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Soilborne diseases caused by *Fusarium* and *Neocosmospora* spp. on ornamental plants in Italy

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Abstract. During surveys conducted in 2010–2014, several disease symptoms were observed on eight ornamental plant species in different nurseries located in Sicily (Southern Italy). Two *Neocosmospora* and 31 *Fusarium* isolates were recovered from symptomatic plants. Fungus identification was based on morphological characteristics and phylogenetic analyses of fragments of the intergenic spacer (IGS), internal transcribed spacer (ITS) and large subunit (LSU) regions of the rDNA; partial fragments of the beta-tubulin (*TUB*), RNA polymerase largest subunit (*RPB1*), RNA polymerase second largest subunit (*RPB2*) and translation elongation factor 1-alpha (*EF-1α*) genes. The *Fusarium* species recovered from ornamental plants were *F. agapanthi* (from *Agapanthus africanus*), *F. anthophilum* (*Dasylirion longissimum*), *F. fujikuroi* (*Trachycarpus princeps*), *F. oxysporum* (*Bougainvillea glabra*, *Cordyline australis* 'Purpurea', *Dasylirion longissimum*, *Eremophila laanii* and *Philoteca myoporoides*) and *F. proliferatum* (*T. princeps*), while *N. solani* was isolated from crown and root rot of *Ficus carica*. The pathogenicity of representative isolates collected from each host was tested on seedlings or cuttings grown in a growth chamber. All the *Fusarium* and *Neocosmospora* isolates tested were pathogenic and reproduced symptoms identical to those observed in the field, except for *F. fujikuroi* on *T. princeps* and *F. oxysporum* on *D. longissimum* that were non-pathogenic.

Keywords. Morphology, multigene phylogeny, pathogenicity, root rot, wilt.

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INTRODUCTION

During the last decade, Italy has significantly increased production of ornamental plants in nurseries, and several new species and products have been introduced for cultivation in greenhouses and open fields. Movement

of ornamental plants through the peninsula led to the spread of pathogens to new areas, and introduction of new pathogens from abroad (Gullino and Garibaldi, 2006; Polizzi *et al.,* 2012; Aiello *et al.,* 2017, 2018).

In Sicily (Southern Italy), production of ornamentals has increased in the eastern area, where it replaced lemon orchards due to decline in demand for these fruits. Plant growth in nurseries is compromised by several foliar and root diseases, and among these diseases those caused by species of Nectriaceae are exceptionally common (Polizzi *et al*., 2007; Vitale *et al.,* 2009; Aiello *et al.,* 2014, 2015; Gullino *et al.,* 2015).

Fusarium Link *sensu lato* was recently segregated into several *Fusarium*-like genera (i.e., *Bisifusarium* L. Lombard, Crous & W. Gams [*Fusarium dimerum* species complex (SC)], *Neocosmospora* E.F. Sm. [*Fusarium solani* SC] and *Rectifusarium* L. Lombard, Crous & W. Gams [*Fusarium ventricosum* SC]). These taxa are among the most important human, animal or plant pathogens, affecting an extensive variety of hosts (O'Donnell *et al.,* 2008, 2010; Lombard *et al.,* 2015). *Fusarium* and *Fusarium*-like genera are well-known as responsible for diseases on ornamental plants, including flowering crops, herbaceous ornamentals such as begonia, carnation and chrysanthemum, woody ornamentals such as *Bougainvillea*, *Hebe*, *Hibiscus* and *Pyracantha* spp. (Horst and Nelson, 1997; Sinclair and Lyon, 2005; Polizzi *et al.,* 2010a, 2010b, 2011; Bertoldo *et al.,* 2015; Lupien *et al.,* 2017), and palms such as *Arecastrum*, *Phoenix* and *Washingtonia* spp. (Elliott *et al.,* 2004).

Considering the importance of diseases caused by *Fusarium*-like fungi, the high economic losses caused by these pathogens and the relevance of these crops, surveys were conducted over a 5-year period in ornamental nurseries located in the Catania province, eastern Sicily, Italy. During the surveys conducted from 2010 to 2014, large numbers of palms, perennial herbaceous shrubs, and young cuttings were detected showing symptoms of crown and root rots, damping-off, wilt and dieback. The aims of the present study were to identify the Fusaria obtained from these affected ornamentals, using morphological characteristics and DNA sequence analyses, and to evaluate the pathogenicity of representative isolates on the hosts from which they were isolated.

