

The challenge of understanding the origin, pathways and extent of fungal invasions: global populations of the *Neofusicoccum parvum*–*N. ribis* species complex

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Abstract

Aim: Cryptic species in the *Neofusicoccum parvum*–*N. ribis* species complex have only recently been described, invalidating previous interpretations on host and geographical distribution. This study aimed to characterize the diversity and distribution of these species and to understand the patterns of host association, likely origins and their patterns of spread.

Location: Australia, Brazil, Cameroon, Chile, China, Colombia, Ethiopia, France, Greece, India, Indonesia, Iran, Italy, Japan, Kenya, Mexico, New Zealand, Panama, Portugal, Puerto Rico, South Africa, South Korea, Spain, Swaziland, Taiwan, Thailand, Uganda, United States of America, Uruguay, Zambia and Zimbabwe.

Methods: Using the unique polymorphisms that separate species within the complex, we evaluated sequence search results available in public and in our own databases. In addition, the global distribution of diversity of *N. parvum* was analysed using seven microsatellite markers.

Results: *Neofusicoccum parvum* is found in 90 hosts across six continents and 29 countries. *Neofusicoccum kwambonambiense* is found on four continents, six countries and on 14 hosts; *N. occulatum* is found on four continents, four countries and on 11 hosts; *N. umdonicola* is found on two continents, countries and hosts; *N. cordaticola* is found on three continents, countries and hosts; *N. batangarum* is found on two continents, three countries and three hosts; and *N. ribis* is found on one host in one country. Population genetic analysis of the global *N. parvum* population reflects admixture and repeat introductions.

Main conclusions: This study illustrates the unfettered and frequent movement of latent pathogens across international borders. Amongst the species in the *N. parvum*–*N. ribis* complex, *N. parvum* is the most widespread and has been reported on the majority of the hosts studied. The current dispersal of *N. parvum* and its sister species is probably due to repeated introductions of plant material into new growing areas, with *Eucalyptus* and *Vitis vinifera* being two prominent candidates for material transfer.

Keywords

Botryosphaeriaceae, Latent pathogen, *Neofusicoccum cordaticola* and *N. batangarum*, *N. kwambonambiense*, *N. occulatum*, *N. umdonicola*, *N. parvum*–*N. ribis* species complex.

Introduction

Invasion and establishment pathways of fungi and Oomycetes are less understood than that of plants and animals. The effects following establishment of serious pathogens is, however, all too evident, for example, the ecological disasters caused by Jarrah Dieback in Western Australia (Shearer & Smith, 2000) and Chestnut Blight in North America and Europe (Dutech *et al.*, 2012). The cryptic nature of fungi and the difficulty in distinguishing species hampers efforts to monitor their presence, define their origin and determine their host and geographical range. This in turn, seriously affects our ability to proactively manage potential invasion pathways, and the processes required to reduce the chances of further catastrophes. The problem is further exacerbated for latent pathogens where, due to their asymptomatic life stage (as an endophyte), disease symptoms may not be apparent on infected plants. In essence, most 'healthy' plant material moving around the world could be colonized by latent pathogens. This problem is highlighted in the *Neofusicoccum parvum*–*N. ribis* species complex, a group of related latent tree pathogens. In this study, we attempt to unravel the questions around their identity, distribution and host range, to better understand the frequency and effect of anthropogenic movement.

Neofusicoccum species (previously known as *Botryosphaeria* species with *Fusicoccum* anamorphs) are commonly associated with numerous woody hosts world-wide (von Arx, 1987). Of these, *N. parvum* Pennycook and Samuels (Pennycook & Samuels, 1985) has the widest distribution, host range and proven ability to cause disease (Slippers & Wingfield, 2007). For example, isolations made from diseased material and subsequent pathogenicity trials have found *N. parvum* to cause lesions on stems of a range of hardwood plantation tree species, native tree species and horticultural plant species (van Niekerk *et al.*, 2004; Sakalidis, 2004; Pavlic *et al.*, 2009; Pérez *et al.*, 2010; Golzar & Burgess, 2011).

Disease and host reports of *N. parvum* prior to the taxonomic revision of *N. parvum*, *N. ribis* and *B. dothidea* are unreliable (Slippers *et al.*, 2004b). *Neofusicoccum parvum* has been frequently confused with *N. ribis* Grossenb. and Duggar and *B. dothidea* (Moug. Fr.) Ces. and De Not. (Slippers *et al.*, 2004b,c). *Neofusicoccum ribis* was described as a species separate from *B. dothidea* by Grossenbacher and Duggar in 1911, however, in 1954, von Arx and Muller synonymized these two species due to the lack of distinct morphological characters and overlapping host ranges. Consequently, for approximately 45 years, many diseases of woody hosts were attributed to *B. dothidea*. A combination of RAPD marker analysis, ISSR fingerprinting, sequence data and detailed morphological work provided support for the separation of *N. ribis* and *B. dothidea* and for the distinction of these two species from *N. parvum* (Smith & Stanosz, 1997, 2001; Jacobs & Rehner, 1998; Zhou *et al.*, 2001; Slippers *et al.*, 2004b). Slippers *et al.* (2004b) selected an epitype for *B. dothidea* and an ex-type culture for *N. ribis* from isolates collected from the location of the holotype. Therefore, only records collected since 2004 with corresponding molecular data, or isolates collected earlier but for which sequence data is available, can be considered reliable.

Since 2004, the use of multiple gene phylogenies to delineate species boundaries has led to the recognition of five additional species within the *N. parvum*–*N. ribis* species complex, namely *N. umdonicola*, *N. cordaticola*, *N. kwambonambiense* (Pavlic *et al.*, 2009), *N. batangarum* (Begoude *et al.*, 2010) and *N. oculatum* (Sakalidis *et al.*, 2011c). These recent descriptions, however, also invalidate the identities assigned to many isolates in GenBank. This misinformation hampers a clear understanding of the host and geographical distribution of the cryptic species, which is crucial for understanding their potential origin,

pattern of spread around the world and impact on various ecologically and commercially important hosts.

In this study, all sequence data for the *N. parvum*–*N. ribis* complex available from GenBank and private databases available to us are reinterpreted in the light of a current phylogenetic framework for this species complex. The aim is to characterize the host and geographical distribution of the individual species. Additionally, polymorphic microsatellite markers are used to characterize the distribution of the diversity in a world-wide collection of the most common species in the complex, *N. parvum*.

Methods

Global species distribution

Isolate information from the population study presented here was pooled with GenBank searches to determine the current known distribution and host range of each species in the *N. parvum*–*N. ribis* complex. Representative sequences for each species in the *N. parvum*–*N. ribis* complex (Pavlic *et al.*, 2009; Begoude *et al.*, 2010; Sakalidis *et al.*, 2011c) were used to perform a BLAST search in GenBank with maximum sequences limited to 500; matches of > 99% homology were aligned with type species in Bioedit v 7.09 (Hall, 1999) using the ClustalW multiple alignment function and default options. This was repeated for up to four gene regions: internal transcribed spacer of the rDNA (ITS), β -tubulin (BT), translation elongation factor 1- α (EF) and RNA polymerase subunit II RPB2 depending upon which loci contained unique polymorphisms that could be used to distinguish the different species (Pavlic *et al.*, 2009; Sakalidis *et al.*, 2011c). *Neofusicoccum parvum* can be separated from all other species based on unique polymorphisms in the ITS region. For *N. parvum*, maximum sequences were limited to 1000; matches of >97% homology (374) sequences were aligned. In some cases, only the genus, for example, *Eucalyptus* sp. is provided for a host on GenBank.

Neofusicoccum parvum population analysis

Origin and identity of isolates

Data from three separate microsatellite studies (Slippers, 2003; Sakalidis, 2004; Pavlic, 2009) conducted prior to the formal description of many cryptic species within the *N. parvum*–*N. ribis* species complex were compiled, isolates that are now recognised as species other than *N. parvum* were removed. These account for some of the unevenness in sampling amongst hosts and countries. Isolates were identified to species level using a combination of available sequence data, RFLP data and unique alleles. Of the 169 verified *N. parvum* isolates from this collection, 38 were isolated from Australia, two from Chile, six from China, 16 from Colombia, 14 from Hawaii, two from Indonesia, 14 from New Zealand and 77 from South Africa. The majority of isolates (81) came from *Eucalyptus* species, 50 isolates came from *Syzygium cordatum* and 38 came from other woody hosts (*Actinidia deliciosa*, *Araucaria* sp., *Cinnamomum camphora*, *Malus sylvestris*, *M. indica*, *Populus nigra*, *Ribis* sp. and *Tibochina lepidota*) (Table 1). Cultures of all isolates are maintained on half strength potato dextrose agar (19.5 g BBL™ PDA, 7.5 g agar and 1 L distilled water) at Murdoch University (MUCC) or in the CMW collection of the Forestry and Agriculture Biotechnology Institute, University of Pretoria, South Africa.

Table 1. Number of haplotypes of *Neofusicoccum parvum* assigned to each group in primary, secondary and tertiary analysis in structure (x denotes isolates that could not be assigned to any group)

Sample	Host	No. isolates	No. Haplotypes	Primar			Secondary			Tertiary						
				y	1	2	x	1	2	3	x	A	B	C	D	E
Australia	<i>Eucalyptus</i> sp.	27	18	3	24	3	24	3	8	16						
	<i>Mangifera indica</i>	3	3	3				3								
	<i>Tibochina lepidota</i>	6	5	6				6		1	5					
	<i>Cinnamomum camphora</i>	1	1	1				1				1				
	<i>Ribis</i> sp.	1	1	1		1									1	
	Total Australia	38	28	3	35	3	1	34	3	12	22	1				
Chile	<i>Eucalyptus</i> sp.	2	2	2		2		2								
China	<i>Eucalyptus</i> sp.	6	4	6			6		6							
Colombia	<i>Eucalyptus</i> sp.	16	9	16		16		16								
Hawaii	<i>Eucalyptus</i> sp.	14	12	12	2	2	11	1	3	8	3					
Indonesia	<i>Eucalyptus</i> sp.	2	2	2			2		1	1						
	<i>Malus sylvestris</i>	1	1	1			1		1							
	<i>Populus nigra</i>	2	2	2			2		2							
New Zealand	<i>Araucaria</i> sp.	2	2	2			2		2							
	<i>Actinidia deliciosa</i>	3	3	3			1	2	1	1	1					
	<i>T. lepidota</i>	6	4	6			6		6							
	Total New Zealand	14	12	14		1	13		7	6	1					
South Africa	<i>Eucalyptus</i> sp.	14	5	14	1	13		3	11							
	<i>Syzygium cordatum</i>	50	18	21	29	21	25	4	11	10	4					25
	<i>M. indica</i>	13	10	6	7	6	7	6	7							
	Total South Africa	77	33	27	50	28	38	11	17	10	14					36
Total		169	102	48	119	2	51	40	77	1	38	10	37	43	38	3

DNA extraction, SSR amplification and visualization

Single conidial isolates were grown on half strength PDA plates for approximately 1 week at 20 °C. The mycelial mass was harvested and placed into 1.5-mL sterile Eppendorf tubes. A modified method from (Raeder & Broda, 1985) was used to extract the DNA (Taylor *et al.*, 2005). DNA was purified using the Ultrabind DNA purification kit in accordance with the manufacturer's instructions (MO BIO Laboratories, Solana Beach, CA, USA).

Seven polymorphic loci that contain SSR sequences were used to amplify DNA from 169 isolates using primers and protocols developed previously (Slippers *et al.*, 2004a). PCR were run on a programme of 94 °C for 2 min then 10 cycles of: 94 °C for 30 s, 60 °C for 45 s, 72 °C for 1 min then 25 cycles of: 94 °C for 30 s, 60 °C for 45 s, 72 °C for 1 min, with a final extension of 72°C for 5 min.

All primer pairs were run at the above conditions with the following exceptions; Expand High™ Fidelity *Taq* polymerase (Roche Biochemicals, Alameda, CA, USA) and Expand PCR buffer (2 mM Tris–HCl, pH 7.5; 1.5 mM MgCl₂; 10 mM KCl) were used to amplify locus *BotF11* and locus *BotF21* was amplified at an annealing temperature of 56 °C instead of 60 °C.

Amplified products that exhibited non-overlapping base pair sizes were combined into two groups, the first containing 0.2 ng of product/ μl of amplicons from *BotF21*, *BotF17*, *BotF37* and *BotF11*, the second with amplicons from *BotF35*, *BotF23* and *BotF15*. One μl of diluted product was added to 2 ml of formamide containing a ROX-labelled GeneScan-500 size standard (Applied Biosystems, Warrington, UK) (14 μl ROX ml^{-1} formamide). These were then run on an ABI PRISM 3100 autosequencer (Perkin-Elmer Applied Biosystems, Warrington, UK). Results were analysed using Gene Mapper software (Perkin-Elmer Applied Biosystems).

Population genetic analyses

Gene diversity, distance analysis, population differentiation, gene flow and mode of reproduction were determined on seven loci of populations of *N. parvum* as outlined in Sakalidis *et al.* (2011b). Chi-squared tests were conducted to determine whether isolates from different hosts within the same region could be combined.

Global population structure

The program structure v 2.2 (Pritchard *et al.*, 2000) was used to assign the global collection of *N. parvum* isolates to distinct populations. structure determines the most likely number of genetic groups (K) using a Bayesian Monte Carlo Markov Chain (MCMC) clustering algorithm. A total of 250000 iterations were performed after a burn-in period of 70000 where K values ranged from 1 to 15. The 'admixture model' was chosen as ancestry model, the correlated allele frequency model for setting the parameter λ (Pritchard *et al.*, 2000). For the best choice of K , the Log likelihood values of K , $L(K)$ (Pritchard *et al.*, 2000) and ΔK values (Evanno *et al.*, 2005) were plotted against the ranging K values (Fig. 1). Isolates were assigned to populations using structure v 2.2 (Pritchard *et al.*, 2000) once the best value of K was determined. CLUMPP (Jakobsson & Rosenberg, 2007) was used to align multiple runs of Structure at the optimum K value using the Greedy algorithm. Distruct (Rosenberg, 2004) was used to generate a visual interpretation of the population assignments of each individual.

