Species of Mycosphaerellaceae and Teratosphaeriaceae on native Myrtaceae in Uruguay: evidence of fungal host jumps

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\textbf{A R T I C L E  I N F O}

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\textbf{A B S T R A C T}

Mycosphaerella species are well-known causal agents of leaf diseases on many economically and ecologically important plant species. In Uruguay, a relatively large number of Mycosphaerellaceae and Teratosphaeriaceae are found on Eucalyptus, but nothing is known of these fungi on native Myrtaceae. The aim of this study was to identify Mycosphaerellaceae and Teratosphaeriaceae species associated with leaf diseases on native Myrtaceae in Uruguay and to consider whether host jumps by the pathogen from introduced Eucalyptus to native Myrtaceae have occurred. Several native forests throughout the country were surveyed with special attention given to those located close to Eucalyptus plantations. Five species belonging to the Mycosphaerellaceae and Teratosphaeriaceae clades were found on native Myrtaceous trees and three of these had previously been reported on Eucalyptus in Uruguay. Those occurring both on Eucalyptus and native Myrtaceous trees included Pallidocercospora heimii, Pseudocercospora norchensis, and Teratosphaeria aurantia. In addition, Mycosphaerella yunnanensis, a species known to occur on Eucalyptus but not previously recorded in Uruguay, was found on leaves of two native Myrtaceous hosts. Because most of these species occur on Eucalyptus in countries other than Uruguay, it appears that they were introduced in this country and have adapted to be able to infect native Myrtaceous. These apparent host jumps have the potential to result in serious disease problems and they should be carefully monitored.

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\textbf{Introduction}

A diverse group of Mycosphaerellaceae and Teratosphaeriaceae has been associated with Mycosphaerella leaf disease (MLD), which are considered particularly important in Eucalyptus plantations worldwide (Park \textit{et al.} 2000; Maxwell \textit{et al.} 2003; Crous \textit{et al.} 2004; Crous \textit{et al.} 2006; Cortinas \textit{et al.} 2006; Hunter \textit{et al.} 2006; Summerell \textit{et al.} 2006; Crous \textit{et al.} 2009; Perez \textit{et al.} 2009a; Hunter \textit{et al.} 2011). These fungi cause leaf spots, leaf blotches, or petiole and stem cankers that often result in stressed and stunted trees, adversely affecting commercial forestry operations (Lundquist & Purnell 1987; Carnegie \textit{et al.} 1994; Carnegie \textit{et al.} 1998; Park \textit{et al.} 2000; Sánchez Márquez \textit{et al.} 2011).

Although most studies on MLD have focused primarily on Eucalyptus, species of Mycosphaerellaceae and Teratosphaeriaceae...
have also been found infecting species of the Myrtaceae other than those on Eucalyptus genus. At least 23 species have been found on non-Eucalyptus species in the Myrtaceae worldwide (Crous 1999; Sivanesan & Shivas 2002; Carnegie et al. 2007). Increased sampling over the last decade has shown that certain species included in these taxa can be found on a wide range of different hosts including different plant orders such as Myrtaceae, Proteales, Fabaceae and Apiales (Hunter et al. 2011). The apparent ease of movement in these fungi between hosts is thus of considerable concern.

Most Eucalyptus species are native to Australia and have been moved extensively around the world. Where Eucalyptus spp. are grown as non-natives, they have largely been separated from their natural enemies (Burgess & Wingfield 2002; Wingfield 2003). This is a situation that is gradually changing with pathogens and pests being brought back into contact with their hosts due to accidental introductions resulting in serious disease problems (Wingfield et al. 2008).

Eucalypts are threatened not only by pathogens that are known to attack them in their native environment but there is also growing evidence of pathogens from native Myrtaceae undergoing host shifts to infect them (Slippers et al. 2005). The best-known example of such a host shift linked to Eucalyptus is that of the Eucalyptus rust pathogen Puccinia psidii. This rust disease is native on Myrtaceae in South and Central America and has adapted to infect Eucalyptus in that region (Coutinho et al. 1998; Glen et al. 2007). In addition, there are many recent examples of members of the Cryphonectriaceae, that are native on members of the Myrtales, adapted to infect Eucalyptus in Africa (Heath et al. 2006) as well as South and Central America and Asia (Hodges et al. 1986; Myburg et al. 2003; Rodas et al. 2005; Gryzenhout et al. 2006).