MATERIALS AND METHODS

Field sampling and pathogen isolations

During 2010–2014, surveys were performed in ornamental plant-producing regions located in eastern Sicily (Table 1). The disease incidence (DI) was recorded for each host, based on the number of symptomatic plants in the total of those present in five investigated nurseries. Additionally, approx. 20 plants per species per nursery showing wilt, crown or root rot or damping-off symptoms, were randomly collected for analysis. Fragments (each 5 × 5 mm) of symptomatic tissues were cut from the margins of lesions, surface-sterilised in a sodium hypochlorite solution (10%) for 20 s, followed by 70% ethanol for 30 s, and rinsed three times in sterilised water. Tissue fragments were dried in sterilised filter paper, placed on 2% potato dextrose agar (PDA) amended with 100 μg mL^{-1} penicillin and 100 μg mL^{-1} streptomycin (PDA-PS), and were incubated at 25°C until characteristic *Fusarium*-like colonies were observed. Pure cultures were obtained by transferring single conidia to fresh PDA, with the aid of a Nikon SMZ1000 dissecting microscope.

Fungal isolates and morphological characterization

The cultural and micromorphological features of all the isolates included in this study were evaluated fol-

Table 1. Hosts, locations, symptoms and incidence (%) of diseases caused by *Fusarium* and *Neocosmospora* in Sicily (Southern Italy).

Hosts	Locations	Geographical coordinates	Collection year	Symptoms	Incidence %[a]
Agapanthus africanus	Carruba, Nursery 1	37.698004, 15.193944	2014	Damping-off	50
Bougainvillea glabra	Carruba, Nursery 1	37.698004, 15.193944	2010	Wilt	30
Cordyline australis 'Purpurea'	Carruba, Nursery 2	37.699090, 15.197300	2014	Wilt	20
Dasylirion longissimum	Riposto, Nursery 3	37.733699, 15.194320	2014	Wilt	10
Eremophila laanii	Carruba, Nursery 1	37.698004, 15.193944	2010	Wilt	50
Ficus carica	Carruba, Nursery 1	37.698004, 15.193944	2013	Crown and Root rot	50
Phyloteca myoporoides	Milazzo, Nursery 4	38.201964, 15.239530	2013	Wilt	30
Trachycarpus princeps	Grotte, Nursery 5	37.681233, 15.180316	2013	Root rot	40

[a] Number of symptomatic plants on the total of those cultivated.

lowing the procedures of Aoki *et al.* (2003), with some modification as described previously (Sandoval-Denis *et al.,* 2018).

DNA extraction, PCR amplification and sequencing

Fungus isolates were grown on PDA for 4-7 d at room temperature, under a natural day/night photoperiod. Total genomic DNA was extracted from fresh mycelium scraped from each colony surface, using the Wizard® Genomic DNA purification Kit (Promega Corporation). Fragments of seven nuclear loci, including the translation elongation factor 1-alpha (*EF-1α*), the intergenic spacer region of the rDNA (*IGS*), the internal transcribed spacer region of the rDNA (*ITS*), the large subunit of the rDNA (*LSU*), the RNA polymerase largest subunit (*RPB1*), RNA polymerase second largest subunit (*RPB2*) and beta-tubulin (*TUB*), were PCR amplified as described previously (O'Donnell *et al.,* 2009; 2010, Sandoval-Denis *et al.,* 2018). The PCR products were sequenced using the following primer pairs: EF-1/EF-2 for *EF-1α* (O'Donnell *et al.,* 2008), iNL11/iCNS1 plus the internal sequencing primer pair NLa/CNSa for IGS (O'Donnell *et al.,* 2009), ITS4/ITS5 for ITS (White *et al.,* 1990), LR0R/LR5 for LSU (Vilgalys and Hester, 1990; Vilgalys and Sun, 1994), Fa/G2R for *RPB1* (O'Donnell *et al.,* 2010), 5f2/7cr and 7cf/11ar for *RPB2* (Liu *et al.,* 1999; Sung *et al.,* 2007), and 2Fd/4Rd for TUB (Woudenberg *et al.,* 2009). Sequences generated in this study were uploaded to the GenBank and the European Nucleotide Archive (ENA) databases.