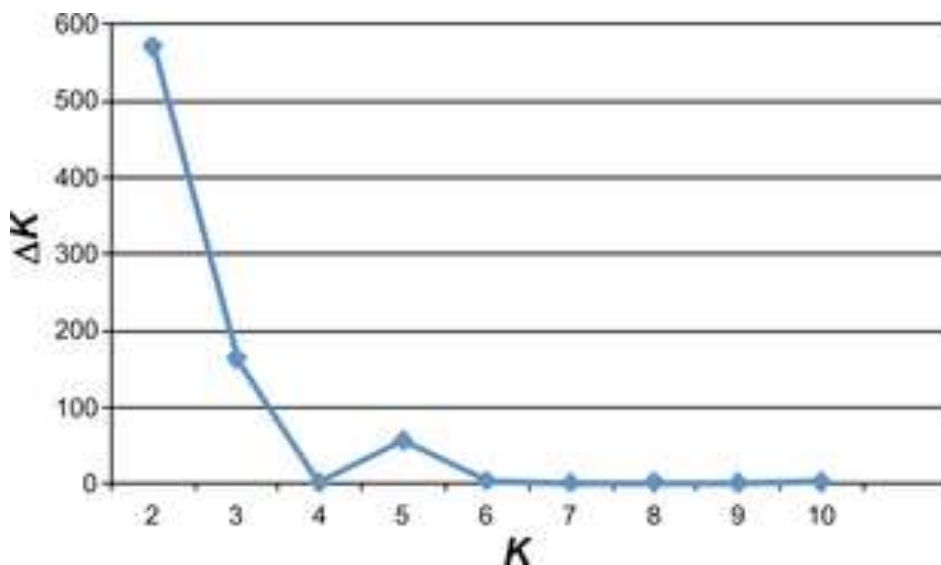


Figure 1. Log likelihood values of ΔK values against the ranging K values for the *Neofusicoccum parvum* population.

Results

Global species distribution

GenBank BLAST search of the ITS sequence of *N. parvum* identified 374 sequence deposits that could be identified as *N. parvum*. Isolates were labelled on GenBank as *N. parvum*, *N. ribis*, *B. parva*, *B. dothidea*, *Botryosphaeria* sp., *Guignardia cryptomeriae*, *Neofusicoccum* sp., fungal endophyte, fungal sp. and uncultured fungus. They were collected from 90 mainly woody plant species, across six continents from 29 countries: Australia; Africa: Ethiopia, Kenya, South Africa, Swaziland, Uganda, Zambia and Zimbabwe; Asia: China, India, Indonesia, Iran, Japan, South Korea, Taiwan and Thailand; Europe: France, Greece, Italy, Portugal and Spain; South America: Brazil, Chile, Colombia and Uruguay; New Zealand; North America: Mexico, USA and Puerto Rico. *N. parvum* has been collected from *Eucalyptus* spp. in 13 countries and from *V. vinifera* in 11 countries (see Table S1 in Supporting Information).

Blast searches of *N. kwambonambiense* sequence matched isolates that were identified on GenBank as *N. parvum*, *N. ribis*, *Botryosphaeria* sp. and *Neofusicoccum* sp. Isolates were collected from six countries: Australia, China, Mexico, South Africa, Uganda, the USA and from 14 host species (see Table S1).

Neofusicoccum occulatum sequences were identified on GenBank as *Botryosphaeria* sp., *B. parva*, *B. ribis*, *Neofusicoccum* sp., *N. parvum* and *N. ribis*. Isolates were collected from four countries: Australia, Uganda, Uruguay and the USA, and from 11 host species (see Table S1).

In addition to the type isolates of *N. umdonicola* obtained from *S. cordatum* in South Africa (Pavlic *et al.*, 2009), one sequence was identified as a 'Fungal sp.' collected from ungerminated seed sampled from Colorado Island in Panama (see Table S1). The only isolates of *N. batangarum* are those collected on *T. catappa* in Cameroon, which were used in the original species description (Begoude *et al.*, 2010), a single isolate collected from *Ficus insipida* seed in Colorado Island in Panama (Kluger *et al.*, 2008) and one collected from *Schinus terebinthifolius* seed in the USA (Shetty *et al.*, 2011). The ex-type isolates of *N. cordaticola* were obtained from *S. cordatum* in South Africa (Pavlic *et al.*, 2009). BLAST searches of *N. cordaticola* sequence matched isolates that were identified on GenBank as *N. parvum* collected from Italy and Australia from two host species (see Table S1). The only isolates of *N. ribis* are those collected on *Ribes* sp. in North America (Slippers *et al.*, 2004b).

Neofusicoccum parvum population analysis

Genetic diversity

Due to the low sample number in some populations, estimates of genetic diversity may be underestimated. However, our focus was on migration pathways of *N. parvum*, and every data point was thus considered valuable and is included. For genetic diversity estimates, please refer to Appendix S1 in Supporting Information.

Of the 169 samples collected, there were a total of 93 multilocus haplotypes. One haplotype was shared between Australia, New Zealand and South Africa. Australia shared another

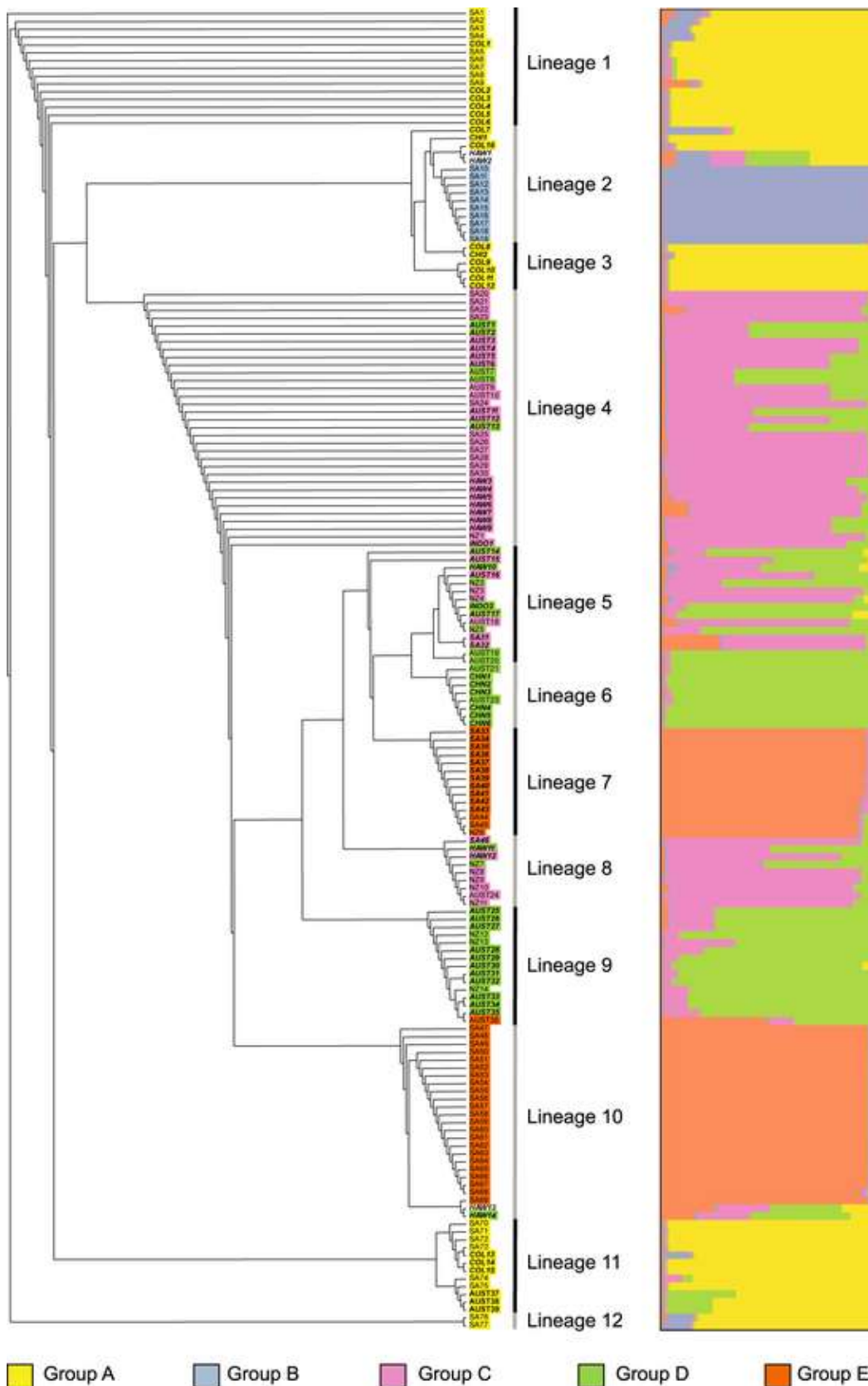


Figure 2. Distance tree and STRUCTURE bar plot of *Neofusicoccum parvum* isolates from Australia (AUST), China (CHN), Chile (CHI), Colombia (COL), Hawaii (HAW), Indonesia (INDO) and South Africa (SA). Colours correspond to groups generated in STRUCTURE. Isolates in bold and italics were collected from *Eucalyptus* species. Isolates without any shading were not assigned to any population.

haplotype with New Zealand, whilst South Africa shared a different haplotype with New Zealand. Hawaii and Indonesia shared one haplotype (Table 1).

STRUCTURE detected three levels of subdivision; isolates were grouped into two (primary division), three (secondary division) and then five groups (tertiary division) (Fig. 2, Table 1). South African and Australian isolates were represented in all groups at all levels of subdivision except in the tertiary division, in group B, there were only South African isolates, whilst in group D, there were no South African isolates (Fig. 2, Table 1). Colombian and Chilean isolates consistently grouped together with South African isolates (although members from Australia, and Hawaii were also present in some cases) (Group A, Table 1). Chinese, Indonesian and New Zealand isolates tended to cluster together in a group with the Australian isolates (Group C and D, Table 1).

Eucalyptus species were sampled 81 times (48% of total samples) in seven countries. Of these, the eight samples taken from *Eucalyptus* species in Chile and Colombia clustered together (Group A, Table 1). Group C contained 30% of Australian *Eucalyptus* samples, 21% of Hawaiian *Eucalyptus* samples, 50% of Indonesian *Eucalyptus* samples and 21% of South African *Eucalyptus* samples (Table 1).

Group D contained 57% of samples taken from *Eucalyptus* species in Hawaii, 50% of Indonesian *Eucalyptus* isolates, 59% of Australian *Eucalyptus* isolates and 100% of Chinese isolates (Table 1). The majority (78%) of South African *Eucalyptus* isolates grouped together in Group E (Table 1).

Distance analysis

Distance analysis resolved 12 lineages (Fig. 2). Isolates identified in groups C and D in the tertiary subdivision by structure were not clearly resolved in the distance analysis. Group A formed five lineages (1, 2, 3, 11 and 12), four of which (1, 3, 11 and 12) contained only members from Group A, and one lineage (2) also contained members from Group B. Group B formed one lineage (2) with members from Group A. Group C formed three lineages (4, 5 and 8) all mixed with members from Group D. Group D formed six lineages (4, 5, 6, 8, 9 and 10); three lineages (4, 5 and 8) were mixed with members from Group C; two lineages (9 and 10) were mixed with members from Group E; and one lineage (6) contained only members from Group D. Group E formed three lineages (7, 9 and 10); lineage 7 containing only members from Group E; whilst lineages 9 and 10 also contained members from Group D.

Population differentiation and gene flow

Chi-squared tests indicate no significant differences ($P > 0.05$) in gene diversity between isolates grouped by host or geographical region from each country, indicating these isolates can be placed into populations according to country of collection. Theta values (θ) between populations comparing Australia and New Zealand and New Zealand and Hawaii were not significant, indicating that there was no population differentiation between Australia and New Zealand and New Zealand and Hawaii. Theta values between all other populations were significant ($P < 0.05$), indicating various levels of population differentiation between these countries (Table 2). A low degree of differentiation was exhibited when comparing South Africa with Australia, Colombia, Hawaii and New Zealand, and when comparing Australia with Hawaii. Moderate to high levels of differentiation occurred between all other

populations, particularly when comparing China with Colombia and Hawaii. This may also be a reflection of small sample size in some of these countries.

Table 2. Pairwise comparisons of population differentiation (θ) (above the diagonal) and gene flow (below the diagonal) among *N. parvum* populations from Australia (AUST), China (CHN), Colombia (COL), Hawaii (HAW), New Zealand (NZ) and South Africa (RSA). Values obtained are for clone-corrected populations

	AUST	CHN	COL	HAW	NZ	SA
1. For θ values, stars and NS indicate significance (* $P < 0.05$, ** $P < 0.001$, ^{NS} $P > 0.05$ -not significant).						
AUST	-	0.309**	0.442**	0.127**	0.007 ^{NS}	0.216**
CHN	1.118	-	0.690**	0.521**	0.412*	0.400**
COL	0.631	0.225	-	0.408**	0.407**	0.153**
HAW	3.437	0.460	0.725	-	0.055 ^{NS}	0.123*
NZ	70.928	0.714	0.728	8.591	-	0.148**
SA	1.815	0.750	2.768	3.565	2.878	-

Mode of reproduction

For Australia, China, Colombia, Hawaii and New Zealand, the I_A of the observed data of individual populations fell within the values produced from the randomized data sets supporting the null hypothesis that alleles are freely recombining (Table 3). The I_A of the observed data of South Africa was greater than that of the values produced from the randomized data sets, indicating predominantly clonal reproduction in this population. Additionally, a significant P -value was produced for the South African and Australian populations, suggesting association between alleles.

Table 3. Index of association for individual data sets from Australia (AUST), China (CHN), Colombia (COL), Hawaii (HAW), New Zealand (NZ) and South Africa (SA)

	Observed (original data set)	Range (randomized data sets)	P -value
1. Values obtained are for clone-corrected populations.			
AUST	0.647	-0.436 to 0.702	0.001
CHN	0.261	-0.783 to 1.304	0.360
COL	-0.034	-0.487 to 1.000	0.570
HAW	0.251	-0.651 to 1.153	0.179
NZ	0.260	-0.477 to 0.712	0.093
SA	0.495	-0.308 to 0.366	<0.001

Discussion

This study shows how widely a generalist, latent pathogen such as *Neofusicoccum parvum* can be distributed across the globe. The re-evaluation of data from GenBank, in conjunction with data from isolates collected as part of this study, confirmed the presence of closely related populations of *N. parvum* in temperate, mediterranean to subtropical climates on 90 different host species. The hosts are mainly woody angiosperms, but isolations were also made from four conifer species and a single monocot species (a lily). Microsatellite analysis suggests two major exchange routes of *N. parvum*; firstly between South Africa, Chile and Colombia and secondly between Australia, China, Indonesia, Hawaii and New Zealand. These routes are not exclusive, and there is evidence of minor incursions between other countries such as South Africa and New Zealand. It is likely that the current dispersal of

diverse populations of *N. parvum* throughout the world is due to repeat introductions of plant material used for agricultural, plantation or horticultural industries, with widely distributed and common hosts of *N. parvum*, such as *Eucalyptus* and *V. vinifera* being two prominent candidates for transfer.

A re-evaluation of GenBank sequence data has significantly expanded the reported host and geographical range of *N. parvum*. This pathogen has previously been reported to cause disease on a range of economically important agricultural, horticultural and forestry plants (van Niekerk *et al.*, 2004; Sakalidis, 2004; Zea-Bonilla *et al.*, 2007; Javier-Alva *et al.*, 2009; Pavlic *et al.*, 2009; Pérez *et al.*, 2010; Golzar & Burgess, 2011). GenBank sequences were associated with fungal samples taken from canker and die-back of stems, various fruit disfigurement and rot, inflorescence abortion and (once) from ungerminated seed. Most GenBank sequences have been deposited from studies involving exotic plants and/or native plants that have commercial value and are grown under human management. The study shows that *N. parvum* has been isolated from 18 fruit and nut crops and numerous tree and shrub species used for wood production, medicinal or ornamental purposes. It should, however, be noted that isolation of *N. parvum* from diseased material alone does not constitute proof of its involvement in causing the symptoms, and further trials are thus required to verify pathogenicity on specific hosts.

