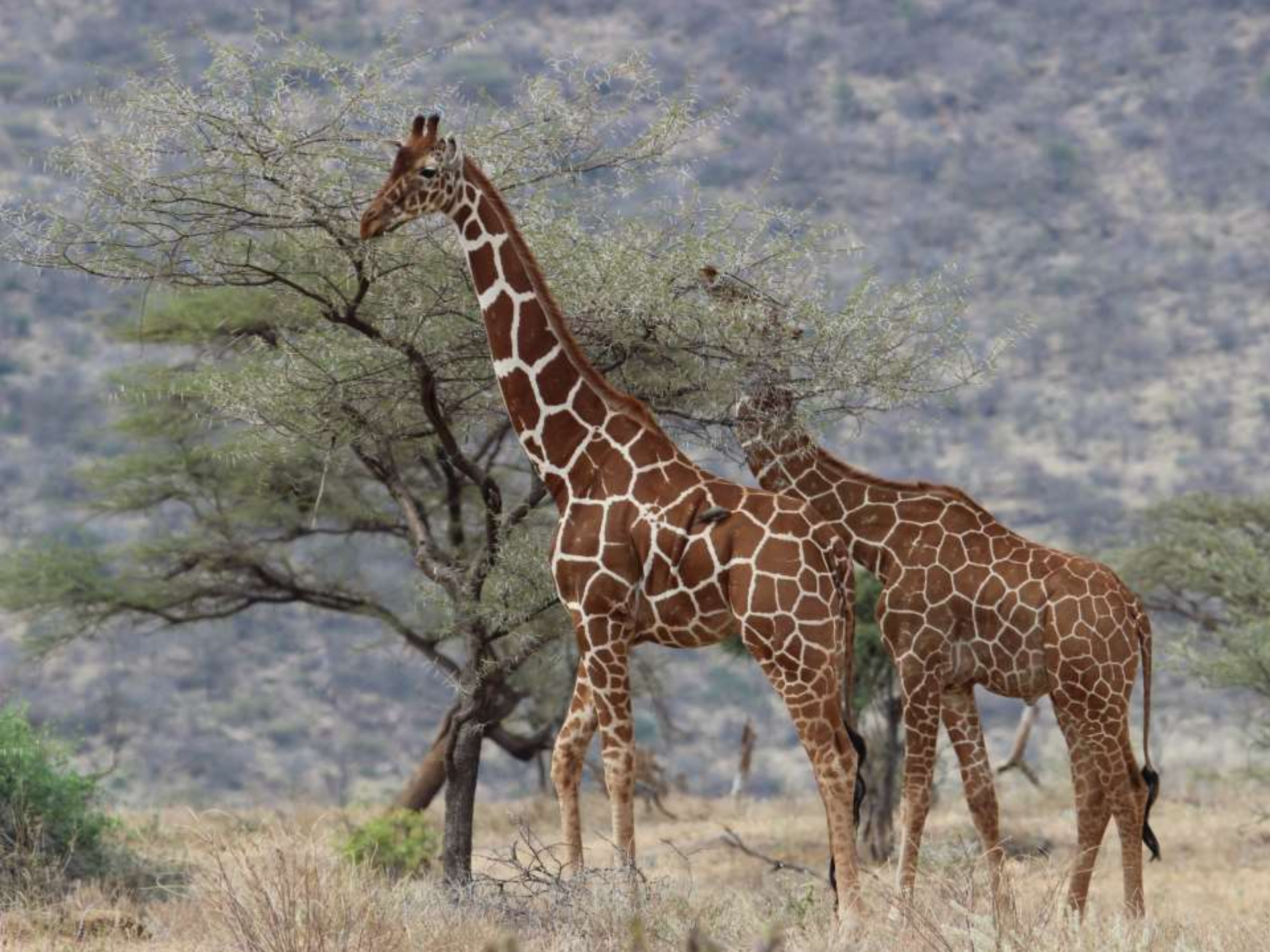
Pantoea ananatis is a Gram-negative plant pathogen that causes disease on a broad range of host plants, including pineapple, maize, rice, onion, melons, and *Eucalyptus*, and has been implicated in several cases of human disease. Here, we report the genome sequence of *P. ananatis* LMG20103 isolated from diseased *Eucalyptus* in South Africa.



AND SOME FINAL THOUGHTS



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The Myrtle rust pathogen, *Puccinia psidii*, discovered in Africa

Jolanda Roux¹, Izette Greyling¹, Teresa A. Coutinho¹, Marcel Verleur², and Michael J. Wingfield¹

¹Forestry and Agricultural Biotechnology Institute (FABI), Department of Microbiology and Plant Pathology, University of Pretoria, Pretoria, South Africa; corresponding author e-mail: jolanda.roux@fabi.up.ac.za