Phylogenetic analyses and molecular identification

Sequence alignments were performed individually for each locus using MAFFT on the European Bioinformatics Institute (EMBL-EBI) portal (http://www.ebi.ac.uk/Tools/msa/mafft/). BLASTn searches on GenBank, and pairwise sequence alignments on the *Fusarium* MLST database of the Westerdijk Fungal Biodiversity Institute (http://www.westerdijkinstitute.nl/fusarium/), were performed using *EF-1α* and *RPB2* sequences. This was to assess the distribution of the Fusaria isolates among the different *Fusarium* species complexes or *Neocosmospora*. Following this preliminary identification, different loci combinations were selected for each of the *Fusarium* species complexes and *Neocosmospora* isolates, according to the phylogenetic informativeness for each locus as compiled in published literature. These combinations were as follows: *EF-1α*, ITS, *RPB1*, *RPB2* and *TUB* for the *F. fujikuroi* species complex (FFSC) (Edwards *et al.* 2016); *EF-1α* and IGS for the *F. oxysporum* species complex (FOSC), and collapsed to haplotypes according to O'Donnell *et al.* (2009); *EF-1α*, ITS, LSU and *RPB2* for the genus *Neocosmospora* (O'Donnell *et al.,* 2008).

The different gene datasets were analysed independently and combined, using Maximum likelihood (ML) and Bayesian methods (BI) as described previously (Sandoval-Denis *et al.,* 2018).

Pathogenicity tests

Pathogenicity tests were performed on potted healthy seedlings or cuttings of all symptomatic species recovered with a subset of 16 representative isolates (Table 2). Each experiment was conducted twice, obtaining similar results in both tests. For each experiment three replicates per isolate were used with 20 to 50 plants per replicate. All plants were inoculated by placing two colonised 1 cm^2 plugs (PDA from 9-d-old mycelium cultures, grown at 25 ± 1°C in the dark) at the base of each plant stem. Uninoculated plants for all the host species served as controls. After inoculation, plants were covered with a plastic bag for 48 h and maintained at 25 ± 1°C and 95% relative humidity (RH) under a 12 h fluorescent light/dark regime until the symptoms were observed. All plants were irrigated two to three times per week, and were examined each week for disease symptoms. Disease incidence (DI) was determined for each host species. Fungi were re-isolated from symptomatic tissues and identified, to fulfil Koch's postulates.

RESULTS

Field sampling and pathogen isolations

Symptoms referable to *Fusarium* spp. were detected on eight ornamental species in five nurseries investigated in Eastern Sicily, Italy (Figure 1). The diseases were observed on seedlings and unrooted and rooted cuttings (1 to 12-month-old) during propagation stages in the greenhouses. Disease incidence varied from 10 to 50%, according to the host species (Table 1). The symptoms observed on ornamental plants consisted of damping-off, crown and root rot, and wilt (Table 1).

Damping-off consisted of root rot and stem decay at soil level, and occurred on young seedlings. Rotted roots were dark brown or black, and were partially or completely destroyed. Crown rot sometimes occurred in association with root rot. As consequence of crown and root rot, basal leaves turned necrotic while infected

Table 2. Collection details and sequence accession numbers of isolates included in this study, as well as disease incidence from pathogenicity tests conducted with the isolates.