The pattern of distribution seen in the *N. parvum*–*N. ribis* complex would appear to reflect the occupation of wild ecosystems and the introduction into managed ecosystems, most likely via human-mediated transfer of germplasm. This is apparent due to the same fungal species occurring on hosts such as *V. vinifera* and *Eucalyptus* spp. in different countries (GenBank). Transfer of *Eucalyptus* spp. has been implicated in the movement of *Teratosphaeria destructans* throughout Southeast Asia (Andjic *et al.*, 2011). *Neofusicoccum oculatum* (Sakalidis *et al.*, 2011c) was described from *Eucalyptus* spp. and *W. nobilis* in Australia but has also been collected from *V. vinifera* in Australia, a *Eucalyptus* sp. in Hawaii, native Myrtaceae species and exotic *E. grandis* in Uruguay and a *Grevillea* sp. and a *Eucalyptus* sp. in Uganda. Similarly, the existence of *N. oculatum* and *N. parvum* on exotic *Eucalyptus* spp. and adjacent native Myrtaceae in Uruguay (Pérez *et al.*, 2010) suggests they have been transferred on *Eucalyptus* germplasm. *Neofusicoccum kwambonambiense*, provides another example of a pathogen that has only been described from native vegetation in South Africa (Pavlic *et al.*, 2009) and China (Table S1), but it has appeared as a serious pathogen on a commercial host elsewhere [i.e. commercial blueberry fields in Florida (Wright & Harmon, 2010) and Mexico (Table S1)]. *Neofusicoccum cordaticola* is present in South Africa (*S. cordatum*) (Pavlic *et al.*, 2009), Australia (*Eucalyptus*) and Italy (*Vitis*) (GenBank), which possibly reflects an endemic range (South Africa) and migration via the plant trade industry.

Extensive sampling of native vegetation in eastern Australia may provide further evidence of when or if *N. parvum* was introduced to Australia; it is known that *N. parvum* has been in eastern Australia for at least 28 years on horticultural crops (Cunnington *et al.*, 2007). Recently, *N. parvum* has been isolated from declining *Araucaria heterophylla* (Norfolk pine-endemic to Norfolk Island) in metropolitan Perth, Western Australia (Golzar & Burgess, 2011). This sudden decline of Norfolk pine might be due to a recent introduction of *N. parvum*, as prior to this report only one record of *N. parvum* had been made in Western Australia despite extensive sampling (Barber *et al.*, 2005; Burgess *et al.*, 2005, 2006; Taylor *et al.*, 2005, 2009; Dakin *et al.*, 2009; Sakalidis *et al.*, 2011d). The single record had been collected from an exotic *E. globulus* species in a plantation (Burgess *et al.*, 2005). This suggests that although Western Australia provides a suitable climate for *N. parvum*, its

geographical isolation and strict quarantine measures has provided an effective barrier to exotic fungi. It is also possible that introduced *N. parvum* is out-competed by the endemic species, *N. australe* (Sakalidis *et al.*, 2011b).

Despite the close genetic relationship of species in the *N. parvum*–*N. ribis* complex and the ability for some species to colonize the same hosts (Sakalidis *et al.*, 2011a; Spagnolo *et al.*, 2011), except for *N. parvum*, all the species from the complex exhibit a relatively restricted geographical range and a preference for certain host species. This is particularly evident for *N. ribis* that have not been recorded beyond the country and host associated with its original description.

The lack of host specificity of many members of the Botryosphaeriaceae (Slippers & Wingfield, 2007), suggests range expansion and speciation within this group are influenced by other environment factors. For example, climate is suggested as a limiting factor in Botryosphaeriaceae colonization of *V. vinifera* in Mexico (Úrbez-Torres *et al.*, 2008), Spain (Úrbez-Torres *et al.*, 2006) and South Australia and New South Wales (Pitt *et al.*, 2010). It is also possible that the dominance of a single species, despite the introduction of multiple species via imported germplasm, is influenced by locally adapted Botryosphaeriaceae already present and environmental factors acting on the host and subsequently on the endophyte. This may account for the dominance of different species of Botryosphaeriaceae collected from *T. catappa* in three different countries; *N. parvum* was dominant in South Africa, *L. pseudotheobromae* was dominant in Cameroon and *L. mahajangana* was dominant in Madagascar (Begoude *et al.*, 2010). Furthermore, in a recent study of *M. indica* in tropical conditions, *N. parvum* was not observed, yet it is often associated with this host in other climates (Slippers *et al.*, 2005). In addition, *M. indica* trees occurring in the Kimberley Region, Western Australia, were found to harbour endemic Botryosphaeriaceae (and not *N. parvum*) (Sakalidis *et al.*, 2011a), suggesting that the microflora in the surrounding environment determines the internal microflora of the exotic host in an environment.

One interpretation of the population genetic analysis (structure and gene flow analyses) of the microsatellite data suggest that a native or naturalized South African *N. parvum* population has moved from native to non-native plant species in South Africa (or vice-versa) and has also been introduced from South Africa to other countries in which *N. parvum* is reported. The founder population within a species' endemic range is generally expected to portray a higher genetic diversity than introduced populations (Nei *et al.*, 1975; Dlugosch & Parker, 2008). Of the seven species in the *N. parvum*–*N. ribis* species complex three have been described from the native *S. cordatum* in South Africa and *N. parvum* is also commonly collected in this host (Pavlic, 2009; Pavlic *et al.*, 2009). Furthermore, isolates of *N. parvum* from both native and non-native plants in South Africa were genetically diverse. They also contained a high number of unique alleles and haplotypes, suggesting South Africa as a possible candidate for the origin of *N. parvum*. However, the lack of detectable sexual reproduction amongst South African strains may conflict with the South African-origin hypothesis. Isolates found in Colombia and Chile grouped with isolates from South Africa in distance and structure analyses, and there was also a low level of genetic differentiation between isolates from these three countries, suggesting South Africa as the source of the populations in South America.

A second interpretation from the population genetic analysis is that *N. parvum* has moved between Australia, New Zealand, China and Hawaii. Isolates from these countries consistently grouped together in the distance and structure analyses and exhibited high levels

of gene flow between them. Also, high genetic diversity in the region may reflect an initial large introduction or multiple introductions, as was evident from the relatively high genetic diversity despite a small number of samples collected in New Zealand.

The genetic composition of *N. parvum* collections in Hawaii and New Zealand probably reflect introductions from both Australia and South Africa. Isolates from Hawaii and New Zealand grouped with isolates from South Africa and also Australia in the distance and structure analyses. In addition to this, despite no significant geneflow between Australia and South Africa, one Australian haplotype and one South African haplotype were identical to one found in New Zealand, and another single haplotype was shared between these three countries.

In most populations, the genetic diversity of *N. parvum* reflects a combined sexual/asexual mating strategy. Mixed reproduction has been observed in the field, as both the teleomorph and anamorph life stages of *N. parvum* were described in New Zealand in 1985 (Pennycook & Samuels, 1985) from introduced *Actinidia deliciosa* (kiwifruit). Most populations exhibited an independent assortment of alleles as expected with sexual recombination (I_A test). Furthermore, recent work by Baskarathevan *et al.* (2011) has demonstrated anastomosis between *N. parvum* strains (outcrossing via hyphal tips) providing another source of genetic variation. Field observations of asexual reproduction, identical haplotypes occurring multiple times within all populations (not accessible in Indonesia as there were only two samples), and significant linkage disequilibrium in the Australian and South Africa populations suggests clonal reproduction in *N. parvum*. The significant linkage disequilibrium occurring in the South African population was surprising considering the high level of genetic diversity in this population. It is possible that sexual reproduction is occurring in South Africa, but our sampling strategy was insufficient to detect it.

The genetic diversity reflected both within and between the *N. parvum* populations may be attributed to a number of factors. Firstly, the genetic composition of a population is a reflection of the original immigrant population introduced to an area, as *N. parvum* populations are genetically diverse, the original immigrant population was probably genetically diverse and may have come from different and/or multiple sources (Goodwin *et al.*, 1994; Dlugosch & Parker, 2008). Considering both the Australian and South African populations are genetically diverse, share haplotypes with other populations, may have mixed reproduction strategies and multiple infections can co-occur in a single host; immigration events from these two countries may well compose a genetically diverse population. Secondly, there may have been singular or repeat introductions (migration events) over time (Milgroom, 1996). There is evidence for extensive geneflow between Australia and New Zealand, also between New Zealand and Hawaii, and the initial establishment of *Eucalyptus* plantations may have involved of the movement of *Eucalyptus* germplasm between countries as has been shown for Southeast Asia (Andjic *et al.*, 2011). Thirdly, variation in well-established populations may be also due to accumulation of mutations over a period of time, although these are expected to play a small role over the time periods of relevance here (Goodwin *et al.*, 1994; Zhan & McDonald, 2004).

This study has used molecular identification techniques to confirm the broad range of hosts that *N. parvum* has been isolated from. The mixed reproduction strategy of *N. parvum* allows for increased genetic variation (sexual reproduction) and rapid dissemination of advantageous genotypes (asexual reproduction) (Zhan & McDonald, 2004; Sakalidis *et al.*, 2011a). These reproductive characteristics when combined with the inherent lack of host specificity

increases the chance of successful establishment when introduced to a new area. This success would also depend on the host health and the ability of *N. parvum* to compete with the native fungal microflora normally present within the host and surrounding environment. The lack of host specificity, common endophytic life stage and reputation as a latent pathogen are a potent combination for potential plant disease; especially when a host is stressed. Stressed hosts may have a reduced ability to combat fungal infection (Schulz *et al.*, 1999; Arnold & Engelbrecht, 2007), and endemic fungi present within the host may be antagonistic to other exotic fungi (Idnurm & Howlett, 2001; Redman *et al.*, 2001).

The ability of *N. parvum* to exist asymptotically as an endophyte and to colonize a wide range of hosts is likely to explain its movement to many locations. It is likely that the current dispersal of *N. parvum* throughout the world is due to repeat introductions of plant material into regions used for agricultural, plantation or horticultural industries, with widely distributed and common hosts of *N. parvum* likely candidates for transfer.

Acknowledgements

The authors would like to thank Chyreene Wingfield for her assistance in extraction of DNA, Draginja Pavlic for the use of some of the microsatellite data, the Forestry and Agricultural Biotechnology Institute, University of Pretoria for the use of facilities for the microsatellite analysis and the Australian Federation of University Women (AFUWA) for the financial assistance in the form of the Jill Bradshaw Bursary.

Biosketch

Monique Sakalidis is a Postdoctoral Fellow in TAIGA (Tree Aggressors Identification using Genomics Approaches) at the Forest and Conservation Sciences Centre at the University of British Columbia. Her research interests include speciation mechanisms, genomics and population genomics of forest pathogens with a special interest in latent pathogens.

Author's contributions: MLS, BS and TIB collected the microsatellite data, MLS collected, analysed and interpreted the remaining data and led the writing, MLS, BS, BW, GH and TIB conceived the ideas and contributed towards the writing.

References

- Andjic, V., Dell, B., Barber, P.A., Hardy, G.E.St.J., Wingfield, M.J. & Burgess, T.I. (2011) Plants for planting: evidence for the movement of serious forest pathogen, *Teratosphaeria destructans* on infected germplasm. *European Journal of Plant Pathology*, 131, 49–58.
- Arnold, A.E. & Engelbrecht, B.M.J. (2007) Understanding the diversity of foliar fungal endophytes: progress, challenges, and frontiers. *Fungal Biology Reviews*, 21, 51–66.
- von Arx, J.A. (1987) *Plant Pathogenic Fungi*. J. Cramer, Berlin, Germany.
- Barber, P.A., Burgess, T.J., Hardy, G.E.St.J., Slippers, B., Keane, P. & Wingfield, M.J. (2005) *Botryosphaeria* species from *Eucalyptus* in Australia are pleoanamorphic, producing *Dichomera* synanamorphs in culture. *Mycological Research*, 109, 1347–1363.
- Baskarathevan, J., Jaspers, M.V., Jones, E.E., Cruickshank, R.H. & Ridgway, H.J. (2011) Genetic and pathogenic diversity of *Neofusicoccum parvum* in New Zealand vineyards. *Fungal Biology*, 116, 276–288.
- Begoude, B.A.D., Slippers, B., Wingfield, M.J. & Roux, Y. (2010) *Botryosphaeriaceae* associated with *Terminalia catappa* in Cameroon, South Africa and Madagascar. *Mycological Progress*, 9, 101–123.
- Burgess, T.I., Barber, P.A. & Hardy, G.E.St.J. (2005) *Botryosphaeria* spp. associated with eucalypts in Western Australia, including the description of *Fusicoccum macroclavatum* sp. nov. *Australasian Plant Pathology*, 34, 557–567.
- Burgess, T.I., Sakalidis, M.L. & Hardy, G.E.St.J. (2006) Gene flow of the canker pathogen *Botryosphaeria australis* between *Eucalyptus globulus* plantations and native eucalypt forests in Western Australia. *Austral Ecology*, 31, 559–566.
- Cunnington, J.H., Priest, M.J., Powney, R.A. & Cother, N.J. (2007) Diversity of *Botryosphaeria* species on horticultural plants in Victoria and New South Wales. *Australasian Plant Pathology*, 36, 157–159.
- Dakin, N., White, D., Hardy, G.E.St.J. & Burgess, T.I. (2009) The opportunistic pathogen, *Neofusicoccum australe*, is responsible for crown dieback of peppermint (*Agonis flexuosa*) in Western Australia. *Australasian Plant Pathology*, 39, 202–206.
- Dlugosch, K.M. & Parker, I.M. (2008) Founding events in species invasions: genetic variation, adaptive evolution, and the role of multiple introductions. *Molecular Ecology*, 17, 431–449.
- Dutech, C., Barrès, B., Bridier, J. et al. (2012) The chestnut blight fungus world tour: successive introduction events from diverse origins in an invasive plant fungal pathogen. *Molecular Ecology*, 21, 3931–3946.
- Evanno, G., Regnaut, S. & Goudet, J. (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology*, 14, 2611–2620.
- Golzar, H. & Burgess, T. (2011) *Neofusicoccum parvum*, a causal agent associated with cankers and decline of Norfolk Island pine in Australia. *Australasian Plant Pathology*, 40, 484–489.
- Goodwin, S.B., Cohen, B.A. & Fry, W.E. (1994) Panglobal distribution of a single clonal lineage of the Irish potato famine fungus. *Proceedings of the National Academy of Sciences of the United States of America*, 91, 11591–11595.
- Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series*, 41, 95–98.
- Idnurm, A. & Howlett, B.L. (2001) Pathogenicity genes of phytopathogenic fungi. *Molecular Plant Pathology*, 2, 241–255.
- Jacobs, K.A. & Rehner, S.A. (1998) Comparison of cultural and morphological characters and ITS sequences in anamorphs of *Botryosphaeria* and related taxa. *Mycologia*, 90, 601–610.