Where pathogens have been introduced into new areas, they also have the potential to cause serious diseases on related native plants. It is for this reason that the severe impact of the recent introduction of P. psidii to Australia has been of such great concern (Grgurinovic et al. 2006; Glen et al. 2007; Carnegie et al. 2010).

Eucalyptus is widely planted in Uruguay and these trees have already been seriously affected by many diseases thought to have been introduced from other areas. Yet almost nothing is known regarding the pathogens of native Myrtaceae in Uruguay, whether these trees might be threatened by Eucalyptus pathogens or possibly the pathogens on the Myrtaceae causing new disease problems on Eucalyptus. Uruguay has a large resource of native Myrtaceae (Brussa & Grela 2007) and the aim of this study was to identify Mycosphaerellaceae and Teratosphaeriaceae species associated with MLD on native Myrtaceae species. Furthermore, we considered their relationships with those species currently affecting Eucalyptus plantations in Uruguay.

### Materials and methods

#### Samples and isolations

Between 2005 and 2008, trees belonging to the Myrtaceae were surveyed in native forests throughout Uruguay and special attention was placed on those located close to Eucalyptus plantations. Leaves showing MLD symptoms were recorded photographically, collected and taken to the laboratory for further study. Samples were collected from a total of 199 trees belonging to 20 native species residing in the Myrtaceae (Table 1). Sampled trees were distributed over the main areas where Eucalyptus is planted (Fig 1).

Lesions on leaves bearing pseudothecia were processed for isolation following the procedure described by Crous (1998). Parts of lesions with mature pseudothecia were soaked in sterile water for 2 h. The leaf pieces were then dried on sterilized paper and adhered with adhesive tape to the underside of Petri dish lids with the pseudothecia facing the surface of 2 % malt extract agar (MEA) (2 % malt extract, 1.5 % agar; Oxoid, Basingstoke, England). Petri dishes were incubated at 17–18 °C in the dark for 24–48 h. Ascospores that had been ejected onto the media and had germinated were observed under a microscope to record the germination patterns as described by Crous (1998). Individual germinating ascospores were lifted from the medium and transferred to new plates to generate monosporic cultures.

Where pseudothecia were not observed, pieces of leaf from the edges of the lesion were cut, surface-disinfested in 70 % ethyl alcohol for 30 s, and rinsed twice in sterile distilled water, blotted dry on sterile filter paper, and plated on 2 % MEA amended with 0.01 g of streptomycin per litre to minimize bacterial contamination. Plates were then incubated at room temperature and emerging colonies were sub-cultured on fresh 2 % MEA plates. Only those cultures with colony morphologies resembling those of species of Mycosphaerellaceae/Teratosphaeriaceae were included in further studies.

### Table 1 – List of Myrtaceae species native to Uruguay sampled in this study. Tree species in bold indicate those where Mycosphaerellaceae or Teratosphaeriaceae species were found associated with MLD symptoms.

<table>
<thead>
<tr>
<th>Tree Species</th>
<th>Fungal species</th>
<th>Province</th>
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<td>Acca sellowiana*</td>
<td>Pseudocercospora norchiensis</td>
<td>Rivera</td>
</tr>
<tr>
<td>Agarita eucalyptides</td>
<td>Passalora loranthi</td>
<td>Rivera</td>
</tr>
<tr>
<td>Blepharocalyx salicifolius*</td>
<td>Mycosphaerella yunnanensis</td>
<td>Rivera</td>
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<td></td>
<td>Teratosphaeria aurantia</td>
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<td>Myrrintinium atropurpureum var. octandrums*</td>
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<td>P. pubifolium</td>
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PCR amplifications were performed in an MJ Research PTC 200 DNA Engine Thermal Cycler PCR (MJ Research, Reno, NV, USA) with the following conditions: initial denaturation for 5 min at 94 °C, then 35 cycles of 1 min at 94 °C, 1 min at 50 °C, 1 min at 72 °C, followed by a final elongation step of 5 min at 72 °C, and hold at 10 °C. The PCRs had a total volume of 25-µl containing 1X of Amplitaq Gold PCR Master-Mix (Applied Biosystems, Foster City, CA, USA), 0.2 µM of each primer and approx. 10 ng µl⁻¹ of DNA template. Deionized-distilled water was added to a final volume of 25 µl.