Species	Culture number[a]	Host	Incidence %[b]	GenBank/ENA accession number[c]						
				ITS	*EF-1α*	IGS	LSU	*RPB1*	*RPB2*	*TUB*
Fusarium agapanthi	CPC 27740#	*Agapanthus africanus*	100	LS422776	LS420058		LS422776	LS420106	LS420122	LS420041
	CPC 27741#	*Agapanthus africanus*	100	LS422777	LS420059		LS422777	LS420107	LS420123	LS420042
Fusarium anthophilum	CPC 27742#	*Dasylirion longissimum*	75	LS422778	LS420060		LS422778	LS420108	LS420124	LS420043
	CPC 27743	*Dasylirion longissimum*		LS422779	LS420061		LS422779	LS420109	LS420125	LS420044
	CPC 27744	*Dasylirion longissimum*		LS422780	LS420062		LS422780	LS420110	LS420126	LS420045
Fusarium fujikuroi	CPC 27719#	*Trachycarpus princeps*	0	LS422781	LS420063		LS422781	LS420111	LS420127	LS420046
Fusarium oxysporum	CPC 27729#	*Philoteca myoporoides*	100		LS420064	LS420138				
	CPC 27730#	*Philoteca myoporoides*	100		LS420065	LS420139				
	CPC 27731	*Philoteca myoporoides*			LS420066	LS420140				
	CPC 27732	*Philoteca myoporoides*			LS420067	LS420141				
	CPC 27733	*Philoteca myoporoides*			LS420068	LS420142				
	CPC 27734#	*Eremophila laanii*	100		LS420069	LS420143				
	CPC 27735#	*Eremophila laanii*	100		LS420070	LS420144				
	CPC 27738#	*Bougainvillea glabra*	100		LS420071	LS420145				
	CPC 27739#	*Bougainvillea glabra*	100		LS420072	LS420146				
	CPC 27745#	*Dasylirion longissimum*	0		LS420073	LS420147				
	CPC 27746#	*Cordyline australis* 'Purpurea'	100		LS420074	LS420148				
	CPC 27747#	*Cordyline australis* 'Purpurea'	100		LS420075	LS420149				
	CPC 27748	*Cordyline australis* 'Purpurea'			LS420076	LS420150				
	CPC 27749	*Cordyline australis* 'Purpurea'			LS420077	LS420151				
	CPC 27750	*Cordyline australis* 'Purpurea'			LS420078	LS420152				
	CPC 27751	*Cordyline australis* 'Purpurea'			LS420079	LS420153				
Fusarium proliferatum	CPC 27711#	*Trachycarpus princeps*	100	LS422782	LS420080		LS422782	LS420112	LS420128	LS420047
	CPC 27712	*Trachycarpus princeps*		LS422783	LS420081		LS422783	LS420113	LS420129	LS420048
	CPC 27713	*Trachycarpus princeps*		LS422784	LS420082		LS422784	LS420114	LS420130	LS420049
	CPC 27714	*Trachycarpus princeps*		LS422785	LS420083		LS422785	LS420115	LS420131	LS420050
	CPC 27715	*Trachycarpus princeps*		LS422786	LS420084		LS422786	LS420116	LS420132	LS420051
	CPC 27716	*Trachycarpus princeps*		LS422787	LS420085		LS422787	LS420117	LS420133	LS420052
	CPC 27717	*Trachycarpus princeps*		LS422788	LS420086		LS422788	LS420118	LS420134	LS420053
	CPC 27718	*Trachycarpus princeps*		LS422789	LS420087		LS422789	LS420119	LS420135	LS420054
	CPC 27720	*Trachycarpus princeps*		LS422791	LS420089		LS422791	LS420121	LS420137	LS420056
Neocosmospora solani	CPC 27736#	*Ficus carica*	100	LT991945	LT991907		LT991952		LT991914	
(= *Fusarium solani*)	CPC 27737#	*Ficus carica*	100	LT991946	LT991908		LT991953		LT991915	

[a] CPC: Culture collection of P.W. Crous, housed at Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; Strains used in the pathogenicity tests are indicated with #.
[b] Percentage calculated from the number of symptomatic plants relative to the total number inoculated.
[c] ENA: European Nucleotide Archive; *EF-1α*: Translation elongation factor 1-alpha; IGS: Intergenic spacer region of the rDNA; ITS: Internal transcribed spacer regions of the rDNA and 5.8S region; LSU: Partial large subunit of the rDNA; *RPB1*: RNA polymerase largest subunit; *RPB2*: RNA polymerase second largest subunit; *TUB*: Beta-tubulin.

Figure 1. Natural and artificial symptoms referable to *Fusarium* and *Neocosmospora* spp. **a, b**. Wilt of *Bougainvillea glabra* cuttings (a) and *Cordyline australis* seedlings (b). **c**. Root rot with subsequent leaf chlorosis of *Trachycarpus princeps*. **d**. Damping-off of *Agapanthus africanus*. **e**. Wilt of *Phyloteca myoporoides.* **F to i**. Vascular discolouration and wilt after *Fusarium oxysporum* inoculation of *Bougainvillea glabra* (f and g), *Eremophila laanii* (h) and *Phyloteca myoporoides* (i). **j**. Crown and root rot caused by *Neocosmospora solani* (= *Fusarium solani*) on *Ficus carica* (left) compared with control plants (right).

Table 3. Characteristics of the data partitions used for phylogenetic analyses in this study.