- Jakobsson, M. & Rosenberg, N.A. (2007) CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics*, 23, 1801–1806.
- Javier-Alva, J., Gramaje, D., Alvarez, L.A. & Armengol, J. (2009) First report of *Neofusicoccum parvum* associated with dieback of mango trees in Peru. *Plant Disease*, 93, 426–426.
- Kluger, C.G., Dalling, J.W., Gallery, R.E., Sanchez, E., Weeks-Galindo, C. & Arnold, A.E. (2008) Host generalists dominate fungal communities associated with seeds of four neotropical pioneer species. *Journal of Tropical Ecology*, 24, 351–354.
- Milgroom, M.G. (1996) Recombination and the multilocus structure of fungal populations. *Annual Review of Phytopathology*, 34, 457–477.
- Nei, M., Maruyama, T. & Chakraborty, R. (1975) The bottleneck effect and genetic variability in populations. *Evolution*, 29, 1–10.
- van Niekerk, J.M., Crous, P.W., Groenewald, J.Z.E., Fourie, P.H. & Halleen, F. (2004) DNA phylogeny, morphology and pathogenicity of *Botryosphaeria* species on grapevines. *Mycologia*, 96, 781–798.
- Pavlic, D. (2009) Taxonomy and population diversity of *Botryosphaeriaceae* associated with woody hosts in South Africa and Western Australia. PhD, University of Pretoria, Pretoria.
- Pavlic, D., Slippers, B., Coutinho, T.A. & Wingfield, M.J. (2009) Molecular and phenotypic characterization of three phylogenetic species discovered within the *Neofusicoccum parvum*/*N. ribis* complex. *Mycologia*, 101, 636–647.
- Pennycook, S.R. & Samuels, G.J. (1985) *Botryosphaeria* and *Fusicoccum* species associated with ripe fruit rot of *Actinidia deliciosa* (kiwifruit) in New Zealand. *Mycotaxon*, 24, 445–458.
- Pérez, C., Wingfield, M., Slippers, B., Altier, N. & Blanchette, R. (2010) Endophytic and canker-associated *Botryosphaeriaceae* occurring on non-native *Eucalyptus* and native *Myrtaceae* trees in Uruguay. *Fungal Diversity*, 41, 53–69.
- Pitt, W.M., Huang, R., Steel, C.C. & Savocchia, S. (2010) Identification, distribution and current taxonomy of *Botryosphaeriaceae* species associated with grapevine decline in New South Wales and South Australia. *Australian Journal of Grape and Wine Research*, 16, 258–271.
- Pritchard, J.K., Stephens, M. & Donnelly, P. (2000) Inference of population structure using multilocus genotype data. *Genetics*, 155, 945–959.
- Raeder, U. & Broda, P. (1985) Rapid preparation of DNA from filamentous fungi. *Letters in Applied Microbiology*, 1, 17–20.
- Redman, R.S., Dunigan, D.D. & Rodriguez, R.J. (2001) Fungal symbiosis from mutualism to parasitism: who controls the outcome, host or invader? *New Phytologist*, 151, 705–716.
- Rosenberg, N.A. (2004) Distruct: a program for the graphical display of population structure. *Molecular Ecology Notes*, 4, 137–138.
- Sakalidis, M.L. (2004) Resolving the *Botryosphaeria ribis*-*B. parva* species complex; a molecular and phenotypic investigation. Honours, Murdoch University, Perth.
- Sakalidis, M.L., Hardy, G.E.St.J. & Burgess, T.I. (2011a) Endophytes as potential pathogens of the baobab species *Adansonia gregorii*: a focus on the *Botryosphaeriaceae*. *Fungal Ecology*, 4, 1–14.
- Sakalidis, M.L., Hardy, G.E.St.J. & Burgess, T.I. (2011b) Class III endophytes, clandestine movement amongst hosts and habitats and their potential for disease; a focus on *Neofusicoccum australe*. *Australasian Plant Pathology*, 40, 510–521.
- Sakalidis, M.L., Hardy, G.E.St.J. & Burgess, T.I. (2011c) Use of the Genealogical Sorting Index (GSI) to delineate species boundaries in the *Neofusicoccum parvum*-*Neofusicoccum ribis* species complex. *Molecular Phylogenetics and Evolution*, 60, 333–344.
- Sakalidis, M.L., Ray, J., Lanoiselet, V., Hardy, G.E.St.J. & Burgess, T.I. (2011d) Pathogenic *Botryosphaeriaceae* associated with *Mangifera indica* in the Kimberley Region of Western Australia. *European Journal of Plant Pathology*, 130, 379–391.
- Schulz, B., Römmer, A.-K., Dammann, U., Aust, H.-J. & Strack, D. (1999) The endophyte-host interaction: a balanced antagonism? *Mycological Research*, 103, 1275–1283.
- Shearer, B.L. & Smith, I.W. (2000) Diseases of eucalypts caused by soilborne species of *Phytophthora* and *Pythium*. *Diseases and Pathogens of Eucalypts* (ed. by P.K. Pj Keane, G.A. Kile, F.D. Podger and B.N. Brown), pp. 259–291. CSIRO Publishing, Melbourne, Australia.
- Shetty, K.G., Minnis, A.M., Rossman, A.Y. & Jayachandran, K. (2011) The Brazilian peppertree seed-borne pathogen, *Neofusicoccum batangarum*, a potential biocontrol agent. *Biological Control*, 56, 91–97.
- Slippers, B. (2003) Taxonomy, phylogeny and ecology of *botryosphaeriaceous* fungi occurring on various woody hosts. PhD, University of Pretoria, Pretoria.
- Slippers, B. & Wingfield, M.J. (2007) *Botryosphaeriaceae* as endophytes and latent pathogens of woody plants: diversity, ecology and impact. *Fungal Biology Reviews*, 21, 90–106.
- Slippers, B., Burgess, T., Wingfield, B.D., Crous, P.W., Coutinho, T.A. & Wingfield, M.J. (2004a) Development of simple sequence repeat markers for *Botryosphaeria* spp. with *Fusicoccum* anamorphs. *Molecular Ecology Notes*, 4, 675–677.
- Slippers, B., Crous, P.W., Denman, S., Coutinho, T.A., Wingfield, B.D. & Wingfield, M.J. (2004b) Combined multiple gene genealogies and phenotypic characters differentiate several species previously identified as *Botryosphaeria* dothidea. *Mycologia*, 96, 83–101.
- Slippers, B., Fourie, G., Crous, P.W., Coutinho, T.A., Wingfield, B.D., Carnegie, A.J. & Wingfield, M.J. (2004c) Speciation and distribution of *Botryosphaeria* spp. on native and introduced *Eucalyptus* trees in Australia and South Africa. *Studies in Mycology*, 50, 343–358.
- Slippers, B., Johnson, G.I., Crous, P.W., Coutinho, T.A., Wingfield, B.D. & Wingfield, M.J. (2005) Phylogenetic and morphological re-evaluation of the *Botryosphaeria* species causing diseases of *Mangifera indica*. *Mycologia*, 97, 99–110.

- Smith, D.R. & Stanosz, G.R. (1997) Heterogeneity among isolates of the *Botryosphaeria dothidea*-*B. ribis* complex is indicated by RAPD marker analysis. *Phytopathology*, 87 (suppl.), S91.
- Smith, D.R. & Stanosz, G.R. (2001) Molecular and morphological differentiation of *Botryosphaeria dothidea* (anamorph *Fusicoccum aesculi*) from some other fungi with *Fusicoccum* anamorphs. *Mycologia*, 93, 505–515.
- Spagnolo, A., Marchi, G., Peduto, F., Phillips, A. & Surico, G. (2011) Detection of *Botryosphaeriaceae* species within grapevine woody tissues by nested PCR, with particular emphasis on the *Neofusicoccum parvum* complex. *European Journal of Plant Pathology*, 129, 489–500.
- Taylor, A., Hardy, G.E.St.J., Wood, P. & Burgess, T. (2005) Identification and pathogenicity of *Botryosphaeria* species associated with grapevine decline in Western Australia. *Australasian Plant Pathology*, 34, 187–195.
- Taylor, K., Barber, P.A., Hardy, G.E.St.J. & Burgess, T.I. (2009) *Botryosphaeriaceae* from tuart (*Eucalyptus gomphocephala*) woodland, including descriptions of four new species. *Mycological Research*, 113, 337–353.
- Úrbez-Torres, J.R., Leavitt, G.M., Voegel, T.M. & Gubler, W.D. (2006) Identification and distribution of *Botryosphaeria* spp. associated with grapevine cankers in California. *Plant Disease*, 90, 1490–1503.
- Úrbez-Torres, J.R., Leavitt, G.M., Guerrero, J.C., Guevara, J. & Gubler, W.D. (2008) Identification and pathogenicity of *Lasiodiplodia theobromae* and *Diplodia seriata*, the causal agents of bot canker disease of grapevines in Mexico. *Plant Disease*, 92, 519–529.
- Wright, A.F. & Harmon, P.F. (2010) Identification of species in the *Botryosphaeriaceae* family causing stem blight on southern highbush blueberry in Florida. *Plant Disease*, 94, 966–971.
- Zea-Bonilla, T., González-Sánchez, M.A., Martín-Sánchez, P.M. & Pérez-Jiménez, R.M. (2007) Avocado dieback caused by *Neofusicoccum parvum* in the Andalucía Region, Spain. *Plant Disease*, 91, 1052–1052.
- Zhan, J. & McDonald, B.A. (2004) The interaction among evolutionary forces in the pathogenic fungus *Mycosphaerella graminicola*. *Fungal Genetics and Biology*, 41, 590–599.
- Zhou, S., Smith, D.R. & Stanosz, G.R. (2001) Differentiation of *Botryosphaeria* species and related anamorphic fungi using inter simple or short sequence repeat (ISSR) fingerprinting. *Mycological Resources*, 105, 919–926.

Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. *Neofusicoccum parvum*-*N. ribis* sequence information as downloaded from GenBank (where possible Australian states are included NSW= New South Wales, QLD= Queensland, VIC= Victoria, WA= Western Australia),- indicates no information was provided in the GenBank record.

Table S2. Allele size (bp) and frequency at seven loci (BOTF11, 15,17, 21, 23, 35, and 37) for *N. parvum* populations collected from Australia (AUST), China (CHN), Colombia (COL), Hawaii (HAW), Indonesia (INDO), New Zealand (NZ) and South Africa (SA).

Table S3. Gene diversity (H) and contingency χ^2 tests for differences in allele frequencies for the seven polymorphic BOTF loci across clone corrected populations of *Neofusicoccum parvum* from Australia (AUST), China (CHN), Colombia (COL), Hawaii (HAW), New Zealand (NZ) and South Africa (SA).

Appendix S1. Genetic Diversity.

Table S1 *Neofusicoccum parvum*-*N. ribis* sequence information as downloaded from GenBank (where possible Australian states are included NSW= New South Wales, QLD= Queensland, VIC= Victoria, WA= Western Australia),- indicates no information was provided in the GenBank record. In some cases data has been retrieved from the associated published manuscript (indicated by an asterisk *).

Correct ID	Isolate Code	GenBank ID	Host	Location	Genbank No.
<i>Neofusicoccum parvum</i>	WAC13360	<i>N. parvum</i>	<i>Araucaria heterophylla</i>	WA, Australia	HM545150
<i>N. parvum</i>	WAC13381	<i>N. parvum</i>	<i>A. heterophylla</i>	WA, Australia	HM545147
<i>N. parvum</i>	WAC13382	<i>N. parvum</i>	<i>A. heterophylla</i>	WA, Australia	HM545148
<i>N. parvum</i>	WAC13383	<i>N. parvum</i>	<i>A. heterophylla</i>	WA, Australia	HM545149
<i>N. parvum</i>	STE-U 3036	<i>N. ribis</i>	<i>Buckinghamia</i> sp.*	Australia*	AF452519
<i>N. parvum</i>	CMW6814 ¹	N/A	<i>Cinnamomum camphora</i>	Australia	N/A
<i>N. parvum</i>	DAR65081	<i>Botryosphaeria parva</i>	<i>Citrus sinensis</i>	NSW, Australia	EF173922
<i>N. parvum</i>	MUCC277	<i>N. parvum</i>	<i>Corymbia citriodora</i>	QLD, Australia	EU339536
<i>N. parvum</i>	MUCC211	<i>N. parvum</i>	<i>Corymbia torreliana</i>	QLD, Australia	EU301017
<i>N. parvum</i>	MUCC239	<i>N. parvum</i>	<i>Eucalyptus camaldulensis</i>	QLD, Australia	EU301023
<i>N. parvum</i>	MUCC240	<i>N. parvum</i>	<i>E. camaldulensis</i>	QLD, Australia	EU301024
<i>N. parvum</i>	MUCC591	<i>N. parvum</i>	<i>E. camaldulensis</i>	QLD, Australia	EU301021
<i>N. parvum</i>	MUCC119	<i>N. parvum</i>	<i>Eucalyptus dunnii</i>	QLD, Australia	EU339540
<i>N. parvum</i>	MUCC124	<i>N. parvum</i>	<i>E. dunnii</i>	QLD, Australia	EU339544
<i>N. parvum</i>	MUCC138	<i>N. parvum</i>	<i>E. dunnii</i>	QLD, Australia	EU339541
<i>N. parvum</i>	MUCC149	<i>N. parvum</i>	<i>E. dunnii</i>	QLD, Australia	EU339539
<i>N. parvum</i>	MUCC150	<i>N. parvum</i>	<i>E. dunnii</i>	QLD, Australia	EU339542
<i>N. parvum</i>	MUCC155	<i>N. parvum</i>	<i>E. dunnii</i>	QLD, Australia	EU339543
<i>N. parvum</i>	MUCC680	<i>Neofusicoccum</i> sp.	<i>E. dunnii</i>	QLD, Australia	EU339549
<i>N. parvum</i>	MUCC145	<i>N. parvum</i>	<i>Eucalyptus globulus</i>	QLD, Australia	EU339548
<i>N. parvum</i>	MUCC673	<i>N. parvum</i>	<i>E. globulus</i>	QLD, Australia	EU339553
<i>N. parvum</i>	CMW15950	<i>B. parva</i>	<i>E. globulus</i>	WA, Australia	DQ093193
<i>N. parvum</i>	MUCC151	<i>Neofusicoccum</i> sp.	<i>Eucalyptus grandis</i>	QLD, Australia	EU339551
<i>N. parvum</i>	MUCC681	<i>N. parvum</i>	<i>E. grandis</i>	QLD, Australia	EU339550
<i>N. parvum</i>	MUCC282	<i>N. parvum</i>	<i>Eucalyptus pellita</i>	QLD, Australia	EU339538
<i>N. parvum</i>	WAC12397	<i>B. parva</i>	<i>E. pellita</i>	QLD, Australia	AY744370
<i>N. parvum</i>	MUCC220	<i>N. parvum</i>	<i>E. pellita</i>	QLD, Australia	EU301022
<i>N. parvum</i>	MUCC312	<i>N. parvum</i>	<i>E. pellita</i>	QLD, Australia	EU301025
<i>N. parvum</i>	MUCC313	<i>N. parvum</i>	<i>E. pellita</i>	QLD, Australia	EU301026