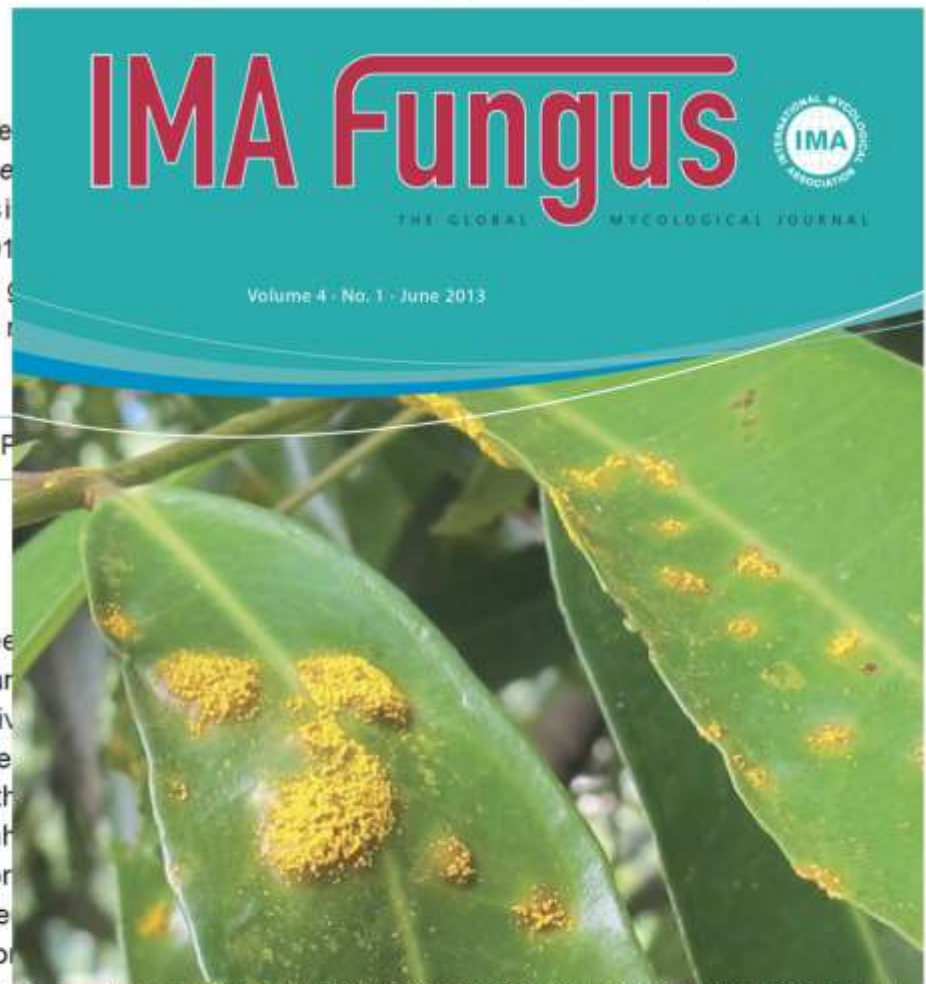
²Sappi Forests Ltd., Pietermaritzburg, South Africa

Abstract: *Puccinia psidii*, the cause of a disease today commonly regarded as a quarantine threat globally. It has a wide host range in the *Myrtaceae* and causes significant damage to native ecosystems where these plants occur. The fungus is a major pest of the forestry industries that propagate Australian *Eucalyptus* species. In May 2013, *P. psidii* were observed on an ornamental Myrtaceous shrub in a garden in Pietermaritzburg, South Africa. This was based on DNA sequence data of the ITS and 5.8S nrRNA gene regions and confirmed by the presence of *P. psidii* in Africa.

Article info: Submitted: 13 June 2013; Accepted: 14 June 2013; Published: 15 June 2013

INTRODUCTION

Puccinia psidii (Uredinales, Pucciniaceae) has been considered as an important quarantine threat to many countries (Glen *et al.* 2007). It was first described from native guava (*Psidium guajava*) in Brazil in 1884 and gained notoriety when it was found to infect various other members of the *Myrtaceae*, an unusual feature for most rust fungi (Coutinho *et al.* 1998, Glen *et al.* 2007, Carnegie *et al.* 2010a, Mordecai *et al.* 2012). *Puccinia psidii* became particularly prominent in the literature when it was found causing disease on non-native *Eucalyptus* species in Brazil (Jolliffe 1944) and it was rapidly considered as a significant threat to the commercial



that it is not phylogenetically related to other members of the genus *Puccinia* (M. Wingfield & W. Maier, unpubl. data), the

“The key point is that the world is not nearly as prepared for a massive epidemic as it needs to be”

Bill Gates



The NEW ENGLAND JOURNAL of MEDICINE

Perspective

The Next Epidemic — Lessons from Ebola

Bill Gates

Perhaps the only good news from the tragic Ebola epidemic in Guinea, Sierra Leone, and Liberia is that it may serve as a wake-up call: we must prepare for future epidemics of diseases that may spread

more effectively than Ebola. There is a significant chance that an epidemic will spread through the air, rather than requiring direct contact.

NATO has a mobile unit that is ready to deploy quickly. Although the system is not perfect, NATO countries participate in joint exercises in which they work out logistics such as how fuel and food will be provided, what language they will speak, and what





nature

THE CHANGING MAP OF SCIENCE

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uses a tree to test
the limits of quantum
mechanics

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A new vaccine
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in the fight against
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