Species[a]	Data partition[b]	ML evolutionary model[c]	Number of characters[d]				
			Total	Conserved	Variable	Informative	BI unique sites
F. fujikuroi SC	ITS	SYM+I	459	420	39	32	50
	RPB1	SYM+I+G	1279	1038	241	148	195
	RPB2	GTR+I+G	1570	1251	319	216	332
	EF-1α	SYM+G	455	317	133	76	148
	TUB	SYM+I+G	507	389	117	65	140
F. oxysporum SC	*EF-1α*	GTR+I+G	591	448	143	101	67
	IGS	GTR+I+G	2190	1420	744	554	218
Neocosmospora	ITS	GTR+I+G	496	404	90	65	117
	LSU	GTR+I+G	481	450	31	14	25
	RPB2	GTR+I+G	1603	1235	365	243	275
	EF-1α	GTR+G	324	222	97	48	107

[a] SC: species complex.
[b] *EF-1α*: Translation elongation factor 1-alpha. IGS: Intergenic spacer region of the rDNA. ITS: Internal transcribed spacer regions of the rDNA and 5.8S region. *RPB1*: RNA polymerase largest subunit. *RPB2*: RNA polymerase second largest subunit. *TUB*: Beta-tubulin.
[c] G: Gamma distributed rate variation among sites. GTR: Generalised time-reversible. I: Proportion of invariable sites. ML: Maximum-likelihood; SYM: Symmetrical model.
[d] BI: Bayesian inference.

plants sometimes wilted and died. Wilted plants had conspicuous vascular brown discolourations from the crown to the canopy.

A total of 33 monosporic *Fusarium*-like isolates were collected (Table 2). Among these, two isolates were obtained from damping-off, 12 from root rot, and 19 were from wilted plants.

Phylogenetic analyses and species identification

Pairwise sequence alignments on the *Fusarium* MLST database and GenBank BLASTn searches demonstrated that 16 isolates belonged to the FOSC and 15 isolates to the FFSC, while two isolates were assigned to the genus *Neocosmospora* (*F. solani* species complex) (Table 2).

Subsequent more inclusive multilocus phylogenetic analyses identified a total of five *Fusarium* spp. and one *Neocosmospora* sp. The alignment characteristics and statistics are summarized in Table 3. The phylogenetic analyses of the 15 FFSC isolates from ornamentals revealed a total of four species (*F. agapanthi* O'Donnell, T. Aoki, J. Edwards & Summerell, *F. anthophilum* (A. Braun) Wollenw., *F. fujikuroi* Nirenberg and *F. proliferatum*) from different hosts (Figure 2). Isolates belonging to FOSC were studied based on a two-gene analysis using *EF-1α* and IGS sequences and incorporated in the original alignments previously published by O'Donnell *et al*. (2009) including representatives of 257 known FOSC haplotypes. The FOSC isolates from ornamentals belonged to 15 different haplotypes: isolates CPC 27748 and 22749, from *Cordyline australis* 'Purpurea' showed identical DNA sequences, and corresponded to haplotype 122 of FOSC; isolate CPC 27733 from *Philoteca myoporoides* belonged to haplotype 188, while each of the remaining isolates corresponded to a previously undescribed haplotype (Figure 3). The phylogeny of the genus *Neocosmospora* was based on *EF-1α*, ITS, LSU and *RPB2* sequences, and showed that two isolates from *Ficus carica* (CPC 27736 and 27737) belonged to *N. solani* (Martius) L. Lombard & Crous (= *F. solani*) (Figure 4).

Pathogenicity tests

Fourteen *Fusarium* and two *Neocosmospora* isolates tested were pathogenic to the different inoculated original hosts, and produced symptoms similar to those observed on diseased plants in nurseries (Figure 1). Two isolates were non-pathogenic. Damping-off occurred on *Agapanthus africanus*, crown and root rot on *F. carica* and root rot with subsequent leaf chlorosis appeared on *Trachycarpus princeps*. The remaining host plants showed vascular discolouration and wilted. The DI (%) caused by *Fusarium* and *Neocosmospora* species on different hosts ranged from 75 to 100%, after 15 d to 3 months (Table 2).