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<i>N. parvum</i>	DAR80006	<i>N. parvum</i>	<i>Vitis vinifera</i>	NSW, Australia	GU944798
<i>N. parvum</i>	DAR77821	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944792
<i>N. parvum</i>	DAR77823	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944800
<i>N. parvum</i>	DAR80003	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944791
<i>N. parvum</i>	DAR80004	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944796
<i>N. parvum</i>	DAR80005	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944797
<i>N. parvum</i>	DAR80008	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944801
<i>N. parvum</i>	DAR77822	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944806
<i>N. parvum</i>	AC45c	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944794
<i>N. parvum</i>	A212a	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944793
<i>N. parvum</i>	B14	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944795
<i>N. parvum</i>	C41	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944799
<i>N. parvum</i>	I21	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944807
<i>N. parvum</i>	H342	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944805
<i>N. parvum</i>	G32	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944802
<i>N. parvum</i>	G33	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia	GU944803
<i>N. parvum</i>	DAR48983	<i>N. parvum</i>	<i>Kolkwitzia amabilis</i>	NSW, Australia	EF173923
<i>N. parvum</i>	CMW7025	<i>B. parva</i>	<i>Mangifera indica</i>	Australia	AY615181
<i>N. parvum</i>	CMW7026	<i>B. parva</i>	<i>M. indica</i>	Australia	AY615182
<i>N. parvum</i>	CMW7798	<i>B. parva</i>	<i>M. indica</i>	Australia	AY615183
<i>N. parvum</i>	BRIP19684	<i>N. parvum</i>	<i>M. indica</i>	Australia	EF585513
<i>N. parvum</i>	DAR41726	<i>B. parva</i>	<i>Olea africana</i>	NSW, Australia	EF173924
<i>N. parvum</i>	CMW7799	<i>B. parva</i>	<i>Persea americana</i>	Australia	AY615184
<i>N. parvum</i>	DAR45915	<i>B. parva</i>	<i>P. americana</i>	NSW, Australia	EF173925
<i>N. parvum</i>	BRIP19486	<i>N. parvum</i>	<i>P. americana</i>	QLD, Australia	EF585515
<i>N. parvum</i>	VPRI32689	<i>B. parva</i>	<i>Pistacia vera</i>	NSW, Australia	EF173926
<i>N. parvum</i>	DAR49440	<i>B. parva</i>	<i>Prunus persica</i>	NSW, Australia	EF173927
<i>N. parvum</i>	CMW9071	<i>N. parvum</i>	<i>Ribis</i> sp.	Australia	EU339552
<i>N. parvum</i>	CMW6967	<i>B. parva</i>	<i>Tibouchina</i> sp.	Australia*	AY194473
<i>N. parvum</i>	CMW6236	<i>B. parva</i>	<i>Tibouchina</i> sp.	Australia*	AY194472
<i>N. parvum</i>	CMW6235	<i>B. parva</i>	<i>Tibouchina lepidota</i>	VIC, Australia*	AY615136
<i>N. parvum</i>	CMW6237	<i>B. parva</i>	<i>Tibouchina urvilleana</i>	VIC, Australia*	AY615137
<i>N. parvum</i>	DAR75339	<i>B. parva</i>	<i>V. vinifera</i>	NSW, Australia*	EF173928
<i>N. parvum</i>	CSU-07-WP-B7A	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia*	EU919700
<i>N. parvum</i>	CSU-07-WP-B12	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia*	EU919694

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<i>N. parvum</i>	CSU-07-WP-B19A	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia*	EU919695
<i>N. parvum</i>	CSU-07-WP-B19B	<i>N. parvum</i>	<i>V. vinifera</i>	Australia*	EU919696
<i>N. parvum</i>	CSU-07-WP-B7B	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia*	EU919701
<i>N. parvum</i>	CSU-07-WP-CB1	<i>N. parvum</i>	<i>V. vinifera</i>	NSW, Australia*	EU919704
<i>N. parvum</i>	CSU-07-WP-B30	<i>N. parvum</i>	<i>V. vinifera</i>	Australia*	EU919697
<i>N. parvum</i>	CSU-07-WP-B31A	<i>N. parvum</i>	<i>V. vinifera</i>	Australia*	EU919698
<i>N. parvum</i>	CSU-07-WP-B31B	<i>N. parvum</i>	<i>V. vinifera</i>	Australia*	EU919699
<i>N. parvum</i>	CSU-07-WP-TS17	<i>N. parvum</i>	<i>V. vinifera</i>	Australia*	EU919706
<i>N. parvum</i>	CSU-07-WP-TS24	<i>N. parvum</i>	<i>V. vinifera</i>	Australia*	EU919705
<i>N. parvum</i>	CSU-07-WP-C9	<i>N. parvum</i>	<i>V. vinifera</i>	Australia*	EU919703
<i>N. parvum</i>	MUCC675	<i>N. parvum</i>	<i>Wollemia nobilis</i>	Australia	EU339535
<i>N. parvum</i>	MUCC674	<i>N. parvum</i>	<i>W. nobilis</i>	Australia	EU339534
<i>N. parvum</i>	MUCC676	<i>N. parvum</i>	<i>W. nobilis</i>	Australia	EU339545
<i>N. parvum</i>	MUCC677	<i>N. parvum</i>	<i>W. nobilis</i>	Australia	EU339546
<i>N. parvum</i>	MUCC678	<i>N. parvum</i>	<i>W. nobilis</i>	Australia	EU339547
<i>N. parvum</i>	MUCC679	<i>N. parvum</i>	<i>W. nobilis</i>	Australia	EU339537
<i>N. parvum</i>	CMM1317	<i>B. parva</i>	<i>M. indica</i>	Brazil	EU938333
<i>N. parvum</i>	CMM1271	<i>B. parva</i>	<i>M. indica</i>	Brazil	EU938335
<i>N. parvum</i>	CMM1276	<i>B. parva</i>	<i>M. indica</i>	Brazil	EU938334
<i>N. parvum</i>	PD299	<i>N. ribis</i>	<i>Vaccinium corymbosum</i>	Chile	GU251147
<i>N. parvum</i>	PD300	<i>N. ribis</i>	<i>V. corymbosum</i>	Chile	GU251148
<i>N. parvum</i>	B02-07	<i>N. parvum</i>	<i>V. corymbosum</i>	Chile	EU833984
<i>N. parvum</i>	B4.2-06	<i>B. parva</i>	<i>V. corymbosum</i>	Chile	EU812205
<i>N. parvum</i>	B1-06	<i>N. parvum</i>	<i>V. corymbosum</i>	Chile	EU856063
<i>N. parvum</i>	CMW10549 ¹	N/A	<i>Eucalyptus</i> sp.	Chile	N/A
<i>N. parvum</i>	HMUC-104(Neo-PD)	<i>N. parvum</i>	<i>V. vinifera</i>	Chile	JF273631
<i>N. parvum</i>	HMUC-105(Neo-PD)	<i>N. parvum</i>	<i>V. vinifera</i>	Chile	JF273632
<i>N. parvum</i>	Fungal endophyte sp. AiS1	fungal endophyte	<i>Artemisia</i> sp.	China	EU054413
<i>N. parvum</i>	clone 35nian-1041	Uncultured fungus	<i>Aquilaria sinensis</i>	China	FN667934
<i>N. parvum</i>	clone 35nian-1007	Uncultured fungus	<i>Aquilaria sinensis</i>	China	FN667928
<i>N. parvum</i>	hsy101	<i>B. parva</i>	<i>Bruguiera sexangula</i>	China	FJ441608
<i>N. parvum</i>	LH107	<i>Neofusicoccum</i> sp.	<i>Camellia sinensis</i>		HQ832811
<i>N. parvum</i>	SXZ-08	<i>Botryosphaeria</i> sp.	<i>Camptotheca acuminata</i>	China	DQ145727
<i>N. parvum</i>	CYN99	<i>N. parvum</i>	<i>Cupressus funebris</i>	China	FJ842961
<i>N. parvum</i>	CYN100	<i>N. parvum</i>	<i>Cupressus funebris</i>	China	FJ842960

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<i>N. parvum</i>	MUCC688	<i>N. parvum</i>	<i>E. globulus</i>	China	EU675676
<i>N. parvum</i>	MUCC689	<i>N. parvum</i>	<i>E. globulus</i>	China	EU675677
<i>N. parvum</i>	MUCC690	<i>N. parvum</i>	<i>E. globulus</i>	China	EU675678
<i>N. parvum</i>	CZ112B	<i>B. parva</i>	<i>Eucalyptus</i> sp.	China	FJ755241
<i>N. parvum</i>	CMW24704	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	China	HQ332201
<i>N. parvum</i>	CMW27110	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	China	HQ332202
<i>N. parvum</i>	CMW27111	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	China	HQ332203
<i>N. parvum</i>	CMW27125	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	China	HQ332204
<i>N. parvum</i>	CMW27135	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	China	HQ332205
<i>N. parvum</i>	MHF-2008	<i>Botryosphaeria</i> sp.	<i>Maytenus hookeri</i>	China	EU523117
<i>N. parvum</i>	SDAU 7-125	<i>N. parvum</i>	<i>P. persica</i>	China	GQ855789
<i>N. parvum</i>	SDAU07-128	<i>N. parvum</i>	<i>P. persica</i>	China	GQ855790
<i>N. parvum</i>	SDAU08-52	<i>B. parva</i>	<i>Punica granatum</i>	China	FJ214100
<i>N. parvum</i>	SDAU07-168	<i>N. parvum</i>	<i>P. granatum</i>	China	GU997684
<i>N. parvum</i>	SDAU08-54	<i>B. parva</i>	<i>P. granatum</i>	China	FJ214102
<i>N. parvum</i>	SDAU07-111	<i>N. parvum</i>	<i>P. granatum</i>	China	GU723470
<i>N. parvum</i>	SDAU07-167	<i>N. parvum</i>	<i>P. granatum</i>	China	GU997685
<i>N. parvum</i>	SDAU08-55	<i>B. parva</i>	<i>Populus</i> sp.	China	FJ214103
<i>N. parvum</i>	SDAU07-16	<i>N. parvum</i>	<i>Populus</i> sp.	China	GU997688
<i>N. parvum</i>	SDAU07-103	<i>N. parvum</i>	<i>Populus</i> sp.	China	GQ865690
<i>N. parvum</i>	SDAU07-118	<i>N. parvum</i>	<i>Populus</i> sp.	China	GQ865691
<i>N. parvum</i>	1	<i>N. parvum</i>	<i>Taxus chinensis</i> var. <i>mairei</i>	China	JN198393
<i>N. parvum</i>	VT-04	<i>N. parvum</i>	<i>Vernicia fordii</i>	China	HQ844226
<i>N. parvum</i>	FG43 18S	<i>N. parvum</i>	<i>V. vinifera</i>	China	EU030352
<i>N. parvum</i>	CDZ1-1s1	<i>N. parvum</i>	<i>V. vinifera</i>	China	HQ840416
<i>N. parvum</i>	CDZ1-1s2	<i>N. parvum</i>	<i>V. vinifera</i>	China	HQ859951
<i>N. parvum</i>	CDZ1-1s3	<i>N. parvum</i>	<i>V. vinifera</i>	China	HQ859952
<i>N. parvum</i>	NW727	<i>N. parvum</i>	-	China	EU520124
<i>N. parvum</i>	T149	<i>N. parvum</i>	-	China	FJ462749
<i>N. parvum</i>	Mht-16	<i>N. parvum</i>	-	China	JF439214
<i>N. parvum</i>	Mht-17	<i>N. parvum</i>	-	China	JN662928
<i>N. parvum</i>	Vega385	<i>Botryosphaeria</i> sp.	<i>Coffea arabica</i>	Colombia	EF672311
<i>N. parvum</i>	CMW8937 ¹	N/A	<i>Eucalyptus</i> sp.	Colombia	N/A
<i>N. parvum</i>	CMW10089	<i>B. parva</i>	<i>Eucalyptus</i> sp.	Ethiopia	AY210477
<i>N. parvum</i>	CMW10094	<i>B. parva</i>	<i>E. saligna</i> *	Ethiopia	AY210478

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<i>N. parvum</i>	CMW10095	<i>B. parva</i>	<i>E. grandis</i> *	Ethiopia	AY210479
<i>N. parvum</i>	CMW11060	<i>B. parva</i>	<i>E. citriodora</i> *	Ethiopia	AY210474
<i>N. parvum</i>	CMW11062	<i>B. parva</i>	<i>E. citriodora</i> *	Ethiopia	AY210475
<i>N. parvum</i>	CMW11064	<i>B. parva</i>	<i>E. citriodora</i> *	Ethiopia	AY210476
<i>N. parvum</i>	CMW11246	<i>B. parva</i>	<i>Pinus patula</i>	Ethiopia	AY210486
<i>N. parvum</i>	CMW11253	<i>B. parva</i>	<i>P. patula</i>	Ethiopia	AY210487
<i>N. parvum</i>	STE-U 4584	<i>B. parva</i>	<i>V. vinifera</i>	France*	AY343471
<i>N. parvum</i>	IGS	<i>B. parva</i>	<i>Actinidia deliciosa</i>	Greece	FN640477
<i>N. parvum</i>	PD6	<i>N. parvum</i>	<i>P. vera</i>	Greece	GU251129
<i>N. parvum</i>	PD62	<i>N. parvum</i>	<i>P. vera</i>	Greece	GU251133
<i>N. parvum</i>	-	<i>N. parvum</i>	<i>P. persica</i>	Greece	JN135282
<i>N. parvum</i>	UAS015	<i>B. parva</i>	<i>Nothapodytes nimmoniana</i>	India	FJ158131
<i>N. parvum</i>	MUCC687	<i>N. parvum</i>	<i>E. grandis</i>	Indonesia	EU675675
<i>N. parvum</i>	CMW4049	<i>B. parva</i>	<i>Eucalyptus</i> sp.	Indonesia	AY236937
<i>N. parvum</i>	IRN1	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121891
<i>N. parvum</i>	IRN10	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121900
<i>N. parvum</i>	IRN11	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121901
<i>N. parvum</i>	IRN12	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121902
<i>N. parvum</i>	IRN2	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121892
<i>N. parvum</i>	IRN3	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121893
<i>N. parvum</i>	IRN4	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121894
<i>N. parvum</i>	IRN5	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121895
<i>N. parvum</i>	IRN6	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121896
<i>N. parvum</i>	IRN7	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121897
<i>N. parvum</i>	IRN8	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121898
<i>N. parvum</i>	IRN9	<i>N. parvum</i>	<i>V. vinifera</i>	Iran	GU121899
<i>N. parvum</i>	CAP247	<i>N. parvum</i>	<i>Olea europaea</i>	Italy	EF638786
<i>N. parvum</i>	BA20	<i>N. parvum</i>	<i>Quercus robur</i>	Italy	HQ893535
<i>N. parvum</i>	DB 05112010	<i>N. parvum</i>	<i>Rhododendron</i> sp.	Italy	HQ589259
<i>N. parvum</i>	B18	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481577
<i>N. parvum</i>	B25	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481578
<i>N. parvum</i>	B27	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481579
<i>N. parvum</i>	B29	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481580
<i>N. parvum</i>	B3	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481576
<i>N. parvum</i>	B30	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481581

