Table 1. MLST gene-based BLAST analysis (Top hit) showing the nearest recognized species and corresponding sequence similarities for individual genes

Proposed species	Strain #	Genome accession	MLST	Closest type-strain	Type / ex-type strain	Reference	Nucleotide	Alignment	Taxonomic interpretation
Cladosporium prattiae	FJI-L7-BK-DG1	JAKLLY000000000	*ITS*	*Cladosporium austrohemisphaericum*	CBS 140482 = CPC 12068; ex-type	KT600382	99.02%	503	A candidate difference from *C. austrohemisphaericum* CBS 140482 was detected in *ITS*, but the species hypothesis was not resolved by *ITS* alone. Additional differentiation was detected in *act* and *tef1-α*, and these sequence comparisons were considered together with the MLSA phylogeny (Fig. 2) in the assessment of the proposed species.
			tef1-α	*Cladosporium cucumerinum*	CBS 171.52 = MUCL 10092; ex-epitype	MW735657	95.30%	914	
			act	*Cladosporium austrohemisphaericum*	CBS 140482 = CPC 12068; ex-type	KT600578	95.54%	224	
			rpb2	*Cladosporium iridis*	CBS 138.40 = MIRRI 0043331; ex-epitype	KT223022	81.24%	1226	
			tub2	*Cladosporium aciculare*	CBS 140488; ex-type	PZ136760	84.59%	370	
Cladosporium crawfordii	FKII-L3-CM-PAB1	JAKLNF000000000	*ITS*	*Cladosporium perangustum*	CBS 125996; ex-type from holotype	HM148121	100.00%	516	No differentiation from *C. perangustum* CBS 125996 was detected over the compared *ITS* interval. The greatest divergence among the three reported loci was detected in *tef1-α*, and additional differentiation was detected in *act*. These differences were interpreted together with the MLSA phylogeny (Fig. 4) in the assessment of the proposed species.
			tef1-α	*Cladosporium cucumerinum*	CBS 171.52 = MUCL 10092; ex-epitype	MW735657	95.73%	914	
			act	*Cladosporium perangustum*	CBS 125996; ex-type from holotype	HM148610	97.79%	226	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	JAKLNE000000000	*ITS*	*Waltergamsia citrina*	CBS 384.96; ex-type from holotype	NR154670.1	94.85%	524	Differentiation from *W. citrina* was detected in *ITS*, and an additional differentiation signal from *W. alkalina* was detected in *rpb2*. Close sequence affinity to *W. alkalina* was detected in *tef1-α*. The *ITS, LSU, rpb2* and *tef1-α* comparisons were interpreted together with the MLSA phylogeny (Fig. 5) in the assessment of the proposed species.
			LSU	*Waltergamsia hennebertii*	CBS 768.69; ex-type from holotype	NG056987.1	98.70%	844	
			rpb2	*Waltergamsia alkalina*	CBS 741.94; ex-type from holotype	OQ454332.1	93.64%	755	
			tef1-α	*Waltergamsia alkalina*	CBS 741.94; ex-type from holotype	OQ471265.1	99.01%	811	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	JAKLNG000000000	*ITS*	*Phaeophleospora eucalypticola*	CPC 26523 = CBS 141294; ex-type	KX228267	99.47%	565	No differentiation from *P. eucalypticola* was detected over the compared *ITS* interval, and only minimal differentiation was detected in *LSU*. The greatest observed divergence was detected in *tef1-α*, by which the principal protein-coding differentiation signal was provided. The proposed species was assessed through joint interpretation of this signal and the MLSA phylogeny (Fig. 6), rather than through *ITS* or *LSU* similarity alone.
			LSU	*Phaeophleospora eucalypticola*	CPC 26523 = CBS 141294; ex-type	KX228318	99.89%	892	
			tef1-α	*Phaeophleospora eucalypticola*	CPC 26523 = CBS 141294; ex-type	KX228374	91.81%	513	
Spissiomyces californiae	FJII-L1-SW-P2	JAKLMF000000000	*ITS*	*Neospissiomyces floridanus*	CBS 152209^{T}	PQ498932	99.10%	558	Close sequence affinity to *Neospissiomyces floridanus* was indicated by *ITS* and *LSU*, whereas high *SSU* similarity was observed in the comparison with *Spissiomyces ramosus*. Differentiation from *S. ramosus* was detected in *tub2*, and a candidate difference from *N. floridanus* was detected in *rpb2*. These comparisons were interpreted together with the MLSA phylogeny (Fig. 7) in the assessment of genus placement and the proposed species.
			LSU	*Neospissiomyces floridanus*	CBS 152209^{T}	PQ498981	99.78%	447	
			SSU	*Spissiomyces ramosus*	CGMCC 3.17076^{T}	KF513497	99.90%	1020	
			rpb2	*Neospissiomyces floridanus*	CBS 152209^{T}	PQ497722	98.64%	516	
			tub2	*Spissiomyces ramosus*	CGMCC 3.17076^{T}	KJ733702	90.59%	829	
Neocatenulostroma huberi	FJI-L3-BK-P2	JAKLLW000000000	*ITS*	*Neocatenulostroma germanicum*	CBS 539.88; ex-type	MH862143	99.05%	526	Close affinity to *N. germanicum* was indicated by *ITS* and *LSU*, and no differentiation was detected over the compared *LSU* interval. A candidate difference from *N. germanicum* was detected over the short *rpb2* interval. Additional differences were detected in *tub2* and *tef1-α* through comparisons with *N. microsporum* and *N. spinulosum*, respectively. These results were interpreted together with the MLSA phylogeny (Fig. 8) in the assessment of the proposed species.
			LSU	*Neocatenulostroma germanicum*	CBS 539.88; ex-type	MH873835	100.00%	891	
			rpb2	*Neocatenulostroma spinulosum*	CBS 150899 = FMR 18793; ex-type	KF902231	95.20%	854	
			tub2	*Neocatenulostroma microsporum*	CBS 101951; ex-type	KF902825	91.76%	255	
			tef1-α	*Neocatenulostroma spinulosum*	CBS 150899 = FMR 18793; ex-type	OX628947	97.52%	806	