PCR products were stained with SYBR Green nucleic acid dye (MBL International, Woburn, MA, USA) and visualized on 1.5 % agarose gels under UV light. Amplicons were prepared for sequencing using ExoSAP-IT PCR clean-up kit (USB Corp., Cleveland, OH, USA) following the manufacturer’s instructions. For sequencing reactions, the same primer pairs were used with the ABI Prism Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, CA, USA) and an ABI Prism 377 automated DNA sequencer. Forward and reverse sequences were assembled using ChromasPro software version 1.33 (Technelysium Pty. Ltd., Eden Prairie, MN, USA).

Sequences were subjected to BLAST searches in NCBI Genbank (http://www.ncbi.nlm.nih.gov/blast/Blast.cgi, verified 26 Jun. 2012), and those of the most closely matching species were downloaded from GenBank. Where available, sequences that represented the ex-type cultures of the closely matching species were used and all species of Mycosphaerellaceae and Teratosphaeriaceae previously reported from Eucalyptus were also included. Following a first preliminary phylogenetic analysis, the alignment was trimmed, discarding those species only distantly related to the sequences under investigation and populating the remainder of the data set with at least two sequences per taxon when possible (Table 2). In addition, sequences of species residing in the Mycosphaerellaceae and Teratosphaeriaceae obtained from Eucalyptus spp. in Uruguay (Perez et al. 2009b) were included in the alignment for comparison. Multiple sequence alignments were made online using the E-INS-i strategy in MAFFT version 6 (http://align.bmr.kyushu-u.ac.jp/mafft/online/server/, verified 4 May 2012) (Katoh et al. 2005).

Neighbour-joining (NJ) and Maximum parsimony (MP) analyses were performed using PAUP v. 4.0b10 (Swofford 2002). The best substitution model for NJ analysis was determined using Modeltest v. 3.7 (Posada & Crandall 1998) from which a general time reversible substitution model including a proportion of invariant sites and gamma-distributed substitution rates of the remaining sites (GTR + I + G) was selected from the Akaiake information criterion (AIC; proportion of invariant sites (I) = 0.3375; gamma distribution shape parameter (G) = 0.8871; base frequencies: pA = 0.2015, pC = 0.2991, pG = 0.2800, pT = 0.2194). Gaps were treated as missing data and all characters were treated as unordered and of equal weight. MP analysis was performed using the heuristic search option with simple addition of taxa and tree bisection and reconnection (TBR) as the branch-swapping algorithm. Support for the nodes of the shortest trees was determined by analyses of 1000 bootstrap replicates (Hillis & Bull 1993) and tree length (TL), consistency index (CI), retention index (RI), and homoplasy index (HI) were calculated.

Part of the translation elongation factor 1-α (EF1-α) region and the Actin (ACT) gene was also amplified for selected isolates to conduct a multiple gene genealogy analysis and thus
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(continued on next page)
to confirm the identity of those species found on both native Myrtaceae and Eucalyptus. EF-1α was amplified using the primers EF1-728F (5′-CAT CGA GAA GTT CGA GAA GG-3′) and EF1-986R (5′-TAC TTG AAG GAA CCC TTA CC-3′) (Carbone & Kohn 1999). Reaction conditions were: an initial denaturation step of 96 °C for 2 min, followed by 35 cycles of denaturation at 94 °C for 30 s, primer annealing at 56 °C for 30 s and primer extension at 72 °C for 30 s. The reaction was completed with a final extension at 72 °C for 7 min. For the ACT gene, the primers ACT-512F (5′-ATG TGC AAG GCC GGT TTC GC-3′) and ACT-783R (5′-TAC GAG TCC TTC TGG CCC AT-3′) were used (Carbone & Kohn 1999). PCR reaction conditions were: an initial denaturation step at 96 °C for 2 min, followed by 10 cycles of denaturation at 94 °C for 30 s, primer annealing at 61 °C for 45 s and extension at 72 °C for 45 s. This was followed by 25 cycles of denaturation at 94 °C for 30 s, primer annealing at 61 °C and elongation at 72 °C for 45 s with an increase of 5 s per cycle. The reaction was completed with a final elongation step at 72 °C for 7 min.