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<i>N. parvum</i>	B31	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481582
<i>N. parvum</i>	B44	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481583
<i>N. parvum</i>	B46	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481584
<i>N. parvum</i>	PVFi-Np3	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187982
<i>N. parvum</i>	PVFi-Np4	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187983
<i>N. parvum</i>	PVFi-Np5	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187984
<i>N. parvum</i>	PVFi-Np9	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187988
<i>N. parvum</i>	PVFi-Np11	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187990
<i>N. parvum</i>	PVFi-Np12	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187991
<i>N. parvum</i>	PVFi-Np14	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187993
<i>N. parvum</i>	PVFi-Np15	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187994
<i>N. parvum</i>	PVFi-Np16	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187995
<i>N. parvum</i>	PVFi-Np17	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187996
<i>N. parvum</i>	PVFi-Np18	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187997
<i>N. parvum</i>	PVFi-Np19	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187998
<i>N. parvum</i>	PVFi-Np20	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187999
<i>N. parvum</i>	PVFi-Np21	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU188000
<i>N. parvum</i>	PVFi-Np30	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU188009
<i>N. parvum</i>	PVFi-Np31	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU188010
<i>N. parvum</i>	PVFi-Np2	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU187981
<i>N. parvum</i>	PVFi-Np29	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	GU188008
<i>N. parvum</i>	<i>Botryosphaeria</i> sp. 67	<i>Botryosphaeria</i> sp.	<i>V. vinifera</i>	Japan	AB034815
<i>N. parvum</i>	<i>Guignardia cryptomeriae</i>	<i>Guignardia cryptomeriae</i>	<i>Cryptomeria japonica</i>	Japan	AB454305
<i>N. parvum</i>	<i>Botryosphaeria</i> sp. 74	<i>Botryosphaeria</i> sp.	<i>Pyrus communis</i>	Japan	AB034818
<i>N. parvum</i>	<i>Botryosphaeria</i> sp. 76	<i>Botryosphaeria</i> sp.	<i>P. communis</i>	Japan	AB034819
<i>N. parvum</i>	<i>Botryosphaeria</i> sp. 77	<i>Botryosphaeria</i> sp.	<i>A. deliciosa</i>	Japan	AB034820
<i>N. parvum</i>	<i>Botryosphaeria</i> sp. 78	<i>Botryosphaeria</i> sp.	<i>Diospyrus kaki</i>	Japan	AB034821
<i>N. parvum</i>	GrF42	<i>N. parvum</i>	<i>Grevillea robusta</i>	Kenya	FJ904817
<i>N. parvum</i>	GrS4	<i>N. parvum</i>	<i>G. robusta</i>	Kenya	FJ904915
<i>N. parvum</i>	Eg36	<i>B. parva</i>	<i>G. robusta</i>	Kenya	FJ904816
<i>N. parvum</i>	Gr78	<i>N. parvum</i>	<i>G. robusta</i>	Kenya	FJ904846
<i>N. parvum</i>	GrY95-7	<i>B. parva</i>	<i>G. robusta</i>	Kenya	FJ904818
<i>N. parvum</i>	Ss57	<i>B. parva</i>	<i>Senna siamea</i>	Kenya	FJ904819
<i>N. parvum</i>	CMW25475/Ec36	<i>Botryosphaeria</i> sp.	<i>E. camaldulensis</i>	Kenya	FJ904820
<i>N. parvum</i>	CRM-152	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647912

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<i>N. parvum</i>	CRM-146	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647911
<i>N. parvum</i>	CMW9077	<i>B. parva</i>	<i>A. deliciosa</i>	New Zealand	AY236939
<i>N. parvum</i>	CMW9078	<i>B. parva</i>	<i>A. deliciosa</i>	New Zealand	AY236940
<i>N. parvum</i>	CMW9079	<i>B. parva</i>	<i>A. deliciosa</i>	New Zealand	AY236941
<i>N. parvum</i>	CMW10120	<i>B. parva</i>	<i>A. heterophylla</i>	New Zealand	AY615160
<i>N. parvum</i>	CMW10121	<i>B. parva</i>	<i>A. heterophylla</i>	New Zealand	AY615161
<i>N. parvum</i>	96-29	<i>B. parva</i>	<i>Malus</i> sp.	New Zealand	AF243395
<i>N. parvum</i>	CMW994	<i>B. parva</i>	<i>Malus sylvestris</i>	New Zealand	AY236883
<i>N. parvum</i>	PD286	<i>N. parvum</i>	<i>Populus</i> sp.	New Zealand	GU251125
<i>N. parvum</i>	CMW9080	<i>B. parva</i>	<i>Populus nigra</i>	New Zealand	AY236942
<i>N. parvum</i>	CMW9081	<i>B. parva</i>	<i>P. nigra</i>	New Zealand	AY236943
<i>N. parvum</i>	10847	<i>N. parvum</i>	<i>Pseudopanax laetus</i>	New Zealand	JN595856
<i>N. parvum</i>	NZFS3125	<i>N. parvum</i>	<i>Rhododendron niveum</i>	New Zealand	JN017921
<i>N. parvum</i>	CMW9952	<i>B. parva</i>	<i>Tibouchina</i> sp.	New Zealand*	AY194471
<i>N. parvum</i>	CMW9945	<i>B. parva</i>	<i>Tibouchina</i> sp.	New Zealand*	AY194470
<i>N. parvum</i>	CMW10117 ¹	N/A	<i>T. lepidota</i>	New Zealand	N/A
<i>N. parvum</i>	STE-U 5253	<i>B. parva</i>	<i>V. vinifera</i>	Portugal*	AY343477
<i>N. parvum</i>	STE-U 5035	<i>B. parva</i>	<i>V. vinifera</i>	Portugal*	AY343473
<i>N. parvum</i>	CBS110301	<i>B. parva</i>	<i>V. vinifera</i>	Portugal*	AY259098
<i>N. parvum</i>	221.IV	<i>N. parvum</i>	<i>Dimocarpus longan</i> L.	Puerto Rico	GU797368
<i>N. parvum</i>	231.I	<i>N. parvum</i>	<i>D. longan</i> L.	Puerto Rico	GU797369
<i>N. parvum</i>	86Q	<i>N. parvum</i>	mango flower	Puerto Rico	GU968434
<i>N. parvum</i>	PD250	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	South Africa	GU251123
<i>N. parvum</i>	PD251	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	South Africa	GU251124
<i>N. parvum</i>	CMW20792	<i>N. parvum</i>	<i>Eucalyptus dorrigoensis</i>	South Africa	FJ752736
<i>N. parvum</i>	BOT21	<i>B. dothidea</i>	<i>E. grandis</i>	South Africa	AF283681
<i>N. parvum</i>	BOT30	<i>B. dothidea</i>	<i>E. grandis</i>	South Africa	AF283682
<i>N. parvum</i>	BOT7	<i>B. dothidea</i>	<i>E. grandis</i>	South Africa	AF283678
<i>N. parvum</i>	CMW20722	<i>N. parvum</i>	<i>Eucalyptus microcorys</i>	South Africa	FJ752727
<i>N. parvum</i>	CMW20727	<i>N. parvum</i>	<i>E. microcorys</i>	South Africa	FJ752735
<i>N. parvum</i>	CMW20735	<i>N. parvum</i>	<i>Eucalyptus nicholii</i>	South Africa	FJ752733
<i>N. parvum</i>	CMW20719	<i>N. parvum</i>	<i>Eucalyptus ovata</i>	South Africa	FJ752724
<i>N. parvum</i>	CMW20726	<i>N. parvum</i>	<i>Eucalyptus robusta</i>	South Africa	FJ752729
<i>N. parvum</i>	CMW20736	<i>N. parvum</i>	<i>E. robusta</i>	South Africa	FJ752730
<i>N. parvum</i>	CMW20720	<i>N. parvum</i>	<i>Eucalyptus saligna</i>	South Africa	FJ752728

Correct ID	Isolate Code	GenBank ID	Host	Location	Genbank No.
<i>N. parvum</i>	CMW20724	<i>N. parvum</i>	<i>E. saligna</i>	South Africa	FJ752726
<i>N. parvum</i>	CMW20725	<i>N. parvum</i>	<i>Eucalyptus scoparia</i>	South Africa	FJ752725
<i>N. parvum</i>	BOT19	<i>B. dothidea</i>	<i>Eucalyptus smithii</i>	South Africa	AF283683
<i>N. parvum</i>	CMW20730	<i>N. parvum</i>	<i>Eucalyptus tereticornis</i>	South Africa	FJ752731
<i>N. parvum</i>	CMW20733	<i>N. parvum</i>	<i>E. tereticornis</i>	South Africa	FJ752734
<i>N. parvum</i>	CMW20734	<i>N. parvum</i>	<i>E. tereticornis</i>	South Africa	FJ752732
<i>N. parvum</i>	STE-U 4417	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343461
<i>N. parvum</i>	STE-U 4420	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343462
<i>N. parvum</i>	STE-U 4424	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343463
<i>N. parvum</i>	STE-U 4431	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343464
<i>N. parvum</i>	STE-U 4437	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343466
<i>N. parvum</i>	STE-U 4438	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343467
<i>N. parvum</i>	STE-U 4439	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343468
<i>N. parvum</i>	STE-U 4530	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343469
<i>N. parvum</i>	STE-U 4534	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343465
<i>N. parvum</i>	STE-U 4540	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343470
<i>N. parvum</i>	STE-U 4589	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343472
<i>N. parvum</i>	STE-U 5049	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343474
<i>N. parvum</i>	STE-U 5130	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343475
<i>N. parvum</i>	STE-U 5142	<i>B. parva</i>	<i>V. vinifera</i>	South Africa*	AY343476
<i>N. parvum</i>	STEU 7036	<i>N. parvum</i>	<i>V. vinifera</i>	South Africa*	JQ038880
<i>N. parvum</i>	STEU 7037	<i>N. parvum</i>	<i>V. vinifera</i>	South Africa*	JQ038881
<i>N. parvum</i>	BOT681	<i>B. dothidea</i>	<i>Heteropyxis natalensis</i>	South Africa	AF283676
<i>N. parvum</i>	CMW10494	<i>N. parvum</i>	<i>Syzygium cordatum</i>	South Africa	EU821912
<i>N. parvum</i>	CMW14029	<i>B. parva</i>	<i>S. cordatum</i>	South Africa	EU821902
<i>N. parvum</i>	CMW14029	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821902
<i>N. parvum</i>	CMW14030	<i>B. parva</i>	<i>S. cordatum</i>	South Africa	DQ316077
<i>N. parvum</i>	CMW14080	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821916
<i>N. parvum</i>	CMW14082	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821907
<i>N. parvum</i>	CMW14085	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821908
<i>N. parvum</i>	CMW14087	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821909
<i>N. parvum</i>	CMW14088	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821910
<i>N. parvum</i>	CMW14089	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821911
<i>N. parvum</i>	CMW14097	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821914
<i>N. parvum</i>	CMW14121	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821917

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<i>N. parvum</i>	CMW14135	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821918
<i>N. parvum</i>	CMW14141	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821920
<i>N. parvum</i>	CMW14143	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821921
<i>N. parvum</i>	CMW27901	<i>N. parvum</i>	<i>S. cordatum</i>	South Africa	EU821927
<i>N. parvum</i>	BOT683	<i>B. dothidea</i>	<i>S. cordatum</i>	South Africa	AF283677
<i>N. parvum</i>	BOT682	<i>B. dothidea</i>	<i>Syzygium guineense</i>	South Africa	AF283680
<i>N. parvum</i>	CMW26714	<i>N. parvum</i>	<i>Terminalia catappa</i>	South Africa	FJ900610
<i>N. parvum</i>	CMW 10337	<i>B. parva</i>	<i>Tibouchina</i> sp.	South Africa*	AY194469
<i>N. parvum</i>	CMW26717	<i>N. parvum</i>	<i>T. catappa</i>	South Africa	FJ900611
<i>N. parvum</i>	CMW26718	<i>N. parvum</i>	<i>T. catappa</i>	South Africa	FJ900612
<i>N. parvum</i>	CMW26720	<i>N. parvum</i>	<i>T. catappa</i>	South Africa	FJ900613
<i>N. parvum</i>	CMW26690	<i>N. parvum</i>	<i>Terminalia sericea</i>	South Africa	GQ471815
<i>N. parvum</i>	CMW26842	<i>N. parvum</i>	<i>T. sericea</i>	South Africa	GQ471821
<i>N. parvum</i>	CMW26844	<i>N. parvum</i>	<i>T. sericea</i>	South Africa	GQ471819
<i>N. parvum</i>	CMW26846	<i>N. parvum</i>	<i>T. sericea</i>	South Africa	GQ471818
<i>N. parvum</i>	CMW26848	<i>N. parvum</i>	<i>T. sericea</i>	South Africa	GQ471816
<i>N. parvum</i>	CMW26851	<i>N. parvum</i>	<i>T. sericea</i>	South Africa	GQ471817
<i>N. parvum</i>	CMW26864	<i>N. parvum</i>	<i>T. sericea</i>	South Africa	GQ471820
<i>N. parvum</i>	Sunchang-P1	<i>Neofusicoccum</i> sp.	<i>Vaccinium</i> sp.	South Korea	HQ384218
<i>N. parvum</i>	Sunchang-P3	<i>Neofusicoccum</i> sp.	<i>Vaccinium</i> sp.	South Korea	HQ384220
<i>N. parvum</i>	Sunchang-P5	<i>Neofusicoccum</i> sp.	<i>Vaccinium</i> sp.	South Korea	HQ384219
<i>N. parvum</i>	MF-20(2)	<i>Neofusicoccum</i> sp.	-	South Korea: Yellow Sea	AB563197
<i>N. parvum</i>	CMW36774	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	Spain	JN119284
<i>N. parvum</i>	CMW37773	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	Spain	JN119283
<i>N. parvum</i>	BON065	<i>N. parvum</i>	<i>Juglans regia</i>	Spain	GU292640
<i>N. parvum</i>	BON066	<i>N. parvum</i>	<i>Juglans regia</i>	Spain	GU292640
<i>N. parvum</i>	IFAPA-CH415	<i>B. parva</i>	<i>P. americana</i>	Spain	AM410966
<i>N. parvum</i>	IFAPA-CH441	<i>B. parva</i>	<i>P. americana</i>	Spain	AM410965
<i>N. parvum</i>	Npa1	<i>N. parvum</i>	<i>Prunus dulcis</i>	Spain	JF330779
<i>N. parvum</i>	UCD578Spa	<i>B. parva</i>	<i>V. vinifera</i>	Spain	DQ356359
<i>N. parvum</i>	CBS121486	<i>N. parvum</i>	<i>V. vinifera</i>	Spain*	EU650672
<i>N. parvum</i>	BOT25	<i>B. dothidea</i>	<i>E. grandis</i>	Swaziland	AF283679
<i>N. parvum</i>	B1001	<i>Neofusicoccum</i> sp.	<i>M. indica</i>	Taiwan	GQ861435
<i>N. parvum</i>	B1174	<i>Neofusicoccum</i> sp.	<i>P. americana</i>	Taiwan	HM015908