All *F. agapanthi*, *F. proliferatum*, and *N. solani* isolates were pathogenic, and caused 100% DI on *A. africanus*, *T. princeps* and *F. carica,* whereas *F. anthophilum*

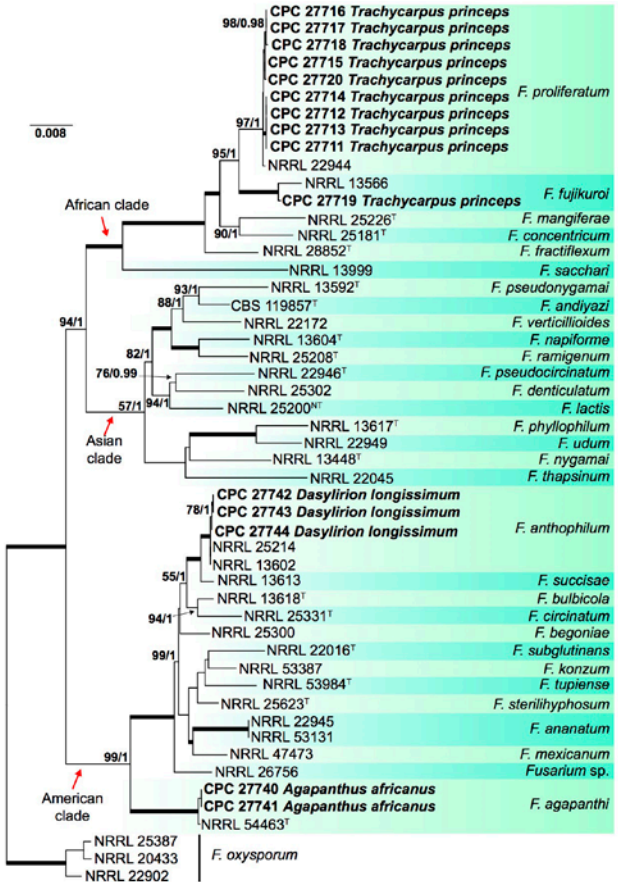

Figure 2. Maximum-likelihood (ML) phylogram of the *Fusarium fujikuroi* species complex obtained from combined ITS, *RPB1*, *RPB2*, *EF-1α* and *TUB* sequences. Branch lengths are proportional to distance. Numbers on the nodes are ML bootstrap values greater than 55%; and Bayesian posterior probability values greater than 0.95. Full supported branches and isolates obtained from ornamentals plants are indicated in bold. Ex-type strains are indicated with T and ex-neotype strains are indicated with NT.

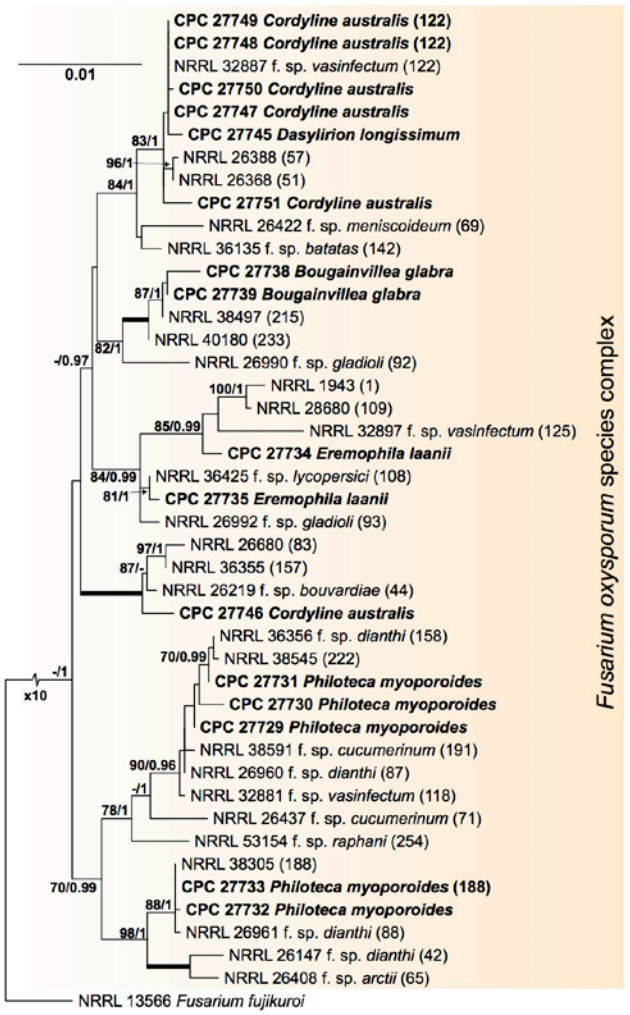

Figure 3. Maximum-likelihood (ML) phylogram of the *Fusarium oxysporum* species complex obtained from combined *EF-1α* and IGS sequences of isolates obtained in this study and representatives of the most closely related haplotypes. Branch lengths are proportional to distance. Numbers on the nodes are ML bootstrap values greater than 55%; and Bayesian posterior probability values greater than 0.95. Full supported branches and isolates obtained from ornamentals plants are indicated in bold. Numbers between parentheses indicate the corresponding haplotype.