ITS, EF-1α, and ACT sequence datasets were examined for congruence using the Partition Homogeneity Test in PAUP (Farris et al. 1995; Huelsenbeck et al. 1996). Selected isolates of Pallidocercospora heimii, Pseudocercospora norchiensis and Teratosphaeria aurantia, obtained from Eucalyptus (Perez et al. 2009b), were included as references to confirm genetic similarity. A combined data set for the ITS, EF-1α, and ACT sequence was analyzed using NJ and MP. Phylogenetic analyses were performed using PAUP Version 4.0b10. Best models for NJ analysis was determined from the AIC Modeltest version 3.7 (Posada & Crandall 1998) as GTR + Γ for the combined dataset (proportion of invariant sites (I) = 0; gamma distribution shape parameter (Γ) = 0.2668; base frequencies: πT = 0.2136, πC = 0.2966, πG = 0.2583, πA = 0.2315). Gaps generated in the alignment process during the comparison were treated as missing data and all characters were treated as unordered and of equal weight. Ties were broken randomly when found.

All the sequences obtained in this study were deposited in GenBank (Table 1). Sequence alignments and trees of the ITS alone and combined analysis have been deposited in TreeBASE (accession number: 13107).

Results

Samples and isolations

Twenty species of Myrtaceae from a wide range of different collection sites in Uruguay were evaluated and sampled during this study. Symptoms resembling MLD were observed on four species namely Acca sellowiana, Blepharocalyx salicifolius, Myrceugenia glaucescens and Myrrium atropurpureum var. octandrum (Table 1). A total of 45 isolates were obtained from lesions on leaves of these trees. Isolates were grouped by culture and conidial morphology, ascospore germination pattern and host species. One isolate was then selected from each of the resulting seven groups for further investigation using DNA sequence comparisons.

DNA comparison and phylogenetic analyses

ITS analysis

ITS sequences were generated in both directions and DNA amplicons of ~550 nucleotides were obtained after assembly. Sequences were deposited in GenBank and accession numbers are shown in Table 2. Following BLAST searches, the 11 sequences obtained in this study were aligned with closest taxa available in GenBank or other species of Mycosphaerellaceae and Teratosphaeriaceae that have been previously reported on Eucalyptus. The alignment consisted of 63 ingroup sequences and Neofusicoccum ribis as the outgroup taxon.

Sequence alignment resulted in a total of 708 characters of which 233 were constant, 111 variable characters were parsimony-uninformative and 364 were parsimony informative. NJ and MP resulted in trees of identical topology. The heuristic search analysis of the data resulted in four most parsimonious trees (TL = 1129 steps; CI = 0.648; RI = 0.841; HI = 0.352). The genetic distance consensus tree obtained with NJ analysis based on the ITS region of the rDNA operon analysis is shown (Fig 2) with the bootstrap values of 1000 replicates of NJ and MP analyses displayed on the branches.

Combined data set analysis (ITS, EF-1α, ACT)

The five sequences of those species previously found on Eucalyptus in Uruguay were subject to a combined analysis to fully verify their identity. The sequence alignment consisted of 12 ingroup sequences and Teratosphaeria nubilosa as the outgroup. A combined dataset of a total of 984 characters was analyzed (474, 227, 283 characters for ITS, EF-1α, and ACT, respectively), of which 532 were constant, 147 were parsimony-uninformative and 305 were parsimony informative. Both NJ (NJ) and MP analyses resulted in trees of identical topology. Heuristic search analysis of the data resulted in one most parsimonious tree (TL = 811 steps; CI = 0.874; RI = 0.905; HI = 0.126). The distance tree obtained from NJ analysis of the combined ITS, EF-1α, and ACT with the bootstrap values of 1000 replicates from NJ and MP analyses displayed on the branches is shown (Fig 3).

Table 2 – (continued)

<table>
<thead>
<tr>
<th>Culture ID</th>
<th>Species</th>
<th>Host</th>
<th>GenBank accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>STE-U348</td>
<td>Zasmidium marassii</td>
<td>Syzygium sp.</td>
<td>AF309591</td>
</tr>
<tr>
<td>CMW3358 T</td>
<td>Zasmidium parkii</td>
<td>Eucalyptus sp.</td>
<td>AF309590</td>
</tr>
<tr>
<td>CMW7777</td>
<td>Neofusicoccum ribis</td>
<td>Ribe sp.</td>
<td>AY236936</td>
</tr>
</tbody>
</table>