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<i>N. parvum</i>	B1118	<i>Neofusicoccum</i> sp.	<i>P. americana</i>	Taiwan	HM015907
<i>N. parvum</i>	TDARES33	<i>N. parvum</i>	<i>Pyrus pyrifolia</i>	Taiwan	GU395186
<i>N. parvum</i>	TDARES37	<i>N. parvum</i>	<i>Pyrus pyrifolia</i>	Taiwan	GU395187
<i>N. parvum</i>	TWFS10	<i>N. parvum</i>	-	Taiwan	JQ408390
<i>N. parvum</i>	CMU37	Fungal sp.	-	Thailand	HM473075
<i>N. parvum</i>	CMW7236	<i>B. parva</i>	<i>E. grandis</i>	Uganda	AY228100
<i>N. parvum</i>	CMW7238	<i>B. parva</i>	<i>E. grandis</i>	Uganda	AY228097
<i>N. parvum</i>	CMW7500	<i>B. parva</i>	<i>E. grandis</i>	Uganda	AY228095
<i>N. parvum</i>	CMW8045	<i>B. parva</i>	<i>E. grandis</i>	Uganda	AY228096
<i>N. parvum</i>	208/1/9/Grevillea	<i>N. parvum</i>	<i>Grevillea</i> sp.	Uganda	GQ922509
<i>N. parvum</i>	196/1/9/Grevillea	<i>N. parvum</i>	<i>Grevillea</i> sp.	Uganda	GQ922512
<i>N. parvum</i>	UY16	<i>N. parvum</i>	<i>Blepharocalyx salcifolius</i>	Uruguay	EU080908
<i>N. parvum</i>	UY37	<i>N. parvum</i>	<i>E. grandis</i>	Uruguay	EU080909
<i>N. parvum</i>	UY129	<i>N. parvum</i>	<i>Myrrhinium atropurpureum</i> var. <i>octandrum</i>	Uruguay	EU860379
<i>N. parvum</i>	UY193	<i>N. parvum</i>	<i>Psidium pubifolium</i>	Uruguay	EU860381
<i>N. parvum</i>	UY1267	<i>N. parvum</i>	<i>B. salcifolius</i>	Uruguay	EU860385
<i>N. parvum</i>	UY1313	<i>N. parvum</i>	<i>Myrciaria tenella</i>	Uruguay	EU860387
<i>N. parvum</i>	UY1325	<i>N. parvum</i>	<i>Myrcianthes cisplatensis</i>	Uruguay	EU860389
<i>N. parvum</i>	UY1609	<i>N. parvum</i>	<i>Eucalyptus cinerea</i>	Uruguay	EU860395
<i>N. parvum</i>	UY1706	<i>N. parvum</i>	<i>E. robusta</i>	Uruguay	EU860398
<i>N. parvum</i>	PD106	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251139
<i>N. parvum</i>	PD140	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251140
<i>N. parvum</i>	PD142	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251141
<i>N. parvum</i>	PD148	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251142
<i>N. parvum</i>	PD17	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251143
<i>N. parvum</i>	PD39	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251144
<i>N. parvum</i>	PD43	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251132
<i>N. parvum</i>	PD57	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251145
<i>N. parvum</i>	PD59	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251146
<i>N. parvum</i>	PD65	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251134
<i>N. parvum</i>	PD81	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251135
<i>N. parvum</i>	PD92	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251136
<i>N. parvum</i>	PD93	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251137
<i>N. parvum</i>	PD94	<i>N. parvum</i>	<i>P. dulcis</i>	USA	GU251138
<i>N. parvum</i>	UCD2393TX	<i>N. parvum</i>	<i>V. vinifera</i>	Texas, USA	FJ790824

Correct ID	Isolate Code	GenBank ID	Host	Location	Genbank No.
<i>N. parvum</i>	I	<i>B. parva</i>	<i>Lilium lancifolium</i>	Georgia, USA	DQ499154
<i>N. parvum</i>	II	<i>B. parva</i>	<i>L. lancifolium</i>	Georgia, USA	DQ499155
<i>N. parvum</i>	UCR1566	<i>N. parvum</i>	<i>Ficus microcarpa</i> var. <i>nitida</i>	California, USA	JN543669
<i>N. parvum</i>	UCR1166	<i>N. parvum</i>	citrus	California, USA	JF271762
<i>N. parvum</i>	UCR273	<i>N. parvum</i>	<i>P. americana</i> Mill.	California, USA	HQ529768
<i>N. parvum</i>	UCR295	<i>N. parvum</i>	<i>P. americana</i> Mill.	California, USA	HQ529765
<i>N. parvum</i>	UCR531	<i>N. parvum</i>	<i>P. americana</i> Mill.	California, USA	GQ857661
<i>N. parvum</i>	UCR735	<i>N. parvum</i>	<i>P. americana</i> Mill.	California, USA	HQ529766
<i>N. parvum</i>	UCR736	<i>N. parvum</i>	<i>P. americana</i> Mill.	California, USA	HQ529767
<i>N. parvum</i>	UCR737	<i>N. parvum</i>	<i>P. americana</i> Mill.	California, USA	GQ857660
<i>N. parvum</i>	UCD1125Na	<i>B. parva</i>	<i>V. vinifera</i>	California, USA	DQ233612
<i>N. parvum</i>	UCD1349So	<i>B. parva</i>	<i>V. vinifera</i>	California, USA	DQ008330
<i>N. parvum</i>	UCD642So	<i>B. parva</i>	<i>V. vinifera</i>	California, USA	DQ008328
<i>N. parvum</i>	UCD646So	<i>B. parva</i>	<i>V. vinifera</i>	California, USA	DQ008329
<i>N. parvum</i>	UCD577Spa	<i>B. parva</i>	<i>V. vinifera</i>	California, USA	DQ356358
<i>N. parvum</i>	UCD759St	<i>B. parva</i>	<i>V. vinifera</i>	California, USA	DQ233611
<i>N. parvum</i>	STE-U 2051	<i>N. ribis</i>	<i>Leucospermum</i> sp.*	Hawaii, USA*	AF452526
<i>N. parvum</i>	STE-U 2057	<i>N. ribis</i>	<i>Protea cynaroides</i> *	Hawaii, USA*	AF452524
<i>N. parvum</i>	STE-U 2100	<i>N. ribis</i>	<i>Telopea</i> sp.*	Hawaii, USA*	AF452521
<i>N. parvum</i>	STE-U 4371	<i>N. ribis</i>	<i>Protea cynaroides</i> *	Hawaii, USA*	AF452518
<i>N. parvum</i>	STE-U 4376	<i>N. ribis</i>	<i>P. cynaroides</i> *	Hawaii, USA*	AF452527
<i>N. parvum</i>	CMW7883 ¹	N/A	<i>Eucalyptus</i> sp.	Hawaii, USA	N/A
<i>N. parvum</i>	STE-U 2055	<i>N. ribis</i>	<i>Leucadendron salignum</i> x <i>L. laureolum</i> *	Florida, USA*	AF452523
<i>N. parvum</i>	96-8	<i>B. ribis</i>	<i>Rhizophora mangle</i> *	Florida, USA*	AF243394
<i>N. parvum</i>	KJ 94.11	<i>B. ribis</i>	<i>R. mangle</i> *	Florida, USA*	AF027744
<i>N. parvum</i>	PD18	<i>N. parvum</i>	<i>Juglans regia</i>	USA	GU251130
<i>N. parvum</i>	PD299	<i>N. parvum</i>	<i>J. regia</i>	USA	GU251131
<i>N. parvum</i>	CMW30144	<i>N. parvum</i>	<i>Eucalyptus cloeziana</i>	Zambia	FJ826610
<i>N. parvum</i>	CMW30143	<i>N. parvum</i>	<i>E. grandis</i>	Zambia	FJ826609
<i>N. parvum</i>	CMW30142	<i>N. parvum</i>	<i>E. grandis</i>	Zambia	FJ826608
<i>N. parvum</i>	STE-U 4381	<i>N. ribis</i>	<i>Protea cynaroides</i> *	Zimbabwe*	AF452522
<i>N. parvum</i>	STE-U 4382	<i>N. ribis</i>	<i>Protea cynaroides</i> *	Zimbabwe*	AF452520
<i>N. parvum</i>	CMW10328	<i>B. parva</i>	<i>Tibouchina</i> sp.	-	AY194468
<i>N. parvum</i>	WF160	<i>Botryosphaeria</i> sp.	<i>Warburgia ugandensis</i>	-	HQ130715
<i>N. parvum</i>	1314	Fungal endophyte	<i>Dendrobium</i> sp.	-	FJ450043

Correct ID	Isolate Code	GenBank ID	Host	Location	Genbank No.
<i>N. parvum</i>	ATCC 58191	<i>B. parva</i>	-	-	FJ545228
<i>N. parvum</i>	Po66	<i>B. parva</i>	-	-	AY206460
<i>N. parvum</i>	SYJM20	<i>N. parvum</i>	-	-	JN222970
<i>N. batangarum</i>	CMW28315	<i>N. batangarum</i>	<i>T. catappa</i>	Cameroon	FJ900606
<i>N. batangarum</i>	CMW28363	<i>N. batangarum</i>	<i>T. catappa</i>	Cameroon	FJ900607
<i>N. batangarum</i>	CMW28320	<i>N. batangarum</i>	<i>T. catappa</i>	Cameroon	FJ900608
<i>N. batangarum</i>	CMW28637	<i>N. batangarum</i>	<i>T. catappa</i>	Cameroon	FJ900609
<i>N. batangarum</i>	222c3b	Fungal sp.	<i>Ficus insipida</i>	Panama: Barro Colorado Island	EU563590
<i>N. batangarum</i>	AR 4676	<i>N. batangarum</i>	<i>Schinus terebinthifolius</i>	USA	HM357636
<i>N. cordaticola</i>	MUCC297	<i>N. parvum</i>	<i>E. pellita</i>	QLD, Australia	EU301020
<i>N. cordaticola</i>	B318s	<i>N. parvum</i>	<i>V. vinifera</i>	Italy	FJ481576
<i>N. cordaticola</i>	CMW13992	<i>N. cordaticola</i>	<i>S. cordatum</i>	South Africa	EU821898
<i>N. cordaticola</i>	CMW14056	<i>N. cordaticola</i>	<i>S. cordatum</i>	South Africa	EU821903
<i>N. cordaticola</i>	CMW14054	<i>N. cordaticola</i>	<i>S. cordatum</i>	South Africa	EU821906
<i>N. cordaticola</i>	CMW14151	<i>N. cordaticola</i>	<i>S. cordatum</i>	South Africa	EU821922
<i>N. kwambonambiense</i>	MUCC206	<i>N. parvum</i>	<i>Corymbia torreliana</i> x <i>C. citradora</i>	QLD, Australia	EU301018
<i>N. kwambonambiense</i>	MUCC210	<i>N. parvum</i>	<i>Corymbia torreliana</i> x <i>C. citradora</i>	QLD, Australia	EU301016
<i>N. kwambonambiense</i>	MUCC209	<i>N. parvum</i>	<i>Corymbia torreliana</i> x <i>C. citradora</i>	QLD, Australia	EU301015
<i>N. kwambonambiense</i>	MUCC140	<i>Neofusicoccum</i> sp.	<i>E. dunnii</i>	Australia	EU339521
<i>N. kwambonambiense</i>	MUCC157	<i>Neofusicoccum</i> sp.	<i>E. dunnii</i>	Australia	EU339522
<i>N. kwambonambiense</i>	MUCC291	<i>N. parvum</i>	<i>E. pellita</i>	QLD, Australia	EU301019
<i>N. kwambonambiense</i>	WAC12727	<i>N. ribis</i>	<i>Sesbania formosa</i>	NW Australia	EF585518
<i>N. kwambonambiense</i>	Mky19	<i>N. parvum</i>	<i>Bruguiera gymnorhiza</i>	China	FJ441610
<i>N. kwambonambiense</i>	ZJ9-4L	<i>Botryosphaeria</i> sp.	Mangrove sp.	China	FJ487915
<i>N. kwambonambiense</i>	ZH4-E1	<i>Neofusicoccum</i> sp.	Mangrove sp.	China	FJ037734
<i>N. kwambonambiense</i>	CRM-35	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JN088050
<i>N. kwambonambiense</i>	CRM-36	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647905
<i>N. kwambonambiense</i>	CRM-20	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647906
<i>N. kwambonambiense</i>	CRM-125	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647907
<i>N. kwambonambiense</i>	CRM-126	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647908
<i>N. kwambonambiense</i>	CRM-18	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647909
<i>N. kwambonambiense</i>	CRM-129	<i>N. parvum</i>	<i>V. corymbosum</i>	Mexico	JQ647910
<i>N. kwambonambiense</i>	CMW7231	<i>Botryosphaeria</i> sp.	<i>E. grandis</i>	Uganda	AY228105
<i>N. kwambonambiense</i>	CMW8286	<i>Botryosphaeria</i> sp.	<i>E. grandis</i>	Uganda	AY228102