caused disease with lower DI on *Dasylirion longissimum* (75%). *Fusarium oxysporum* isolates gave high DI (100%) on *Bougainvillea glabra*, *C. australis* 'Purpurea', *Eremophila laanii* and *P. myoporoides*, but was non-pathogenic on *D. longissimum*. Similarly, *F. fujikuroi* caused no symptoms on the original host *T. princeps*. The pathogens were re-isolated from the artificially inoculated plants, and were identified as previously described, fulfilling Koch's postulates. No symptoms were observed on control (uninoculated) plants.

DISCUSSION

The most important plant pathogenic *Fusarium* species is the soil-borne *F. oxysporum* Schltdl. (Gordon and Martyn, 1997; Gullino *et al.*, 2012), currently encompassing nearly 150 *formae speciales* (ff. spp.) and races. The broad host plant range of this fungus includes valuable ornamental plants such as *Chrysanthemum*, *Dianthus*, *Gerbera*, *Gladiolus*, and *Lilium* spp. (Engelhard and Woltz, 1971; Linderman, 1981; Farr and Rossman, 2018), on which it causes symptoms ranging from vascular wilt to crown and root rot (Engelhard and Woltz, 1971; Linderman, 1981).

Fusarium proliferatum (Matsush.) Nirenberg ex Gerlach & Nirenberg is another important species, which has

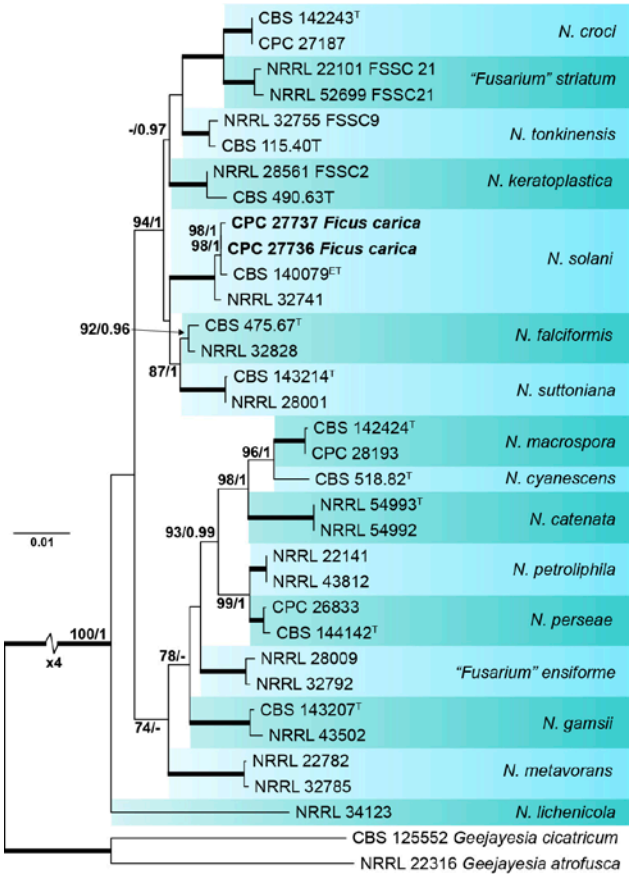

Figure 4. Maximum-likelihood (ML) phylogram of *Neocosmospora* (= *Fusarium solani* species complex) obtained from combined *EF-1α*, ITS, LSU and *RPB2* sequences. Branch lengths are proportional to distance. Numbers on the nodes are ML bootstrap values greater than 55%; and Bayesian posterior probability values greater than 0.95. Full supported branches and isolates obtained from ornamentals plants are indicated in bold. Ex-type and ex-epitype strains are indicated with ^{T} and ^{ET} respectively.

been described as the causal agent of blight, dieback and wilt of several palms belonging to the genera *Chamaerops*, *Phoenix*, *Ravenea*, *Trachycarpus* and *Washingtonia* (Polizzi and Vitale, 2003; Armengol *et al.,* 2005).