*ex-type cultures.*
Fig 2 – Genetic distance consensus tree obtained with NJ analysis based on the ITS region of the rDNA operon. Species name and GenBank accession number are shown for each sequence. Sequences labelled with a ‘T’ at the end correspond to the ex-type culture. Bootstrap values of 1000 replicates of NJ and MP analyses are shown above and below branches, respectively. Only bootstrap values higher than 75 % are shown. *Neofusicoccum ribis* was used as outgroup taxon. Uruguayan isolates are indicated with the prefix ‘UY’ and sequences corresponding to isolates obtained from native Myrtaceous trees are in bold. Underlined sequences correspond to isolates obtained from *Eucalyptus* spp. in Uruguay, and included for reference.
Species identified

A diverse group of Mycosphaerellaceae and Teratosphaeriaceae were found to occur on diseased leaves of native Myrtaceae in this study. Phylogenetic analyses revealed a total of five distinct species residing in the Mycosphaerellaceae and Teratosphaeriaceae. These included *Mycosphaerella yunnanensis*, *Pallidocercospora heimii*, *Passalora loranthi*, *Pseudocercospora norchensis*, and *Teratosphaeria aurantia*.

Three of these species were previously found on Eucalyptus by Perez et al. (2009b). *Teratosphaeria aurantia* was found associated with leaf spots on Blepharocalyx salicifolius, in the northern region (i.e. province of Rivera). The sequence of this isolate was identical to that of UY372 obtained from Eucalyptus *grandis* by Perez et al. (2009a,b,c) and was confirmed in the multigene analysis.

*Pallidocercospora heimii* was associated with leaf spots only on Myrciaria glaucescens in Rio Negro, and the sequence of this isolate was identical to that for the isolate obtained from Eucalyptus *dunnii* by Perez et al. (2009b), whereas *Ps. norchensis* was found on leaves of two native tree species, Acca sellowiana and *B. salicifolius*, also in the province of Rivera, and obtained sequences grouped with sequences UY1528 and UY1561 obtained from *E. dunnii* and *E. grandis* also in Rivera by Perez et al. (2009b). *Passalora loranthi* was found on leaf spots on *A. sellowiana* in the province of Rivera. Surprisingly, *M. yunnanensis*, not previously reported in Uruguay, was found on leaves of *B. salicifolius* and Myrhinium *atropurpureum* var. *octandrum* in Rivera. Phylogenetic grouping was strongly supported by both NJ and MP analyses and sequences differed only at one base from the sequence for the ex-type culture of this fungus.

### Discussion

Results of this study clearly showed that there is a relatively diverse group of species belonging to the Mycosphaerellaceae and Teratosphaeriaceae associated with leaf spots on native Myrtaceae in Uruguay. Three species, *Pallidocercospora heimii*, *Pseudocercospora norchensis* and *Teratosphaeria aurantia*, are well-known Eucalyptus leaf spot associated fungi, previously reported to infect Eucalyptus in Uruguay (Balmelli et al. 2004; Crous et al. 2006; Perez et al. 2009b). An important and intriguing aspect of this study was the clear evidence of fungi previously thought to be specific to Eucalyptus, occurring on the leaves of native trees in Uruguay. These fungi are all known on Eucalyptus leaves in countries other than Uruguay and it seems most likely that they were introduced into Uruguay on Eucalyptus and have subsequently undergone a host shift to native tree species. Such host shifts have recently been shown in Uruguay for *Quambalaria* leaf disease caused by *Quambalaria eucalypti* (Perez et al. 2008) and *Neofusicoccum eucalyptorum* (Perez et al. 2009c). This is, however, the first evidence of species associated with MLD of Eucalyptus undergoing such host shifts.

*Teratosphaeria aurantia* (syn. *Mycosphaerella aurantia*) was found associated with leaf spots on Blepharocalyx salicifolius. Although there has been some confusion regarding the identification of this species, with Hunter et al. (2006) suggesting that it is likely the same as *Teratosphaeria africana*, isolate UY1382 obtained from *B. salicifolius* grouped strongly with other *T. aurantia* isolates, including that of the ex-type (Maxwell et al. 2003). Morphological characteristics of ascospores observed in this study also showed they did not have constrictions at the median septum, as described for *T. aurantia* (Maxwell et al. 2003). To date, this species has only been known to occur in Australia and Uruguay (Andicic et al. 2010; Hunter et al. 2011; Perez et al. 2009b) and this study represents the first report on a host other than Eucalyptus.