Correct ID	Isolate Code	GenBank ID	Host	Location	Genbank No.
<i>N. kwambonambiense</i>	CMW8041	<i>Botryosphaeria</i> sp.	<i>E. grandis</i>	Uganda	AY228101
<i>N. kwambonambiense</i>	CMW7230	<i>Botryosphaeria</i> sp.	<i>E. grandis</i>	Uganda	AY228098
<i>N. kwambonambiense</i>	CMW8036	<i>Botryosphaeria</i> sp.	<i>E. grandis</i>	Uganda	AY228099
<i>N. kwambonambiense</i>	T4B1/16/1Eucalyptus	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	Uganda	GQ922510
<i>N. kwambonambiense</i>	108/2/6/Grevillea	<i>N. parvum</i>	<i>G. robusta</i>	Uganda	GQ999854
<i>N. kwambonambiense</i>	GAC1	<i>N. ribis</i>	<i>Vaccinium darrowii</i>	Florida, USA	GQ336828
<i>N. kwambonambiense</i>	WRS1	<i>N. ribis</i>	<i>V. darrowii</i>	Florida, USA	GQ336829
<i>N. kwambonambiense</i>	WWC38	<i>N. ribis</i>	<i>V. darrowii</i>	Florida, USA	GQ336830
<i>N. kwambonambiense</i>	MixSuC4	<i>N. ribis</i>	<i>V. darrowii</i>	Florida, USA	GQ845092
<i>N. kwambonambiense</i>	UFO440	<i>N. ribis</i>	<i>V. darrowii</i>	Florida, USA	FJ877139
<i>N. kwambonambiense</i>	WFF9	<i>N. ribis</i>	<i>V. darrowii</i>	Florida, USA	GQ845089
<i>N. kwambonambiense</i>	ARS	<i>N. ribis</i>	<i>Vaccinium</i> sp.	Florida, USA	GQ845088
<i>N. kwambonambiense</i>	RBE2	<i>N. ribis</i>	<i>Vaccinium</i> sp.	Florida, USA	GQ845087
<i>N. kwambonambiense</i>	CMW26856	<i>N. kwambonambiense</i>	<i>Terminalia sericea</i>	South Africa	GQ471843
<i>N. kwambonambiense</i>	CMW26860	<i>N. kwambonambiense</i>	<i>Terminalia sericea</i>	South Africa	GQ471844
<i>N. kwambonambiense</i>	CMW26865	<i>N. kwambonambiense</i>	<i>Terminalia sericea</i>	South Africa	GQ471845
<i>N. kwambonambiense</i>	CMW26850	<i>N. kwambonambiense</i>	<i>Terminalia sericea</i>	South Africa	GQ471846
<i>N. kwambonambiense</i>	CMW26853	<i>N. kwambonambiense</i>	<i>Terminalia sericea</i>	South Africa	GQ471847
<i>N. kwambonambiense</i>	CMW26855	<i>N. kwambonambiense</i>	<i>Terminalia sericea</i>	South Africa	GQ471848
<i>N. kwambonambiense</i>	CMW14025	<i>N. ribis/N. cordaticola</i>	<i>S. cordatum</i>	South Africa	DQ316080/ EU821901
<i>N. kwambonambiense</i>	CMW14031	<i>N. kwambonambiense</i>	<i>S. cordatum</i>	South Africa	DQ316076
<i>N. kwambonambiense</i>	CMW14023	<i>N. kwambonambiense</i>	<i>S. cordatum</i>	South Africa	EU821900
<i>N. kwambonambiense</i>	CMW14123	<i>N. kwambonambiense</i>	<i>S. cordatum</i>	South Africa	EU821924
<i>N. kwambonambiense</i>	CMW14140	<i>N. kwambonambiense</i>	<i>S. cordatum</i>	South Africa	EU821919
<i>N. kwambonambiense</i>	CMW14155	<i>N. kwambonambiense</i>	<i>S. cordatum</i>	South Africa	EU821923
<i>N. occulatum</i>	CMW3388	<i>Botryosphaeria</i> sp.	<i>A. cunninghamii</i>	QLD, Australia	AY615154
<i>N. occulatum</i>	MUCC158	<i>Neofusicoccum</i> sp.	<i>E. dunnii</i>	QLD, Australia*	EU339532
<i>N. occulatum</i>	MUCC270	<i>B. ribis</i>	<i>E. grandis</i>	QLD, Australia*	EU339529
<i>N. occulatum</i>	MUCC225	<i>Neofusicoccum</i> sp.	<i>E. grandis</i> hybrid	QLD, Australia*	EU339530
<i>N. occulatum</i>	MUCC227	<i>N. ribis</i>	<i>E. grandis</i> hybrid	QLD, Australia*	EU339509
<i>N. occulatum</i>	MUCC286	<i>N. ribis</i>	<i>E. pellita</i>	QLD, Australia*	EU736947
<i>N. occulatum</i>	MUCC296	<i>N. ribis</i>	<i>E. pellita</i>	QLD, Australia	EU301034
<i>N. occulatum</i>	MUCC317	<i>Neofusicoccum</i> sp.	<i>E. pellita</i>	QLD, Australia	EU339533
<i>N. occulatum</i>	MUCC683	<i>Neofusicoccum</i> sp.	<i>Eucalyptus</i> sp.	QLD, Australia	EU339531

Correct ID	Isolate Code	GenBank ID	Host	Location	Genbank No.
<i>N. occulatum</i>	PD289	<i>N. ribis</i>	<i>Eucalyptus</i> sp.	Australia	GU251788
<i>N. occulatum</i>	PD288	<i>N. ribis</i>	<i>Eucalyptus</i> sp.	Australia	GU251259
<i>N. occulatum</i>	MUCC232	<i>N. ribis</i>	<i>Eucalyptus urophylla</i> x <i>E. camaldulensis</i>	QLD, Australia	EU301031
<i>N. occulatum</i>	H73-1	<i>N. ribis</i>	<i>V. Vinifera</i>	Australia	HQ392733
<i>N. occulatum</i>	W45-3-2	<i>N. ribis</i>	<i>V. Vinifera</i>	Australia	HQ392765
<i>N. occulatum</i>	CMW3389	<i>Botryosphaeria</i> sp.	<i>W. nobilis</i>	QLD, Australia*	AY615155
<i>N. occulatum</i>	CMW9070	<i>Botryosphaeria</i> sp.	<i>W. nobilis</i>	E Australia*	AY615164
<i>N. occulatum</i>	CMW7885	<i>B. parva</i>	<i>Eucalyptus</i> sp.	Hawaii, USA	AY236944
<i>N. occulatum</i>	107/2/6/Grevillea	<i>B. parva</i>	<i>Grevillea</i> sp.	Uganda	GU130544
<i>N. occulatum</i>	MT9B2/32/2/Masaka2	<i>N. parvum</i>	<i>Eucalyptus</i> sp.	Uganda	GU130543
<i>N. occulatum</i>	UY52	<i>N. parvum</i>	<i>E. grandis</i>	Uruguay	EU080912
<i>N. occulatum</i>	UY231	<i>N. parvum</i>	<i>Blepharocalyx salicifolius</i>	Uruguay	EU863164
<i>N. umdonicola</i>	Fungal sp. 222c3b	Fungal sp.	seed	Panama	EU563590
<i>N. umdonicola</i>	CMW13990	<i>B. ribis</i>	<i>S. cordatum</i>	South Africa	DQ316074
<i>N. umdonicola</i>	CMW14011	<i>B. ribis</i>	<i>S. cordatum</i>	South Africa	DQ316072
<i>N. umdonicola</i>	CMW14012	<i>B. ribis</i>	<i>S. cordatum</i>	South Africa	DQ316073
<i>N. umdonicola</i>	CMW14058	<i>N. umdonicola</i>	<i>S. cordatum</i>	South Africa	EU821904
<i>N. umdonicola</i>	CMW14060	<i>N. umdonicola</i>	<i>S. cordatum</i>	South Africa	EU821905
<i>N. umdonicola</i>	CMW14096	<i>N. umdonicola</i>	<i>S. cordatum</i>	South Africa	EU821913
<i>N. umdonicola</i>	CMW14079	<i>N. umdonicola</i>	<i>S. cordatum</i>	South Africa	EU821915
<i>N. umdonicola</i>	CMW14106	<i>N. cordaticola</i>	<i>S. cordatum</i>	South Africa	EU821899
<i>N. umdonicola</i>	CMW14127	<i>N. umdonicola</i>	<i>S. cordatum</i>	South Africa	EU821926
<i>N. ribis</i>	CMW7772	<i>N. ribis</i>	<i>Ribes</i> sp.	New York, USA	AY236935
<i>N. ribis</i>	CMW7773	<i>N. ribis</i>	<i>Ribes</i> sp.	New York, USA	AY236936
<i>N. ribis</i>	CMW7054	<i>N. ribis</i>	<i>Ribes rubrum</i>	New York, USA	AF241177

¹There is no associated DNA sequence data for this isolate; instead it was identified in the population analysis.

Table S2 Allele size (bp) and frequency at seven loci (BOTF11, 15,17, 21, 23, 35, and 37) for *N. parvum* populations collected from Australia (AUST), China (CHN), Colombia (COL), Hawaii (HAW), Indonesia (INDO), New Zealand (NZ) and South Africa (SA).

Locus	Allele	AUST	CHN	COL	HAW	INDO	NZ	SA
<i>BotF11</i>	421	-	-	-	0.143	-	-	-
	426	-	-	-	-	-	0.071	-
	427	0.026	0.167	-	-	0.500	-	-
	428	0.895	0.834	0.750	0.714	0.500	0.929	0.675
	432	0.053	-	0.250	0.143	-	-	0.026
	434	0.026	-	-	-	-	-	0.026
	Null	-	-	-	-	-	-	0.273
<i>BotF15</i>	365	-	-	-	-	-	-	0.117
	374	-	-	-	-	-	-	0.013
	377	0.868	-	1.000	1.000	1.000	1.000	0.779
	378	-	-	-	-	-	-	0.013
	387	0.105	1.000	-	-	-	-	-
	389	-	-	-	-	-	-	0.052
	390	-	-	-	-	-	-	0.026
395	0.026	-	-	-	-	-	-	
<i>BotF17</i>	230	0.105	1.000	-	-	-	-	-
	232	0.026	-	0.938	-	-	-	0.143
	236	0.079	-	-	-	-	-	-
	240	0.632	-	-	0.571	1.000	0.643	0.013
	242	-	-	-	0.071	-	0.071	-
	244	0.026	-	-	-	-	-	0.065
	246	0.026	-	-	-	-	0.143	0.143
	248	-	-	-	0.214	-	0.143	0.208
	250	-	-	-	-	-	-	0.299
	252	0.079	-	-	-	-	-	-
	256	-	-	-	0.143	-	-	0.065
	259	-	-	-	-	-	-	0.065
Null	0.026	-	0.062	-	-	-	-	
<i>BotF21</i>	196	0.026	-	-	-	0.500	-	-
	199	0.026	-	-	0.143	-	-	-
	203	0.316	0.667	-	-	-	0.286	-
	204	-	-	-	-	-	-	0.039
	207	0.263	-	0.938	0.357	-	0.357	0.260
	208	0.132	-	0.062	-	-	0.071	0.065
	209	-	-	-	-	-	-	0.078
	217	-	-	-	-	-	-	0.039
	219	0.210	0.167	-	0.071	0.500	0.214	0.520
	231	-	-	-	0.214	-	-	-
Null	0.026	0.167	-	0.214	-	0.071	-	
<i>BotF23</i>	415	-	-	-	-	-	0.071	-
	420	-	-	-	-	-	0.071	-
	422	0.921	0.500	-	0.857	1.000	0.857	0.649
	423	0.079	0.500	0.375	-	-	-	0.013
	424	-	-	0.062	-	-	-	0.026
	425	-	-	0.500	0.143	-	-	0.221
	426	-	-	0.062	-	-	-	0.091

Locus	Allele	AUST	CHN	COL	HAW	INDO	NZ	SA
<i>BotF35</i>	221	0.737	1.000	-	0.500	1.000	0.357	0.156
	224	0.026	-	-	0.286	-	0.071	0.480
	227	0.105	-	-	0.143	-	0.509	0.078
	230	-	-	-	0.071	-	-	-
	237	0.105	-	-	-	-	-	0.091
	241	-	-	0.062	-	-	-	-
<i>BotF35</i>	244	--	-	0.812	-	-	-	0.130
	247	-	-	0.125	-	-	0.071	-
	261	-	-	-	-	-	-	0.026
	263	0.026	-	-	-	-	-	-
	265	-	-	-	-	-	-	0.013
	Null	-	-	-	-	-	-	0.026
<i>BotF37</i>	310	0.053	-	-	-	-	-	-
	311	0.447	1.000	-	-	-	0.357	0.026
	312	0.474	-	1.000	1.000	1.000	0.643	0.948
	314	0.026	-	-	-	-	-	0.026
No. Isolates		38	6	16	14	2	14	77
No. Haplotypes		25	4	9	11	2	12	33
Unique Haplotypes		23	4	9	10	1	9	31
No. Alleles		31	10	14	19	9	20	38
Null Alleles		2	0	2	1	0	1	2
Unique Alleles		5	0	1	3	0	3	13
Polymorphic loci		7	3	5	5	2	6	7

Table S3 Gene diversity (H) and contingency χ^2 tests for differences in allele frequencies for the seven polymorphic BOTF loci across clone corrected populations of *Neofusicoccum parvum* from Australia (AUST), China (CHN), Colombia (COL), Hawaii (HAW), New Zealand (NZ) and South Africa (SA). Stars and NS indicate significance level (* P<0.001, ^{NS}P>0.05) numbers in superscript indicate standard deviation.

Locus	Gene Diversity						χ^2	df
	AUST	CHN	COL	HAW	NZ	SA		
BotF11	0.221	0.560	0.444	0.430	0.153	0.291	43.4 ^{NS}	30
BotF15	0.218	0.320	0.000	0.000	0.000	0.572	90.3*	35
BotF17	0.625	0.320	0.000	0.546	0.597	0.834	171.5*	60
BotF21	0.749	0.625	0.198	0.735	0.694	0.680	87.1*	50
BotF23	0.147	0.320	0.667	0.165	0.292	0.709	73.8*	30
BotF35	0.510	0.320	0.531	0.678	0.639	0.813	106.4*	45
BotF37	0.536	0.320	0.000	0.000	0.486	0.117	52.7*	15
MEAN	0.432 ^{+/-} 0.235	0.398 ^{+/-} 0.134	0.263 ^{+/-} 0.283	0.365 ^{+/-} 0.310	0.409 ^{+/-} 0.265	0.574 ^{+/-} 0.272		

Appendix S1

Genetic Diversity

The seven primer pairs produced 58 alleles across seven loci; amplifying fragments ranging from 196 - 434 bp (Table 2). *BotF11* and *BotF21* were polymorphic in all populations. *BotF15* and *BotF37* were monomorphic in six and four populations, respectively. *BotF17* and *BotF35* were fixed in two populations, whilst *BotF15* was fixed in one (Table S2).

Isolates from the South African and the Australian populations contained the most alleles (38 and 31, respectively), whilst those from the Indonesian and Chinese populations contained the least (9 and 10, respectively). Isolates from the remaining countries contained 14- 20 alleles (Table S2).

All geographically defined populations (populations verified in the chi-squared analysis) exhibited high haplotype diversity; the lowest was exhibited by South Africa (43 % of isolates exhibited a different haplotype). The highest haplotype diversity was exhibited in New Zealand (85 % of isolates exhibited a different haplotype) (Table 1).

Isolates from Indonesia and Chile were not considered as there were only two samples from each of these countries. Chi-squared tests across all populations and all loci indicated that at all loci frequency of alleles were significantly ($\chi^2=43.4$, $p>0.05$) different for all populations except at *BotF11*. The mean total gene diversity across all loci was $0.585^{+/-0.212}$. This was similar to the gene diversity of South Africa (0.574); lower gene diversities was exhibited by all remaining countries (Table S3). Some

populations had a small sample number and gene diversity values must be treated with caution as they would probably be an underestimate of the true gene diversity present in these populations.