In the present study, two *Neocosmospora* and 31 *Fusarium* isolates were recovered from eight ornamental species in Sicily over a 5-year period. Disease symptoms were observed in five ornamental nurseries, and included damping-off, crown and/or root rot, and wilt. The isolates obtained from symptomatic tissues were identified based on single and multilocus phylogenetic analyses of seven loci (*EF-1α*, IGS, ITS, LSU, *RPB1, RPB2,* and *TUB*), as well as morphological characters. Our study revealed considerable diversity in the composition of *Fusarium*-like fungal populations recovered from nurseries.

As confirmed in the pathogenicity tests, all the *F. oxysporum* isolates caused symptoms except on *D. longissimum*. However, this host showed disease symptoms when inoculated with *F. anthophilum*. The inoculated isolate of *F. fujikuroi* produced no symptoms on *T. princeps*, while the remaining *Fusarium* species investigated, *F. agapanthi, F. proliferatum* and *N. solani*, were pathogenic to the respective tested hosts from which they were isolated.

Fusarium and *Neocosmospora* species are widespread in nurseries in Italy (Polizzi *et al.,* 2003; 2010a; 2010b; 2011; Bertoldo *et al.,* 2015), where they represent a limiting factor for production of ornamental plants cultivated in Sicily. These pathogenic species have very broad host ranges worldwide (Farr and Rossman, 2018). However, there are no known reports of diseases caused by *F. anthophilum* on *D. longissimum*. Moreover, *F. agapanthi* was originally described as pathogenic on *Agapanthus praecox* in Australia and Italy (Edwards *et al.,* 2016). However, this pathogen was isolated in the present study, causing serious seedling damping-off of *A. africanus*, suggesting that it may also be more prevalent on other species of *Agapanthus*. Previous studies have reported *F. proliferatum* associated with palms belonging to the genera *Chamaerops*, *Phoenix*, *Trachycarpus* and *Washingtonia* (Polizzi and Vitale, 2003; Armengol *et al.,* 2005). Our study presents a new report for *F. proliferatum* as a pathogen of *T. princeps*.

The FOSC includes soil-borne pathogens responsible for vascular wilts, stem cankers, rots, and damping-off of a wide range of agronomical and horticulturally important crops (Baayen *et al.,* 2000; Michielse and Rep, 2009; O'Donnell, 2009). Members of this complex collectively represent the most commonly found and economically important species complex within *Fusarium*. *Fusarium oxysporum* was the predominant species found in all the nurseries sampled, and unlike other species, it was recovered from multiple hosts. Recently, Polizzi *et al.* (2010a; 2010b; 2011) identified *F. oxysporum* associated with wilt diseases of *B. glabra*, *E. laanii* and *P. myoporoides*. However, no reports were previously known of diseases caused by *F. oxysporum* on *C. australis*, as reported here.

The present study is also the first report of *N. solani* causing crown and root rot of *F. carica* cuttings. This plant species is often cultivated for fruit production, and thousands of cuttings cultivated for ornamental purposes were investigated because serious losses were observed from of crown and root rot, leading to plant death. *Neocosmospora* is a species-rich genus containing at least 60 phylogenetically distinct species (O'Donnell, 2000; Zhang *et al.,* 2006; O'Donnell *et al.,* 2008; Nalim *et al.,*

2011). These fungi generally cause crown and/or root rot of infected host plants, while symptoms on aboveground plant portions may manifest as cankers, wilting, stunting and chlorosis, or as lesions on stems and/or leaves (Coleman, 2016; Guarnaccia *et al*., 2018).

The high disease incidence observed in the investigated ornamental nurseries probably depends on the prevailing climatic conditions, farming practices and environmental conditions such as temperature, humidity, irrigation systems or the use of non-disinfected plant growth substrates. Potted plant production could promote infections, since plants are frequently stressed due to being containerised during the production processes. Moreover, several wounds can occur during transplanting. Thus, prevention is a major strategy to control *Fusarium* diseases, and an accurate diagnosis of *Fusaria* species occurring in a particular area is significant for the selection of effective disease management strategies.

This study provides the first overview of *Fusarium* and *Neocosmospora* diversity associated with diseased ornamental plants in Southern Italy, and includes information on the pathogenicity of these fungi. It also provides the first reports of several new pathogen/host combinations, such as *N. solani* associated with crown and root rot of *F. carica*, and *F. agapanthi*, *F. anthophilum*, *F. oxysporum* and *F. proliferatum* as pathogens, respectively, of *A. africanus*, *D. longissimum*, *C. australis* and *T. princeps*.

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