*Pallidocercospora heimii* was found associated with leaf lesions on Myrciaria glaucescens. *Pallidocercospora* is a novel genus to accommodate former 'Mycosphaerella' species with pale brown Cercospora-like conidia, and includes *Pallidocercospora norchensis* to represent a member of a species complex due to the difficulty differentiating this species from *Pallidocercospora heiminoidea*, *Pallidocercospora crystallina* and *Pallidocercospora irregulariaramosa*, we found that isolate UY322 consistently grouped with *Pallidocercospora norchensis* sequences and it was clearly separate from other related species of this complex. The ITS sequence for this isolate was also identical to isolate UY423 obtained from Eucalyptus *dunnii* in Uruguay by Perez et al. (2009b).

*Pallidocercospora heimii* is known from Australia, Brazil, Madagascar, Portugal, Uruguay, and Venezuela (Hunter et al. 2004; Crous et al. 2006; Crous et al. 2007; Perez et al. 2009b) where it has been found only on Eucalyptus. However, it was also found on *Acacia auriculiformis* and *Acacia* sp. in Thailand (Crous & Groenewald 2005). Our results support this data and demonstrate that it is able to cross hosts and all indications are that in Uruguay, it has moved from Eucalyptus onto native Myrtaceae. *Pseudocercospora norchensis*,

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**Fig 3** – NJ tree from the combined analysis based on partial ITS, Actin, and EF1-α sequence data. Bootstrap values of 1000 replicates of NJ and MP analyses are shown above and below branches, respectively. Only bootstrap values higher than 75% are shown. Sequences corresponding to isolates obtained from native Myrtaceae trees are in bold.
found on Acca sellowiana and B. salicifolius in this study, was very recently described by Crous et al. (2007) on leaves of Eucalyptus collected in Italy. Very little is known regarding this fungus but Perez et al. (2009b) found it on E. dunnii, Eucalyptus globulus and Eucalyptus grandis in the northern region of Uruguay. Although Pseudocercospora luzardi grouped closely with Ps. norchiensis, the morphology of sequences of isolates UY1436 and UY1484 and the species were described for Ps. norchiensis as well as the DNA sequence data (100% similarity with the ex-type sequence of Ps. norchiensis) supports the identification of these isolates as Ps. norchiensis. In addition, the reference sequence of Ps. luzardi (AF362057) in GenBank differed from Ps. norchiensis (EF394859) at three nucleotides in the ITS2 region. The former species has been reported only on Hancornia speciosa (Apocynaceae) in Brazil (Furnaletto & Dianese 1999) and it probably represents a distinct species.

Mycosphaerella yunnanensis found on native Myrtaceae in this study has been described by Burgess et al. (2007) from Eucalyptus urophylla in China. We found this species associated with leaf spots on the native B. salicifolius and Myrrhinum atro-purpureum var. octandrum in Uruguay. To the best of our knowledge, this is the first report of M. yunnanensis outside China. Although it has not been found on Eucalyptus in Uruguay, it seems likely that its origin is on that host.

Passalora loranthi appears to be a species in the Mycosphaerellaceae with a wide host range. The fungus has been previously recorded in two unrelated hosts, namely Citrus sp. and Musa (Arzanlou et al. 2008). We found Pa. loranthi associated with leaf disease on A. sellowiana. This finding adds a member of the Myrtaceae to the list of hosts that can be infected by this fungus.

This study is the first to broadly consider the MLD on native Myrtaceae growing in association with non-native Eucalyptus plantations. Four species previously only known from Eucalyptus were found on native Myrtaceae. This suggests strongly that these fungi are moving from non-native Eucalyptus to native trees. Our findings support the views of Crous & Groenewald (2005) and Hunter et al. (2011) that some leaf-infecting fungi previously thought to be specific to Eucalyptus, have wider host ranges than was thought in the past. Almost nothing is known regarding the etiology and impact of these species, other than the fact that they are associated with leaf spot diseases on native trees. There is currently no evidence to suggest that they are causing serious disease problems on the native trees on which they were found, but their potential to result in serious disease situations such as those observed on Eucalyptus in Uruguay and around the world must be considered. Continued monitoring of these disease situations is essential.

While there are growing numbers of examples of pathogens of native Myrtaceae moving to Eucalyptus where these trees are grown as exotics (Rodas et al. 2005; Glen et al. 2007; Coutinho et al. 2011), there are far fewer examples of movement of apparently introduced Eucalyptus pathogens to native plants (Crous & Groenewald 2005). Results of this study provide important new information that this movement is far more common than has been previously thought. Although the consequences have yet to be realized, the results illustrate the danger of moving crop plants between countries together with pathogenic fungi that are poorly understood.

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References


